Towards a Framework for Observing Artificial Evolutionary Systems

Janardan Misra
HTS Research, Bangalore, India 560076
Email: janardan.misra@honeywell.com

Abstract
Establishing the emergence of evolutionary behavior as a defining characteristic of 'life' is a major step in the Artificial life (ALife) studies. We present here an abstract formal framework for this aim based upon the notion of high-level observations made on the ALife model at hand during its simulations. An observation process is defined as a computable transformation from the underlying dynamic structure of the model universe to a tuple consisting of abstract components needed to establish the evolutionary processes in the model. Starting with defining entities and their evolutionary relationships observed during the simulations of the model, the framework prescribes a series of definitions, followed by the axioms (conditions) that must be met in order to establish the level of evolutionary behavior in the model. The examples of Cellular Automata based Langton Loops and $\lambda$ calculus based Algorithmic Chemistry are used to illustrate the framework. Generic design suggestions for the ALife research are also drawn based upon the framework design and case study analysis.

Keywords: Artificial Life, Evolution, Observations, Formal Framework, Evolutionary Processes.
1 Background

The phenomenon of “life” on earth is one of the most intriguing one with vast variety and complexity of forms in which it is found on multiple levels ranging from microbiological scale to higher taxa exhibiting a wide array of characteristics. Although we can explain several aspects of life around us in the light of existing theories for real-life evolution, we do not yet have a comprehensive understanding of the principles underlying the emergence of life and the conditions that led to the diversity and complexity of life on earth [Fut98]. Experimental methods to understand biological processes are usually difficult and error prone because living systems are by nature complex in design and usually hard to manipulate. Evolution is even more difficult to study experimentally since experiments may span over several generations and are usually difficult to control.

Artificial life (ALife) is an elegant methodology to complement real life theories to study the principles underlying the complex phenomena of life without directly working with the real-life organisms. For example, ALife studies can complement theoretical biology by uncovering detailed dynamics of evolution where real life experiments are not possible, and by developing generalized formal models for life to determine criteria of life in any arbitrary model can be observed.

Cellular Automata based models are one of the earliest attempts of synthesis to understand the underlying logic of self reproduction [Sip98]. Later attempts in the field have considered several new kinds of synthetic structures including programs, λ terms, strings, graphs, automata’s etc (see for overview [DZB01]) and have demonstrated that one or the other observable properties of real-life are shared by all of these models, though the parallel diversity and robust evolving structures which we find in real-life are yet to be designed. One of the guiding principles of ALife research behind these novel class of synthetic structures is that - “life is a property of form and organization rather than the matter used to build it” [Lan95]. This criterion to identify life in these novel synthetic structures in turn poses further questions as to which kind of organizational structures possess life? Which properties should we be looking at in those structures? and most importantly how can we recognize life in any arbitrary model?

To partly address these questions, in this paper, we proceed with the hypothesis that one of the possible ways life can be recognized in an arbitrary ALife model during its simulations is by observing population of entities undergoing evolution in the spirit of evolution by natural selection, which demands the presence of reproduction, heredity, variation owing to mutational changes, and finally natural selection based reproductive success. (See also [Daw82]). Though the criterion to equate life with the presence of evolutionary processes excludes other plausible properties including metabolism [BFF92], complexity [AOC00], self organization [Kan93], autonomy and autopoiesis [Zel81], yet captures a wide class of interesting phenomena related to population level evolution of entities [SH00]. Such a identification of population level evolutionary phenomena in arbitrary ALife models critically depends upon the observations carried out over simulations as we discuss next.

1.1 Motivations

Observations play a fundamental role both in real life studies as well as in ALife research. In case of real-life studies the role of observations is usually limited to an experimental analysis to uncover the specific dynamics underlying the observed life forms and their properties using natural observations or controlled experiments. On the other hand, in case of ALife studies, in general there is no known method to decide beforehand the kind of entities, which might demonstrate non-trivial life-like behavior, without closely observing the simulations of the model.

The very identification of life is thus an existential problem for ALife studies and we need some sound formal framework to address this problem. In absence of a formal framework, we often encounter intuitive and informal arguments, which remain useful only to specific models and do not always have the generic perspective. We question whether these model-specific arguments are sufficient to support the presence of an extremely complex phenomenon such as evolution in ALife models. Without formal foundations to ascertain these (informally presented) claims, there is always a danger to run into conflicting arguments, which might, for example, be based upon observations of the simulations on different levels. Nehaniv and Dautenhahn [ND98] specifically discuss that identification of time varying entities is a deep rooted problem in the context of formal definitions for self-reproduction and add that in absence of observers it is problematic to decide whether an instance of artificial self-replication be treated at all a life-like one.
In an attempt to provide a formal platform for observations in ALife studies, a high level abstraction mechanism is presented for characterizing the observations needed to establish the evolutionary behavior in ALife studies. Initial concepts in this direction appeared in [Mis06a, HM07]. The central concept of the framework is the formalization of the observation process, which we believe is essential, but most often remains implicit in ALife studies. The observation process leads to abstractions on the model universe, which are consequently used for establishing the necessary elements and the level of evolution in that model. Examples of Cellular Automata based Langton Loops (Section 3.2) and λ calculus based Algorithmic Chemistry (Section 3.3) are used to demonstrate the applicability of the formalism. Importantly the framework does not build upon the low-level dynamics or the “physical laws” of the underlying universe of the particular ALife model at hand, and thus permits the study of higher-level observationally “emergent” phenomena as a basis of evolution.

1.2 Contributions
The paper brings the implicitly assumed notion of observations to be carried out independent of the underlying structure of the model into main focus of ALife studies. It was not clear before that observational processes can be independently studied in their own right and the work presented in this paper makes it clear by placing observations into distinct formal platform. The work can also be seen as an attempt to fulfill the need for explicitly separating the design of the ALife models from the abstractions used to describe their dynamic progression.

The approach has helped us to formalize certain aspects of life including recognition of reproductive relationships under parental mutations as well as reproductive mutations in children along with their epigenetic developments, which were believed to be difficult to formalize before [ND98, Neh05]. The formalism captures wide range of reproductive instances including the case of multi parent reproduction (without resorting to the concept of species), and the case of reproduction without overall growth of the population (cf. [ND98]). Finally framework design and analysis of the case studies are used to draw useful design suggestions for the ALife research so that interesting evolutionary phenomena involving life-like entities can be better synthesized and analyzed.

The paper is organized as follows: In Section 2 we will formally elaborate the framework. Case studies will follow in Section 3. Section 3.2 applies the framework on cellular automata based Langton’s Loops and Section 3.3 on λ calculus based Algorithmic chemistry. Section 4 presents a discussion of related work, and is followed by concluding remarks in Section 5 along with the discussion on design suggestions for the ALife researchers in Section 5.2. Limitations of the framework and pointers for further work are discussed in Sections 5.3 and 5.4 respectively.

2 The Framework
In the ensuing discussion, we will use “ALife model” and “model”, “Observation process” and “Observer” interchangeably to add convenience in presentation. Similarly “real-life” is used in the paper to refer to organic life on earth in contrast with the “artificial-life”. Also, Observer Abstractions will refer to specific observations and corresponding abstractions made upon the ALife model during its simulations. Axioms are used to specify conditions which need to be satisfied in order to infer various components of evolution. Thus for each fundamental component of evolution: self reproduction, mutation, heredity, and natural selection, framework specifies certain Axioms constraining what is needed to be observed and consequently inferred in a formal way if any claim towards presence of any of these evolutionary components has to be substantiated. The aim is to define these formal Axioms such that only valid claims for evolutionary processes in a model can be entertained. Auxiliary formal structures are used in the intermediate stages of analysis. E.g., distance measure for determining dissimilarity between entities for their specific characteristics (see Section 2.1.3).

2.1 The Formal Structure of the Framework
To illustrate the framework, we will use a simple example of a binary string based chemistry whenever required in the discussion to assist the intuition behind the formalism. The chemistry will be referred as CBS (Chemistry of Binary Strings). Specifics of the design and structure of the chemistry will be explained as we proceed.
2.1.1 Observation Process and the Model Universe

We define the observation process as a transformation from the underlying universe of the ALife model to a set of observed abstractions as follows:

**Observation Process.** $\Gamma \mapsto Obj: \Pi$: An observation process $Obj$ is defined as a computable transformation from the underlying model structure $\Gamma = (\Sigma, T)$ to observer abstractions $\Pi = (E, F, Y, D, \delta_{mut}, \delta_{rep,mut}, C)$ and represented as $\Gamma \mapsto Obj\Pi$. $\Gamma$ and $\Pi$ are defined below.

The condition of computability is to ensure that the framework is decidable (or feasible [Bed99]), that is, the observation process only involves feasible computable steps, which can also be algorithmically programmed by the designer of the model and that infeasible observations defined in terms of non verifiable claims (e.g., ‘meta - information’ based claims) can be avoided.

**States.** $\Sigma$: set of observed states of the model in a simulation.

The exact definition of a “state” would vary from one model to the other due to their irreducible design differences as well as the level at which observations are being made. A multiset\(^1\) can sometimes be used to represent state of a model by defining it as a collection of observable basic structures and their corresponding multiplicities in the model at any instance during its simulation. As an example, we can consider an observed state in the case of our example chemistry of binary strings, CBS, as a multiset - such that some specific state could be:

$$\{(00101, 2), (10101, 1), (010, 1), (0100, 1)(10100, 1)\}$$

Further illustrative examples can be seen in the case studies appearing in Section 3.

**Observed Run.** $T$: set of observed sequences of states, ordered with respect to the temporal progression of the model. Each such sequence represents one observed run of the model. A sequence of states is formally represented as a mapping: $N \rightarrow \Sigma$, where $N$ is the set of non negative integers acting as a set of indexes for the states in the sequence.

A temporally ordered state sequence is one of the basic building blocks in the framework upon which all other observed abstractions are made. Such a definition of a run of model implicitly implies that the framework is fundamentally based upon the dynamic simulations of the model and not upon static analytical inferences. This is in accord with the notion of “weak emergence” [BMP+00], which is a generic characteristic of most of the ALife studies.

For a state $S$, $S-1$, and $S+1$ would denote the the states just before and after $S$ in a state sequence.

$\Sigma$ and $T$ thus define the underlying dynamic structure of the model $\Gamma = (\Sigma, T)$. Using $\Sigma$ and $T$, sometimes, a state machine model can also be used to define $\Gamma$.

2.1.2 Entities and Their Characteristics

**Observer Abstraction 1 (Entity Set).** $E$: set of entities observed and uniquely identified by the observer within a state and across the states of the model.

The criterion to select the set of uniquely identifiable entities in a given state of the ALife model is entirely dependent on the observation process as specified by the ALife researcher. Thus for the same set of simulations of a model, there may exist very different observed states as well as entities. Nonetheless, same observation process must not yield different sets of entities in two identical states.

Defining sound criterion to identify entities often requires a careful attention since arbitrariness in defining entities might well lead to the problem of false positives as discussed later (see Section 5.3.)

“Tagging” can be sometimes used as a mechanism for the identification of individual entities whenever there exist multiple entities in the same state which are otherwise indistinguishable. Thus an observer may associate and correspondingly identify every entity in a state using a unique tag. In

---

\(^1\)A multiset $M$ on a set $E$ is a mapping associating nonnegative integers (representing multiplicities) with each element of $E$, $M : E \rightarrow N$. Informally a multiset may contain multiple copies of its elements.
cases, where tags are selected such that they remain invariant under time progression of the model (i.e., do not change owing to reactions or interactions of the entities), the tags can as well be used for recognition of the persistence of these entities across the states of the model.

For example, in case of CBS, an observer might identify individual strings as entities such that to distinguish syntactically identical strings, we can associate with every string an integer tag such that with tag $i$, an entity corresponding to the binary string $s$ can be represented as $[s]_i$. Thus a possible set of entities corresponding to the example state given above becomes

$$
\{[00101], [00101], [10101], [010], [010], [01000], [01000]\}
$$

Alternately another observer may choose to define entities as a tuples consisting of strings with three identical leftmost bits - giving the set of entities for the same state as

$$
\{[00101], [00101], [10101], [10100], [010], [0100], [0100]\}
$$

Observer Abstraction 2 (State Function). $F \subseteq E \times \Sigma$ returns the state(s) in the state sequences in which a particular entity is observed. For a specific state sequence $F$ can be treated as a function.

The state information provided by $F$ for entities will be used later to define valid evolutionary relationships among them. In general observers may use different mechanisms based upon the nature of model as well as the entities defined, to determine the state for a given entity. For example, as a simple mechanism, in case of CBS, the observer can maintain a table mapping entities to their corresponding states in order to define $F$.

Having defined the sequence of states with temporal ordering and the entities identified by their tags, we will now proceed to discuss how an observer might define the detailed observable characteristics for such entities. Using these characteristics it can draw descendent relationship, as well as can establish presence of other components of evolution, e.g., heredity and variation. To this aim, we will define ‘character space’, as set of values for the observed characteristics. These values might be purely symbolic without any relative ordering or can be ordered using suitable ordering relation.

Observer Abstraction 3 (Character Space). The observer should define the set of all possible orthogonal and measurable characteristics for possible entities in the model as a multi dimensional character space $\Upsilon = \text{Char}_1 \times \text{Char}_2 \times \ldots \times \text{Char}_n$, where each of $\text{Char}_i$ is the set of values for $i^{th}$ characteristic. Each of $\text{Char}_i$ make one dimension in the space $\Upsilon$. Each entity $e \in E$ is thus a point in $\Upsilon$, say $e = (v_1, v_2, \ldots, v_n)$, where $v_i \in \text{Char}_i$.

For a vector $x = (a_1, a_2, \ldots, a_n)$, $i^{th}$ element $(a_i)$ will be denoted as $x[i]$. For some of the characteristics observer might define a ‘partial ordering’ ($\leq_i$ for $\text{Char}_i \in \Upsilon$), which can be used to compare values for those characteristics. The absence of any characteristics in an entity is represented by special zero element $0_{\text{char}}$, such that if $\text{Char}_i$ is(partially) ordered then $\forall v \in \text{Char}_i$, $0_{\text{char}} \leq_i v$.

Notice that, observable characteristics need not to be limited to syntactic level or structural properties and can also include semantic properties - observable patterns of behaviors. Though semantic properties are much more difficult to observe and measure than the syntactic ones since they require abstracting the patterns of reactions over a range of states.

In case of CBS, for simplicity we may assume that model consists of binary strings of size $n$. In that case each position of the string can represent one orthogonal dimension and we have only two binary values ($\{0, 1\}$) at any position in a string for corresponding dimension. Thus character space $\Upsilon$ in CBS is $n$ dimensional binary hypercube with each string occupying a possible diagonal end point. We will represent this hypercube as $\{0, 1\}^n$. The ordering relation $\leq$ for all dimensions is the same and defined as $0 < 1$.

In terms of such character space $\Upsilon$, an entity set $E$ at any state can be defined by annotating the points in $\Upsilon$ with integer constants denoting the multiplicity of the entities present in $E$ with characteristics defined by the point.

2.1.3 Distance Measures

Another important structure in the framework is the “dissimilarity measure” $(D)$ to define the “observable differences” $(\text{Diff})$ between the characteristics of the entities in a population. The distance
measure defined below can be used by the observer to distribute entities into separate clusters such that entities in the same cluster are sufficiently similar while entities from different clusters are distinguishably different in their characteristics. Again exact definition of distance function is model dependent.

Observer Abstraction 4 (Distance Measure). An observer defines a decidable clustering distance measure \( D : E \times E \rightarrow \text{Diff} \), where \( \text{Diff} \) is the set of values to characterize the observable “differences” between entities in \( E \).

Examples include the Hamming distance to define distance between genomic strings in the Eigen’s model of molecular evolution [Sch01], set of points where two computable functions differ in their function graphs, or the set of instructions where two programs may differ. One of the known criterions to define the concept of species is “phenotype similarity” [Rid96], which can also be seen as another example for distance measure.

In case of CBS, we can define an auxiliary function \( \oplus : \{0,1\} \times \{0,1\} \rightarrow \{0,1\} \) as a binary \( XOR \) such that we have \( 0 \oplus 0 = 1 \oplus 1 = 0 \), and \( 1 \oplus 0 = 0 \oplus 1 = 1 \). Thus the clustering distance measure \( D : E \times E \rightarrow \{0,1\}^n \) is defined such that \( \forall i. D(e_1, e_2)[i] = e_1[i] \oplus e_2[i] \), which implies that \( \text{Diff} = \{0,1\}^n \).

For example in case of two \( n = 3 \) bit binary entities \( e_1 = [001] \) and \( e_2 = [101] \), \( D(e_1, e_2) = 100. \) Other alternatives may include Hamming distance measure \( D(e_1, e_2) = \sum_{i=1}^{n} (e_1[i] \oplus e_2[i]) \) with \( \text{Diff} = \{0,1,\ldots,n\} \).

2.1.4 Observable Limits on Mutational Changes

The observer needs to specify the limits under which it can recognize an entity across states even in the presence of mutational changes in the entity owing to its interactions with the environment. This is an inherent limiting property on the part of the observer and could vary among observers. Based upon the choice of clustering distance measure \( \text{Diff} \), an observer can establish whether two entities in different successive states are indeed the same with differences owning to mutations or not. The smaller the limit, the harder it will be for an observer to keep recognizing entities across states and he would be counting mutated entities as the new entities. As entities are observed in more and more refined levels of details, their apparent similarities melt away and differences become sharply noticeable.

Another type of mutations arise during reproduction, in which case an observer has to identify whether an entity is indeed an descendent of another entity even though they might not be similar. This necessitates us to introduce another bound on observable reproductive mutations as \( \delta_{\text{rep,mut}} \). This limit on observable reproductive mutations is indeed crucial while working with models where epigenetic development in the entities can be observed [MB97]. This is because in such chemistries including examples from real life, the “child” entity and the “parent” entities do not resemble with each other at the beginning and observer has to wait until whole epigenetic developmental process gets unfolded and then compare the entities for similarities in their characteristics. \( \delta_{\text{rep,mut}} \) assists an observer to establish whether a particular entity could be treated as a “descendent” of another entity or not.

Another reason for introducing the limit \( \delta_{\text{rep,mut}} \) is that from the view point of an high level observation process not recording every micro level details, it is quite essential to distinguish between parent entities and other secondary entities involved in the reproductive process. Consider, for example, a model where entity \( A \) reproduces according to reaction \( A + B \rightarrow 2A' + C \), where \( A' \) is mutant child entity of \( A \), which can be determined by an observational process only when it can establish that \( A \) and \( A' \) are sufficiently similar with respect to their characteristics, while \( A' \) and \( B \) are not. These limits on observable differences are formally defined as follows:

Observer Abstraction 5 (Mutation Bounds). Based upon the choice of clustering distance measure \( D \), the observer selects some suitable \( \delta_{\text{mut}}, \delta_{\text{rep,mut}} \in \text{Diff} \), which will be used later to bound mutational changes (both reproductive and otherwise) for proper recognition. \( \delta_{\text{mut}} \) and \( \delta_{\text{rep,mut}} \) are vectors such that each element specifies an observer-defined threshold on the recognizable mutational changes for corresponding characteristics.

It is important to note that the choice of \( \delta_{\text{mut}}, \delta_{\text{rep,mut}} \) critically affects further inferences. For example, a choice of very large values would result in the lack of identification of variability in characteristics and thus make it difficult to infer natural selection (discussed later). On the other hand if an
observer decides to select very small values for $\delta_{mut}$ then it cannot recognize persistence of an entity across states under changes, similarly small values for $\delta_{rep,mut}$ make it harder to establish reproductive relationship among entities and for such an observer every new entity would seem to be appearing _de novo_ in the model.

2.2 Evolutionary Components

Having defined the observation process as a computable transformation from the underlying sequence of observed states of the model to the set of components involving entities and their observable characteristics with measurable differences as well as observable limits on such differences, we will now proceed with formalization of the fundamental evolutionary components: mutations, reproduction, heredity and natural selection.

2.2.1 Mutations

For evolution to be effective entities should change (mutate) over the course of their interaction with the environment (or other entities.) Moreover, there can also be observable differences between the child and the parent entities arising out of reproductive processes. These changes in the characteristics of the entities may or may not be inheritable based upon the design of the model and the simulation instance.

Mutations can be considered of carrying two kinds of effects in the entities: one where mutations change the values for specific characteristics, secondly where after mutation an entity has at least one new character not present before or when certain characteristics are lost. We define a Recognition relation to establish the non reproductive mutational changes in the entities:

**Definition 1 (Recognition Relation).** The observer establishes recognition of entities across states of the model with (or without) mutations by defining the function $R_{\delta_{mut}} : E \rightarrow E$, which is a partial function and satisfies the following axioms:

**Axiom 1.** $\forall e, e' \in E \cdot R_{\delta_{mut}}(e) = e' \Rightarrow F(e') = F(e) + 1$.

Informally, the axiom states that entities to be recognized as the same even with mutational changes have be observed in successive states. $R_{\delta_{mut}}$ is defined antisymmetric to ensure that entities are recognized based upon the time progression of the model not in any other arbitrary order.

**Axiom 2.** $R_{\delta_{mut}}$ is an injective function, that is, $\forall e, e' \in E \cdot R_{\delta_{mut}}(e) = R_{\delta_{mut}}(e') \Rightarrow e = e'$

Informally, the axiom states that no two different entities in one state can be recognized as the same in the next state.

**Axiom 3.** $\forall e, e' \in E \cdot \forall Char_i \in \Upsilon \cdot R_{\delta_{mut}}(e) = e' \Rightarrow 0_{\text{diff}, i} \preceq_i D(e, e')[i] \preceq_i \delta_{mut}[i]$.

Informally $R_{\delta_{mut}}(e)$ is that $e' \in E$, which is recognized in the next state by the observer as $e$ in the previous state with possible mutations bounded by $\delta_{mut}$. In other words if entity $e$ mutates and changes in the next state and identified as $e'$, then observer might be able to recognize $e$ and $e'$ as the same if these changes (between $e$ and $e'$) are bounded by $\delta_{mut}$.

2.2.2 Reproduction

Reproduction is one of the fundamental components of evolution. Through reproduction, entities pass on their characteristics to the next generation and increase the population size. Reproduction is possiblly the only way by which abstract entity structures can persist across generations in case of those Alife models, where entities do not persist forever. In our framework, the way an observer establishes reproduction is by providing observed evidence for it. This is done by defining causal descendence relationships among the entities across states. The parent and the child entities are recognized by the observer as being sufficiently similar and “causally” connected across the states:
Observer Abstraction 6 (Observed Causality). \( C \subseteq E \times E \). \( C \) establishes the observed causality among the entities appearing in the successive states. \( C \) satisfies the following axiom:

**Axiom 4 (Causality).** \( \forall e, e' \in E \cdot (e, e') \in C \Rightarrow [F(e') = F(e) + 1] \land [\exists e'' \in E \cdot F(e'') = F(e) \land R_{\delta_{\text{mut}}} (e'') = e'] \)

Informally, the axiom on causal relationship \( C \) states that, if an entity \( e \) is causally connected to another entity \( e' \), then the observer must observe \( e' \) in the next state of \( e \) and never before. This is to ensure that mutations are not confused by the observer with reproductions. Notice that in order to establish causal relation between entities, observers need not necessarily know the underlying reaction semantics or the micro level dynamics of the model. Only requirement is that the observer’s claimed causality conforms with the stated axiom. In essence, this formulation of causality is an abstract specification which demands observers to identify the entities which have been observed to be causal sources for the appearance of a new entity. Only then proper descendence relation for the new entity can be established.

Apart from causality \( C \) we also need auxiliary relation \( \Delta \) to determine that the differences due to the reproductive mutations are also bounded by \( \delta_{\text{rep,mut}} \).

**Definition 2.** \( \Delta \subseteq E \times E \) such that \( \forall e, e' \in E \cdot (e, e') \in \Delta \Leftrightarrow \forall \text{Char}_i \in \Upsilon \cdot i \text{Char}_i \text{ has an ordering then } D(e, e')[i] \leq_i \delta_{\text{rep,mut}}[i] \).

Informally for \((e, e')\) to be in \( \Delta \), their differences for each single characteristic \( \text{Char}_i \) must be bounded by \( \delta_{\text{rep,mut}}[i] \).

Based on the thus established notion of “causal” relationships between entities and \( \Delta \), we will define \textbf{AncestorOf} relation, which connects entities for which an observer can establish descendence relationship across generations.

**Definition 3.** \textbf{AncestorOf} = \((C \cup R_{\delta_{\text{mut}}})^+ \cap \Delta)^+

In this definition the (inner) transitive closure of \((C \cup R_{\delta_{\text{mut}}})\) captures the observed causality \( (C) \) across multiple states even in cases when “parent” entities might undergo mutational changes \( (R_{\delta_{\text{mut}}}) \) before “child” entities complete their “epigenetic” maturation with possible reproductive mutations. Intersection with \( \Delta \) ensures that causally related parent and child entities are not too different from each other, that is, reproductive mutational changes are under observable limit. Outer transitive closure is to make \textbf{AncestorOf} relationship transitive in nature so that entities in the same lineage can be related with each other. For \( e, e' \in E \), \((e, e') \in \textbf{AncestorOf}\), describes that \( e \) is observed as an ancestor of \( e' \).
Figure 1 depicts graphically the relationships between entities in successive states. Vertical lines represent the states \((S_0, S_1, S_2, S_3, S_4)\). Various kinds of arrows represent different relationships: recognition relation \(R_{\delta_{\text{mut}}}\), causal relation \(C\), and \textbf{AncestorOf}. The end points of the arrows on state lines represent entities.

\textbf{Claim 1. Case of Reflexive Autocatalysis.}

\textit{Proof.} In the simplest form, a reflexive autocatalytic cycle is represented as a system of reaction equations:

\[
A + X_1 = A_1 + Y_1 \\
A_1 + X_2 = A_2 + Y_2 \\
\vdots \\
A_{n-1} + X_n = mA' + Y_n
\]

where \(m\) copies of entity \(A'\) are produced at the end and that entity \(A'\) is a variation of entity \(A\), i.e., \((A, A') \in \Delta\). Such autocatalytic cycles are supposed to be the chemical basis of biological growth and reproduction. Examples include the Calvin cycle, reductive citric acid cycle, and the formose system. Competing cycles of this sort can even undergo limited evolution, though they are supposed to have very limited heredity [SS97].

In the current framework suppose an observer could determine the causal relations - \((A, A_1), (A_1, A_2), \ldots, (A_{n-1}, A')\). Also assume that entity \(A\) does not undergo any changes before \(A'\) is produced, that is, \((A, A) \in R_{\delta_{\text{mut}}}\). Then \((C \cup R_{\delta_{\text{mut}}}^+)\) would contain \((A, A')\) so also would \((C \cup R_{\delta_{\text{mut}}}^+ \cap \Delta)\) establishing the reproduction of \(A\) through reflexive autocatalytic cycle and with variation.

\textbf{Claim 2. Recognition of reproductive relationships under parental mutations together with reproductive mutations and epigenetic developments in the child entities.}

\textit{Proof.} Let us see what it requires for establishing reproductive relationship when (parent) entities might be undergoing changes across states and child entities not only differ from the parent entities owing to reproductive mutational changes but also that there exist epigenetic developments in the child entities, which make it harder for any observer to establish similarities between child and parent entities by observing the child entities only in the beginning (i.e., in the state when child entities were observed for the first time.) Naturally it would require that an observer observes child entities so long that their epigenetic development unfolds completely - since in general there cannot be any fixed limit on the number of states required for such epigenetic development, we capture this requirement of observations across states using transitive closure - \((C \cup R_{\delta_{\text{mut}}}^+)\), where \(R_{\delta_{\text{mut}}}^+\) ensures that (mutational) changes in the parent entities and also the changes in the child entities during epigenetic development are accounted for.

Let us assume that in a state \(S_i\), a child entity \(c\) was observed for the first time and (parent) entity \(p\) present in the state \(S_{i-1}\) was observed to be casually connected to it. Suppose that for entity \(e\) its epigenetic development unfolds through states \(S_{i+1}, S_{i+2}, \ldots, S_{i+r}\) such that with changes owing to the development \(c\) was observed as \(c_1, c_2, \ldots, c_r\) in these states with \((c, c_1), (c_1, c_2), \ldots, (c_{r-1}, c_r) \in R_{\delta_{\text{mut}}}^+\). Similarly suppose that parent entity \(p\) undergoes mutations in these successive states and observed as \(p_1, p_2, \ldots, p_r\) such that \((p, p_1), (p_1, p_2), \ldots, (p_{r-1}, p_r) \in R_{\delta_{\text{mut}}}^+\). It is clear that \((C \cup R_{\delta_{\text{mut}}}^+)\) would contain \((p, c), (p, c_1), \ldots, (p, c_r), (p_r, c), (p_r, c_1), \ldots, (p_r, c_r)\) among other tuples implying that the intersection of \((C \cup R_{\delta_{\text{mut}}}^+)\) with \(\Delta\) would result in those tuples \((p_m, c_n)\), where \(p_m\) and \(c_n\) are sufficiently similar in their characteristic. Therefore if the resultant set \((C \cup R_{\delta_{\text{mut}}}^+ \cap \Delta)^+\) is not empty, the observer can establish the reproductive relationship between entities \(p\) and \(c\) even under parental mutational changes and the epigenetic changes and reproductive mutations in the child entity.

Using \textbf{AncestorOf} relation, we now can consider the cases of \textit{entity level reproduction} and \textit{Fecundity}:
Case 1: Entity Level Reproduction

We consider the case where instances of individual entities can be observed as reproducing even though there might not be any observable increase in the size of the whole population.

For a given simulation of the model, an observer defines the following Parent relation:

**Definition 4.**

\[
\text{Parent}_\Delta = \{(p, c) \in \text{AncestorOf} \mid \nexists e \in E . ((p, e) \in \text{AncestorOf} \land (e, c) \in \text{AncestorOf})\}
\]

The condition in defining Parent is used to ensure that \( p \) is the immediate parent of \( c \) and thus there is no intermediate ancestor \( e \) between \( p \) and \( c \). Using Parent relation, in order for the observer to establish reproduction in the model, the following axiom should be satisfied:

**Axiom 5 (Reproduction).** \( \exists \text{state sequence } T \in T . \text{Parent}_\Delta \neq \emptyset \)

This means, if there is reproduction in the model, then there should exists some simulation \( T \in T \) of the model, where at least one instance of reproduction is observed.

In case of CBS, we consider a very simple model of reproduction, where at any state of the model some of the strings are randomly chosen and are copied with some random errors. How it is done remains hidden from the observer but the observer can observe which parent entities are chosen for copying and can establish causal relation between these parent and their copied child entities if the random errors occur only at even positions as the way \( \delta_{\text{rep,mut}} \) has been defined in Section 2.1.4. It can be easily seen that under such construction scheme Axiom of Reproduction will be satisfied.

Case 2: Population Level Reproduction - Fecundity

Though entity level reproduction is essential to be observed, for natural selection it is the population level collective reproductive behavior (fecundity), which is significant owing to the carrying capacity of the environment. Since carrying capacity is an limiting constraint on the maximum possible size of population, an observer needs to establish that there is no perpetual decline in the size of the population. In other terms for all generations, there exists a future generation that is of the same size or larger. This allows cyclic population sizes where the cycle mean grows (or stays steady) over time. Also in case of fecundity, an observer need not to observe all the parents in the same state, nor do children need to be observed in the same states of the model. Formally we require the observer to establish Fecundity by satisfying the following axiom:

**Axiom 6 (Fecundity).** There exist infinitely many different generations of entities in temporal ordering \( G_1, G_2, \ldots \) such that \((\forall G_i \subseteq E)(\exists G_{j+i} \subseteq E) . |G_{j+i}| \geq |G_i| \) where \( G_i = \{c \in E \mid \exists a \in G_i . (a, c) \in \text{AncestorOf}\}, \) (operator |\( . \mid \) returns the size of a set.)

Informally, the axiom states that for every generation of entities \( (G_i) \), in future there exist generation of its descendents entities \( (G_j) \) such that the size of descendents generation must be equal or more than current generation. Note that the granularity of the time for determining generations is entirely dependent on the design of the model and the observation process.

We can now formulate another important axiom from evolutionary perspective, which asserts that reproduction in the model should not entirely cease because of the (harmful) mutations.

**Axiom 7 (Preservation of Reproduction under Mutations).** Some mutations do preserve reproduction. Formally, \( \exists e \in E . Ch_e = \{e' \in E : (e, e') \in \text{Parent}_\Delta \cup R_{\text{mut}}\} \neq \emptyset \Rightarrow \exists e'' \in Ch_e . \{e' \in E : (e'', e') \in \text{Parent}_\Delta\} \neq \emptyset \)

Informally, this means, there exists entity \( e \in E \), which reproduces (with mutations) and one of those (mutant) children of \( e \) can also further reproduce. \( Ch_e \) denotes the set of children of \( e \).

In case of CBS, since copying mechanisms do not work differently based upon selected entities, hence the errors during copying process do preserve the above axiom of Preservation of Reproduction under Mutations.
2.2.3 Heredity

Heredity, yet another precondition for evolution, can in general be observed in two different levels: Syntactic level and Semantic level. On syntactic level, entity level inheritance is implied by the structural proximity between parents and their progenies ranging over several generations - though in case of continuous structural changes in the parental entities and epigenetic development in progenies, this would require an observer to establish structural similarities over a range of states as discussed earlier with the definition of AncestorOf relation. Also for syntactic inheritance to persist, design of the model needs to ensure that environment, which controls the reaction semantics of entities, remains approximately constant over a course of time so that structural similarities also result into continued reproductive behavior.

Difficulty arises primarily on the level of multi parental reproduction - in this situation an observer might have to stipulate some kind of gender types and might have to relax the mechanism of recognizing the parent-child relationship in a way as happens for example in case of organic life, where male-female reproductive process (often) gives birth to a progeny belonging to “only” one gender type. In such a case, for heredity, an observer need to ensure that, over a course of time all the gender types are sufficiently produced in the population.

On the other hand it is also possible to observe inheritance on the semantic level (ignoring structural differences) in terms of semantic relatedness between entities, whereby an observer can observe that progenies and their parental entities exhibit similarities in their (reproductive) behaviors under near identical set of environments. This in turn would require an observer to identify the possible sequences of observable reactions between existing entities, which appear to be yielding new set entities (children) and in the child generation as well there exist a similar observable reproductive process, which enables the (re)production of entities. Such an observation would enable the observer to abstract the reproductive processes currently operational in the model. The inherent difficulties in this view are obvious - in essence an observer needs to abstract the reproductive semantics from observable reactions in the model, which in turn might require non trivial inferences in absence of the knowledge of the actual design of the model.

Considering the case of real-life from an observational view point, semantic view is in fact an abstraction over all the reproductive processes existing across various species and levels including the case of bacterial organisms, where next generation of bacteria may contain a mix of genetic material from various parental bacterium of previous generation through the process of horizontal transmission. So while in case of syntactic inheritance an observer would only be able establish inheritance across organisms belonging to same species, using semantic view, he could expand his horizon to the all organic life as a whole.

However, heredity as a mechanism of preservation of syntactic structures, appears to be crucial for those ALife models where entities have very limited set of reproductive variations possible, that is, where environment supports only rare forms of entities to reproduce and any changes in the syntactic structure of these reproductive entities may result in the elimination of the reproductive capability. Real-life on earth as well as the model of the Langton loops (as discussed further in Section 3.2) are definitive examples where most of the variations in the genetic structure, or the loops geometry/transition rules result in the loss of reproductive/replicative capabilities.

Also heredity usually requires further mechanisms to reduce possible undoing of current mutations in future generations owing to new mutations. Therefore, in order to establish inheritance in ALife models, sufficiently many generations of reproducing entities need to be observed to determine that the number of parent-child pairs where certain characteristics (both syntactic and semantic) were inherited by child entities without further mutations is significantly larger than those cases where mutations altered the characteristics in the child entities. We can express it as the following axiom:

Axiom 8 (Heredity). Let a statistically large observed subsequence of a run $T$: $\Omega = \lim_{N \to \infty} \{S_n, \ldots S_N\}, n \ll N$

Consider $\text{Parent}_{\Delta} = \{(e, e') \in \text{Parent}_{\Delta} | F(e) \in \Omega \land F(e') \in \Omega\}$ to be the set of all parent - child pairs observed in $\Omega$. Again let $\text{Inherited}_{\Delta} = \{(e, e') \in \text{Parent}_{\Delta} | \exists \text{Char}_i \in \mathcal{Y}, D(e, e')[i] = 0_{\Delta}\}$ be the set of those cases of reproduction where $i^{th}$ characteristics were inherited without (further) mutation. Then high degree of inheritance for $i^{th}$ characteristics $\text{Char}_i$ implies that $|\text{Parent}_{\Delta}/|/\text{Inherited}_{\Delta}|$
\( \simeq 1 \). For syntactic inheritance to be observed in a population of entities, we should have some such characteristics which satisfy this condition.

The axiom of heredity together with the axiom of preservation of reproduction under mutation ensures that reproductive variation is maintained and propagated across generations.

2.2.4 Natural Selection

There are several existing notions of selection in the literature on evolutionary theory [Fut98, Rid99, Rid97, SH00, MB97, Kim83]. In case of our observation based framework we choose to define natural selection as a statistical inference of average reproductive success, which should be established by an observer on the population of self reproducing entities over an evolutionary time scale i.e., over statistically large number of states in a state sequence. Other notions of selection using fitness, adaptedness, or traits etc. are rather intricate in nature because these concepts are relative to the specific abstraction of “common environment” shared by entities and “the environment-entity interactions”, which are the most basic processes of selection. Nonetheless selecting appropriate generic abstraction for these from the point of view of an observation process is not so simple. Therefore we consider more straightforward approach based upon the idea that on evolutionary scale the relative reproductive success is an effective measure, which is also an indicator of better adaptedness or fitness. We thus define the following (necessary) axioms for the natural selection:

**Axiom 9 (Observation on Evolutionary Time Scale).** An Observer must observe statistically significant population of different reproducing entities, say \( \Lambda (|\Lambda| \gg 1) \), for statistically large number of states in a state sequence \( T \in T \). That is, for a statistically large subsequence \( \Omega \) of \( T \), \( \Omega = \lim_{n \to \infty} (S_n, \ldots, S_N), n \ll N \), the observer defines the set of reproducing entities \( \Lambda \subseteq \bigcup_{S_j \in \Omega} SR(S_j) \), where \( SR(S_j) = \{ e \in E | [F(e) = S_j] \land \exists \epsilon' \in E \cdot (e, \epsilon') \in Parent_\Delta \} \) is the set of all reproducing entities in state \( S_j \in \Omega \).

**Axiom 10 (Sorting).** Entities in \( \Lambda \) should be different with respect to characteristics in \( \Upsilon \) and there should exist differential rate of reproduction among these reproducing entities. Rate of reproduction for an entity is the number of child entities it reproduces before undergoing any mutations beyond observable limit.

In other words, \( \text{Rate}_{\text{rep}} : E \to N^+ \) defined as \( \forall e \in E \cdot \text{Rate}_{\text{rep}}(e) = |\text{Child}_e| \) where \( \text{Child}_e = \{ \epsilon' \in E | \exists \epsilon'' \in E \cdot (\epsilon'', \epsilon') \in Parent_\Delta \text{ and } |\epsilon''| \leq |\epsilon'| \} \).

The above two axioms though necessary are not sufficient to establish natural selection since these cannot be use as such to distinguish between natural selection with neutral selection [SH00]. The following axioms are therefore needed to sufficiently establish natural selection.

**Axiom 11 (Heritable Variation).** There must be variation in heritable mutations in population of \( \Lambda \). Formally, let

\[
\text{Child}_\text{mut} = \{ e \in \Lambda | \exists \epsilon' \in \Lambda \cdot (e, \epsilon') \in Parent_\Delta \land \exists \text{Char}_i \in \Upsilon \cdot 0_{\text{diff}} < D(e, \epsilon')(i) \}
\]

be the set of child entities carrying reproductive mutations. Let \( \text{Var}_\text{Child}_\text{mut} \subseteq \text{Child}_\text{mut} \) be the set of those child entities which carry different mutations with respect to characteristics in \( \Upsilon \), that is,

\[
\forall e, \epsilon' \in \text{Var}_\text{Child}_\text{mut} \text{ we have } \exists \text{Char}_i \in \Upsilon \cdot 0_{\text{diff}} < D(e, \epsilon')(i)
\]

Then axiom of heritable mutation demands that \( |\text{Var}_\text{Child}_\text{mut}| \gg 1 \), that is, there are significantly many child entities carrying different mutations.

**Axiom 12 (Correlation).** There must be non zero correlation between heritable variation and differential rate of reproduction. Formally,

\[
\forall \text{Char}_i \in \Upsilon \cdot \forall e, \epsilon' \in \text{Var}_\text{Child}_\text{mut} \cdot \text{the following two conditions should hold:}
\]

\[i) \ e[i] \leq e'[i] \Leftrightarrow [\text{Rate}_{\text{rep}}(e) > \text{Rate}_{\text{rep}}(e') ] \lor [\text{Rate}_{\text{rep}}(e) < \text{Rate}_{\text{rep}}(e')] \]

\[ii) \ e[i] = e'[i] \Leftrightarrow \text{Rate}_{\text{rep}}(e) = \text{Rate}_{\text{rep}}(e') \]
Informally, this means as the value of characteristics inherited by the child entity changes, rate
of reproduction also changes. Based upon the environmental pressures with respect to a particular
characteristics, rate of reproduction might either increase or decrease as the characteristic changes.

The last two axioms state that there must be significant variation in population (in characters) of
entities which must be maintained for evolutionarily significant periods and that this variation must be
caused by the differences in inheriting mutations from the parent entities, which in turn directly affect
the rate of reproduction.

Having formalized the fundamental component of evolutionary processes to be observed in a model,
we will illustrate the framework on two important ALife models in the following Section. These
illustrations will later be used in concluding Section 5 to extract generic design principles for ALife
research.

3 Case Studies

3.1 General Considerations

Having described the generic formal framework in Section 2 which formalizes the concept of observa-
tions and consequent axiomatic inferences to establish the level of evolution for ALife studies, in the
following sections, we will apply the formalism to different models as case studies. These case studies
include Cellular Automata based Langton Loops [Lan97] and λ Calculus based Algorithmic Chemistry
[Fon92]. The case studies elaborate the steps and technical details specific to the example universe of
the model, which remained implicitly defined in the generalized description of the framework.

For a given model, the steps to instantiate the framework can be described as follows: The obser-
vation process works on the simulations of the model which iteratively change the underlying states
based upon the application of the updation rules of the model. The observation process starts with
the identification of states of the model (Σ) during its simulations (i.e., state sequences \( T \)). Usually
any change in the model (i.e., the changes in the set of basic units) may give rise to a change of the
observed state. It is important to note that in some cases there might be any changes in the observable
state of the model even tough there is ongoing underlying activity in the model, that is, when model
reaches, for example, a fix point.

For every state in the state sequence, the observation process (or the observer) needs to identify a
set of well defined entities with suitable tagging for individual identification (\( E \)). These entities need
to be described in terms of their characteristics (\( \Upsilon \)). Next important task is to define the limits on the
observable mutational changes in individual characteristics of the entities (\( \delta_{\text{mut}}, \delta_{\text{rep,mut}} \)), which will
in turn define the recognition relation (\( R_{\delta_{\text{mut}}} \)) to relate entities persisting across states of the model
as well to determine whether two entities might be considered related under descendent relationship.

Once the sets of entities in various successive states of the model as well as their characteristics
are known, important evolutionary relationships need to be established between them. These evolu-
tionary relationship depend upon the intermediate causal relation (\( C \)) between the entities as observed
under the mechanics of observation process. Using the limits on mutational changes as well as causal
relationship between entities, we proceed to define the Ancestor (\( \text{AncestorOf} \)) and the Parent sets
(\( \text{Parent}_\Delta \)). These sets determine whether there are entities which might be potentially reproducing
in the model, even with observable changes between parent and child entities (\( \Delta \)).

Next stage of the observation process is to ascertain the level of effectiveness of evolution in the
model. Using the long term observations on the model for statistically large number of generations,
one can infer some statistical patterns for degree of heredity and variation. For natural selection
to be effective, there should exist large number of reproducing entities with significant variation in
their characteristics such that there exists correlation of this variation in the characteristics with the
reproductive success of the entities.

This process at the end establishes the validity of all or some axioms of the framework for the given
model which provides clues to the degree upto which evolutionary processes might be effective in that
model universe. The case studies in the following sections will illustrate this process in detail.

In these case studies, constructs not explicitly defined are assumed to be same as what is defined
in the framework.
3.2 Case Study 1: Langton Loops

Research on the self reproduction has a long cherished history starting in early fifties [Bur70, Sup98, FM04]. After the pioneering work of Alan Turing in early 40s to define the mechanical meaning of ‘computation’ as a Turing machine transitions, John von Neumann defined Cellular Automata (CA) [vN65] to explain the generic logic of self reproduction in mechanical terms. His synchronous cellular automata model was a two dimensional grid divided into cells, where each cell would change in parallel its state based upon the states of its neighborhood cells, its own state and its transition rule. For such CA model, von Neumann defined a virtual configuration space where he demonstrated analytically that there exists some universal replicator configuration which could replicate other configurations as well as itself. Though universal replicators are not found in nature and such self replicator was extremely large in its size, nonetheless the underlying logic of treating states of cells in the grid both as ‘data’ as well as ‘instruction’ was very fundamental contribution of this model and that was exactly was was discovered later in case of real life where DNA sequences specify both transcription as well as translation for their own replication in a cell. Another strength of von Neumann’s formulation was its ability to give rise to unlimited variety of self replicators [McM00a, McM00b]. Over the years this model was simplified and reduced in size considerably [Cod68, 81-105].

Finally Langton introduced loop like self replicating structures in [Lan84], which retained the ‘transcription - translation’ property of von Neumann’s model excluding the capability of universal replication and symbolic computation. Langton’s original self-replicating structure is a 86-cell loop constructed in two-dimensional, 8-state, 5-neighborhood cellular space consisting of a string of core cells in state 1, surrounded by sheath cells in state 2. These loops have since then, been extended into several interesting directions including evolving Evoloops in [Say98].

These cellular automata based ALife models offer the ideal example for our observer (observation process) based framework since these replicating loops and their variations evolve only with respect to some high level observation process, which can be used to define entities (loops) and their evolution. We will illustrate the formal framework by instantiating it on the Cellular automata based Langton loop model. Further details on the model itself can be found in the above references.

Instantiating the Framework

We consider the case of two dimensional CA lattice based model. An observation is defined on the CA model by assuming an underlying coordinate system such that each cell in a two dimensional cellular automata (CA) lattice can be associated with unique coordinates (represented as \((x, y)\)). A cell is then completely represented as \((x, y, s)\), where \(s \in [0, 7]\) is the state of the cell. When a cell is in state 0, it is also known as a quiescent cell. Let us denote the set of all cells of a CA model as \(Cell\), which is a potentially infinite set.

For a given cell \(((x, y), s) \in Cell\), its coordinates can be accessed as follows: \(co_x(((x, y), s)) = x\), \(co_y(((x, y), s)) = y\), which can be extended to the set of cells: \(\forall Z \subseteq Cell, \ co_x^Z(Z) = \bigcup_{c \in Z} co_x(c)\), \(co_y^Z(Z) = \bigcup_{c \in Z} co_y(c)\).

\(Neigh : Cell \rightarrow 2^{Cell}\) gives the coordinate wise non quiescent cells in the surrounding neighborhood of a cell. Formally, \(\forall (c = ((x, y), s)) \in Cell\) we have

\[Neigh(c) = \{((x \pm 1, y), s'), ((x, y \pm 1), s') | s' \neq 0\}\]

The model Structure

A CA-based model is usually initialized by setting some finite number of selected cells to non-quiescent states. At each step, state of every cell of the model is changed as per the state transition rules. Therefore we define for an observer state of the Langton’s model as the subset of \(Cell\) consisting of only non quiescent cells. It is clear that for the observer change in a state is observable only if there is a change in the set of non quiescent cells. The state of the model for the observer will also be referred to as configuration. Thus \(\Sigma\) denotes the set of all possible different configurations and a state sequence in \(T\) is a sequence of configurations observed in temporal order by the observer starting from some specific configuration. In the following discussion we will consider a fixed sequence given as \(T \in T\), starting with a specific initial state given in Figure\[Time\] (Time 0). For the fact that there exist a temporal (total) ordering of states in \(T\), we can also associate an integer sequence \(I = [0, 1, 2, \ldots]\) with \(T\), which works as an indexing for the states. With the above structure of Langton’s CA model, the observer takes the following decisions.
Entities

Each entity in some state is characterized by two values - the connected set of non quiescent cells and the associated pivot. Two cells are connected only if there exists a consecutive sequence of neighboring non quiescent cells joining them in the lattice. The (function) pivot gives the coordinates for a cell uniquely associated with an entity in CA lattice in a particular state. Formally, the set of entities (loops) in the model is defined as follows:

\[ E = \{ \{Z, \text{pivot}(Z)\} \mid \exists \text{ a configuration } S \in T . \{Z \subseteq S \land Z \neq \emptyset \} \land \{\forall c \in Z . \exists c' \in \text{Neigh}(c) . c' \in Z\}\} \]

To define pivot, an observer may choose the coordinates of top left hand corner cell of an entity as the pivot for it. Formally

\[ \text{pivot}(Z) = (\min\{\text{co}_x(Z)\}, \max\{\text{co}_y(Z)\}) \forall (e = [Z, \text{pivot}(Z)]) \in E \]

This gives an obvious characterization for a two dimensional character space \( \Upsilon = \text{Char}_1 \times \text{Char}_2 \) with \( \text{Char}_1 \) being the set of all non quiescent connected set of cells and \( \text{Char}_2 \) being the set of corresponding pivots. We do not associate additional tags with entities because pivots can be used to uniquely identify them in any state of the model.

State Function

\( F : E \mapsto I \) is defined using a table which associates with each entity \( e \in E \), the index \( i \in I \) for the state in which \( e \) is observed.

Distance Measure

Distance function \( D : E \times E \rightarrow \{0,1\} \times \{0,1\} \) is defined such that \( \forall e, e' \in E . D(e, e') = [d_g, d_p] \) where \( d_g \) and \( d_p \) are defined as follows: \( d_g \) is 0 only if both entities have the same number of cells arranged identically or else it returns 1. \( d_p \) is 0 when the pivots for both the entities are same and 1 otherwise.

Limits on Observable Mutations

The observer next selects \( \delta_{mut} = [1,0] \), which means that observer can recognize an entity in future states even with mutations (changes in the states, number, or the arrangement of cells comprising the entity) provided that the pivot remains the same. Select \( \delta_{rep,mut} = [0,1] \) which implies that for reproduction observer strictly demands identical geometrical structure of the parent and child entities, though may have different pivots - this is essential to capture exact replication of the loops.

Observing Reproduction and Fecundity

Recognition relation \( R_{\delta_{mut}} : E \rightarrow E \) is defined as follows:

\[ \forall e, e' \in E, R_{\delta_{mut}}(e) = e' \iff [F(e') = F(e) + 1] \land [D(e, e') \leq \delta_{mut}] \]

Informally this means two entities in consecutive states are recognized same only if they have the same pivots. Which also means observer can recognize entity even with change in the number, state, and geometrical arrangement in the cells of an entity across states provided that entity does not shift in CA lattice altogether (which would result in the change of the pivot.)

Lemma 1. \( R_{\delta_{mut}} \) satisfies Axiom 1, Axiom 2, and Axiom 3.

Proof. Axiom 1 and Axiom 3 are satisfied by definition. Axiom 2, which states that \( R_{\delta_{mut}} \) is an injective function holds because no two entities in the same state share the same pivot. This is because pivot as defined above is connected to all other cells of the entity and all the non quiescent cells which are connected in any state are taken together as one entity. Thus two different entities in the same state always consist of cells such that cells in one entity are not connected with the cells of second entity, and hence always have different pivots.
Causal relation

The relation $C$ between entities in consecutive states is defined as follows: $C \subseteq E \times E$ such that $\forall e,e' \in E$ where $e = [Z_e, \text{pivot}(Z_e)]$ and $e' = [Z_{e'}, \text{pivot}(Z_{e'})]$ we require

$$(e, e') \in C \iff \begin{cases} 
1. & \text{co}^x_e(Z_e) \supset \text{co}^x_{e'}(Z_{e'}) \\
2. & \text{co}^y_e(Z_e) \supset \text{co}^y_{e'}(Z_{e'}) \\
3. & \text{pivot}(Z_e) \neq \text{pivot}(Z_{e'}) \\
4. & F(e') = F(e) + 1
\end{cases}$$

Intuitively what we demand with above definition of causal relation $C$ is that child entity was part of the parent entity and at certain stage it “breaks off” from the parent entity, as can be seen in Figure 2 at time step 127.

Lemma 2. Causal relation $C$ defined above satisfies the Causality Axiom.

Proof. Condition $F(e') = F(e) + 1$ insures that $e$ and $e'$ are not observed in the same state. To establish that $e'$ is not the result of mutations in some other entity $e''$ observed in past (i.e., $[F(e'') = F(e)] \land [\text{Rec}(e'') = e']$) we note that because of the definition of $\text{Rec}$, $e''$ and $e'$ would otherwise have the same pivots, which means pivot of $e''$ will be included in the set of cells in $e$ (since $[\text{co}^x_e(Z_e) \supset \text{co}^x_{e'}(Z_{e'})] \land [\text{co}^y_e(Z_e) \supset \text{co}^y_{e'}(Z_{e'})]$), which is not possible because $e$ and $e''$ being different entities in the same state cannot have cells in common including pivot as argued above in the proof of previous lemma.

Figure 2: Self-Reproduction in Langton loops; screen shots from [Bac07]

Lemma 3. Axiom of Reproduction and the Axiom of Fecundity are satisfied by the entities and abstractions on Langton Loops described above.

Proof. These two axioms can be established by the observer in a specific state sequence as exemplified in Figure 2 and Figure 3 by repeatedly applying the recognition relation $\text{Rec}$ when entities are changing in number and states of cells (retaining the pivots) and applying the causal relation when a parent entity splits (e.g. at Time=127). The relation $\Delta$ connects the initial parent entity and the child entity at Time=151.

With respect to Figure 2 an entity is identified at Time=0 with associated pivot. Between time steps [1...126] entity changes in number and states of its cells but the pivot remains the same, hence as per the definition of $\text{Rec}$, the observer can recognize the entity in these successive states. At Time=127, the (parent) entity is observed to be splitting into two identical copies. One of these is again recognized as the original parent entity because of its pivot and the second entity would be claimed to be causally related with the parent entity as per the definition of $C$. To see this, notice that the parent entity at Time=126 contains all the cells of the child entity appearing at Time=127, which satisfies the definition of $C$. Between time steps 128 and 151 both parent and child entities undergo changes in the number and states of their cells but their pivots remain fixed. Hence they can again be recognized. Finally at Time=151 the child entity becomes identical to the original parent entity, therefore the parent entity at Time=0 and the child entity at Time=151 are related using $\Delta$. The transitive closure finally give us the final descendence relationship between the parent and the child entity.
Mutations, Inheritance, and Natural Selection

Primary focus of Langton while defining the CA based replicating loop model was to demonstrate that genotype - phenotype based coding decoding scheme can be captured in CA universe as well [Lan97]. And we have seen that this can be observed by the observer as defined above. Nonetheless, Langton loops do not exhibit mutations and indeed if we analyze the underlying state transitions defined for the cells in the model, it becomes clear that the transition behavior required for the reproduction changes immediately if any changes are introduced in an entity and resulting entity is no longer capable of reproduction or in other terms, none of the mutations in existing replicating loops preserve reproduction and in terms of the current framework Axiom of Preservation of Reproduction under Mutations is not valid. Because of the enormity of possible configurations and transition dynamics it is not easy to analyze which kind of replicating loops can ever withstand certain mutations and can preserve replicating functionality. Heredity of course is worth considering only when entities mutate and continue reproduction. Thus with existing Langton loops, an observer cannot observe heredity and subsequent natural selection.

The extension of Langton loops defined by Sayama as Evoloops in [Say98] is one such attempt, where not all the loops in the model are of the same type with respect to the number and geometrical arrangement of cells and final population witnesses (small) variety of different kinds (in size) of reproducing loops scattered on the lattice forming colonies. The Evoloops and their evolution can be formulated in the framework by suitably modifying the definition of the distance measure $D$ to measure the differences between the entities in the number and geometric arrangement of cells and by changing limit $\delta_{rep,mut}$ such that the observer is able to establish descendence relationship even when the parent and the child entities (loops) are not identical. Since evoloops of different types replicate at different rates, where rate of replication is measured in terms of number of state transitions, we can infer that the loops satisfy the axiom of sorting. Indeed in a weak sense with available simulation results it appears that evoloops can be observed demonstrating heredity as well as selection.

Conclusion

We have seen that we can formally define an observation process on the CA universe which discovers the self replication of so called Langton loops during the simulation of model. The specific observer presented here follows the intuition that Langton implicitly stated when describing the loops. We also noted that mutations, heredity, and selection based axioms are not met in the model where this limitation can be attributed to underlying transition rules of the model. Evoloops, which were designed as extensions of Langton loops with mutations can be seen to be evolving with variation in the sizes and rates of reproduction.
3.3 Case Study 2: Algorithmic Chemistry

Algorithmic Chemistry (AlChemy) was introduced in [FB94b] and further discussed in [FB94a, FB94c, FB94r, FB96]. The main focus of the AlChemy is to study the principles behind the emergence of biological organizations with the approximate abstraction of real chemistry as λ calculus with finite reductions. Starting with a random population of λ terms (molecules), using different filtering conditions on reactions, authors describe the emergence of different kinds of organizations: Level 0 organization consisting of a set of self copying λ terms and hypercycles with mutually copying λ terms. Level 1 self maintaining organizations consisting of λ terms such that every term is effectively produced as a result of reaction between some other terms in the same organization and lastly Level 2 organization consisting of two or more Level 1 sub organizations such that molecules migrate between these self maintaining sub-organizations. They also provide detailed algebraic characterization of Level 1 and Level 2 organizations without referring to the underlying syntactical structure of the λ terms (molecules) or the micro dynamics (reduction semantics and filtering conditions) governing the output of reactions.

Instantiating the Framework

In view of the proposed observer based framework, characterization of self replicating molecules and hypercycles consisting of mutually copying molecules is achieved by defining an observation process, which focusses on individual λ terms as entities and identifies hypercycles as a set of individually replicating λ terms in a sequence of reaction steps (reflexive autocatalysis).

Since Level 1 and Level 2 organizations emerge only when self copying reactions are filtered out (i.e., self reproduction is not allowed) to ensure that Level 0 organizational structures do not become the fixed points, these cannot be analyzed under the current framework design because we only consider reproduction, mutation, inheritance, and selection based evolution and emergence of organizations.

The Chemistry Structure

A chemical soup of AlChemy consisting of λ terms as molecules is usually initialized with a population of large number of randomly generated λ terms. A state of the chemistry could, therefore, be considered as the collection of all these λ terms (with multiplicity). Since every non elastic reaction results into introduction of output λ term into the soup and possible removal of some other randomly chosen terms, it is natural to consider such succession of states after every reaction step as a state sequence \( T \in T \).

The components of the observation process defined next are based upon the assumption that it is possible to observe the inputs terms for a reaction (collision), resultant output term to be added to the soup, and the randomly deleted terms from the soup, without knowing the actual reaction details or the reduction semantics.

Entities

For a given state of the chemistry, let the observation process identify each λ term as a separate entity associating an unique integer tag with it. Each such entity is represented as \([w,i]\) where \(i\) is the tag uniquely associated with λ term \(w\). \(E\) is the set of all such entities in the chemistry.

Tagging: Suitable tagging mechanism needs to be defined by the observer to recognize whether two λ terms in successive states are the same and to distinguish between multiple syntactically identical copies of a λ term in the soup at any state. We can associate tags of the form \((i_{size}, i_{lex}, i_{mul})\) \((i_{size}, i_{lex}, i_{mul} \in N)\) with the individual molecules in the following way: for the initial population of λ terms, they are arranged with respect to their sizes and we assign the size of these terms as the first component in their tags \((i_{size})\) and for terms of same size arrange them lexicographically and assign in increasing order second component of their tags \((i_{lex})\) such that multiple copies of a term have the same first two components of their tags and then assign increasing integers to each of these as their third component of the tag \((i_{mul})\). Under such tagging scheme a small population of λ terms \(\{\lambda x.x, \lambda y.x, \lambda x_1.\lambda x_2.x_2\}\) defines the state - \(\{[\lambda x.x, (3, 1, 1)], [\lambda x.x, (3, 1, 2)], [\lambda x_1.\lambda x_2.x_2, (5, 1, 1)]\}\) . For a given tag \(tg = (i, j, k)\) its components are accessed as \(i = tg[1], j = tg[2],\) and \(k = tg[3]\).

Next we discuss the mechanism for updating these tags after reaction and elimination steps. We increment by one the third component of the tags for each entity, which was not deleted from the soup from previous state and give new unique tag to the new terms added to the soup with respect to their position in the list of terms based on their size and lexicographic order such that third component of the
newly added terms is always given value 1. This numbering scheme reliably maintains the recognition of terms across states of the chemistry.

**Distance Measure**

Distance function $D : E \times E \rightarrow \{0, 1\} \times \{0, 1\}$ is defined such that $\forall (e = [w, t_g], e' = [w', t_g']) \in E$. $D(e, e')[1] = 0$ if $w$ and $w'$ are the same with respect to $\alpha$ renaming implying that entity $e'$ is the same entity $e$ in the previous state; otherwise $D(e, e')[1] = 1$. $D(e, e')[2] = 0$ if $t_g'[3] - t_g[3] = 1$ indicating that entity $e$ is observed in the next state as entity $e'$, otherwise $D(e, e')[2] = 1$. The distance function $D$ has been defined keeping in mind the use of these distances in defining recognition relation later.

**The Limits on Observable Mutations**

Let $\delta_{\text{mut}} = [0, 0]$, indicating that syntactically different $\lambda$ terms (under $\alpha$ renaming) are treated as different entities. Also let $\delta_{\text{rep,mut}} = [0, 1]$ indicating that reproductive mutations resulting into syntactically different term are not observable. This is primarily because under $\beta$ reduction semantics of Alchemy, even changes in the syntactical representations result into very different reaction behaviors.

**Observing Self Replicating Hypercycles**

We can observe the self-replicating elementary hypercycles as sets of self-replicating entities. Let us define, for that purpose, the recognition relation $R_{\delta_{\text{mut}}} : E \rightarrow E$ as follows: $\forall e, e' \in E$, $R_{\delta_{\text{mut}}}(e) = e' \Leftrightarrow [F(e') = F(e) + 1] \land D(e, e') \leq \delta_{\text{mut}}$. Informally this means two entities in consecutive states are recognized same only using their tags.

**Lemma 4.** $R_{\delta_{\text{mut}}}$ satisfies Axiom 1, Axiom 2, and Axiom 3.

**Proof.** Axiom 1 and Axiom 3 are satisfied by definition. Axiom 2, which states that $R_{\delta_{\text{mut}}}$ is an injective function holds because of the specific construct of tagging mechanism and the definition of Distance function $D$ which is such that two entities in successive states are recognized as same only when the difference between their third components of tags is 1, and we know that the observer selects new tags in such a way that this difference is 1 only when same entity was present in the previous state.

Next let us defines $\Delta \subseteq E \times E$ such that $\forall e, e' \in E, (e, e') \in \Delta \Leftrightarrow D(e, e') \leq \delta_{\text{rep,mut}}$. In order to define causal relation between entities in the AlChemy, we assume that observer has the knowledge of the reacting entities and the output term at any state. Therefore if entities $e_1$ and $e_2$ react in some state and yield $e_o$, the observer defines causal relation $C$ so that $(e_1, e_o) \in C$ and $(e_2, e_o) \in C$ with
\[ F(e_1) = F(e_2) = F(e_o) - 1. \]

**Lemma 5.** Causal relation \( C \) defined above satisfies Axiom 4.

*Proof.* First condition of Axiom 4 is satisfied by definition since \( F(e_o) = F(e_1) + 1 = F(e_2) + 1 \). The second condition \[ \{ e' \in E. F(e_1) = F(e') \land R_{\text{mut}}(e') = e_o \} \], that is, there does not exist any third entity \( e' \) in the previous state, which has mutated into \( e_o \), again follows from the specific construct of tagging as well as the distance function because as per the tagging mechanism explained before \( e_o \) being newly added entity in the chemistry will have the 3\textsuperscript{rd} component of its tag as 1 and all previously present entities, including \( e_1, e_2 \), in the chemistry would have their tags in new states updated such that their 3\textsuperscript{rd} components are always greater than 1.

Relations \textit{AncestorOf} and \textit{Parent} can be defined same as in the framework.

**Lemma 6.** Axiom of Reproduction and the Axiom of Fecundity are satisfied by the entities and corresponding abstractions discussed above.

*Proof.* These two axioms depend upon the examples of self replicating \( \lambda \) terms as well as elementary hypercycles. In case of hypercycles, the observer establishes multi-step reproduction using transitive closure of causal relation for each of the entities in the hypercycle. A quite well known example of self replicating \( \lambda \) term is \( \lambda x.(x)(x) \) since \( (\lambda x.(x)(x))(\lambda x.(x)(x)) \Rightarrow (\lambda x.(x)(x))(\lambda x.(x)(x)) \). Though in case of Alchemy, the level 0 organization consists of self-copiers like \( \lambda x.x \) and hypercycles like \{ \( \lambda x_1.\lambda x_2.x_2 \), \( \lambda x.x \) \} as illustrated in Figure 3. As per the definition of causal relation, entity instances of \( \lambda x_1.\lambda x_2.x_2 \) and of \( \lambda x.x \) are causally related to past instances of each other and therefore of themselves.

**Mutations, Inheritance, and Natural Selection**

As emphasized in [FB94a], primary goal of AlChemy is to study alternative pathways in which higher level organizations (i.e., hypercycles, self maintaining organizations) can emerge starting with a random set of molecules. Therefore it appears that there is no explicit notion of mutations present in the chemistry. To see this notice that every new entity in the population is the result of reaction between two other entities. Therefore if one particular observer decides that one of the reacting entities is mutating into the resulting entity, it is still difficult to decide which of the two reacting entities should be considered as mutating into the new one. Even if such a view is adopted, the observer will observe that if a self-copying entity at any reaction step mutates into another entity then most often the new entity can no longer self-copy. Thus Axiom 7 (Preservation of Reproduction under Mutation) would be violated. Finally as discussed at the beginning of the section, owing to the focus of our framework on the evolutionary processes, self-maintaining organization of the kind that arise in AlChemy are beyond the scope.

**Conclusion**

Thus we have demonstrated that, based upon the knowledge of reacting terms and outputs, a precise observation process can be defined to work with AlChmey, which can be used to discover the self replicating \( \lambda \) terms as well as hypercycles in the model. We also noted that mutations, heredity, and selection based axioms are not met in the chemistry where this limitation should be attributed to underlying reaction semantics of the chemistry as well as its design. This study highlights the fact that not all interesting dynamic processes are evolutionary in nature and therefore some of these non evolutionary processes are out of scope of the framework at present.

**4 Related Work**

Because of the presence of sufficiently many biology-specific criterion (e.g., morphological characters, bio-molecular structures etc.) to distinguish life from non-life, in biological literature there is little formal work on recognizing life \textit{per se}. There is, however some recent work on defining and developing
methods to analyze genotype space structure based upon the macroscopic observations on phenotype characteristics (mainly morphological and reactive characteristics) \cite{LG98, GCKV03, LGC04}.

To the authors’ knowledge, there is not much work focussing on the observation process for ALife studies reported in literature. Though there exist proposals to define ‘numerical parameters’ or ‘statistics’ \cite{Bed99} to recognize life in a model. However, it is not clear whether there can be simple numerical definitions capturing the essence of life in arbitrary models and even if so does not seem to be the case with the existing proposals. The difficulty arises out of intricate nature of reproduction and selection inevitably involving non trivial identification of the population of evolving entities. Langton defined in \cite{Lan90} a quantitative metric, called \textit{lambda} parameter to detect life in any generic one dimensional cellular automata model based upon the characteristics of its transition rules. This lambda parameter based analysis is based upon the assumption that any self organizing system can be treated as living and does not consider population centric evolutionary behavior as characteristic of life. In \cite{BSP98} there is a discussion on the classification of long term adaptive evolutionary dynamics in natural and artificially evolving systems. This they achieve by defining activity statistics for the components, which quantifies the adaptive value of components (characteristics in our model). They employ similar mechanism as of ours by associating activity counters (tags) with all the components present in the system during simulation.

Self-reproduction, which has a long history of research starting from the late 1950s \cite{Bur70, Sip98, FM04} has evaded precise formal definition applicable to a wide range of models \cite{ND98} in the sense of observable characterization of the reproducing entities. Though there is enough work on mathematical analysis of replication dynamics (fecundity) in various natural systems or the systems where environmental constraints governing the rate of reproductions are known (see for overview \cite{FM04, Chap5}.) In some of the discussions related to self-replication in cellular automata models \cite{Say98, Mor98}, formalizations of reproducing structures are presented, but they do not attempt to provide a general framework for observing reproduction or other components of evolutionary processes. These attempts at formalizing reproduction in CA models are reminiscent of our definition of entities (loops) in Section 3.2.

In other work \cite{Mis06b}, we proposed a multi-set theoretic framework to formalize self reproduction (with mutations) in dynamical hierarchies in terms of hierarchal multi-sets and corresponding inductively defined meta-reactions. The “self” in “self-reproduction” was defined in terms of \textit{observed structural equivalences} between entities. We also introduced constraints to distinguish a simple “collection” of reacting entities from genuine cases of “emergent” organizational structures consisting of \textit{semantically coupled} multi-set of entities.

\section{Conclusion}

\subsection{General Remarks}

This paper formalizes an implicit underlying component of ALife studies, namely the observation process, by which entities are identified and their evolution is observed in a particular ALife simulation. Under the assumption that the essence of life-like phenomena is their evolutionary behavior, we developed a framework to formally capture basic components of evolutionary phenomena. This work, in essence, brings insights from evolutionary theory for real-life into the realm of artificial-life for defining a formal framework for observational processes, which are needed for the identification of life-like phenomena in the ALife studies. We have argued that without such a formalism, claims pertaining to the evolutionary behavior in ALife studies will remain inconclusive.

We formally elaborate in algebraic terms the necessary and sufficient steps for an observational process, to be employed by an ALife researcher upon the time progressive model of his model universe, to uncover (hidden) life-like phenomena in the light of Darwinian evolution as defining characteristics of life. The observation process as specified in our framework may be carried out manually or can be alternatively algorithmically programmed and integrated within the model.

To define inference process we specify necessary conditions, as axioms, which must be satisfied by the outcomes of observations made upon the model universe in order to infer whether life-like phenomena is present in the model (Section 2.2). These axioms also specify the experimental work necessary in order to observe and lay claims for the presence of life in the model universe.

The case studies on Langton loops (Section 3.2) and Algorithmic Chemistry (Section 3.3) highlight the contributions that such an approach can make to the discussion of specific ALife experiments. An
important property of such a study is to make explicit “multi-level observations”, where entities and their relationship can be observed and defined on separate organizational levels.

The framework design and the case study analysis also provide us clues for ALife research designs so that to be better able to witness evolutionary phenomena in the model during its simulations. This is discussed next:

5.2 Design Suggestions for ALife Researchers

As the framework is based upon the Darwinistic concepts of defining life in terms of evolutionary processes, the design suggestions we describe here are rather more suitable for those studies which aim to complement real life studies in an evolutionary framework.

- Sufficient Reproduction with Variation: The model must be designed such that there exist potentially large set of reproducing entities with significant variation in their characteristics. Quite often this hinges upon the choice of reaction rules or the semantics of the model and indeed it is a serious challenge for any model designer to define the reaction semantics which permits potentially large set of reproducers with significant variation. Another interesting aspect is that these reproducers must be relatively closely related to each other under the reaction semantics. This means that sufficiently many variations of reproducers should also be reproducers in themselves otherwise the axiom of preservation of reproduction under mutation will not effectively hold in the model and most of the reproducers would have to appear de novo during simulations. We encounter this problem in both of the case studies discussed in Section 3. In case of Langton loops, any kind of change in the loop structure would cause cessation of replication. The work on designing Evoloops is therefore based upon the redefinition of the reaction semantics or transition rules which permit variation in replicating loops. Similarly in the case of Algorithmic chemistry, almost all of the single replicating $\lambda$ terms arise de novo and their variations do not replicate under $\beta$ reaction semantics.

- Measurable Rates of Reproduction: The model should be designed such that it is possible to impose some valid measure of determining the rates of reactions which in turn can be used to estimate differences in the rates of reproduction of different entities. This measurement of reproductive rates must be independent of the updation algorithm which selects entities for reaction. Therefore it can be argued that the models, where all (reproductive) reactions take place in a single step would be difficult to observe for natural selection, which works only when different entities reproduce at different rates. For example, it is not possible to infer differences in the rates of reproduction among different reproducing elementary hypercycles in the Algorithmic Chemistry consisting of the same number of $\lambda$ terms because every reaction between any two $\lambda$ terms occurs in a single step. On the other hand natural selection can be observed in case of Evoloops precisely because different types of loops consisting of different number of cells reproduce at different rates based upon the number of state transitions.

5.3 Limitations

The decision to equate life with evolutionary processes also excludes some of the interesting complex phenomena that are not evolutionary in nature from the scope of this work. Indeed, we have shown in Section 3.3 that the framework cannot account for the dynamic non-evolutionary behavior of Level 1 and Level 2 organizations emerging in the Algorithmic Chemistry. We limit our attention to only those observations having evolutionary significance, though other observations can also be made upon the model including metabolism [BFF92], emergence of complexity [AOC00], self organization [Kau93], and autonomous and autopoietic nature of life [Zel81] etc.

We have not placed direct emphasis on certain concepts widely associated with ALife studies including the notion of “emergence”. In our current setting the notion of “strong emergence” is only implicitly present and indeed “the element of surprise” [BE97] often associated with emergence is not immediate in the framework. Similarly “the element of autonomy” of emergent processes with respect to the underlying micro-level dynamics is not addressed in our framework. Indeed, the spirit of the high level of observations and corresponding abstractions upon which the framework rests, may preclude such inferences. Nonetheless the idea of “weak emergence” [Bed97], which lays emphasis on the simulations of the model for the emergence of high level macro-states is fundamental to our framework, where
the observation process is by default based upon the simulations of the model and not on analytical derivations.

Another limitation of the framework in its current state is that it cannot be used effectively to make predictions regarding the possible observable evolutionary dynamics in a ALife model during simulations. This limitation though carries forward from the nature of Darwinian theory which is too generic in its conceptualization and based upon random sources of change that make it difficult to derive useful predictions.

Similarly analysis of Gödelian type conjunctures to counter possibility of strong Alife, stating the impossibility of formalizing life in general because that would imply formalizing “mathematically intelligent” entities like ourselves, which could in turn prove the Gödel theorems in their own “mathematical universe” having correspondence with ours, is also beyond the scope of the current limits of the framework. See [III97, Ras92].

### Problem of False Positives

Terms ‘false positive’ and ‘false negative’ are used in general to highlight the limitations of ‘observation - inference’ based methodologies. False positive refers to a situation where observations and consequent inferences on a model result into a claim of the presence of certain property in the model which actually does not exist, while false negative is used to refer the situation where observations do not yield required support for the presence of certain property, which is actually present in the model. False negatives are usually the result of incomplete observations while false positives indicate arbitrariness in the observation/inference process.

Like any other generic specification framework, current framework also suffers from the weakness of administering false positives. False negatives are also possible, whereby an observation process is defined such that it does not infer evolution, even though there might actually be evolution present in the model.

The case of false negatives, however will not concern us since our focus is to establish the presence of evolution in a given ALife model and not whether it is absent with respect to certain observations. The problem of false positives stems due to the fact that the framework permits arbitrariness in the definition of entities and their causal relationships. In case of causal relationships, they are defined in the framework as observation dependent and might not be consistent with the underlying micro-level dynamics of the model (Section 2.2.2). This arbitrariness might give rise to false claims on the presence of evolution in the model though there might be none actually.

For example, an observer (say ob) might decide to “ignore” entities in some states in the beginning and then choose later on to observe them in some other states so that to use them for establishing (false) evolutionary relationships, which would not have been possible had he not preferred to ignore them earlier. This problem of selectively observing entities in various states requires additional constraints in the framework. We may add the following constraint by considering another observer ob′ with same universe of observation as ob. Let us consider a particular simulation of a model as a state sequence $T$. For a state subsequence $S$ of $T$, let $E_{ob}^S$ and $E_{ob'}^S$ denote the set of entities observed by ob and ob′ respectively. Consider that ob′ observes some entities $X \subseteq E_{ob}^S$, which were ignored by ob, that is, $X \not\subseteq E_{ob}^S$. Now consider the case when ob chooses to observe $X$ in some later subsequence $S'$ of $T$, $S \neq S'$, that is, $X \subseteq E_{ob}^{S'}$, and also $X \subseteq E_{ob'}^{S'}$, where $E_{ob}^{S'}$ and $E_{ob'}^{S'}$ are the sets of entities observed by ob and ob′ in $S'$. Now if ob establishes evolutionary relationships using entities in $X$, which cannot be established by ob′, then we say that ob has drawn illegitimate conclusions.

### 5.4 Further work

Framework can be further extended in several interesting directions, including the following: We need to capture the essence of strong emergence by considering several observation processes at different organizational levels of the model. We can also study overlapping evolutionary processes - examples from real life include co-evolution, and sexual selection versus environmental selection. Framework ought to be extended so that fruitful predictions for a given ALife model regarding the nature of evolutionary dynamics can be made. We also need to introduce more strict constraints to overcome the problem of false positives by limiting as to what could be claimed as observed. Further insights can be gained by applying the framework to novel classes of ALife models to refine the framework further, which we are currently involved with.
References

[AOC00] Christoph Adami, Charles Ofria, and Travis C Collier. Evolution of biological complexity. Proceedings of National Academy of Science, 97:4463–4468, 2000.

[Bac07] Eli Bachmutsky. Java applet: Self-Replicating Loops in Cellular Space. Available at http://necsi.org/postdocs/sayama/sder/java/ 06/08/2007.

[BE97] N. A. Baas and C. Emmeche. On emergence and explanation. Intellectica, 1997/2(25):67–83, 1997.

[Bed97] M. A. Bedau. Weak emergence. In James Tomberlin, editor, Philosophical Perspectives: Mind, Causation, and World, volume 11, pages 375–399. Blackwell Publishers, 1997.

[Bed99] Marc A. Bedau. Can unrealistic computer models illuminate theoretical biology? In Proceedings of the 1999 Genetic and Evolutionary Computation Conference Workshop Program, pages 20–23, Orlando, Florida, 1999.

[BFF92] Richard J. Bagley, J. Doyne Farmer, and Walter Fontana. Evolution of a metabolism. In Christopher G. Langton, Charles Taylor, J. Doyne Farmer, and Steen Rasmussen, editors, Artificial Life II, pages 141–158, Redwood City, CA, 1992. Addison-Wesley.

[BMP+00] M. A. Bedau, J. S. McCaskill, N. H. Packard, S. Rasmussen, C. Adami, D. G. Green, T. Ikegami, K. Kaneko, and T. S. Ray. Open problems in artificial life. Artificial Life, 6(4):363–376, 2000.

[BSP98] M. A. Bedau, E. Snyder, and N. H. Packard. A classification of long-term evolutionary dynamics. In C. Adami, R. Belew, H. Kitano, and C. Taylor, editors, Artificial Life VI, pages 228–237. Cambridge: MIT Press, 1998.

[Bur70] A.W. Burks. Essays on Cellular Automata. University of Illinois Press, 1970.

[Cod68] E.F. Codd. Cellular Automata. Academic Press, 1968.

[Daw82] Richard Dawkins. Universal darwinism. In D.S.Bendall, editor, Evolution from Molecules to Men, pages 403–25. Cambridge University Press, (Cambridge, 1982.

[DZB01] P. Dittrich, Jens Ziegler, and Wolfgang Banzhaf. Artificial chemistries—a review. Artificial Life, 7(3), 2001.

[FB94a] W. Fontana and L. W. Buss. 'The arrival of the fittest': Toward a theory of biological organization. Bull. Math. Biol., 56:1–64, 1994.

[FB94b] W. Fontana and L. W. Buss. What would be conserved if ‘the tape were played twice’? Proc. Natl. Acad. Sci. USA, 91:757–761, 1994.

[FB96] W. Fontana and L. W. Buss. The barrier of objects: From dynamical systems to bounded organization. In J. Casti and A. Karlqvist, editors, Boundaries and Barriers, pages 56–116, Redwood City, MA, 1996. Addison-Wesley.

[FM04] Robert Freitas and Ralph Merkle. Kinematic Self-Replicating Machines. Landes Bioscience, 2004.

[Fon92] W. Fontana. Algorithmic chemistry. In C. G. Langton, C. Taylor, J. D. Farmer, and S. Rasmussen, editors, Artificial Life II, pages 159–210, Redwood City, CA, 1992. Addison-Wesley.

[Fut98] Douglas J. Futuyma. Evolutionary Biology. Sinauer Associates, 3 edition, 1998.

[FWB94] W. Fontana, G. Wagner, and L. W. Buss. Beyond digital naturalism. Artificial Life, 1/2:211–227, 1994.

[GCKV03] M. Gamez, R. Carreno, A. Kosa, and Z. Varga. Observability in strategic models of viability selection. Biosystems, 71 (3):249–255, 2003.
[HM07] Martin Henz and Janardan Misra. Towards a framework for observing artificial life forms. In Proceedings of the 2007 IEEE Symposium on Artificial Life (IEEE-ALife’07), pages 23–30. IEEE Computational Intelligence Society, 2007.

[III97] John P. Sullins III. Godel’s incompleteness theorems and artificial life. Society for Philosophy and Technology, 2(3-4):141–157, 1997.

[JG98] M. B. Garay J. Garay. Genetical reachability: when does a sexual population realize all phenotypic states. J. Math. Biol., 37:146–154, 1998.

[Kau93] S. A. Kauffman. The Origins of Order: Self-Organization and Selection in Evolution. Oxford University Press, New York, 1993.

[Kim83] Motoo Kimura. The Neutral Theory of Molecular Evolution. Cambridge University Press, 1983.

[Lan84] C. G. Langton. Self-reproduction in cellular automata. Physica D, 10D(1-2):135–44, 1984.

[Lan90] C. G. Langton. Computation at the edge of chaos: Phase transitions and emergent computation. Physica, D 42:12–37, 1990.

[Lan95] C. G. Langton. Artificial life: An overview. In Complex Adaptive Systems. MIT Press, Cambridge, MA, 1995.

[Lan97] C. G. Langton. Artificial life. In Artificial Life VI: Proceedings of an interdisciplinary Workshop on the Synthesis and Simulation of Living Systems, pages 1–47. SFI Studies in the Sciences of Complexity, 1997.

[LGC04] I. Lopez., M. Gamez, and R. Carreno. Observability in dynamic evolutionary models. BioSystems, 73:99–109, 2004.

[MB97] M. Mahner and M. Bunge. Foundations of Biophilosophy. Springer, 1997.

[McM00a] Barry McMullin. John von Neumann and the evolutionary growth of complexity: Looking backward, looking forward. Artificial Life, 6:347–361, 2000.

[McM00b] Barry McMullin. The von Neumann self-reproducing architecture, genetic relativism and evolvability. In Evolvability Workshop at Artificial Life VII: Proceedings of the Seventh International Conference on Artificial Life, 2000.

[Mis06a] Janardan Misra. Artificial life evolution: Can we observe it or not. In The International European Conference on Computing and Philosophy (ECAP’06). Extended Abstract at http://www.anvendtetikk.ntnu.no/ecap06/program/Mishra.pdf, 2006.

[Mis06b] Janardan Misra. An inductive formalization of self reproduction in dynamical hierarchies. In Proceedings of ALIFE X: 10th International Conference on the Simulation and Synthesis of Living Systems, pages 553–558, Bloomington, US, 2006. MIT Press.

[Mor98] Kenichi Morita. Cellular automata and artificial life: Computation and life in reversible cellular automata. In E. Goles and S. Martinzez, editors, Complex Systems, pages 151–200. Kluwer Academic Publisher, 1998.

[ND98] C. L. Nehaniv and K. Dautenhahn. Self-replication and reproduction: Considerations and obstacles for rigorous definitions. Third German Workshop on Artificial Life: Abstracting and Synthesizing the Principles of Life, pages 283–290, 1998.

[Neh05] C. L. Nehaniv. Self-replication, evolvability, and asynchronicity in stochastic worlds. Proc. 3rd Symposium on Stochastic Algorithms, Foundations and Applications, 3777:(in press), 2005.

[Ras92] S. Rasmussen. Aspects of information, life, reality, and physics. Artificial Life II, SFI Studies in the Science of Complexity, 10:767–773, 1992.

[Rid96] Mark Ridley. Evolution. Blackwell Science, 2 edition, 1996.
[Rid97] Mark Ridley, editor. *Evolution*. Oxford University Press, 1997.

[Say98] Hiroki Sayama. *Constructing Evolutionary Systems on a Simple Deterministic Cellular Automata Space*. PhD thesis, Department of Information Science, Graduate School of Science, University of Tokyo, December 1998.

[Sch01] Peter Schuster. Mathematical challenges from molecular evolution. In Björn Enquist and Wilfried Schmid, editors, *Mathematics Unlimited - 2001 and Beyond*. Springer, 1 edition, 2001.

[SH00] Stephen C. Stearns and Rolf F. Hoekstra. *Evolution—An Introduction*. Oxford University Press, 2000.

[Sip98] Moshe Sipper. Fifty years of research on self-replication: An overview. In *Artificial Life IV*, pages 237–257, 1998.

[SS97] John Maynard Smith and Eors Szathmary. *The Major Transitions in Evolution*. Oxford University Press, reprint edition edition, 1997.

[vN66] J. von Neumann. *Theory of Self-Reproducing Automata*. University of Illinois Press, 1966.

[Zel81] M. Zeleny, editor. *Autopoiesis: A Theory of Living Organization*. North Holland, New York, 1981.