

Complexity-invariant dynamics: a recipe for an open-ended increase in complexity in evolution

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A major goal of artificial life is to obtain a system whose evolution is open-ended in some way — something which, if permitted to run for longer and longer spans of time, will continue to deliver new things to an observer without requiring further human intervention. Various kinds of open-endedness have been achieved in simulations, but this raises the further complication of deciding what exactly one means when talking about the open-endedness observed in biological evolution and what the target should be (Banzhaf, 2015). Often, this involves some concept of an open-ended increasing complexity of the system (with varying definitions of complexity available).

In this talk, I'll describe previous work (Guttenberg and Goldenfeld, 2008; Guttenberg, 2009) developing a recipe for constructing systems with open-ended increase of complexity, using the idea of a critical point phase transition to drive the divergence. In second-order phase transitions, the system enters into a scaling regime near its critical point in which fluctuations become structured at all spatial and temporal scales. This leads to phenomena such as critical opalescence, where the usually microscopic hydrodynamic fluctuations in a liquid are able to grow in size to be big enough to see with the naked eye. The reason for this is that as one approaches the critical point, factors in the dynamics which are strongly bound to specific spatiotemporal scales become asymptotically suppressed relative to the dynamics associated with the phase transition, which (in a second order transition) have no intrinsic spatiotemporal scale.

However, the scale-free structure at a critical point can be fragile to certain factors which are connected directly to the phase transition in question. For example, even a tiny external magnetic field can 'poison' the criticality in an Ising model's critical point, creating a cutoff at finite scale. Therefore, to create a scaling regime one must suppress those things which could poison the criticality due to directly coupling to the phase transition in question.

In evolutionary terms, we take the analogy to having structure at all spatiotemporal scales to be having an ecology which spans all scales of complexity. The effects which can poison this scaling are all the things which interact di-

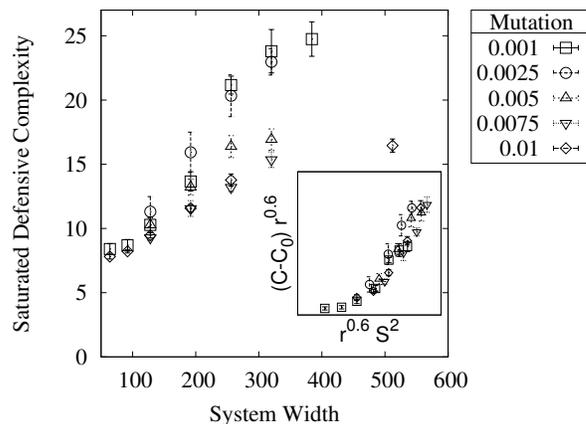


Figure 1: Scaling of complexity in the predator-prey model as a function of point mutation rate and system size. The inset shows that the two scalings can be collapsed onto a single curve in terms of a variable which measures the normalized distance from the critical point.

rectly with an organism's absolute complexity rather than its relative complexity compared with the rest of the ecosystem. Systems are never fully scale-invariant, but even at some distance away from criticality there is a partial scaling regime that can be detected which is then cut off by the scale-dependent terms. Critical point theory makes predictions for the approach to scale invariance, and so even if we cannot actually measure an infinity directly in artificial evolutionary systems due to limitations of system size and computer power, we can check to see whether the behavior is consistent with an asymptotic approach to infinite complexity in particular well-defined limits (Fig. 1).

So, in order to construct systems with open-ended complexity growth, we should try to remove any effects which explicitly depend on the absolute value of an organism's complexity. That is to say, factors such as finite mutation rate and optimal complexities for 'solutions' to fixed fitness landscapes specified by particular 'problems' naturally tend to disrupt the emergence of a scale-invariant regime. On

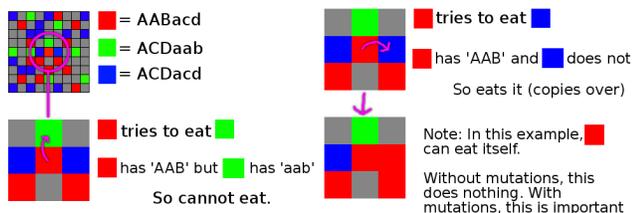


Figure 2: Schematic of the predator-prey model. Organisms live on a grid and compare their genomes to their neighbors to figure out who can eat who. As such, fitness is completely dependent on the local environment and has no explicit absolute character.

the other hand, if the interactions between organisms were a stronger contributor to organismal fitness than these absolute considerations, that should lend itself more towards finding scale-invariant regimes.

To do that, we focus on things with more of an ecological character — fitnesses which are defined only relatively between pairs or sets of organisms and which have no intrinsic factors at all and using horizontal gene transfer (which is genetically scale-invariant) instead of point mutation as the source of genetic variation. Furthermore, by analogy to critical point systems, we also expect to see a limit to the asymptotic complexity due to finite population size effects. In previous work, we have used these ideas to construct three distinct model systems which all appear to have open-ended complexity growth (at least, for system-appropriate proxies for complexity) — a predator-prey model with a divergent competitive arms race (Guttenberg and Goldenfeld, 2008), a forest growth model with competition for sunlight and the formation of increasingly complex 3D forms (Guttenberg, 2009), and a collaborative symbiotic model with open-ended increase in the diversity and complexity of the model's ecosystem (Guttenberg, 2009).

For example, in the predator-prey model (Fig. 2), organisms are genomes living on a grid where each base of the genome can function as an attack, a defense, or be inert. All of an aggressor's strings of contiguous attack bases are compared against the defender's defense strings, and if any attack string is not matched by a conjugate defense string, the aggressor eats the defender and replicates into their space. In this way, fitness is based on the appropriateness of an organism's defense strings to the ambient attack strings, and an organism having an attack that is not matched among the defenses. This naturally encourages exploration of longer attacks and defenses to try to find an un-protected vulnerability; however, as the strings get longer, a single point mutation at any location within a string can disrupt the entirety of its function (so in this case, we think of string length as a proxy for complexity). In this simulation, attack and defense string lengths asymptotically increase towards infinity, but

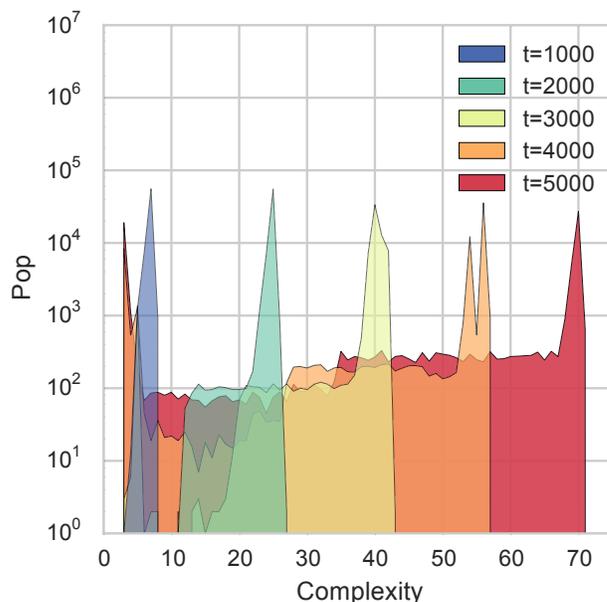


Figure 3: Distribution of complexities in the symbiosis model as a function of time. The population peak continually moves to higher complexity, supported by the ecosystem created in its wake.

the fluctuations become greater as the complexity increases (and therefore, the system size must be larger for those fluctuations to not result in a collapse of the ecosystem) (Fig. 1). In genetic space, these dynamics are sort of reminiscent of travelling wave solutions.

In the symbiotic model, the dynamics are similar, except that organisms must be primed by interaction with a nearby partner in order to replicate. An organism is primed by a partner if it entirely matches one of the partner's contiguous functional strings, but is exactly one functional character longer. The metaphor here is that each organism processes food and turns it into some chemically more inaccessible byproduct, requiring increasingly specialized machinery (e.g. longer specific strings) to get any more utility out of the byproduct. In this simulation, rather than getting meta-stable packets of co-evolving pairs, a range of organisms at each complexity must be supported in order for the most complex organisms to persist. So rather than getting a travelling peak in the sequence length distribution, we get a broad distribution (Fig. 3).

The forest model works somewhat differently, with trees existing in a shared 3D environment in which they grow, receive light, and cast shadows (Fig. 4). The 3D shapes of each tree are defined by a sequential building process, reading out the tree's genome one character at a time and attempting to express an associated building block wherever it would fit in the growing tree. Overlaps block growth (or, alternatively, introduce a fitness penalty), and so as the tree gets bigger the

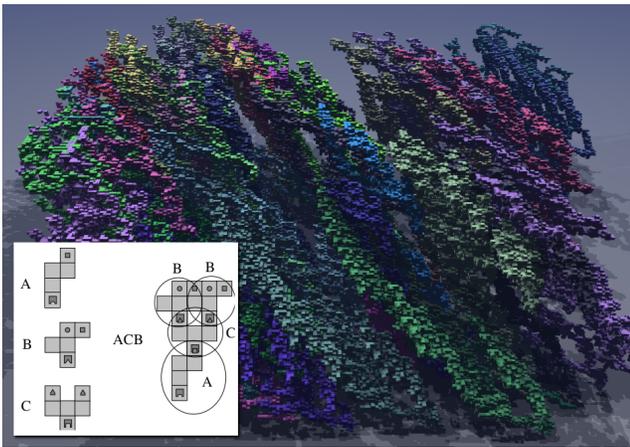


Figure 4: An example forest from the PlantNet model. The inset shows a schematic of how the shapes of trees are determined from the tree's genome.

problem of not colliding with itself during growth becomes more difficult. When trees have received a certain amount of light they replicate and replace a random other tree in the forest, and so while there is a competition for light, trees receive no direct fitness benefit from being tall.

In these models, we measure the asymptotic complexity with respect to system size, mutation rate, and other deviations from criticality. We show that the dependencies of the complexity on these multiple factors can be collapsed onto a single shared scaling curve in terms of scaled distance from the critical point (which is a usual signature of critical point phenomena in general). From this, we argue that these models likely have a true open-ended growth of complexity.

However, at the end of the day, this kind of open-endedness also proves to be different than the diversity of evolution on Earth. In our models, we require fairly restrictive conditions in order to achieve the open-ended regime — point mutation must be asymptotically driven to zero, the interactional aspect of the fitness must be infinitely more important than any absolute considerations, etc. Furthermore, no matter how long we wait, none of these models will change the rules of the game, develop a new mode of interaction, or undergo a major evolutionary transition. Those features appear to be distinguishable from simply increasing the complexity of forms, even if the complexity of forms is highly internally contingent and has other promising-looking properties. That is to say, by doing these simulations, we've identified that for us at least, what we really wanted to achieve was not complexity but rather an open-ended generation of novelty — of new ways that the system as a whole can be organized.

References

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