Inducing Modular Reusability in Neural Cellular Automata through Hierarchical Control

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Research Proposal for Ph.D. in Computer Science
2026

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Abstract

Current research in Neural Cellular Automata (NCA) has successfully modelled morphogenesis as a self-organizing process capable of generating complex anatomies from a single seed cell. These models function as flat, fully connected architectures that are capable of distorting morphologies. While NCAs reuse developmental strategies by conserving early factors, this reuse relies on growing and pruning entire structures rather than composing explicit modules. Standard NCAs fail to produce homeotic phenotypes, structures developed in the wrong anatomical positions, because they lack metameric structures and reusable modules. This proposal outlines a Hierarchical NCA architecture. By introducing a Gene Regulatory Network (GRN) abstraction layer to govern cellular update rules, this research aims to enforce modularity through architectural constraints and connection costs. The methodology involves implementing high-level controllers, penalizing connectivity to force decoupling, and utilizing dynamic environments to incentivize the mathematical conservation of organ modules. This approach seeks to move NCA from static image regeneration to true artificial biological development capable of open-ended evolution.

Introduction & Background

The paradigm of biology-as-computation serves as the foundational philosophy for this proposal, aligning with a lineage of work that views morphogenesis as a striking example of self-organization governed by localized communication and feedback loops [12]. Within this framework, Neural Cellular Automata (NCA) have emerged as a robust tool for studying how cell collectives specify large-scale anatomy [12, 19]. Foundational models such as in Mordvintsev et al. [12] demonstrated that differentiable update rules can reliably self-assemble into complex anatomies resistant to traumatic tissue loss. Subsequent advancements, including Randazzo et al. [15], introduced cellular chirality to break symmetries in organ development, while findings in Stovold [19] demonstrated how specific identity channels could prevent the breakdown of natural organism boundaries in multi-agent environments [19].

My previous research supports the efficacy of bio-mimetic architectures in solving these types of high-dimensional problems. In developing Visual Cortex Network, I demonstrated that modelling the primate visual cortex's dual-stream architecture could improve accuracy on light field classification [10]. Similarly, my work on Structurally Adaptive Predictive Inference Network showed that introducing biological principles like structural plasticity and active inference allowed agents to solve control tasks purely through homeostatic drive, without external rewards [8]. These projects confirm that architecting systems based on biological constraints, such as cortical hierarchy or homeostatic plasticity, can yield robustness that standard flat architectures lack.

Despite these strides, the current state of the art faces a structural limitation. Chow and Bentley [3] comprehensively interrogated the hidden representations of NCA morphogenesis. While they successfully identified hidden units functionally analogous to biological transcription factors, no homeotic phenotypes were observed during functional knock-out experiments. They hypothesized that this failure to produce homeosis, defined biologically as the development of body structures in the wrong places, was due to the model's lack of metameric structures and reusable modules. Currently, NCAs recycle anatomical modules

(such as legs) by growing the original form and then pruning off unnecessary structures, rather than possessing a modular library of parts that can be re-deployed. This research proposes to bridge this gap by architecting a hierarchical system where modularity is an inherent structural requirement rather than a secondary observation.

Problem Statement: Lack of Modularity

Standard NCAs are characterized by a flat organizational structure where every cell executes an identical neural network rule based on a local 3x3 Moore neighborhood [12, 19]. While this promotes self-organization, it leads to a fully connected behavioural dependency where structural changes are often cancerous or distortive rather than modular [3, 19]. Biological modularity assumes that functionality can be seamlessly partitioned into discrete entities of elementary components that perform identifiable tasks separable from other modules [16]. In contrast, the lack of architectural constraints in standard NCAs prevents the emergence of these reusable modules [3]. This issue mirrors a challenge I encountered researching AI in industry, where standard state estimation failed due to sensor noise and high dimensionality. I resolved this by developing a manifold disentanglement algorithm that reframed the problem onto a robust, lower-dimensional manifold [7].

Modularity does not evolve for free in artificial or natural systems. As argued in Clune et al. [4], it requires specific selection pressures or architectural constraints. Standard NCAs lack connection costs, allowing for monolithic, entangled networks that are slow to adapt to new environments compared to modular counterparts. In the absence of a direct pressure to reduce the cost of information transmission or connection number, NCAs gravitate toward non-modular, high-cost attractors.

Furthermore, true homeosis must be distinguished from mere distortion or cancerous overgrowth. Biologically, homeosis occurs when a mutation in selector genes (such as Hox genes) directs a cell lineage to adopt an alternative developmental fate, such as transforming an antenna into a leg [1]. These master control genes act as stable switches that integrate positional information [1]. Without a hierarchical layer to act as these selector switches, current NCAs cannot achieve the build an eye here subroutine activation that is the hallmark of natural developmental software [12].

Proposed Methodology: The Hierarchical NCA

I propose three investigations to induce modularity and homeosis in NCAs.

Investigation A: The Abstraction Layer. I propose the implementation of a higher-level controller, a simplified Gene Regulatory Network (GRN) abstraction layer, that sits above the standard NCA update rule. This design is motivated by the regulatory structures described in Davidson and Erwin [5] and the separation of genotype and phenotype explored in Montero et al. [11].

To design this controller, I will leverage insights from my MARL communication research where I found that agents sharing high-level plans and intentions achieved greater success in coordination tasks, compared to only those sharing raw percepts [9]. In this Hierarchical NCA, the upper layer will function similarly to that high-level communication channel. It will act as a kernel of the network, performing essential upstream functions to specify the domains of body parts in the spatial coordinate system [5]. Rather than explicitly modelling cells, this layer will dictate the weights of the lower-level cellular update rules based on spatial

regions. By separating the DNA (global instructions) from the phenotype (the cell-level execution), I can enable state-dependent decoding of a shared genome, a concept aligned with the metalearning approaches in Montero et al. [11]. This allows different parts of the organism to attend to different subroutines within the DNA, effectively creating a library of reusable modules.

Investigation B: Penalizing Connectivity. To force the decoupling of these modules, I propose introducing an L1 regularization or connection cost to the loss function. This methodology is inspired by the findings of Clune et al. [4], who demonstrated that modularity arises from the pressure to minimize connection costs.

This work will drawn on my experience engineering optimization passes for quantum compilers that identified and removed redundant topological patterns to reduce circuit depth [6]. Just as minimizing gate depth was essential for quantum fidelity, I will mathematically penalize the length and number of connections used in the cellular communication protocol. By requiring the system to maximize performance while minimizing these costs, I predict the emergence of functional modularity where the system is forced to solve subproblems (e.g., leg development) using sparsely connected clusters of nodes, replicating the evolutionary dynamics observed in Clune et al. [4]. This directly counters the tendency of NCAs to remain in high-cost, low-modularity regions of the parameter space.

Investigation C: The Tierra and Virtual Creature Test. Finally, I propose moving beyond static image targets (like the gecko) to a dynamic, behaviour-driven environment inspired by Sims [18]. Drawing on the resource-limitation principles of Tierra [17], I will implement a system where CPU time and memory serve as the digital analogues of energy and space. To automate the generation of these environmental demands, I will adapt insights from my adversarial curriculum generation research, where an adversarial generator drove performance increases in agent strategies by dynamically creating novel challenges [9]. Here, a similar adversary will perturb the environment to select for robust, homeotic modularity. In a task-driven scenario, such as evolving locomotion, reusing a leg module should confer a mathematical advantage by reducing the genetic information required to specify multiple appendages [18]. I will utilize a sample pool strategy where final states are subjected to metamorphosis perturbations, forcing the NCA to re-classify and re-configure its shape to meet new environmental demands [12, 14].

Expected Outcomes & Impact

The primary expected outcome is the emergence of master control units within the upper hierarchy of the model that function analogously to biological Hox genes [5, 1]. I predict that by perturbing these high-level units, I will observe true homeosis, such as the activation of a tail module in the anterior region of the organism, without destroying the structural integrity of the individual modules. This would address the specific developmental deficits identified in standard NCAs by Chow and Bentley [3].

This work will contribute to Dr. Peter Bentley's vision of using artificial life systems to determine whether fundamentally novel living organizations can exist [2]. By inducing modular reusability, I aim to move NCAs from the realm of digital image processing to artificial biological development, resolving the "cancerous" growth modes critiqued in Chow and Bentley [3]. This architecture provides a pathway toward the open-ended evolution

seen in Sims [18], where complexity can grow beyond a predefined genetic space [17, 18, 13]. Ultimately, this research offers a roadmap for rationally editing the information structures of cellular collectives, which is essential for the future of synthetic bioengineering and regenerative medicine [3, 12, 14].

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