Complex ALife Simulations: From Generating Life-like Behaviors to Predicting Real-life Phenomena

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Abstract

Artificial Life relates to the study of life-like processes or methods for generating behaviors that may be interpreted as life-like. ALife Computer simulations constitute a significant scientific tool for promoting scientific understanding of biological phenomena and complex natural dynamic processes. Significant leaps in computational force and software engineering methodologies now allow the design and development of large-scale biological models, which– when combined with advanced graphics tools–produce realistic biological scenarios. In some cases, these scenarios may reveal new scientific explanations and knowledge about real life phenomena.

Three state-of-the-art simulation projects are examined in the context of the contemporary philosophical debate on the scientific value of simulations, as we demonstrate the ability of some of these simulations to generate new emergent behaviors, making possible the prediction or hypothesis about the equivalent modeled real-life phenomena. Various considerations in the construction process of the simulation and its user-interface allow the formation of new features and unexpected behaviors, which may serve as speculations in the scientific sense and as a basis for further laboratory research.

Extended Abstract

Computer models, whose dynamic application are termed "simulations", constitute a significant scientific tool for promoting scientific understanding of natural phenomena and dynamic processes in diverse disciplines, including biology. The emerging need of culling significant knowledge and insights from vast amounts of empirical data, generated in recent decades about biological molecules and the millions of interactions among them, has generated innovative sophisticated computational methods. Significant leaps in computational force and software engineering methodologies now allow the design and development of large-scale biological models, which– when combined with advanced graphics tools– may produce realistic biological scenarios, that reveal new scientific explanations and knowledge about real life phenomena.

The living biological structures (which are commonly divided into hierarchical levels of organization, from the chemical-genetic level, through the molecular level to the cells, tissues, organs, organisms and on to populations and ecosystems), clearly represent the idea of *Emergence*. Each level represents a whole, whose functional, structural and behavioral properties are derived from properties and interactions that take place at lower levels of the organization, but cannot be simply explained by them. According to the holistic systematic approach, which underlies modern biological research, only an integrated view of complex entities allows their true understanding, as well as the detection of emergent novel features and behaviors, which cannot be predicted or viewed at lower hierarchical levels. The fact that biological systems are extremely dynamic, whereas data derived from laboratory experiments are mostly static, requires the use of simulations, to merge the data into an integrated whole, in a parallel, multi-layered, dynamic (and often interactive) manner, in order to allow scientists to yield valuable knowledge.

In recent years there has been an awakening among philosophers of science, seeking to clarify the role played by simulations and their epistemological standing within the space defined by theories, models and scientific experiments, as well as the ability of simulations to scientifically explain real-world phenomena (e.g. (Callebaut 2012), (Eckhart 2010), (Lenhard 2007), (Morrison 2009), (Pennock 2007), (Winsberg 2010)). Following this contemporary philosophical debate, the model construction process is carefully examined for three state-of-the-art test cases, in order to determine its ability to generate novel emergent behaviors that make it possible to predict or make solid hypothesis about equivalent real-life phenomena.

The selected test cases are computer simulations of unprecedented scale of complex biological systems, developed by three leading research groups and involved the development of sophisticated computer models and tools.

Reactive Animation (RA). A group of researchers in Weizmann Institute (Israel) developed a computational approach termed Reactive Animation for simulating the developmental and behavioral processes of an organism (and organs within) (Vainas, Harel et al. 2011). The dynamic characteristics of the biological objects are described based on cellular and molecular data collected from real lab experiments. These data are integrated bottom-up by computational tools and methods to create a comprehensive, dynamic, interactive simulation (with front-end animated visualization) of biological systems behavior and development, in which the "simulationist" may intervene on-line and observe in-silico, on the artificial life-like system, the effects of what may be considered as thought experiments.

In particular, the RA system was reported to have revealed several unexpected emergent properties that were not overtly preprogrammed in the molecular and cellular data included

during the construction of the simulation (e.g. competition between thymocytes for sites of stimulation in the thymus). These behaviors may be considered as "weakly emergent" phenomena, meaning that they are incompressible and "cannot be derived except by crawling through all of the gory details of the interactions in the causal web" (Bedau 2013). The discoveries consequently alerted biologists and prompted real lab experimentations of phenomena previously unknown. This renewed investigation of the real world is a process which, according to the researchers, highlights the explanatory power and the potential aid to experimentation offered by an animated interactive ALife simulation of complex sets of data (Efroni, Harel et al. 2005). According to the developers, these models enable in-silico experiments at run-time and produce results that are similar to in-vivo experiments and suggest new intriguing hypotheses (Setty, Cohen et al. 2010).

Digital Organisms of Avida. A research group in DevoLab, Michigan, developed the Avida platform, on which populations of digital organisms evolve under various evolutionary conditions, which leads to the emergent formation of complex traits (Lenski, Ofria et al. 2003), (Ofria, Huang et al. 2008). Through a large series of different experimental environment simulations, performs on these digital organisms (which are self-replicating and evolving computer programs), the researchers demonstrated the ability of the simulated population to dynamically and spontaneously develop novel behaviors and capabilities, not programmed for, which may, again, be considered as weakly emergent.

A major goal of these simulations is to test specific hypotheses related to the theory of evolution and population genetics. However, we claim that due to specific issues related to the modeling process and to the extent of idealization, these simulations should be classified as "how possibly" simulations (Craver 2006), models that are not necessarily based on actual real-world knowledge. Despite the life-like behaviors they produce, they are not sufficiently qualified to scientifically explain or predict real-life phenomena.

Blood clotting nanobots. A UK-based research group developed a series of simulations of coagulation processes, as a basis for physical-medical implementation using nano-robots (Polack, Andrews et al. 2010). A major goal of the group was to develop nature-inspired methodologies to engineer complex emergent phenomena with assurance of functionality and safety. Despite the agent-based simulation' impressive results, producing life-like blood clots, we claim that these are merely phenomena-generating simulations, that cannot be used to predict or enable biologists to gain insight about the actual modeled biological system.

Summary. Based on the above-described test cases, a distinction is made between phenomena-generating models and phenomena-inducing models, and it is shown how the development and execution of a simulation can create actual scientific knowledge, that enables scientific explanation of the phenomenon being modeled.

Simulations, it is claimed, have a "life" of their own, characterized by complexity, creativity and dynamic interactive computational power, which exceeds the standard Turing computation. These features, along with various considerations in the construction process of the simulation and its user-interface, allow the formation of new features and unexpected behaviors, which may serve as speculations in the scientific sense and as a basis for further research. Specifically, the distinction, present in most relevant publications, between bottom-up models and those constructed from the top downwards is, we claim, fictitious. This insight, according to which these two directions merge into a single whole, underlies the ability of simulations to produce emergent phenomena, which involve complex causal relations, upstream and downstream alike. It is the verification and validation processes integrated into the simulations, the usefulness and contribution of the models in scientific discourse and the cumulative reliability of the applied techniques, which ultimately provide simulations their credibility and scientific significance.

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