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A biological perspective on evolutionary computation

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Abstract

Evolutionary computation is inspired by the mechanisms of biological evolution. With algorithmic improvements and increasing computing resources, evolutionary computation has discovered creative and innovative solutions to challenging practical problems. This paper evaluates how today's evolutionary computation compares to biological evolution and how it may fall short. A small number of well-accepted characteristics of biological evolution are considered: openendedness, major transitions in organizational structure, neutrality and genetic drift, multi-objectivity, complex genotype-to-phenotype mappings and co-evolution. Evolutionary computation exhibits many of these to some extent but more can be achieved by scaling up with available computing and by emulating biology more carefully. In particular, evolutionary computation diverges from biological evolution in three key respects: it is based on small populations and strong selection; it typically uses direct genotype-to-phenotype mappings; and it does not achieve major organizational transitions. These shortcomings suggest a roadmap for future evolutionary computation research, and point to gaps in our understanding of how biology discovers major transitions. Advances in these areas can lead to evolutionary computation that approaches the complexity and flexibility of biology, and can serve as an executable model of biological processes.

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Ethics declarations

Competing interests

The authors declare no competing interests.

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