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LATE-BREAKING ABSTRACTS

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A proposition of Intra- and Interspecies Cell-Cell Communication System

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Abstract

All living organisms depend on highly complex networks of intercellular signals to coordinate cell-cell communication in various physiological functions. A large number of mechanisms that rely only on cell signaling are capable of development, collective behavior, self-repair and immunity. This abstract proposes the use of an ANN-based GRN model to orchestrate cell-cell communication in two contexts: unicellular organism via Quorum Sensing and multicellular organisms via Notch signaling pathway. A simple grammar inspired from membrane computing is proposed to describe the dynamic cell-like structure.

Introduction

Communication is vital to life. It represents the coordination of cells and tissues to accomplish various physiological functions as well as the adaptation to the environment. All forms of life on earth (eukaryotes, prokaryotes and metazoan organisms) need to communicate to survive.

Over hundreds of millions of years, evolution of metazoan organisms has produced a complexity both in phenotypes as well as the developmental mechanisms by which this complexity is generated. It is now known, in developmental biology, that this process is based on good coordination of intra and intercellular communication signals. Indeed, a small toolkit of cell signaling co-opted recurrently during development is sufficient for tissue morphogenesis, angiogenesis and metastasis.

Cell-cell communication occurs when a molecular signal is emitted by a cell called emitting cell and recognized by another cell called receiving cell. Basically, signals are composed of growth factors, hormones, cytokines, and neurotransmitters that bind to specific cell receptors. This ligand-receptor interaction then generates several types of intracellular signals that may be relayed by downstream signaling and by protein phosphorylation cascades. Finally, these intracellular signals lead to the activation of transcription factors that regulate target genes responsible for the expression of diverse biological outcomes: activation of cell cycle, proliferation, differentiation.

It does not come as a surprise that “Unicellular organisms including both eukaryotes (e.g. yeast) and prokaryotes (e.g. bacteria) utilize similar communication systems as multicellular organisms. For example: receptors for insulin are present in *Drosophila* which are similar to their vertebrate counterparts in binding properties, general structure, and insulin-stimulated enzyme activity.” [1]

In the artificial life community, cellular interactions have been investigated using cellular automata [2, 3], agent-based

models [4], and GRN-based dynamics [5]. In most of these models, cell-cell interactions are abstract and they do not rely on an advanced exploration of the underlying biological mechanisms. In fact, communications between cells are based on: a diffusion system, information pathway passed through neighboring cells, or the concentration of a molecule that has a direct effect in regulating gene expression and cell behavior. Moreover, communication between unicellular organisms like bacteria Quorum Sensing has not been well investigated by the Artificial Life community. Here, we assume that more realistic unicellular and multicellular approaches must involve more investigation of, the architecture of the chemical communication network, how chemical information is transduced to control gene expression; how intra- and interspecies cell-cell communication is accomplished; and the fascinating option of unicellular-multicellular crosstalk.

ANN Based GRN Model

Various modeling techniques have been developed to simulate the functioning of the GRN. They can be divided into two classes. The first class: logical models, including Boolean networks and their variants. Although effective in dealing with noise, they fail to consider temporal dynamic aspects that are important features of regulatory network [6]. The second class: Continuous models based essentially on differential equations allow more detailed descriptions of GRN dynamics.

To describe the dynamics of a generic GRN supervising cell-cell communication, we use an Artificial Neural Network (ANN) modeling technique introduced by Vohradsky [7]. Formally, an ANN is defined by:

$$dX_i/dt = v_i f \left(\sum_{j=1}^N w_{ij} X_j - \vartheta_i \right) - k_i X_i \quad \vartheta_i v_i k_i > 0$$

- X_i , with $i = 1, \dots, N$, is the i -th gene product concentration.
- v_i : is the maximal expression rate of gene i .
- w_{ij} is the connection weight of control of gene j on gene i . Positive values of w_{ij} indicate enhancing influences while negative values define inhibiting influences.
- ϑ_i : is the influence of external input on gene i , which modulates the gene's sensitivity of response to activating or repressing influences.
- f : Represents a non-linear sigmoid transfer function modifying the influence of gene expression products X_i and

external input ϑ_i to keep the activation from growing without bounds.

- k_i Degradation of the i -th gene expression product.

We extend the formula to take into account cellular processes (e.g., signal translation) that influence the gene sensitivity.

Dynamic cell-like structure

Based on the idea that a cell is a complex structure, we consider a cell as a multi-set of objects arranged in regions and delimited by another main object which is the membrane. Each object within the cell is composed of a multi-set of objects also. An object can be: a lipid, a protein, a receptor, a cytoplasm or a nucleus. So, the model of the cell-like structure is a hierarchical arrangement of multi-sets of objects.

To simulate this hierarchical arrangement of the cell structure, we introduce a simple cellular grammar inspired from formal grammars like in Membrane Computing [8]. However, rules of the grammar don't govern (in any way) development. Development occurs through cellular interactions that lead to gene expression and regulation. Thus, rules are just a formal description of the cell-like structure. This formal description can be used to observe the resulting changes in the cell structure and deduce the resulting grammar. Membrane computing is a computational model that solves NP complete problems. This can be used to investigate the computational power of the resulting digital organisms.

Application on unicellular organisms (Quorum Sensing)

Bacterial cell-cell communication, termed Quorum Sensing (QS), is a signal-response process that regulates gene expression according to the cell density in order to coordinate collective behaviors. In [9], we have introduced a molecular network that uses Ordinary Differential Equations (ODEs) to calculate the concentration of Gram negative bacteria QS components. The simulation shows that bacterial cells are able to form micro-colonies and behave like a multicellular organism (figure 1). The principal limitation of the model resides in the use of a proposed algorithm of QS to simulate bacteria cells communication instead of a regulation mechanism that describes the mutual enhancing-inhibiting influences in genes of a GRN. Moreover, bacterial response to QS is various and includes biofilm formation, bioluminescence, drug-resistance... Our work focuses on investigating the underlying mechanisms behind these phenomena; how chemical information is transduced to control gene expression, and observing in simulation the emerging phenotypic traits.

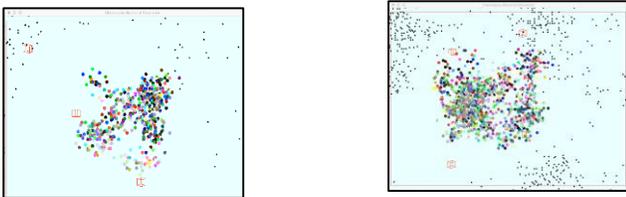


Figure 1: Micro-colonies of moving bacteria emerged from QS communication [9].

Application on multicellular Organisms (Notch signaling pathway)

Notch signaling plays a central role in cell differentiation decision via the lateral inhibition process, which is a common phenomenon during selection of neural and muscle precursor cells [10]. Briefly, two or more equivalent cells express both the receptor Notch and the ligand. A negative feedback loop operates so that ligand expression became repressed in some cells which will be specialized on receiving cells, and this will lead to asymmetry. Despite the fact that the Notch pathway has a myriad of roles in different developmental and disease contexts, it is relatively simple in its functioning. This is why, we made the choice of using specifically this signaling pathway as instance of our model.

Conclusion

In the lineage of our previous work [11], we use Generative Developmental Systems (GDS) that consist of a grammar inspired by membrane computing to simulate the dynamic structure of the cell. This is made to explore the computational power of the emerged organisms.

Multicellular organisms are ecosystems that cohabit cells of the organism and other microorganisms that are bacteria. We assume that a link must be made for a future study of both the artificial ecosystem and the pathological context (QS virulence pathway) considering the two species.

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Constructing Minimal Synthetic Ecosystems: Emergent Properties from Biotic and Abiotic Interactions within a Mutualistic Microbial Consortium

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Abstract

The field of synthetic ecology involves the design and construction of multispecies microbial consortia to perform complex metabolic functions. Consortia are commonly designed considering organisms as modules providing fixed sets of chemical reactions. However even simple consortia are more properly considered as ecosystems. Their stability and function depends on their ecological and evolutionary dynamics and emergent properties of their interactions. To illustrate our point, we discuss work on a synthetic, obligate mutualism created between the yeast *Saccharomyces cerevisiae* and the alga *Chlamydomonas reinhardtii*: an example of a minimal synthetic ecosystem. This simple system clearly shows a “synergistic homeostasis” arising without prior co-evolution of the two partners, which may be akin to rein control. It is the interaction of abiotic and biotic dynamics in this system that stabilize the system. Thus, even in this simple 2 species system the influence of abiotic effects cannot be discounted. Such emergent, synergistic effects are likely to affect synthetic consortia in ways which impact their function and stability. They must therefore be taken into account in consortium design. More than this however, they provide an opportunity. Manipulating the attractor structure and emergent properties of microbial communities is a potentially powerful tool for generating consortia which are not just functionally useful, but also robust and usable in real contexts.

Extended Abstract

Within synthetic biology, the construction of multi-species microbial consortia has been recognized as a route to engineering complex metabolic processes. Work in “synthetic ecology”, however commonly ignores the ecological and evolutionary dynamics of constructed consortia (Escalante *et al.* 2015). Although these synthetic consortia are often unstable when realized, they are commonly designed considering only fixed chemical reactions of a given set of organisms which are assumed to be unchanging.

To understand the stability, function and evolution of both synthetic and natural microbial consortia it is crucial to think of them as ecosystems. That is, systems in which abiotic and biotic interactions combine to determine the system’s behavior (Penn *et al.* Forthcoming). Construction of synthetic consortia has focused thus far simply on the reactions and interactions of direct interest and excluded additional and indirect interactions, including those mediated by the abiotic environment or through modifications of a shared environment. Despite this such additional interactions are ubiquitous and may qualitatively as well as quantitatively change the system dynamics. We propose that to be most effective, synthetic ecology must become a genuine study of ecosystems rather than simply collections of species.

To illustrate our point, we discuss work on a synthetic, obligate mutualism created between the yeast *Saccharomyces cerevisiae* and the alga *Chlamydomonas reinhardtii* (Hom and Murray 2014). Essentially a minimal synthetic ecosystem. Here, the yeast produces CO₂ to feed the alga, while the alga releases NH₃ to feed the yeast in return. A crucial factor in the stability of this synthetic mutualism is the active maintenance of pH in a zone of co-viability in which both organisms can co-exist and in which their relative population sizes are stabilized at a lower level. In this seemingly homeostatic system, the interaction of both the mutualistic cross-feeding dynamics and the species effect on and tolerance to environmental pH is required to maintain a stable and persistent ecosystem.

Each mutualistic partner has opposite pH preferences and opposite directions of environmental (pH) forcing. Crucially, both organisms force pH in the direction of their own preference (and beyond it), resulting in an unstable equilibrium in the absence of the obligate mutualism. Thus, without mutualism, we would expect to see the system run away to extreme pH, resulting in extinction of one of the species. In conditions of obligate mutualism, the co-culture system becomes homeostatic with respect to pH: if either partner grows too rapidly, moving the pH out of the co-

viability zone and thus reducing the growth of its mutualistic partner, its growth will be constrained by a negative feedback resulting from the reduction of an essential nutrient provided by the mutualism. The addition of these extra constraining feedbacks transforms the unstable equilibrium into a dynamically stable “homeostatic” state in which pH is maintained within a tolerable, but sub-optimal, range for both species, allowing them to stably coexist.

This simple system clearly shows an emergent “synergistic homeostasis” arising without prior co-evolution of the two partners, which may be akin to rein control (Harvey 2004, 2015). Models of multi-species, rein control homeostasis have demonstrated a large range of dynamical behaviors can be possible (Dyke and Weaver 2013). The existence of such dynamics and the overall structure of the system’s stability landscape depend strongly on the relative natures of forcing and preference functions over all species. In our system, the mutualistic interaction between species and its connection to other environmental variables render the dynamics even more complex.

Within even this minimal Algal-Yeast system, it is the interaction of abiotic and biotic dynamics in this system that stabilize the system. Thus, even in such simple 2 species consortia, the influence of abiotic effects cannot be discounted. Such systems must be understood as “ecosystems”. The abiotic interactions in this case provide additional constraining feedbacks which modify the consortium’s fitness and stability landscapes. The existence of emergent effects such as this in even simple ecosystems is likely to influence the stability and composition of the microbial communities which constitute the biotic element. The biotic-abiotic dynamics may simply modify biotic interactions in unexpected ways which may alter how they respond to change, or may provide higher level system properties and contexts that may modify evolutionary selection pressures.

These emergent interactions may provide “zones of stability” or areas of phase space in which species co-existence is expanded with respect to what we might expect considering only direct biotic interactions. Such increased stability (expanded zones of viability) may potentially function to bootstrap the evolution of mutualisms. We speculate on the potential consequences for the resilience and evolvability of such mutualisms, wherein extended persistence and co-evolution of species plus potential discontinuous change in values of environmental and population variables provide a system-level context that may significantly alter the outcome of selective processes.

In general, such emergent, synergistic effects are likely to affect synthetic consortia in ways which impact their function and stability. They must therefore be taken into account in consortium design. More than this however, they provide an opportunity. Manipulating the attractor structure and emergent properties of microbial communities is a potentially powerful

tool for generating consortia which are not just functionally useful, but also robust and usable in real contexts.

We propose and discuss an alternative approach to synthetic ecology. One which aims to construct and steer stable, functional synthetic ecosystems via the design and manipulation of stability landscapes and selective contexts (Penn 2016).

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Fractal Artificial Life: Looking for Creativity at the Edge of Chaos

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Abstract

The goal of this article is to outline a new research framework at the intersection of artificial life and computational arts and design, and was originally motivated on the one hand by an artistic fascination for the presence of fractal patterns in nature and the universe at all scales, and on the other hand by the intuitive assumption that such patterns are indicators of some very universal self-organization principles leading to situations known as criticality at the edge of chaos. In this paper, we formulate several hypothesis as to how these situations might be reproduced using computer simulations and discuss the possible impacts of this field of research for computational art and creation.

Introduction

Scientists and artists have long shared a common fascination for the diversity of shapes, structures and phenomena found in nature, a diversity that is all the more striking since it arises from a relatively limited set of rules. One of the recurring pattern that has attracted considerable interests from both communities are fractals. They seem to pervade our universe at all scales: from quantum systems (Satija, 2016),(Morris et al., 1987),(Jadczyk, 2008) to geographical features, population dynamics (Newman et al., 2002), the human nervous system (Losa, et al. 2011), galaxy clusters (Borgani, 1995), and many other examples which list is too long to be detailed here. Such patterns are often the sign of an underlying complexity with self-organising properties.

Mathematical and computational models like power laws, L-systems, iterated function systems or logistic maps can be empirically built to describe fractal-generating processes, but give little information as to where those processes originate (Brown et al. 2002), and do not account for phenomena of emergence and self-organization.

As artists and scientists, shedding light on the source of those processes is a major goal, because the insights it would provide on the mechanisms of “nature’s creativity” could then be leveraged to build and explore new realms of inspiration and nurture countless developments in biomimetic or bio-inspired engineering, design and art.

Observations regarding biologically-inspired models of creativity

Among the biologically-inspired approaches to modelling creativity that have been explored over the past decades, genetic algorithms have arguably drawn most of the attention (Dennis & Stella, 2011), (Boden, 2009). The argument for their relevance as computational models of “nature’s creativity” builds on the assumption that generating novelty is essentially an adaptive process, and that the search for novelty amounts to the stochastic exploration of a solution space. (see Figure 1 for example).

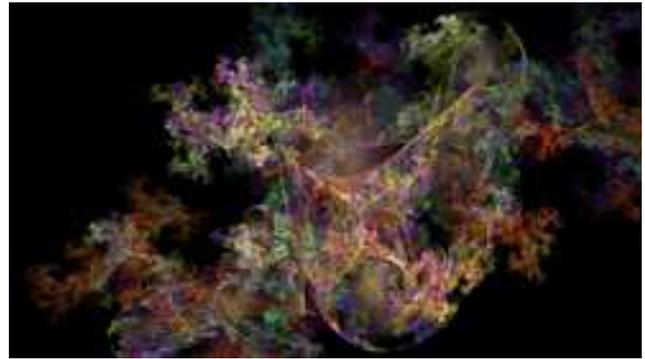


Figure 1 : Fractal Morphogenetic Experimentation. © Alain Lioret 2017.

However, generating novelty and/or complexity using such methods has an obvious shortcoming: In order to explore a solution space, one needs a problem to solve. Yet not every novelty-generating process can be viewed as a problem-solving strategy, let alone a darwinian strategy (Gabora, 2005). One of the most generic example may be the emergence of life itself (Pascal, 2013), which precedes the very notion of evolutionary adaptation . It has been proposed that life emerges and maintains itself through self-organized criticality at the edge of chaos, i.e. it spontaneously evolves towards a region of the phase space located at the boundary between the chaotic and non-chaotic regimes (Mora, 2011). Another important argument for non-adaptive evolutionary innovation can be found in the concept of exaptation, coined by Gould & Vrba (1982) to describe innovations that arise as by-products of other adaptive traits, but aren’t themselves adaptation strategies. A recent study by Barve & Wagner (2013) suggests that

metabolic processes are inherently suited to produce novelty through exaptation.

Hypothesis

These observations provide the basis for the following set of hypothesis:

- Nature-inspired creativity (and inspired creativity in general) is essentially a process of exaptation, in which pre-existing innovations are re-purposed for a need that didn't exist at the time of their emergence.
- Furthermore, based on recent models of emergent self-organizing metabolic systems (Tkachenko & Maslov, 2015), we argue that self-organized criticality at the edge of chaos is a major source of latent exaptations, and is better suited than random combinatorial processes at spontaneously producing novelty.
- Complexification through self-organized criticality generates an increasing number of competing processes at different scales, each of which is associated with an attractor basin, and the resulting partitioning of the phase space by these basins can - under certain conditions - exhibit a fractal geometry.

Review of possible approaches

In the following paragraph, we review several computational models that we think could be interesting starting points for investigating the possibilities of self-organized criticality at the edge of chaos as a source of creative exaptations.

The historical approaches by Lohn & Reggia (1997), Reggia et al. (1998) and Chou (1998) based on cellular automata, provide an efficient proof of concept of replicating structures appearing and growing spontaneously from randomly occurring interactions in a disordered initial state, and have laid the groundwork for interesting developments, a good example of which can be found in the works of Ishida (2011) which demonstrates the ability of cellular automata to realize cell-like self-replication. A possible direction for refining this model and achieving more complexity and realism is to use a Voronoi automata such as may be found in Adamatzky et al. (2011), instead of a traditional grid-based cellular-automata. To our knowledge, this approach has not been studied from the perspective of self-organized criticality at the edge of chaos.

Artificial chemistry and physics are another possibly useful framework to study the emergence of complexity, as demonstrated by the works by Hutton (2002, 2004), and Smith et al. (2003) on simulating the emergence, growth and replication of membranes and information carriers.

Sayama (2008) more recently introduced another take on the simulation of chemical processes by proposing that chemical structures are themselves an emergent manifestation of lower-order behaviors, in this case the

kinematics of chemical particles. Swarm systems being known to exhibit self-organization and emergent behaviors, it seems reasonable to consider that such a model could provide an interesting framework to simulate a fairly sophisticated artificial life.

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Reverse engineering biological complexity in artificial evolution

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INTRODUCTION

In biology, the scientific community has widely adopted evolution as the essential concept for explaining the emergence of diversity and adaptability of life forms. However, current artificial evolutionary systems are still a simple imitation of real biological organisms and a further exploration on simulating more complex evolutionary processes may not only extend our understanding on biological evolution but also help us to improve the efficiency of our evolutionary algorithms. Actually, based on observations in evolutionary biology, researchers have recently suggested that some of the essential principles of natural evolution have been too often ignored, and rethinking those principles may help us to obtain a more comprehensive view on artificial evolution (Pigliucci 2007, Wade 2011). One thing we could learn from recent evolutionary biology studies is that evolution in Nature always encompasses many dynamic interactions at different levels and any of these interactions may create a corresponding domino effect. These effects connect all different components subjected to the evolutionary process into a co-evolutionary process and creates an immensely complex context.

Based on complexity theory, complex biological systems are formed on the basis of coherent interactions between its multiple interactive components. Here, “large numbers of functionally diverse, and frequently multifunctional, sets of elements interact selectively and nonlinearly to produce coherent rather than complex behaviour” (Kitano 2002). Important features of biological organisms such as robustness and flexibility are based on emergent self-organized patterns and these patterns dynamically form through complex interactions rather than through predefined models (Csete and Doyle 2002). These features of biological systems have been well-known for a long time but at the same time it has been difficult to accurately describe the formation of these features because of the complexity behind the evolutionary process. However, simulating such complexity (complex interaction context) during evolution is an essential step to better understand and utilize evolutionary principles. As Clune suggested in (Clune, Mouret et al. 2013), one major contributor to robustness of biological systems is modularity. Biological systems or evolutionary processes usually consist of highly modular structures that can be modeled as networks at different levels, such as metabolic pathways, gene regulatory networks, protein interaction networks or the network formed by the animal brain (Wagner, Pavlicev et al. 2007, Cain, Conte et al. 2008, Hintze and Adami 2008,

Pigliucci 2008). High modularity in complex systems means that the interactive components of the systems only interact with a few fixed targets rather than with everything else in the system randomly. Therefore, to simulate biological complexity, we have to simulate the intricate interactions between different components, such as genes, networks, organisms, and populations, to evolve self-organization depending on the evolutionary context rather than using some predefined model. Here, we study the biological complexity as discussed above by simulating the interaction of various components in an artificial evolution experiment. By dispensing the interactive functions into various autonomous virtual robots, swarm robots in our simulation can interact with each other as interactive components while their interactive behavior provides a simplified imitation of the evolutionary context. In this research, we try to further investigate the emergence of complexity which has also been regarded as evolutionary transitions during evolution. We discuss the possible effects of ubiquitous interactions among emergent modules at different levels and propose a nested architecture model to describe the corresponding co-evolutionary framework.

EXPERIMENTS & RESULTS

Based on the similar simulation platform that we used in previous research (Yao, Marchal et al. 2014, Yao, Storme et al. 2016), We have run our artificial evolution in a virtual ecological environment. From the experiment results of 50 independent runs, we have observed two interesting tendencies at the ecological level and genetic level.

More complex adaptation and more intensive interaction between organism robots increase the complexity of swarm behaviour of robots

To observe how such complexity evolves during simulation, we have tracked and analyzed the emerging patterns during robot swarm behaviour. In the simulation, we observed that the equilibrium between the number of food sources and the robot population is fragile. For surviving under an expedient balance, as shown in Figure. 1, some robots start to attack other robots and plunder energy as predators rather than to gain energy from searching for food.

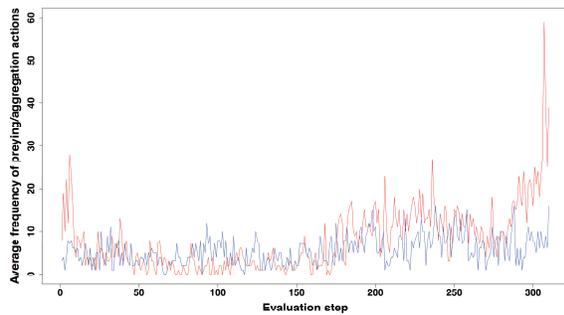


Figure 1. The comparison between the frequency of prey behavior and aggregation behavior.

Such phenomenon only has been observed during later phases of the simulation when food becomes scarce and therefore we assume this pattern to be evolved as an adaptation to the new food scarced environment. To confirm our assumption, we have repeated the simulation for 50 times and found a clear correlation between prey behaviour pattern and food scarce.

The preservation and recede of complexity in GRNs

To evaluate the change of complexity in GRNs, we have recorded the average number of different kinds of 'active agents' in every GRN at every 10 time steps, the result of which has been shown in Figure. 2.

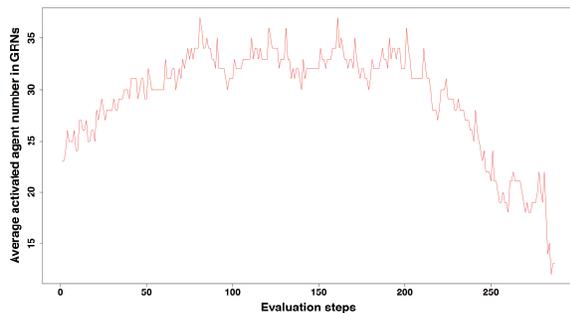


Figure 2. The average agent number in one simulation experiment.

In our simulation, the robot behaviour is determined by its GRN and the output control signal from the GRN is based on the swarm behaviour of the agents in the GRN. Therefore, the average number of different agents in a GRN represent the complexity of the robot controller. Although the average complexity of the GRNs gradually increase at the early stages of the simulation, we observed an apparent decrease at later stages when food become scarce.

DISCUSSION

Self-organizing structure has been well investigated in evolutionary studies and many scientists believe that the high modular structures organized within a nested architecture can

accelerate the evolutionary rate while efficiently preventing the fragility caused by the cost of complexity (Bolker 2000, Welch and Waxman 2003, Clune, Mouret et al. 2013). Inspired by these ideas, we have developed a simulation based on swarm robotic models acting at multiple levels to reengineer the complexity in biological evolution. The results indicate that the complexity encapsulated in each module actually can be adjusted through the interaction between modules and such interaction makes the hierarchical structure of evolution to become a co-evolving framework (Tavares, da Gama et al. 2008). Finally, through interaction and multiple level selection, all selected modules will be optimized for more robust and complex co-adaptation within the whole system.

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A Multi-Level Autopoietic System to Develop an artificial Organism

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Abstract

We present a new model for the self-creation of an artificial embryogenesis, using a new kind of organization, The Autopoietic System Theory, at different levels. The development is dependent on a global function in the environment and the regulation of the Artificial GRN policy enzyme inside the cells.

Introduction

Natural systems distinguish themselves by their high morphogenetic ability, and show the possibility of combining self-organization with complex architecture[4]. The exportation of these living system characteristics is desirable as their self-formation capabilities to generate automatic design of complex system such as artificial multicellular organism is one of the most considerable challenges in artificial life. Many developmental models have been designed to simulate the growth of virtual multicellular starting with one cell.

The biologists Adrian P. Bracken et al. [2], confirm that even if cells have identical genomes, they can respond differently to the same stimulus because of their preprogrammed memory considered by “Polycomb group (PcG)”. Moreover, cells are considered as an autopoietic system. In which the external events (the outside of the cell) have only a partial effect inside the system, and the total and significant effect of the changes is defined by the internal dynamics of the system and not by the external [3]. Many natural systems such as cells, chemical compounds, galaxies, organisms and planets show self-organized construction. Maturana and Varela describe the autopoietic machine as an organization of living system which define the universal self-organization [1]. Since the autopoietic machine defines the organization of living system, we adopt this theory in our model to develop an artificial multi-cellular organism. That has the capacity to create and organize itself without any external driver.

We propose an “A Multi-Level Autopoietic System” with different levels of organization (cell level, tissue level and organ level), where each different individual is an autopoietic machine figure1 (1). A GRN policy enzyme controls cell fate during development figure1 (2), where the morphogens in the environment have a partial effect in the cell decision. The direct effect is from the interior of the cells (memory system and policy enzyme), which are inspired in their role by the PcG protein.

A Multi-Level Autopoietic System (MLAS)

Maturana and Varela provide the following definition : “An autopoietic machine is a machine organized (defined as a unity) as a network of processes of production (transformation and destruction) of components that produces 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.”[1]. Despite the fact that the theory of autopoietic system was originally proposed in biology, we will use an interpretation of the autopoietic theory in artificial embryogenesis, that combines self-organization and an architecture system.

At initialization, the environment has a single concentration of an artificial protein. This protein represents the global function that the whole process attempts to achieve. The environment also has energy, one stem cell that contains an irregular GRN policy enzyme, and an empty memory system. The global function presented in the environment as a concentration of protein at the organ level has the following properties:

- The protein identifier (ID) is coded as an integer between 1 and p that represents the identifier of the organ.
- Individual Reports(I_R) are coded as a float between 0 and 1 and the concentration I_R expresses the success rate of the component. They work to achieve the global function. I_R is initialized by 0.
- Autopoietic factor (A_F) is coded as a float between 0 and 1 and initialized by 1. This A_F represents the new function and it will be sent to the sub level. These two initial concentrations (I_R at 0 and A_F at 1) demonstrate that the organ doesn't exist yet.

This protein is the beginning of the network of processes of production of the first autopoietic machine (organ) that produces the components (tissues), and the reason for all the other autopoietic machines that will appear in the system.

When the concentration of this autopoietic factor is superior to a threshold, this will create the beginning of new tissues. The production of new tissues (the components of the first autopoietic machine) is done by generating another protein in the environment, in which the structure of this protein

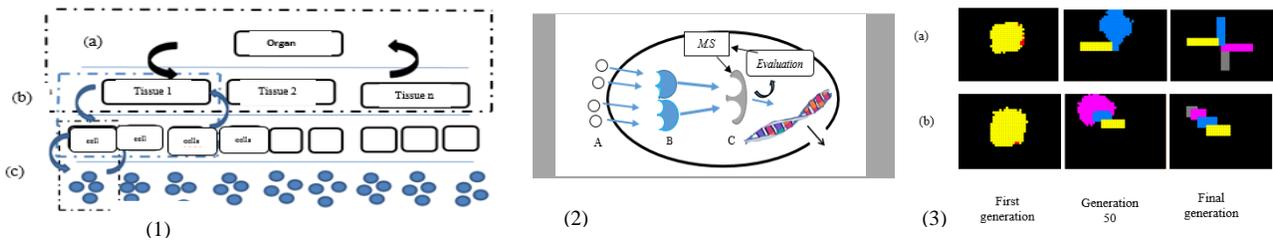


Figure 1 : (1) Autopoietic system in different levels; In (a), first organ level with tissue, the interaction and transformation generate a network that stimulates the organ to produce itself. The same process happens in (b), at the tissue level, the number of tissues is proportional to the number of the autopoietic systems in this level. In (c), a network is generated between cells and genes level which stimulates the cell to regulate its GRN. (2) GRN Policy Enzyme Architecture. (A) Represents morphogens in the environment, (B) the first layer or regulation (gene action). (C) The second layer of regulation (policy enzyme), (M.S) the Memory system. (3) The evolution in the development of two different organ with different global functions diffused in the environment, (a) the first protein of the global function (protein organ) was initialized by $\{ID =1, I_R=0, A_F=1\}$, and in (b) $\{ID =3, I_R=0, A_F=1\}$. with energy equal to 250 and α equal to 0.01 for both.

(function in tissue level) is different from the previous protein only at protein identifier level. This new protein has the ID of the organ and the ID of the tissue that is coded as an integer between 1 and P. The initialization of the concentration of the two reports of this protein (I_R, A_F) is the same than the organ protein. This protein can be received by one type of cells that is stem cell, the cell will know the function that allows her to work for its global interest for all its lifetime. Thus, the interaction between each of the two levels in our system is made by these two reports, individuals show their level of success in fulfilling its function.

At the cell level, the first report (I_R), is the total of the evaluation of each action. The evaluation of an action : $Eva(Action_i[t])$ is equal to 1 if it is a “good” action support the global interest of the cell, else it is equal to 0, divided by the number of the action which are executed. This report is in $[0..1]$, the optimal result is one, where individual executes only the good actions, if the number action “ N_A ” equal to 0, the individual report for the cell is one.

$$I_R_m = \sum_{i=1}^{N_A} Eva(Action_i[t])/N_A$$

For the other levels, tissue and organ, the individual report I_R_n is the total of all their individual reports I_R_i divided by the number of their individuals, if they are more than the minimal number, else by the minimal number of individual “ Nb_m ”.

$$I_R_n = \sum_{i=1}^{N_ind} I_R_i / ((N_ind + Nb_m) + |(N_ind + Nb_m)|) / 2$$

The second report between an higher level and a sub level is calculated by the difference between the optimal value, and its individual report : $A_F_n = 1 - I_R$.

We define α as a threshold. If $A_F_n < \alpha$, the functions are accomplished.

On-line GRN Policy Enzyme

To achieve an embryogenesis process, we must know how the tissues and organs of the developing embryo take their miraculous forms, we use an Artificial GRN with new additions in order to obtain an on-line learning process with memory concept. Our proposed model is defined as follows:

1. Reinforcement learning realized by an Artificial GRN.
2. A policy enzyme that accelerates the activation of one of the potential actions using the memory system.

3. Memory system, represented by two matrices: “best action” and “worst action”.
4. Evaluation module with two evaluation functions, the first against local interest, and the second against the global interest, initialized at the genesis of the individual.

Morphogens in our model are obtained from neighbors as a signal of the individual, the energy, responsible for achieving an action, and signals from the upper level. These morphogens can activate more than one action at the same time in the first layer. With a GRN, an individual can activate the right action in the right place using reinforcement learning. Two regulation layers are used here; the first one assures that all the necessary morphogens of the environment are present for each action. If the gene action of the first layer is active, they pass to the second layer (policy enzyme), where it chooses between the actions activated to select the right action according to the memory. These two layers regulate the output of the GRN.

Conclusion

We presented a new model of artificial embryogenesis. We used in our model the concepts of the autopoietic theory that we interpreted in different levels coupled with the use of a new On-line GRN Policy Enzyme. Our model exhibits the self-organization of natural system shown to be organizationally closed.

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A Study on Evolutionary Dynamics of Mating: Appearance and Distance

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Abstract

Mating is an essential behavior for animals including humans who rely on sexual reproduction. Here we present the design and some results of our multi-agent-based simulation targeting an evolutionary process of appearance, preference, and mating strategies, as a model of human life. A person's evaluation for neighbors to find the best partner does not always depend on the matching degree between the subject's appearance and the observer's preference. We introduce two kinds of interpersonal attractiveness, which stand for "distance" and "appearance" in our simulation. Our simulation result showed that, in mating, we should not stick to how close to the candidates of our partner and how good appearance they have.

Introduction

There has been much discussion in recent years about evolutionary psychology, such as human's sex differences and mating strategies. Darwin's work has had a huge influence on various fields, specifically in animal's instinct characters. Individual differences in psychology are also traits inherited from their ancestors through the evolutionary process (Darwin, 1871). Additionally, attractiveness of appearance is an important evaluation criteria in human sexual selection (Walster and Berscheid, 1969). However, there is no clear explanations how the human's appearance is involved with interpersonal attraction, and how the appearance is important compared to other factors.

We tried to make an artificial society using multi-agent system to investigate population dynamics on mating and reproduction, which is often used to simulate a complex evolutionary ecological system. A person's evaluation for neighbors to find the best candidate of partner does not always depend only on the matching degree between the subject's appearance and the observer's preference, but an acceptable neighbor is often better than the best look far away. We make a comparison between visual attractiveness and distance attractiveness, and considered which attractiveness we should take priority.

Agent Model

The system we designed here includes a collection of hundreds of individual agents that moves in the world of square shape interacting each other. Each agent has its own life span, and has a chance of reproduction. The following subsections describe the specification of individual agent.

Agent's parameter

In this simulation, agent's appearance and preference are specified by RGB color. Agents have parameters of

- gender
- age
- appearance color (f_R, f_G, f_B)
- preference color (p_R, p_G, p_B) .

Appearance and preference inherit the descendants.

Mating

Every agent of the age between 15 and 50 years tries to make a proposal to the best candidate as a partner every step if it has no partner. To choose the best, each agent calculates two kinds of attractiveness for each candidate of the opposite gender positioned within a given visible range S . First one is l_{fm} standing for agent's appearance, and second attractiveness standing for agent's appearance l_{fm} . Second one is d_{fm} standing for intersexual distance, defined as

$$l_{fm} = 1 - (|f_R - p_R| + |f_G - p_G| + |f_B - p_B|) \quad (1)$$

$$d_{fm} = 1 - \frac{D_{fm}}{S}, \quad (2)$$

where D_{fm} is the distance to the candidate. The comprehensive interpersonal attractiveness L_{fm} weighted summation between these two values by using a weighting coefficient "appearance bias" α . If the proposal is accepted, the proposer and the acceptor make a child together. The child agent's appearance and preference are inherited from its parents. Each component of RGB color data is randomly inherited from mother or father with crossover and mutation in a given probability.

Move

Each agent is subjected to the force \vec{F}_f from neighbors depending on matching degree. \vec{F}_f is defined as

$$\vec{F}_f = \sum_m (L_{fm} - C_{fm}) \cdot \frac{\vec{a}_f \vec{a}_m}{|a_f a_m|}, \quad (3)$$

where C_{fm} is a variable that works to prevent agents from overlapping each other.

Simulation

We conducted ten simulation processes with different random number sequences for each value of appearance bias α from 0 to 1 stepping by 0.1, that is 1,100 processes in total. The other parameter settings are:

1. The number of agents is at most 1000.
2. Agent's life is fixed at 1000 steps (10 steps = 1 year).
3. There are two distinct genders, which are chosen randomly at birth with equal probability.
4. Every female can give a birth to one child per step.
5. Agents accept proposals from others if their evaluation value of proposer's comprehensive attractiveness is over 0.7.

Figure 1 shows how the simulation goes. Round shapes stand for females, and square shapes stand for males. Small ones are 0 to 20 years old. The inside color of each agent is its preference, and the outside is its appearance.

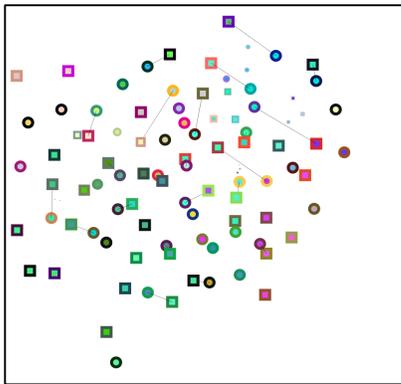


Figure 1: Simulating window

Figure 2 shows the number of married agents ratio to population which is averaged in each value of α . When α is 0.6, the ratio of married agents reaches the maximum except the case α is 1.0. In the case α is 1.0, the acceptance ratio becomes higher because the average of population is smaller than other cases.

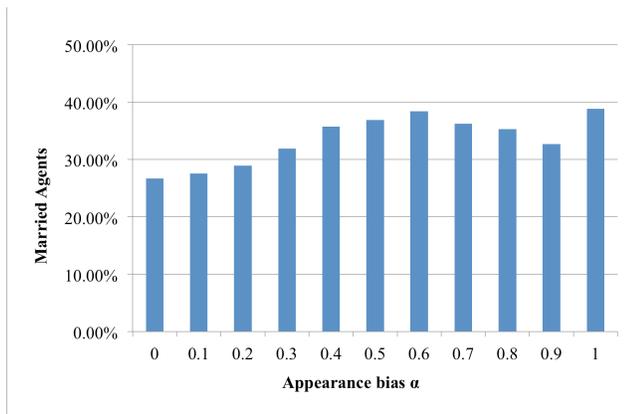


Figure 2: The averaged number of married agents ratio to population in each value of α .

Conclusion

We confirmed evolutionary dynamics of agent's appearance and preference in different strategies of mating. The simulation results indicate that sticking to the degree of matching in appearance or distance decreases the possibility of mating. Under the environment that every agent chooses their partner depending on physical distance ($\alpha = 0$), agents cannot easily get their partner, and as the value of appearance bias increases, the number of married agents ratio to population increased as well. However, if the value gets over 0.6 except the case it is 1.0, the number of married agents ratio begins to decline. This is because, we assume that, as observers evaluate matching degree depending on subject's appearance, acceptor's preference does not match proposer's appearance often. This phenomenon looks close to reality. We predicted before this experiments that, as the value of α increases, the number of married agents ratio also decreases. It is because the degree of distance attractiveness is often larger than appearance attractiveness. Contrary to our expectations, however, the number of married agents ratio increases as the α increases in the cases α is 0 to 0.6. The reasons we discussed are as follows.

- Many couples divorce by the approach of a third agent.
- Many proposes are refused because of triangular relationships.

These results suggest that in reality, we should not stick to how close to the candidates of our partner and how good appearance they have. To simplify the simulation, this paper has only defined two criteria so that agents can select the best candidate of partner. In reality, of course, there are many more than two factors, for example, degree of similarity to observer's family, observer's past experiences. Actually, in this paper, female agents can give a birth to over 10 children. That is an example of unreal setting, so we need to restrict the number of children that an female agent can give a birth in its life. Our future task is to review the simulation settings and make it close to real human society model.

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An approach of model evaluation improvements for classification in kidney cancer prediction

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Abstract

This paper, presenting a work in progress, discusses an approach to a relevant supervised learning method from the art of machine learning field: classification. Various aspects are considered, as preprocessing of the input data; selection of the model applied to the data; evaluation of the model; improving the performance of a model, selection of the most relevant features to be included in the model and also learning a model that is able to perform well on new data. The computed metrics for performance evaluation of a model are also highlighted. In this paper, the selected models are ensembles of decision trees such as Random Forest and Gradient Boosted Regression Trees. The model evaluation, the model improvements and feature selection ultimately lead to building models able to generalize to new data with a high value of accuracy. All these represent an added value in fields where patterns are important.

Introduction

We are living in an age in which we are invaded by the amount of available data. These data are increasing in an exponential way. The art of making sense of all the data represent an issues nowadays. Moreover, the ability to deal with different types of these data require new approaches in the field of exploratory analysis. Therefore the extraction of relevant information, the discovery of relations between data and the ability to generalize to new data represent a continuous challenge.

Exploratory data analysis becomes an impressive area of concern for certain domains such as education, healthcare, biology, economics, geography, geology, history or agriculture. Particularly, the purpose of this paper is related to medicine and psychology. Some machine learning advantages are being investigated in order to improve a treatment, a diagnosis of a patient.

The data sets used in our analysis are data from medical field and also are suitable for multiclass classification.

Methods and results

The data set used in our experiments is data set Kidney-Cancer, a data set which contains 155 items denoting pa-

tients analyzed for kidney health, and 19 variables denoting medical analysis like the age, sex, value of albumin, liver and spleen dimensions, histology and fatigue. The decision variable represents the patient diagnosis given as 1 and 0 (0 representing benign and 1 representing malignant) [Breiman, 1996].

As a preprocess of this data set we had the following aspects, first, in the numerical feature, there are some missing values. In order to deal with this missing values, we have compute the mean of the existing values for this feature and after that we just replaced the missing values with the computed mean, and the second, the ordinal features were encoded such as these can be used in our models, the encoding methods was to use a one-of-K, that is the transformation of each ordinal feature with m possible values into m binary features, with only one active, once.

Using this data set, our goal is to build models that generalize to some new observations. A model evaluation method allow us to use our existing labeled data to estimate how well our models are likely to perform on our new observation.

Some methods used to compute the values of parameteres a powerful hyper parameter optimization technique called grid search that can further help to improve the performance of a model by finding the optimal combination of hyper parameter values.

The approach of grid search performs an exhaustive search paradigm where we specify a list of values for different hyper parameters, and the computer evaluates the model performance for each combination of those to obtain the optimal set. Although grid search is a powerful approach for finding the optimal set of parameters, the evaluation of all possible parameter combinations is also computationally very expensive [Mueller et al., 2013]. An alternative approach to sampling different parameter combinations is randomized search. Randomized search is a randomized search over parameters, where each setting samples from a distribution over possible parameter values. Using k-fold cross-validation in combination with grid search methods is a useful approach for fine-tuning the performance of a machine learning model by varying its parameters values. And this

also was an approach that we have choose to be investigated. This paper is a working project [COROIU et al., 2016].

In our experiments, we have used an approach of the standard k fold cross-validation, called stratified k-fold cross validation, in order to produce better bias and variance estimates, especially in cases of using the unequal class proportions [Chau et al., 2012].

After we have selected a model that has been fitted on the training dataset, we can use the test dataset to estimate how well it performs on this unseen data to estimate the generalization error.

If we are satisfied with its performance, we can now use this model to predict new, future data. It is important to note that the parameters for the previously mentioned procedures, such as feature scaling and dimensionality reduction, are solely obtained from the training dataset, and the same parameters are later reapplied to transform the test dataset, as well as any new data samples - the performance measured on the test data may be overoptimistic otherwise.

Conclusion

We have perform the procedure of determining the values for the parameters with the search methods: conventional grid search, randomized grid search. To quantify the performance of a model, we used the accuracy metric.

Comparing conventional grid search and randomized search for parameter estimation we have the following conclusions. All search methods explore exactly the same space of parameters.

The run time for randomized search is drastically lower than for grid search. The run time is lower for randomized search, and this reveals that from the point of view of time, the conventional is better than randomized grid search methods. General, the run time increases for the data sets with a greater number of observations.

From the point of view of model selection, we can conclude that for our data set the model, with an appropriate value of accuracy is Gradient Boosted Regression Trees.

The model evaluation, the model improvements and feature selection ultimately lead to building models able to generalize to new data with a high value of accuracy. All these represent an added value in fields such us medicine and psychology, where a physician or a psychologist may use pattern and information as input in the treatment of a patient.

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Odometry in swarms of e-puck robots cooperatively transporting a heavy object

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Abstract

A swarm of physical e-puck robots is required to transport a heavy object as far as possible from its initial position in an arbitrarily chosen direction. One robot of the group is also required to estimate its final position using odometry. The odometry process is performed using four sensory set-ups: 1) wheel encoders, 2) optic-flow sensors, 3) wheel encoders with gyroscope, 4) optic-flow sensors with gyroscope. We find that frequent wheel slippage caused by the robot pushing the static object, and later displacements caused by collisions with other robots severely disrupt the precision of the position estimates generated by 1) and 2). The support of the gyroscope's reading used to measure the robot angular displacements improves the position estimates of the optic-flow sensor based odometry more than the estimates generated by the wheel encoders based odometry.

Introduction

This paper describes a set of experiments in which odometry is performed by a physical e-puck robot while transporting a heavy object in cooperation with other e-puck robots. Odometry refers to the process of estimating change in the robot's position and orientation over time by using data extracted from the movement of the robot actuators. Odometry is particularly useful for navigation in indoor environments where GPS is not available. In most wheeled robots, where wheels are linked to a common axle, odometry is achieved by using sensors (e.g., wheel encoders) that measure how far the wheels have rotated in a given interval of time. The precision of wheel encoders based odometry is undermined by both systematic errors (e.g., differences in the wheels diameter), and by non-systematic errors (e.g., wheel slippage) which accumulate over time in an unbounded fashion often leading to inaccurate and unreliable localisation estimates.

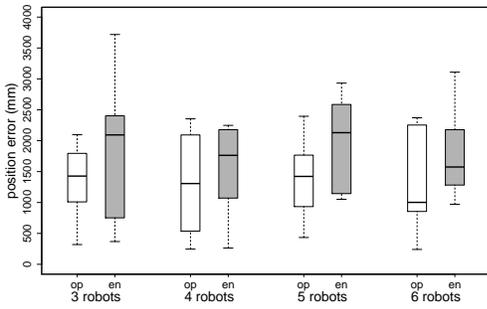
Odometry can also be performed using alternative sensors to wheel encoders, such as camera modules that use ground texture and visible features to determine the agent's ground velocity. These sensors, known as optic-flow sensors, are immune to some of the non-systematic error that affect wheel encoders based odometry. The results discussed in (Sorensen et al., 2003) show that odometry with a single

optic-flow sensor can be sufficiently accurate for small differential drive robots, for which the kinematics constraints of differential drive hold during the navigation.

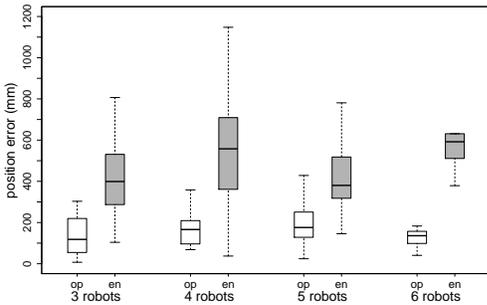
In this study, we first compare the position estimates of a single robot generated by using wheel encoders, and by using the optic-flow sensor mounted underneath the e-puck chassis. We show that, in the context of cooperative object transport scenarios, the precision of both types of estimates is severely disrupted by the dynamics of the transport, which result in quite a lot of wheel slippage (e.g., due to pushing forcing exerted on a static object and collisions), and robot's lateral displacements with a consequent violation of the differential drive constraints (e.g., due to collisions with other robots). In a second set of experiments, we show that the precision of both optic-flow and wheel encoders based odometry can be improved by combining the reading of these sensors with those of a gyroscopes, used to detect changes in robot orientation. We show that the optic-flow sensor based odometry with gyroscope corrections is more accurate than the wheel encoders based odometry with gyroscope corrections.

Methods and Results

4 homogeneous groups of 3, 4, 5 and 6 physical e-puck robots are required to push a cuboid object as far as possible from its initial position in an arbitrary direction. The object's mass is set in a way that the transport requires the cooperative effort of all the robots of the group. Robots are controlled by artificial neural networks synthesised using evolutionary computation techniques. The characteristics of the robot controllers, the evolutionary process used to set the controllers' parameters, and other methodological details of the object transport task are described in (Mohammed Alkilabi and Tuci, 2017). In each group, there is a robot, referred to as *R-robot*, whose final position in the arena at the end of the transport is estimated using the readings of its optic-flow sensor, and using the readings of its wheel encoders. Both types of final position estimates are compared with the ground truth generated with a Vicon system. Each group is evaluated for 10 trials. Video of a trial



(a)



(b)

Figure 1: Graphs showing the position errors referring to the Euclidean distances (in millimetre) between the final *R-robot*'s positions recorded by the Vicon (i.e., ground truth) and the final *R-robot*'s positions estimates generated by: (a) the optic-flow sensor (op, white box) and by the wheels encoder (en, grey box); (b) by the optic-flow sensor with gyroscope corrections (op, white box), and by the wheels encoder with gyroscope corrections (en, grey box). Tests are run for homogeneous groups of 3, 4, 5, and 6 physical e-puck robots, for 10 trials per group. Each point in the box refers to the position error in a single trial. Boxes represent the inter-quartile range of the data, while dashed horizontal bars inside the boxes mark the median value. The whiskers extend to the most extreme data points within 1.5 times the inter-quartile range from the box.

with 6 robots can be found at <https://www.youtube.com/embed/8wCs07KUT5I>. The results of these tests are shown in Figure 1a, where the white boxes refer to the errors corresponding to the position estimates generated with the optic-flows sensor, and the grey boxes refer to the errors corresponding to the position estimates generated with wheel encoders. We noticed that the errors for both types of position estimates are quite high. We also notice that errors corresponding to estimates generated by the wheel encoders are slightly higher than the error corresponding to position

estimates generated by the optic flow sensor. Wheels slippage occurring anytime while the *R-robot* pushes a static element of the transport scenario—that can be the cuboid object or another static robot—severely deteriorate the precision of the position estimates generated by wheel encoders. The optic-flow sensor is relatively immune from the consequence of wheel slippage. Unfortunately, in the collective object transport task wheel slippage events are associated to rather frequent lateral sliding of the robot body (i.e., robot movements in the direction perpendicular to the wheel direction of rotation), which are a consequence of pushing forces mainly exerted by other robots. Lateral sliding events disrupt the precision of the optic-flow estimates relative to changes of the *R-robot*'s orientation more than the estimates relative to change in position (data not shown).

In order to overcome the disruptive effects on odometry associated to the object transport scenario, we run a further set of tests, in which the changes in orientation estimates for both the optic-flow sensor and the wheel encoders are generated using the gyroscope mounted in the *R-robot*. This means that, the optic-flow sensor and the wheels encoders are used only to estimate the linear displacements (i.e., translational movements) in the two-dimensional navigation space. The results of this set of tests are shown in Figure 1b. We notice that, for both types of final position estimates and for all groups, the errors are much smaller. Moreover, the errors corresponding to the position estimates generated by the optic-flow sensor with gyroscope corrections (see white boxes in Figure 1b) are significantly lower (Wilcoxon rank-sum test, $p < 0.001$) than the errors corresponding to position estimates generated by the wheel encoders with gyroscope (see white boxes in Figure 1b). We conclude that, in this cooperative object transport scenario, the optic-flow sensor with gyroscope is a better means for odometry than wheels encoder with gyroscope.

Conclusions

Cooperative object transport scenarios are particularly challenging for odometry since frequent wheel slippage and lateral displacements severely disrupt the precision of changes in position and orientation estimates. We showed that optic-flow based odometry with gyroscope correction for estimating angular displacements works significantly better than the classic wheel encoders based odometry.

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Local entropy patterns in continuous cellular automaton models

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Abstract

The article presents the results of the simulation of a cellular automaton model whose cells assume continuous values. The described experiment examined the behaviour of local entropy and showed the occurrence of its three qualitatively different images with their character resembling Turing patterns. The hypothesis, according to which the behaviour of local entropy might be identified with an image created in a reaction-diffusion process, was presented.

Problem

The research study concerning the mathematical foundations of creating cultures (Zgrzebnicki, in press-a) considers a continuous cellular automaton model as a hypothetical framework. Although there have been many studies on the properties of discrete cellular automata published so far, the models whose cells assume any values limited only by floating point precision have been much less discussed in scientific works. The research presented herein assumed that the discussed automaton may change values of its cells according to any function transforming the values of neighbours in the neighbourhood of a certain radius, and that this radius and weight of the neighbours' contribution to a cell's change may also be arbitrarily defined for the purposes of a certain experiment. In comparison with discrete automata (Wolfram, 1984), such assumptions imply a much broader class of solutions. The conducted research is aimed at finding an answer to the question whether there are any general regularities or patterns describing the dynamics of the assumed model.

Method

Let there exist a matrix M , whose components are called cells. Let there exist a function G , which transforms matrix M into matrix M' in a way that:

$$c'_i = G(\delta_i^j c_j, r)$$

, where c stands for the cell's value, while i and j mean coordinates, and r means a radius within which the neighbourhood of a certain cell has an influence on its value's transformation. Furthermore, to eliminate the problem of boundary values, let us assume that the boundaries of the matrix

are glued together so that topology of the described space is identical with a torus.

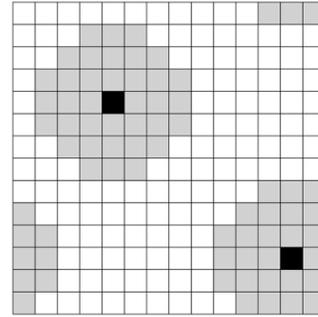


Figure 1: The value of cells established on the basis of the values of their neighbours located within the radius $r = 3$. Topology of glued boundaries guarantees continuity of solutions on the edges of the matrix.

Finally, let us consider process P in which values of all the cells are changed so that a matrix obtained after the change becomes a source matrix for the next step:

$$P: M \rightarrow M' \rightarrow M'' \rightarrow M''' \rightarrow \dots$$

Experiment

The following experiment was done. In matrix M of a size of 512×512 components, a random value from the range of $[0, 1]$ was attributed to each cell. In each subsequent time step, arithmetical mean α of a value of neighbouring cells within radius r was calculated for each cell. Subsequently, on the basis of the following functions, the weight with which the neighbourhood contributes to the later change was calculated:

$$w_1: \omega = e^{-\frac{(\alpha - c_i)^2}{2\sigma^2}}, w_2: \omega = -e^{-\frac{(\alpha - c_i)^2}{2\sigma^2}} + 1, w_3: \omega = 1$$

, where c_i stands for the value of the cell whose neighbourhood is analysed, while σ constitutes a parameter of the experiment defined *a priori*.

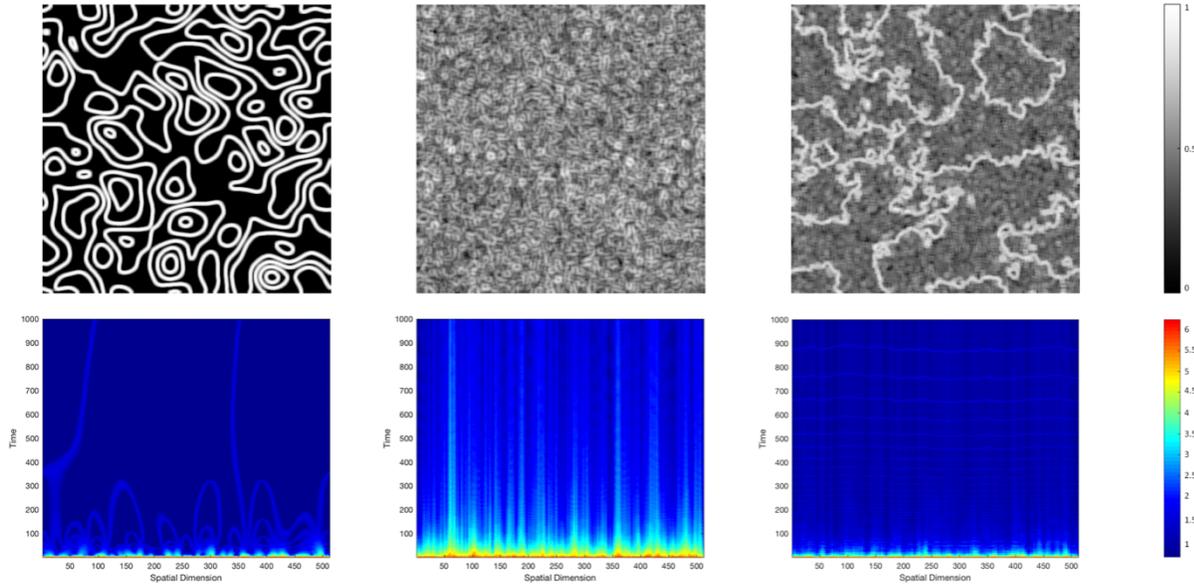


Figure 2: Normalized local entropy of the matrix (top) and local entropy in a time slice across the whole matrix and along cell no. 128 (bottom) in the experiments of the following parameters: $[G_1, w_3, r=4, \text{step of the process: } 150]$ (left), $[G_2, w_2, \alpha=0.5, r=4, \text{step of the process: } 800]$ (middle), $[G_2, w_2, \alpha=0.1, r=48, \text{step of the process: } 285]$ (right).

The value of each cell in a subsequent time step was calculated with the use of the following functions:

$$G_1: c'_i = \frac{c_i + \omega\alpha}{1 + \omega}, \quad G_2: c'_i = \frac{c_i + \omega(\alpha - c_i)}{1 + \omega}$$

Results

By means of the aforementioned transformations, the value of the cells of matrix M in the subsequent steps of process P was calculated. Subsequently, for each P process, proper L matrix was obtained whose every cell assumes the value equal to local entropy (MathWorks, 1994-2017) in the neighbourhood of an analogous cell of matrix M . The process of qualitative evaluation of the results distinguished three images of changes occurring within the frameworks of local entropy. Each of the obtained result could be attributed to one of these three groups. The first image is a fine, tangled pattern, almost unchanged over time; the second image is a pattern similar to broadly scattered contour lines and it varies over time in a cyclical fashion; while the third pattern is the two aforementioned patterns — unchanged and cyclical — overlapping.

Discussion

The distinguished images resemble Turing patterns occurring, among others, as the result of reaction-diffusion processes (Turing, 1952). According to the proposed hypothesis, the analysed systems might be treated as reaction-diffusion ones if

low local entropy is understood as a high concentration of one component, while high local entropy as mapping of a near homogeneous mixture. Observation of a time change of Turing patterns in the dynamics of a continuous cellular automaton may show that the mechanism of imitating the neighbourhood, on which its operation relies, may imply waves of ordering patterns recurrent over time.

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Hybrid topology in GrowCut algorithm

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Abstract

This paper presents the results obtained by investigating a new hybrid topology for the GrowCut algorithm. The main purpose is to study whether choosing neighbors situated at a certain distance from a pixel (in addition to the pixels from a classical neighbourhood) can influence the results of image segmentation. Experiments were performed on real and synthetic images and the results were evaluated using different performance measures. Some of the results were unexpected and worth studying in the future.

Introduction

Image segmentation is an important part of image processing which consist in partitioning an image into two or more regions. The purpose of image segmentation is to isolate different regions of interest and further analyze them. The task of segmenting an image becomes harder when the dimension of the image or the number of partitions increases.

In this paper, we approach the image segmentation by using the GrowCut algorithm Vezhnevets and Konouchine (2005) which provides multi-label segmentation for N -dimensional images. It uses local information on each pixel and uses Cellular Automata as a parallelization tool. One of the reasons for choosing this algorithm is the fact that it is very easy to implement and use and provides good segmentation results in a reasonable amount of time. The algorithm needs user interaction because it starts with some user-defined seeds which are considered to be correct from the beginning. The process is iterative.

The purpose of this paper is to explore a new type of neighborhood which contains, besides the classical neighbors, pixels situated at a certain distance from the current pixel, to evaluate and interpret the results obtained on a set of images using some performance measures and compare them with results obtained using standard neighborhoods.

The paper is organized as follows: Section 3 studies different topologies and neighborhoods for Cellular Automata, Section 4 contains a short description of the proposed approach and Section 5 includes several obtained performance measures and some examples of the images segmented with different neighborhoods.

Related work

This section begins with an introduction to Cellular Automata topology which is necessary for understanding the GrowCut topology presented further.

The CA topology and neighborhood structure used for a cell in applying the rule are crucial elements in the process of rule discovery and impact directly the rule performance. In the case of an one-dimensional lattice of N cells, the neighborhood of a cell is usually given by the cell itself and its r neighbors on both sides of the cell, where r represents the radius of the CA. The regular lattice topology and the described induced neighborhood are engaged in most studies tackling 1D Cellular Automata.

In the case of 2D Cellular Automata, the topology is usually a two-dimensional grid that allows the definition of different neighborhood schemes. The most popular neighborhoods used in this case are the von Neumann and the Moore neighborhoods. The von Neumann neighborhood is given by the set of all cells that are orthogonally-adjacent to the core cell (the core cell itself may or may not be considered part of the neighborhood, depending on context). The Moore neighborhood is the set of all cells that surround the core cell.

In the case of 1D Cellular Automata, different neighborhood schemes have been investigated in order to study their influence on the rule performance. In Watts and Strogatz (1998); Watts (1999); Darabos et al. (2007, 2011); Tomassini et al. (2005), network topologies are evolved for cellular automata. In these studies it is shown that, compared to regular lattices, the evolved topologies have better performance for the CA majority and synchronization tasks.

A node-weighted network model proposed in Gog and Chira (2012) and extended in Andreica and Chira (2013b) allows the use of weights for each node in the network topology. As already mentioned, the state of each cell in CA changes according to a function depending on the current states in the neighborhood. The neighborhood of a cell is given by the cell itself and its neighbors. Each neighbor (including the cell itself) has the same vote weight when deciding which is the next state of the current cell. The network

topology allowed the introduction of neighbors with different vote weights when deciding the next state of the current cell. Thus, a node-weighted network is obtained where each node has a certain associated weight reflecting the varying importance represented by nodes.

A new hybrid topology and a mixed induced neighborhood that keeps invariable the number of neighbors was also proposed in Andreica and Chira (2013a). The neighborhood of a node is given by the radius r . Each node has r neighbors on the left hand side and r neighbors on the right hand side, which gives a neighborhood of $2 * r + 1$, because we also consider the node itself. In order to create the new topology of radius r , the authors started with a regular ring lattice of radius $r - n$. The other $2 * n$ nodes that node i is connected to, are long distance neighbors. They are randomly chosen from the rest of the nodes, but following some rules that ensure the equilibrium of the neighborhood. This means that i always remains the central node of the neighborhood and the distance between node i and the long distance neighbors places half of them (n nodes) on the left hand side and the other half (n nodes) on the right hand side of i .

The hybrid topology described before allowed the enhancement of the neighborhood scheme with neighbors having different vote weights when deciding the next state of the current cell Andreica and Chira (2013b). The hybrid topology involves the presence of two kinds of neighbors: local and far neighbors. The proposed rule gives different vote weights to local neighbors and to far neighbors.

The computational experiments performed for the density task have emphasized that the proposed topologies and neighborhoods induce an improved performance of the considered rules, compared to the standard ones. Moreover, the CA performance remains stable when dynamic changes are introduced in the neighborhood structure.

Proposed topology

Our current research is based on the studies presented in Andreica et al. (2016a) and Andreica et al. (2016b) where several different neighborhood schemes were investigated for the image segmentation task within the framework of the popular GrowCut algorithm. While most of the implementations of the GrowCut algorithm use the Moore neighborhood, the authors proposed to study the image segmentation task using various neighborhoods which are formalized below.

The experiments were carried for von Neumann and Moore neighborhoods of radius 1 and 2 and the results showed that in some cases, the extended neighborhoods of radius 2 provide better results than those of radius 1. In the proposed approach we introduce new neighborhoods which contain, besides the regular pixels (of von Neumann or Moore neighbourhoods), some pixels that are situated at a certain distance from the current pixel to be updated (their number was chosen to be 1 or 3). The purpose of this ex-

tended neighborhood is to check whether the distanced pixels can influence the results of the segmentation task and to what extent, in the context of the GrowCut algorithm. The algorithm starts with seeds chosen by the user with a defined label and strength. At each time step pixels will be labeled based on their neighbors which in our case will be a combination of pixels situated near and at a certain distance from the pixel. The process stops when there are no more pixels left to modify.

Numerical experiments

Details about data

We have carried out experiments using some synthetic data and some real images. A first experiment was dedicated to analyze the performance of segmentation obtained by GrowCut with different neighborhood schemes for two-dimensional synthetic images. Several regular geometric shapes (square, rectangle, circle) were automatically generated as foreground in images, with uniform intensity and with noise.

Regarding the real-world image, Berkeley Segmentation Dataset Martin et al. (2001) and The Interactive Segmentation (IcgBench) Dataset Santner et al. (2011) contain natural images with corresponding human segmentations (ground-truth) and we used some of them in order to validate our approach.

Performance measures

In order to interpret the results of the segmentation, we chose some supervised performance measures such as DICE coefficient Dice (1945), AUC (area under curve) measure Fielding and Bell (1997), Hausdorff distance Hausdorff (1914), precision, specificity and sensitivity Yeghiazaryan and Voiculescu (2015).

Numerical results

Since GrowCut algorithm requires some initial seeds, 30 generated sets of seeds have been considered for each image and for each neighbourhood type. For each set of seeds, the GrowCut algorithm has been run more iterations, until no pixel changes its state. After the last iteration, the segmented image is compared to the corresponding ground truth and the evaluation measure is determined.

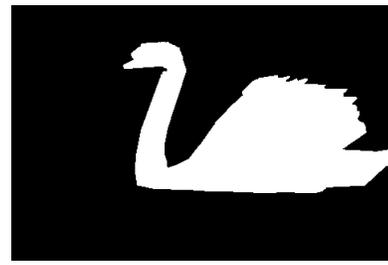
In Figure 1 we present a real image and the associated ground truth while in Figure 2 we present the results of the segmentation algorithm for various neighborhoods on this particular image.

In Table 1 we present the supervised performance measures over all the images tested with this algorithm.

Comparing the classical neighborhood for Moore and Neumann with radius $r = 1$ and $r = 2$ with the neighborhoods that contain 1 distanced neighbor, we can observe, both visually and from the numerical results from Table 1,

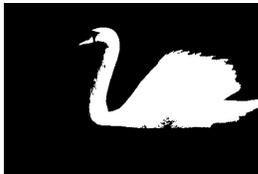


(a) Original image

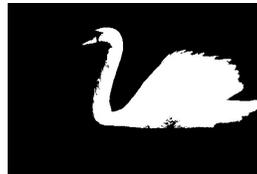


(b) Ground truth

Figure 1: An image from Berkley dataset



(a) Moore neighborhood



(b) Moore with 1 distanced neighbor



(c) Moore with 3 distanced neighbors

Figure 2: Segmentation results of GrowCut with variations of Moore neighborhood with $r=2$

that there is no significant difference between the obtained segmentations.

At the same time, if we compare classical neighborhoods with the ones containing 3 distanced neighbors, we observe that there are some important changes.

First of all, visually, by using distanced neighbors the algorithm not only isolates the object from the background, but also finds details of the image which we cannot see in the ground truth. These details may not be useful when we desire to have only the main object in the segmented image, but could come in hand when we wish to have more information on the image.

Second of all, the evaluation obtained with the performance measures is not very relevant for this case because the images obtained with 3 distanced neighbors are very different from the ground truth.

In Figure 3 we present some segmentations obtained for medical images.

Conclusions and further work

The image segmentation problem solved with GrowCut algorithm was considered in this paper. Several neighborhoods (classical and new proposed) have been considered and tested on a database containing real and synthetic images. The segmentation performance has been evaluated using different supervised performance measures.

Future work will consist in measuring the segmentation performance with unsupervised measures, due to the fact that supervised performance measures have proven to be insufficient for the images obtained with proposed extended neighborhoods.

Acknowledgment

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	Synthetic images			Real-world images		
	DICE	AUC	HDRFDST	DICE	AUC	HDRFDST
Moore	0.69	0.79	52.74	0.82	0.89	56.77
Neumann	0.69	0.79	53.07	0.81	0.89	59.09
Moore Ext	0.69	0.79	52.65	0.81	0.89	63.68
Neu Ext	0.69	0.79	52.66	0.82	0.89	59.65
Moore 1 r	0.69	0.79	52.74	0.82	0.89	56.77
Moore 3 r	0.97	0.97	8.75	0.46	0.72	208.65
Neu 1 r	0.69	0.79	53.07	0.81	0.89	59.05
Neu 3 r	0.97	0.97	8.75	0.44	0.70	206.16
Moore Ext 1 r	0.69	0.79	52.65	0.81	0.89	63.68
Moore Ext 3 r	0.97	0.97	8.74	0.44	0.70	206.03
Neu Ext 1 r	0.69	0.79	52.66	0.82	0.89	59.65
Neu Ext 3 r	0.97	0.97	8.75	0.44	0.70	206.10

Table 1: Supervised performance measures (average over all considered images)

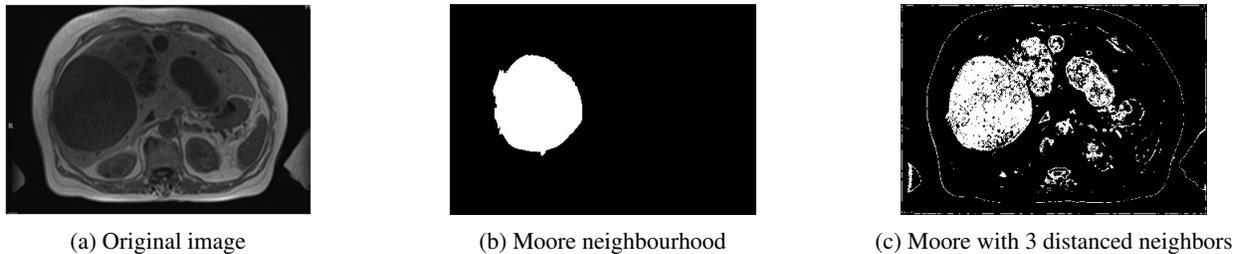


Figure 3: Segmentation results of GrowCut – liver image

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VAEGAN as a New Perception Model

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Abstract

The Variational Autoencoder Generative Adversarial Network (VAEGAN) uses image datasets as input to gradually learn to generate realistic images. The Generator maps the continuous vectors to corresponding images, so the system does not simply memorize all images in the dataset; rather, it reconstructs those images in continuous space. Through this process, structures emerge in the image space. We investigated these structures in detail, using VAEGAN and a dataset of images from a first-person perspective, especially from a dynamical systems point of view.

Introduction

In studying artificial life, it is necessary to discuss internal perspectives, not only in apparently life-like forms but also in terms of the origin of the perceptions that have evolved in artificial life systems. Also, perceptions should be regarded as generative, not as passive filters. In this paper, we discuss an artificial system for generative perception, using the methodology of deep learning, which has recently advanced significantly.

In particular, we focus on the following points to investigate how artificial life systems can evolve perceptions:

- 1) Using the Variational Autoencoder Generative Adversarial Network (VAEGAN)(Larsen and Winther, 2015), we enabled a network inside an agent to learn sequential visual images and then investigated in detail what type of cognitive map was self-organized in the network. A cognitive map is a spatial map generated from a first-person point of view instead of a third-person point of view. Different cognitive maps can be generated from the same real space using different agents.

- 2) In the hippocampus of a real brain system, it has been shown that rats rehearse the acquired cognitive map by compressing time length (Diekelmann and Born, 2010). This implies that replaying or preplaying simulations of sequential visual images from an acquired cognitive map can be a function of dreaming. We tested this hypothesis by simulating image processing using VAEGAN modeling.

Generative Deep Neural Networks

Recently, some deep neural network architectures were discovered to be good at image-generating tasks. Deep Convolutional Generative Adversarial Network (DCGAN)(Radford and Chintala, 2015) is one example of such a network, as it can learn from unlabeled image datasets and generate realistic images resembling those in the original dataset. DCGAN also includes two deep-convolutional neural networks, the Generator(Gen) and the Discriminator(Dis). The Generator is trained to generate realistic images that look like those in the dataset, while the Discriminator is trained to discriminate the images generated from those in the original dataset. Through a learning process, these two networks compete and coevolve with each other, and the Generator gradually acquires the ability to generate realistic images.

VAEGAN (Larsen and Winther, 2015) is similar to DCGAN but includes another neural network, the Encoder(Enc), in addition to the Generator and the Discriminator. Using images as inputs, the Encoder outputs the corresponding latent vectors, which are transformed into images similar to those in the input by the Generator.

Dataset

Here, we adopted a dataset that has characteristics of our everyday visual inputs, including images in the first-person perspective, for the training. The dataset consisted of 4888 frames of videos (at 30 fps) from a first-person perspective, which we shot while walking around campus. Due to the constraints of the learning abilities of VAEGAN, the resolution of each image was 64×64 .

Cognitive Map in the VAEGAN Latent Space

The Generator uses continuous vectors as input and outputs images, so the network does not simply remember the images in the dataset; rather, it reconstructs these images in continuous latent space. This image structure in latent space is self-organized during the learning process.

We trained VAEGAN using the dataset and investigated how images in the original dataset were placed in latent

space. Figure 1 shows one example trajectory in the latent space obtained using this procedure. The original image sequence was converted into points in the latent space using the Encoder, and the trajectory was drawn in the latent space. The content of each frame changed frame by frame, so a moving average of one second was used. Although the shape of the trajectory in the latent space was complicated—partly due to the space’s high dimensionality—the continuous spatial trajectory in the real world was also embedded as a continuous trajectory in the latent space.

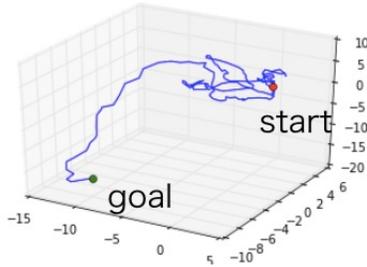


Figure 1: An example of the trajectory of the original dataset in the latent space. In the figure, the original image sequence starts at start and ends at goal. The latent space dimension was set at five coordinates, and this figure shows only three of the five coordinates.

VAEGAN Model for Preplay/Replay

By modifying the original VAEGAN, we were able to construct a simple prediction network, imposing the network $\text{Gen}(\text{Enc}(\text{image}(t))) = \text{image}(t + \tau)$ instead of $\text{Gen}(\text{Enc}(\text{image}(t))) = \text{image}(t)$. This was quite simple, but it worked.

Performing this prediction iteratively generated images sequentially (Fig.2) or obtained a trajectory in the latent space. We call this method the closed loop. In this procedure, first, we converted the latent-space vectors into images using the Generator, then converting the images back to latent-space vectors using the Encoder, thereby constructing a map in the latent space, $z(t + 1) = \text{Enc}(\text{Gen}(z(t)))$, and treating the latent space as a dynamic system.

First, we constructed this map using VAEGAN without the prediction model. In this case, after the training, repeating the loop usually resulted in convergence on either a single attractor or a small number of attractors.

In contrast, in the prediction model, in addition to the attractors, we observed limited cycles or chaotic behavior in the closed-loop analysis. We investigated these features systematically, changing the dimension of the latent space and the number of learning epochs, and found that about 20% showed the chaotic behavior. We calculated the embedding dimension and the Lyapunov exponent following the method



Figure 2: Two examples of sequential image generation using the closed loop method and the prediction model. In the upper example, images converge on certain scenes, while, in the lower example, the sequence does not converge on a single scene.

of Rosenstein et al. (Rosenstein et al., 1993) and found that the embedding dimensions were $\sim 5-10$ and the Lyapunov exponents were 0.07 ± 0.03 , regardless of the dimension of the latent space. This universality might imply that these values reflect the structure behind the original dataset.

Discussion

This study used a dataset close to everyday visual input to train networks to reconstruct the visual experience in continuous latent space. The way these images were continuously placed in the space was self-organized, and as we also observed, in some cases, the components of the latent-space vector show place cell-like location specificity (in prep.). These results suggest that the generative nature of perception is the origin of cognitive maps in our brains.

Also, our closed loop method enables us to treat the system as a dynamic one. These looping pictures in the system provide an example of how an artificial brain might construct an internal model and simulate the external world.

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