Temporal Patterns in Artificial Reaction Networks

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Abstract. The Artificial Reaction Network (ARN) is a bio-inspired connectionist paradigm based on the emerging field of Cellular Intelligence. It has properties in common with both AI and Systems Biology techniques including Artificial Neural Networks, Petri Nets, and S-Systems. This paper discusses the temporal aspects of the ARN model using robotic gaits as an example and compares it with properties of Artificial Neural Networks. The comparison shows that the ARN based network has similar functionality.

Keywords: Artificial Neural Networks, Artificial Reaction Networks, Cellular Intelligence, Biochemical Networks.

1 Introduction

When Artificial Intelligence (AI) researchers want to develop connectionist models of intelligence, it is only natural that they should look to the brain for inspiration. The result, of course, is the Artificial Neural Network (ANN). However, as discussed in this paper, there is an alternative, biologically inspired, connectionist paradigm based on the emerging field of Cellular Intelligence – the Artificial Reaction Network (ARN) [1].

In recent years, researchers have become increasingly interested in the behaviors displayed by single celled organisms, in particular protists. These eukaryotes, display an astonishing array of complex behaviors. Some can avoid light with photo-sensitive spots; some actively hunt prey; while others can build protective shelters [2].

These complex behaviors have led researchers to investigate how such traits of primitive intelligence might arise. Well known examples of such work are that by Nakagaki and Yamada, who demonstrated that the slime-mould *Physarum polycephalum* was able to solve a simple maze [3]. Similar research by Saigusa et al showed that this same organism was able to learn and change its behavior in anticipation of the next environmental stimuli [4].

These high level behaviors are mediated by Cell Signaling Networks (CSNs) which, as this paper will discuss, are analogs to ANNs. Such networks are composed of interacting proteins within the cell's cytoplasm that function to regulate virtually all cellular activity.

The ARN is a new representation based on CSNs. This paper explores the ARNs ability to generate temporal oscillations in protein species – a common theme in CSNs. It discusses its similarities and differences to ANNs by comparing them in similar

applications - specifically in the generation of robotic gaits. The aim of this research is firstly, to explore the mechanisms of cell intelligence in order to broaden understanding of intelligence in its widest sense as well as have possible applications in biological modeling. Secondly, to investigate the resulting representation in terms of its possible application for use as an AI technique.

1.1 Mechanisms of Cellular Intelligence

CSNs consist of different protein species, the interactions of which are shown by connecting lines in a similar way to a neural network. Via a system of complex mechanisms, CSNs adjust their set of protein activation levels to fine tune cellular activity appropriate to current conditions. An instantaneous set of these protein concentrations serves like a memory, containing an imprint of the current environmental state [5]. Individual spatio-temporal activation patterns of protein concentrations emerge from a multitude of low level interactions and result in a range of cellular responses and behaviors [6-8]. The network therefore represents cascades of numerous protein coupled interactions with topological features such as feedback loops and interconnectivity, forming highly complex systems [5, 8].

Bray claims that the processing performed by individual CSN units is similar to Boolean and fuzzy logic and further speculates that these networked logical units can perform computational processing equivalent to a Turing machine [5]. Similar reports were documented by a number of other researchers [9-11].

Many researchers highlight the similarities between CSNs and ANNs [5-7, 12]. Bray, observes both networks are made up of highly connected parallel distributed units, where each unit simultaneously integrates and processes signals. Both are able to recognize patterns, and provide the correct response in the presence of noise and loss of units, and are therefore robust [5, 12]. One difference is that while simple traditional ANNs like the perceptron lack an explicit time dimension, CSN functionality incorporates this in a similar way to spiking neuron models. Bhalla notes that the high level cellular behavior is encoded by temporal spatial patterns of intracellular species generated in this way [12]. One such common motif is oscillating patterns, resulting from feedback structures and cyclic loops [8].

2 The Artificial Reaction Network

2.1 Techniques Used to Develop Model

The ARN representation was designed to incorporate the previously discussed mechanisms of cell intelligence. Our previous paper provides a complete description, and verification of the ARNs accuracy and biological plausibility [1].

There are many methods used to model biochemical reactions, some are very simple Boolean-based techniques, others complex quantum mechanical abstractions [13], here the two most relevant adopted techniques are described. The first is S-Systems; these have proven themselves accurate and provide a similar degree of system abstraction to an ANN. They comprise sets of ordinary differential equations

(ODEs) that exploit a power law representation to approximate chemical flux [13]. Similarly to traditional rate law [13], each ODE is equal to the difference between two conceptually distinct functions; the first function includes all terms contributing to system influx, the second to decay. S-systems provide simple but accurate representations of temporal dynamics, including both steady and transient state. However, in their general form, terms are highly coupled, and therefore are difficult to manipulate without interference.

Like an ANN, Petri Nets (PNs) offer a modular approach. PNs are a graphical and mathematical modeling tool used to study processes characterized as parallel, distributed, concurrent, and asynchronous [14]. They are used extensively in several types of information processing, including modeling CSNs. Each PN is a networked structure of separate self-maintaining units called "places", where movement between connections is defined by separate transitions, thus PNs exploit benefits of modularization.

2.2 The Artificial Reaction Network Model

The authors combined the continuous mathematical nature of S-systems, the modular properties of PNs, and weighted connections of ANNs. The ARN, as shown in Figure 1, is a modular and expandable S-System. It comprises a set of connected reaction nodes (circles), pools (squares), and inputs (triangles). Each pool represents the current available protein species concentration (avail) and each circle corresponds to a reaction unit, representing an interaction (reaction) between a numbers of proteins. For example, Figure 1 shows the reaction between species A and B to produce species C. Connections symbolize the flow of species into and out of reaction units and their weight (W) corresponds to reaction order. This structure can be compared to a perceptron, where the pools correspond to inputs, the reaction units to the weighted sum function, and these are joined together by weighted connections. Both are instances of highly connected parallel distributed networks, where units simultaneously integrate and process signals.

$$\Delta C = \left(K_{f(C)} \left(A_{avail}^{W_A} B_{avail}^{W_B} \right) - K_{r(C)} \left(C_{avail}^{W_C} \right) \right) \Delta t$$
(1)

Where:

A, B, C = Species Concentrations avail = available species concentration W = reaction order ΔC = Change in species concentration C K_f = Forward rate constant K_r = Reverse rate constant Δt = time step

Each reaction unit calculates flux ($\Delta A/\Delta B/\Delta C$) at Δt as given by Equation (1), and is equal to an aggregate of connected contributing (incoming) pools and connected decay (outgoing) pools raised to n powers of weighted connections and multiplied by pseudo rate constants. This can be compared to the Sigma-pi ANN model, where the output

depends on a function of the product of the inputs. Unlike the feedforward perceptron, species can flow in either direction, depending on the sign of the flux calculated by Equation 1. Dissimilarly to a perceptron, the ARN incorporates a temporal dimension, where at time interval Δt , each reaction unit's temporal flux value is calculated, which then is used to update the current concentration values of each reaction's connecting pools. Thus the complete set of pool concentrations at time t corresponds to the current state of the system. Euler's approximation was adopted in favor of other evaluation methods because it supports modularization. Its disadvantage is that net error accumulates with every cycle; however by decreasing step size error is reduced. The intention however, is to characterize high-level system properties and thus requires only sufficient low level detail to represent its contributing mechanisms such as temporal dynamics and complex network topologies.



Fig. 1. The Artificial Reaction Network (ARN)

3 Experiments

As previously discussed, complex mechanisms found in CSNs lead to stable temporal patterns of species concentrations, where each relates to a high-level behavior. One way to investigate the ability of the ARN to produce such temporal oscillatory patterns is by applying it to generate those associated with robotic gaits. Furthermore, this allows comparison with similar results obtained using ANN models.

Terrestrial locomotion of limbed animals is achieved by multiple phase locked patterns of limb movements known as gaits. For example, depending on speed of locomotion and terrain, quadrupeds commonly walk, trot and gallop [15]. The gait phase is a value that ranges from 0 to 1 as the gait cycle proceeds. Therefore, the motion of each limb can be described relative to the gait phase. The ideal quadrupedal gaits are described by Dagg [15] and others [16], and are used as a standard for comparison here and similarly in other studies [17]. The walk gait is characterized where, each leg is a quarter cycle out of phase; in the trot gait each pair of diagonal limbs move half a cycle out of phase with one another. An ARN based robotic controller was implemented, to produce trot and walk gaits of a simulated Lynxsmotion dual-servo quadruped 2 (Q2) robot. The structure of the ARN controller

was designed to include abstractions of regulatory mechanisms found in CSNs including inhibitory/excitatory reactions, cyclic loops, and feedback structures.

3.1 The Robot and the ARN Controller

Each robotic leg is controlled by two servo motors, one for each degree of freedom (DOF), where one raises the leg, the other turns it. Signals are sent by the ARN to each motor and control the angle of the rotor for each DOF, using a simple position to pulse width modulator interface circuit to control the servo. The physical structure and control are described in detail in other papers [18].



Fig. 2. The ARN based controller displayed contains 4 identically structured modules, a module is shown surrounded by a dashed line

Figure 2 illustrates the structure of the ARN controller, it comprises four identical modules (a module is highlighted by a dashed line) each controlling the motors for a separate leg. Each module contains 3 reaction units, and 3 pools: A, B and C. Pool A controls the up/down (U/D) motor, Pool B the back/forward (B/F) motor and Pool C controls the off period for both motors. The activity of pools is regulated by a series of excitatory and inhibitory connections between reaction units. These connections represent properties of specialized regulatory proteins common to CSNs such as enzymes. The connection weights were hardcoded using the same method as used in the Billard and Ispeert model [19]. The entire structure is organized as a closed loop, allowing chemical species to be recycled to the first module, and thus generate a stable repeating temporal pattern. The type of robot gait is easily modified by a simple adjustment of the initial pool values. For example, by initializing a C pool, a walk gait will be generated, where the C pool chosen will determine the starting leg. Similarly, a trot gait is achieved by initializing 2 C pools within alternate modules. In this particular design, the value to which the C pool(s) are initialized determines the DOF angle and were set specifically for the physicality of the particular robot, although it can be freely varied.

4 Results

The ARN controller was considered to generate a specific gait if the relative phases of the respective oscillatory signals were within 2% of the standard gait cycle described previously. Higher values of 10% were used in other studies [17], and this was

considered reasonable due to the variation found in real animal gaits [20]. In each case, the controller first generates the U/D motor oscillation and on reaching the maximum value the B/F motor is initiated. As can be seen the walk gait results (Figure 3) show legs are a quarter cycle out of turn, with phases of 0.0, 0.25, 0.5, 0.75 between limbs in clockwise order from FL leg. Similarly the trot gait shows opposite legs are half a cycle out of turn with phases respectively of 0.0, 0.5, 0.0, 0.5. Both phase locked limb patterns match the standard, and compare well with other connectionist models. For example, Billard and Iispeert present a CPG (central pattern generator) based neural controller for a quadrupedal AIBO robot, similarly with 2 DOFs for each leg [19]. Here, the network is composed of 8 coupled non-linear oscillators and each oscillator consists of 6 leaky integrator neurons (total of 96 neurons). Each neuron implements an activation approximately as complex as the ARN reaction unit function. Thus the complexity of this network is equivalent to approximately 96 ARN reaction units. The oscillatory signals produced by this network for both walk and trot gaits show that the limb phases correspond to the standard and to those produced by the ARN. Similar correspondence is found in numerous other sources. For instance, Collins explores a CPG based neural controller for a quadrupedal robot with 1 DOF per limb, and compares 3 types of activation function models. The controller is composed of a network of 4 coupled non-linear oscillators [17], where each oscillator controls a separate limb. The reported limb phases correspond to the standard, although those reported for the trot were within 10% of the ideal, whereas the ARN matches the standard for both gaits. Each model has approximately twice the complexity of the ARN reaction unit and, unlike the ARN, all require a pulsing signal to drive the network. Overall the ARN affords a higher degree of accuracy where fine tuning of parameters can provide finite levels of control. For instance, the frequency of oscillations and therefore the gait speed can be easily modified by uniform increase or decrease of K_f of each unit. Similarly, independent variation of speed for each type of DOF (B/F or U/D) or for a specific leg DOF motor. These results show the ARN has a very similar capacity in robotic control tasks as other connectionist robotic controllers, where it can offer reduced computational complexity. Furthermore the ARNs ability to produce gaits illustrates how cellular networks can generate the complex temporal patterns necessary in emergent behavior.



Fig. 3. Output generated by ARN controller for walk gait. Solid lines are legs up/down motor, dashed lines are back/forward motor. Legs move independently in order: FL (front left), FR (front right), RR (rear right), RL (rear left).



Fig. 4. ARN controller output for trot gait. Diagonal legs are in phase and operate in order FL and RR then FR and RL.

5 Conclusions

The ARN is a bio-inspired connectionist representation based on mechanisms found in CSNs that contribute to the emergence of cell intelligence. One feature of CSNs is the ability to generate high level behavior by regulating temporal activation patterns of its component proteins. The ARN was tested as a means to artificially produce similar pattern regulation, and its potential applicability was explored. Here an ARN based control system was designed to exploit topological features such as negative feedback, and cycles found in real CSNs. The controller was applied to produce the temporal oscillatory patterns associated with quadrupedal trot and walk gaits. The results confirmed the ability of the ARN to regulate temporal oscillating patterns with applicability in robotic control. These results are in good correspondence with ANN models, where both generate very similar spatial temporal patterns. A significant number of parallels between ARNs and ANNs were highlighted, suggesting the nature of cell intelligence may not be that different from neural intelligence. These similarities highlight the potential of single celled organisms to produce complex behavior similar to that produced by a neural network. This will be explored further, in particular by generating more complex temporal patterns, regulating composite behavior and chaotic components.

References

- Gerrard, C.E., McCall, J., Coghill, G.M., Macleod, C.: Artificial Reaction Networks. In: Proceedings of the 11th UK Workshop on Computational Intelligence, UK, pp. 20–26 (2011)
- 2. Ford, B.J.: Are cells Ingenious? The Microscope 52, 135–144 (2004)
- 3. Nakagaki, T., Yamada, H., Toth, A.: Maze-solving by an amoeboid organism. Nature 407(6803), 470–470 (2000)
- Saigusa, T., Tero, A., Nakagaki, T., Kuramoto, Y.: Amoebae Anticipate Periodic Events. Phys. Rev. 100(1), 1–4 (2008)
- 5. Bray, D.: Protein molecules as computational elements in living cells. Nature 376(6538), 307–312 (1995)
- Helikar, T., Konvalina, J., Heidel, J., Rogers, J.A.: Emergent decision making in biological signal transduction. Proc. Natl. Acad. Sci. USA. 105, 1913–1918 (2008)
- Hjelmfelt, A., Ross, J.: Mass Coupled Chemical Systems with Computational Properties. J. Phys. Chem. 97, 7988–7992 (1993)
- Kholodenko, B.: Cell Signaling dynamics in Time and Space. Nature Rev. Mol. Cell Biol. 7(3), 165–176 (2006)
- Stadtman, E.R., Chock, P.B.: Superiority of interconvertible enzyme cascades in metabolic regulation: analysis of multicyclic systems. Proc. Natl. Acad. Sci. USA 74, 2766–2770 (1977)
- Arkin, A., Ross, J.: Computational functions in biochemical reaction networks. Biophys. J. 67, 560–578 (1994)
- 11. Wang, B., Kitney, R.I., Joly, N., Buck, M.: Engineering Modular and Orthogonal genetic logic gates for robust digital-like synthetic biology. Nat. Commun. 2, 508 (2011)
- Bhalla, U.S.: Understanding complex signaling networks through models and metaphors. Prog. Biophys. Mol. Biol. 81, 41–65 (2003)
- Savageau, M.A., Voit, E.O.: Recasting Nonlinear Differential Equations as S-Systems: A Canonical Nonlinear Form. Math. Biosci. 87(1), 83–115 (1987)
- Baldan, P., Cocco, N., Marin, A., Simeoni, M.: Petri Nets for Modeling Metabolic Pathways: A Survey. Natural Computing 9(4), 955–989 (2010)
- 15. Dagg, A.I.: Gaits in mammals. Mammal Rev. 3, 135–154 (1973)
- 16. Hildebrand, M.: Analysis of asymmetrical gaits. J. Mammal. 58, 131–156 (1977)
- 17. Collins, J.J., Richmond, S.A.: Hard-wired central pattern generators for quadrupedal robots. Biol. Cybern. 71, 375–385 (1994)
- Macleod, C., Maxwell, G., Muthuraman, S.: Incremental Growth in Modular Neural Networks. Eng. Appl. Artif. Intel. 22(4-5), 660–666 (2009)
- Billard, A., Ijspeert, A.J.: Biologically inspired neural controllers for motor control in quadruped robot. In: Proceedings of the IEEE-INNS-ENNS International Joint Conference on Neural Neural Networks, pp. 637–641. IEEE, Italy (2000)
- Afelt, Z., Blaszczyk, J., Dobrzecka, C.: Speed control in animal locomotion: transitions between symmetrical and nonsymmetrical gaits in the dog. Acta. Neurobiol. Exp. 43, 235– 250 (1983)