

Is non-parametric Bayesian MCMC a good model of evolutionary computation?

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Nature gives us two remarkable adaptive algorithms in asexual and sexual evolution. These algorithms produce radically different types of organisms. Simple considerations about fossil ancestry show that sexual evolution can be impressively fast.

What is the source of these two algorithms' computational effectiveness, and how should these two natural algorithms be computationally modelled? Many people have approached these questions – yet it is curious that there is so little communication between the machine learning and evolutionary computation communities, and it is also curious that evolution has been so little considered using the tools of machine learning.

Starting from first principles, I will propose models of both sexual and asexual evolution that are, at the same time, plausible computational abstractions of natural evolution, and also non-parametric Bayesian MCMC algorithms. They are genetic algorithms that satisfy detailed balance, and for which the stationary distribution over populations (also known as mutation-selection equilibrium) can be written in closed form for a general class of fitness functions.

Basic properties of the two models will be considered. The asexual and sexual models have structurally different 'prior' distributions, with radically different properties. There are also natural scaling relationships among parameters.

The relationship between individual learning and evolution can be modelled by placing both individual and evolutionary learning within one probability model in this framework.

Lastly, the "Bayesian" interpretation of evolution applies only when individual fitnesses do not depend on other individuals in the population. A natural question is whether group-dependent fitness, or coevolution, are essentially more powerful processes.