SCBCS - Applied Coevolution

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May 14, 2016

1 An Introduction to Coevoluion

Coevolution, the reciprocal adaptation between interacting populations, is not just a simple generalization of single-population evolution [20]. Because adaptations in one population alter what is selectively favorable for the other, coevolution is typified by an inherent feedback between populations [11, 10]. This unique push and pull of coevolution is responsible for an expanded range of potential evolutionary outcomes compared to single-population evolution [21]. Indeed, coevolutionary hypotheses are strong contenders for many of the biggest open questions in evolutionary biology [8].

2 Microbial Coevolution

Coevolutionary hypotheses are starting to be tested in the lab with microbial communities [3]. Microbes have the major advantage of fast generation times, which allow evolutionary changes to occur on observable timescales [12]. In addition to their speed, laboratory environments can be manipulated with a level of control impossible to replicate in the field. Together, these properties make it possible to directly test the causal relationship between coevolution and broader biological patterns [3].

In addition to the level of environmental control afforded by laboratory populations, synthetic biologists are now able to rationally engineer microbes that perform novel functions [14]. Thus, synthetic biology enables experimental coevolutionary biologists to *design* the biotic interactions between populations of microbes [2, 17].

3 Computational Coevolution

Even more controllable are computational systems that allow open ended evolution [16]. Both Tierra and Avida, artificial-life platforms where individual computer programs must self-replicate and compete for resources, have been used to study fundamental questions in coevolutionary biology [13, 22]. In fact, the first time Tom Ray ran Tierra he noticed that his populations of programs began to fall victim to "parasites" that stole costly replication code from their "hosts"; however, they didn't last long as resistant organisms evolved and eventually took over [19]. At the same time that Tom Ray was exploring biological coevolution using computers, others like Daniel Hillis of Thinking Machines were using coevolution as inspiration for new types of genetic algorithms that solve computational problems better and faster [9, 18].

Hillis implemented a traditional GA to find minimal sorting networks with 16 inputs for a description of sorting networks). Sorting networks are still a topic of active research in theoretical computer science, where the optimality of sorting networks has been proven for up to 10 inputs as of 2014 [4]. In 1962, Bose and Nelson introduced the 16 input sorting network and a 65-step solution that they posited was the optimal solution[1]. Hillis's traditional GA performed well, finding a solution to the 16-input network also requiring only 65 steps. However, when Hillis examined each run carefully, he found that the GA was plagued by a classic problem – populations becoming trapped on local optima that would require a reduction in fitness to escape [9, 7]. In part, these local optima were occurring because many of the test cases used to evaluate fitness were satisfied after just a few generations. Unfortunately, which test cases were satisfied depended on what solutions were evolved, so eliminating the "easy" test cases was not an option. Hillis tried several ways of improving his GA including varying test cases over time as well as varying them over space in a 2D grid. However, it was when he allowed the test cases to *evolve* against the evolving solutions (*i.e.,* to coevolve) that solutions with as few as 61 steps were found [9].

The success of Hillis's experiments inspired others to implement coevolutionary inspired processes in genetic algorithms. One of the more striking examples of coevolution being harnessed was in Floreano and Nolfi's predator-prey robots that chased each other around a mini battlefield [15]. The researchers outfitted a predator robot with a simple visual system that was able to see prey robots within a 36° field of vision up to 100 cm away. The prey were only able to detect predators within 1.5 cm, but could outrun them with a top speed twice that of the predators [5]. Because of the placement of sensors, the prey had a *blind spot* which the predators evolved to exploit. Eventually the prey evolved coping strategies such as staying near the battlefield walls or spinning to avoid leaving the blind spot exposed for too long. Several other strategies evolved, but the researchers noticed that these behaviors cycled, thus exhibiting Red Queen dynamics [6]. In an attempt to encourage arms races rather than cycling, Nolfi and Floreano implemented a *hall of fame*, where previously high-performing predator or prey robots were saved and used as part of the fitness evaluations in the future [15].

4 A Proposed Synthesis

The ability to control exactly how selection works in these artificial populations is a feature evolutionary biologists certainly wish their biological populations possessed. On the other hand, this control means computer scientists are exploring ways of harnessing coevolution in ways biologists could never have imagined. Is there a role for cross-talk between coevolutionary biology and coevolutionary computation? I would argue the answer is a resounding yes, especially as synthetic biology continues to open up radically new ways of testing coevolutionary hypotheses and even controlling coevolution.

At the same time, computational studies of coevolution are sometimes asking questions that biologists may already understand deeply, or entirely missing the large open questions interesting to biologists. With this proposed paper, we would expand our review on the relevant work from both empirical and computational studies of coevolution. We would similarly expand our synthesis and include specific examples of how biological coevolution could learn from computational systems and vice versa. One example of such crosstalk is a microbial implementation of Nolfi and Floreano's *hall of fame.*

References

[1] R C Bose and R J Nelson. "A Sorting Problem". In: *Journal of the ACM (JACM)* 9 (Apr. 1962), pp. 282–296.

[2] Katie Brenner, Lingchong You, and Frances H Arnold. "Engineering microbial consortia: a new frontier in synthetic biology". In: *Trends in biotechnology* 26 (Sept. 2008), pp. 483–489.

[3] Michael A Brockhurst and Britt Koskella. "Experimental coevolution of species interactions". In: *Trends in ecology & evolution* 28 (June 2013), pp. 367–375.

[4] Daniel Bundala and Jakub Závodný. "Optimal Sorting Networks". In: *Language and Automata Theory and Applications.* Cham: Springer International Publishing, Jan. 2014, pp. 236–247.

[5] Dario Floreano and Laurent Keller. "Evolution of Adaptive Behaviour in Robots by Means of Darwinian Selection". In: *PLoS Biology* 8 (Jan. 2010), e1000292.

[6] Dario Floreano and Stefano Nolfi. "God save the red queen! Competition in co-evolutionary robotics". In: *Genetic Programming 1997: Proceedings of the Second Annual Conference.* Morgan Kaufmann, 1997, pp. 398–406.

[7] James A Foster. "Evolutionary computation". In: *Nature Reviews Genetics* 2 (June 2001), pp. 428–436.

[8] D J Futuyma and Andre Levy. *Coevolution.* 1983.

[9] W Daniel Hillis. “Co-evolving parasites improve simulated evolution as an optimization procedure”. In: *Physica D: Nonlinear Phenomena* 42 (June 1990), pp. 228–234.

[10] D H Janzen. “When is it coevolution”. In: *Evolution* (1980).

[11] Stuart A Kauffman and Sonke Johnsen. “Coevolution to the edge of chaos: Coupled fitness landscapes, poised states, and coevolutionary avalanches”. In: *Journal of Theoretical Biology* 149 (Apr. 1991), pp. 467–505.

[12] Tadeusz J Kawecki et al. “Experimental evolution”. In: *Trends in ecology & evolution* 27 (Oct. 2012), pp. 547–560.

[13] A R Kraaijeveld. “Cost of resistance to parasites in digital organisms”. In: *Journal of Evolutionary Biology* 20 (May 2007), pp. 845–853.

[14] Ryan McDaniel and Ron Weiss. “Advances in synthetic biology: on the path from prototypes to applications”. In: *Current Opinion in Biotechnology* 16.4 (Aug. 2005), pp. 476–483.

[15] Stefano Nolfi and Dario Floreano. “How co-evolution can enhance the adaptive power of artificial evolution: Implications for evolutionary robotics”. In: *Evolutionary Robotics*. Berlin, Heidelberg: Springer Berlin Heidelberg, Jan. 1998, pp. 22–38.

[16] Bill O’Neill. “Digital Evolution”. In: *PLoS Biology* 1 (Oct. 2003), e18.

[17] Csaba Pal, Balázs Papp, and György Pósfai. “The dawn of evolutionary genome engineering”. In: *Nature Reviews Genetics* 15 (July 2014), pp. 504–512.

[18] J Paredis. “Coevolutionary computation”. In: *Artificial Life* (1995).

[19] Thomas S Ray. “An Evolutionary Approach to Synthetic Biology: Zen and the Art of Creating Life”. In: *Artificial Life* 1 (Apr. 2010), pp. 179–209.

[20] John N Thompson. “Concepts of coevolution”. In: *Trends in ecology & evolution* 4 (June 1989), pp. 179–183.

[21] John N Thompson. *The Coevolutionary Process*. Chicago: University of Chicago Press, 1994.

[22] Luis Zaman, Suhas Devangam, and Charles Ofria. *Rapid host-parasite coevolution drives the production and maintenance of diversity in digital organisms*. New York, New York, USA: ACM, July 2011.