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Analysing the Mutational Pathways of a von Neumann Self-reproducer within the *Avida* World

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Abstract: *The architecture of machine self-reproduction proposed by John von Neumann is studied within an artificial life platform known as Avida. To shed light on the evolutionary potential of the von Neumann style self-reproduction within the Avida world, we preliminarily characterise a hand-designed self-reproducer by extensive single-point mutation analysis. Although not surprisingly, the vast majority of the single-point mutants were classified as infertile, whereas the rest minorities as fertile and as yet unclassified. We conclude this paper by suggesting the possible enhancement of the analysis.*

Keywords: John von Neumann, Avida, Self-reproduction, Genotype-phenotype mapping, Evolutionary growth of complexity

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1. Introduction: The Architecture of Machine Self-reproduction

In the late 1940s and early 1950s, John von Neumann substantially theorised machine self-reproduction (von Neumann, 1966). His theory implicates that the world of machines can have potential for the evolutionary growth of complexity, like in real biological evolution where the degree of complexity (in an abstract sense) can not only decrease but also maintain or even increase (McMullin, 2000). The proposed architecture of machine reproduction characteristically comprises active and passive components. The active component includes a *programmable constructor*, a *copier* and a *control*. These subcomponents collaborate to reproduce an arbitrary machine described by the passive component, a *description tape*. If the description tape describes the active component that works on itself, then the reproduction amounts to machine self-reproduction. This architecture by von Neumann, based on copying and decoding of the passive component using the active component, was subsequently found to have an interesting parallel with a biological mechanism of self-reproduction where genotype is translated into phenotype. The active and the passive components of von Neumann's architecture can be considered as analogous to phenotype and genotype, respectively.

In terms of von Neumann's architecture, the decoding rule is implemented by the programmable constructor and it must be represented in the description tape in some encoded form, in a totally self-consistent way. This resonates with the biological mechanism (e.g., DNA as a symbolic description, transcribed as mRNA, is eventually translated into arbitrarily complex proteins). Importantly, it is pointed out that with this architecture, a genotype-phenotype mapping may evolve (McMullin, Taylor, & von Kamp, 2001). This evolvability is underpinned by the description tape which can undergo inheritable variation (*mutation*): if a mutation occurs in the programmable constructor but does not destroy the reproductive function, it is theoretically possible for an offspring machine to be self-reproducing with a different decoding mechanism, hence with a different genotype-phenotype mapping from that of the parent machine (i.e., in a way that the mapping is “backward compatible”). It appears, however, that such evolvability of the genotype-phenotype mapping was not particularly emphasised by von Neumann himself. Nevertheless, for better understanding of the evolvability, it is worthwhile to implement a von Neumann style self-reproducer and investigate its potential mutational pathways within such an established platform as *Avida.* The present paper briefly summarises a preliminary empirical study of analysing the single-point mutational pathways.

2. The *Avida* World and the Single-point Mutation Analysis

The *Avida* world is an artificial life platform which has been widely used in evolutionary research (Adami, 1997). The platform is designed to observe spontaneous evolutionary dynamics of a population of virtual organisms. The world is represented as a two-dimensional lattice of computational nodes. Each node is a virtual CPU (as opposed to a finite-state machine as in cellular automata) with a local memory. A node can represent an organism which “metabolises” by executing the program. An organism can overwrite or replace another program on a neighbouring node. When successfully programmed, an organism can repeatedly self-reproduce. A typical Avida simulation run is initiated with a single, self-reproducing seed program (*ancestor*) designed by the experimenter. Over time, a population grows, filling up the world in the manner of bacteria in a petri dish. Organisms compete for limited resources such as CPU time and memory space. Certain errors may be set in CPU operations, which serves as mutation and can diversify the population. As a result, the Darwinian evolution is expected to be observed. (For a detailed description, see Ofria and Wilke (2004)).

The self-reproduction in the Avida world is, by default, achieved through self-copying based on self-inspection. By contrast, in the previous study, we hand-designed and studied a prototype ancestor with von Neumann's architecture instantiated within the Avida world (Hasegawa & McMullin, 2012). The prototype design incorporates the decomposition into the *phenome* segment and the *genome* segment (corresponding to phenotype and genotype, respectively). The phenome segment is sequentially executed, decoding and copying the genome segment to reproduce the identical set of phenome and genome (i.e. an identical offspring). Decoding is designed to proceed using a simple, one-to-one translation table incorporated in the phenome segment.

Contrary to our first expectation that we might be able to explore the evolutionary potential of the ancestor in the Avida world, an unexpected finding was that such a self-reproducer can degenerate into a standard self-copier through only one step of single-point mutation. Since it is not obvious how typical this phenomenon is, the self-reproducer needs to be further investigated by analysing the mutational pathways. In the current study, we systematically counted out possible single-point mutants of the prototype ancestor (*candidates* for having interesting evolutionary potential) and preliminarily classified the candidates based on fertility with the help of a built-in automated analysis tool in the Avida system.

3. Discussions: Fertility Classification

Preliminary fertility classification showed that, not surprisingly, the vast majority of the candidates are infertile, implying no evolutionary potential. On the other hand, fertile ones turn out to be minority. There are also some that are yet to be classified, due to the limitation of the search using the built-in automated analysis tool. The analysis was limited in that lineage pathways are not extensively traced, but only a single pathway.

It is an ongoing, next step to enhance the analysis so that all lineage pathways that an arbitrary organism potentially exhibits can be traced. With it, the unclassified candidates can be reclassified as either fertile or infertile. Importantly, it should be noted that although self-reproduction requires fertility by definition, fertility does not necessarily follow evolutionary potential (e.g. exponential population growth). Nevertheless, once fertile candidates are revealed, their evolutionary potential can be further investigated by classifying reproduction “modes”. Reproduction modes can be so diverse, ranging at least from standard self-copying to von Neumann style self-reproduction, that more case studies may be required than automated classification. Thus, we intend to better characterise the prototype in the particular setting of Avida in hopes that insights from the characterisation will help design different von Neumann style ancestors with more interesting evolutionary potential.

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