

On the task to create the minimum mathematical model for open ended evolution [closed]

I'd like to create a model of Open Ended Evolution (Then test it on the PC. May be even with hardware random number generator). The good overview of the Open Ended Evolution problem is given by Alastair Channon: <http://www.channon.net/alastair/>. This name states for an artificial life that don't stop it's evolution on a fixed level of complexity but instead progresses further. The only difference seems to be that the model I'd like to create is planned to be the simplest model. So my task is about creation of a mathematical dynamic model that satisfies the specific constraints (start from the simplest structure, no predetermined structures except natural selection postulates, no environment, only individuals, ...).

The constraints are described further. This task is actually derived from the question *Intuitions for the simplest model in which the evolution of the laws of nature arises from the natural selection of structures* <http://math.stackexchange.com/questions/1611737/>

The constraints:

1. The model describes process of discrete changes of the graph-like structure.
2. The process starts from the graph consisting of the only one vertex. There are no edges.
3. The predetermined rules are applied to the existing graph to get the next graph.
4. The predetermined rules should include the rules that resemble the postulates of natural selection:
 - Reproduction (may be: spontaneous events of doubling of the vertices).
 - Heredity (may be: conservation or invariability of some subgraph of the graph. Or subset of the set of edges of a particular vertex)
 - Variation (may be: spontaneous events of changing the vertices' edges during reproduction. There are more than one such events so there are random choices in most cases)
 - Selection (I'm not sure but there also may be the events of joining two vertices into one. May be this event is applied only to the two vertices that share in their history the same event of doubling)
5. As I see it now the edges of the vertices appear to be the structure of the individuals in the natural selection. But I may be wrong.
6. There are two ways of imagining this process:
 - 6.1 Do not draw the history of rules application. First step: o, Second step: o—o. Here the rule of reproduction was applied.
 - 6.2 Do draw the history of rules application. First step: o, Second step:



In this picture the history of reproduction was taken into account. And directed edges are used to denote events of application of the rules to the graph (or to the subgraph of it).

7. During the process of rules application (partially randomly) we get the history of graph changes. The process of creating such a history is an infinite process.
8. In the history of this process should be patterns in the graph that are isomorphic to each other in some sense. If we are imagining the process like in 6.2 then the isomorphic patterns should be found both in time direction and in graph structure. The simplest analogue to this is the waves propagating in the medium.
9. Moreover there should be the evolution of such patterns that lead to their complication and incorporation the information about the graph structure or about other patterns. Presumably this evolution is led by competition for "staying alive" of such patterns with each other.
10. This evolution should not stop at the fixed level of pattern complexity. So it should be the case of Open Ended Evolution.

The model to be built should satisfy the 1, 2, 4, 8, 9, 10 constraints. Other constraints may be altered to fit the 1, 2, 4, 8, 9, 10 constraints.

So my question is request for formalisations that satisfy the constraints mentioned. Actually it would be much easier to check whether formalisation satisfies the constraints than to create such a formalisation. I understand that this is a hard question so the partially formalised ideas (but formalised to some degree) are also very welcome.

The question is also a request for convincing arguments in favor that the model satisfying the constraints is impossible.

PS

1. Presumably, there are many "layers" on which populations exist. The vertices themselves are the atomic individuals that are characterised by their edges. All the vertices are the basic population (basic level). But the goal of the model is to get the individuals at next levels: as patterns in the graph (there may be even cycles of patterns changing to each other, like wave). The interesting individuals are patterns (subgraphs that persist in the changing graph during time). And there expected layers on layers.
2. From some point of view my task to create this specific model is an attempt to figure out whether postulates of natural selection are sufficient for evolution with endless complication (given the simplest beginning structure possible) or not sufficient.

UPD

Examples of the models that resemble the desired model:

Here is the a try to create a mathematical dynamic model that satisfies some of the constraints mentioned. I doubt that it would succeed. But

closed as too broad by [AMR](#), [rg255](#), [James](#), [Christiaan](#), [fileunderwater](#) Jan 15 at 11:55

There are either too many possible answers, or good answers would be too long for this format. Please add details to narrow the answer set or to isolate an issue that can be answered in a few paragraphs.

If this question can be reworded to fit the rules in the [help center](#), please [edit your question](#).

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1 Vote to Close as Too Broad. There are either too many possible answers, or **good answers would be too long for this format**. Please revise your question to narrow the answer set or to isolate an issue that can be answered in a few paragraphs. – [AMR](#) Jan 15 at 9:07

2 I'm voting to close this question as off-topic because it's about alife simulation not biology. meta.biology.stackexchange.com/questions/32777/... – [rg255](#) Jan 15 at 9:17

@AMR Why do you think that good answers would be too long? In case of existence of such a model the answer would be surprisingly short. The reasons why the model is impossible can also be put in a short words. The formal proof is impossible because the formalisation is absent at the moment. – [Peter Zagubisalo](#) Jan 15 at 9:38

@PeterZagubisalo This sounds like an interesting project, but your question doesn't appear to be about biology. I've also voted to close. I think the biology would come into play when analysing the results of such a simulation. – [James](#) Jan 15 at 10:06

@James The questions are asked not for the goal of fitting the criteria. They are asked for the answers form the people that may have the answers. And people read the questions and answers to get information. And I assume that the people who are experienced in researching the mechanism of natural selection are of competence to answer the questions like mine. – [Peter Zagubisalo](#) Jan 15 at 10:19

1 It is also to be noted that alife simulations imitate a biological phenomena and not really the mechanism. Therefore IMO they cannot be called models of biological systems. Just the way ANN has got nothing to do with actual neural network. – [WYSIWYG](#) Jan 15 at 10:19

@WYSIWYG What do you mean by mechanism? – [Peter Zagubisalo](#) Jan 15 at 10:22

@PeterZagubisalo The actual underlying mechanism that leads to evolution. Alife is bio-inspired; it is not IMO a representation of the biological phenomenon. Like GA is genetics-inspired but it is an optimization algorithm and not really a model for genetic interactions. I could be wrong.. this is what I think.. – [WYSIWYG](#) Jan 15 at 11:07

@WYSIWYG From some point of view my task to create this specific model is an attempt to figure out whether postulates of natural selection are sufficient for evolution (given the simplest beginning structure possible) or not sufficient. – [Peter Zagubisalo](#) Jan 15 at 11:15

2 Evolution by Alife standards certainly doesn't match well to the biological definition. Alifers (is that the word for Alife people?) tend to define evolution as only a selection driven process of change, and that selection is for greater complexity. Biologists would tend to define evolution simply as a process of change, and that selection favours improvement but not necessarily complexity. – [rg255](#) Jan 15 at 11:17

@rg255 Yes. And the results of constructing the proposed model (fail or success) give some evidence on the topic you mentioned. As I think: there are good chances that in the lack of environment constraints the natural selection would lead to the unlimited complication because of the black queen hypothesis. – [Peter Zagubisalo](#) Jan 15 at 11:54

Your constraint 4 sounds very strange, if the purpose is to mimic natural selection. As I understand your Q, the complexity of the graph is a representation of the complexity of the "organism" (am I mistaken?). At the same time, you define 'reproduction' as the duplication of vertices, which to me sounds like an bipedal organism growing a third leg, if the graph is supposed to model the "complexity" of the "organism". How is the population size represented in the proposed model? – [fileunderwater](#) Jan 15 at 12:01

@PeterZagubisalo You might want to see this post about the conditions for evolution given from the perspective of an evolutionary biologist (me). – [rg255](#) Jan 15 at 12:09

@fileunderwater Presumably, there are many "layers" on which populations exist. The vertices themselves are the atomic individuals that are characterised by their edges. All the vertices are the basic population. But the goal of the model is to get the individuals at higher levels: as patterns in the graph (there may be even cycles of patterns changing to each other, like wave). The interesting individuals are patterns (subgraphs that persist in the changing graph during time). And there expected layers on layers. – [Peter Zagubisalo](#) Jan 15 at 12:25

To me, it is still unclear how individuals, individual traits and the population is represented in your model. It would probably be useful if you clearly defined how 'individual', 'individual properties' (which represent individual 'complexity') and 'population' are represented in the model directly in your question, e.g. vertex = xxx, graph = yyy, edge = zzz. – [fileunderwater](#) Jan 15 at 12:51

@fileunderwater Current assumption: vertexes=individuals, edges=individual traits and the graph=population. But this is only at the "basic level". Patterns are also individuals but on the "next level". – [Peter Zagubisalo](#) Jan 15 at 13:21

The edits don't improve the flaws in the question, and adding more material to an already long and convoluted question is not particularly useful - try to streamline the question to focus on the biological aspects. I'm not voting to reopen as it stands. – [rg255](#) Jan 15 at 20:56

@rg255 This is not for reopening. This is because I really forgot to clear this moment at all. The questions of fileunderwater are reasonable. – [Peter Zagubisalo](#) Jan 16 at 4:17
