

Evolution and Problem Decomposition

summary of ongoing dissertation research for GECCO'99 student workshop

Richard A. Watson

Dynamical and Evolutionary Machine Organization
Volen Center for Complex Systems, Brandeis University, Waltham, MA, USA.
richardw@cs.brandeis.edu
<http://www.cs.brandeis.edu/~richardw>

Motives - Natural Evolution and Artificial Evolution

Whereas natural evolution is prolific and diverse, artificial evolutionary algorithms (EAs) model a convergent process—the adaptation of a species within a fixed environment. The broader, long-term view of natural evolution includes diversification, co-adaptation, and mutually beneficial relationships as well as local competitive pressures. Enlightened evolutionary theory recognizes symbiosis as an integral process in evolution. *Symbiogenesis*, the genesis of new species via the genetic integration of symbionts, is responsible for some of the major transitions in evolutionary history [6], [7]. This genetic integration of distinct pre-adapted organisms is a fundamentally different source of innovation from the Darwinian accumulation of small random variations and neo-Darwinian sexual recombination modeled in EAs. What algorithmic advantage does such a mechanism offer and how might it be incorporated in artificial evolution?

My working hypothesis attributes the utility of symbiogenesis to its ability to decompose a problem and perform localized optimization (adaptation of distinct species), and to the subsequent construction of composite solutions from these building-blocks (integration of mutually beneficial symbionts). But, is this not exactly what recombination in the canonical GA is supposed to do, as per the building-block hypothesis (BBH)? [4], [5]

Problem Decomposition and the Regular GA

The tangle of controversy surrounding the BBH and the utility of recombination in the regular GA, e.g. [2], became clear for me by recognizing the difference between *decomposable* and *separable*. Separable problems such as the Royal Roads [8] and concatenated trap functions, e.g. [3], consist of sub-problems that can be solved optimally without regard for how other sub-problems are solved—searching combinations of sub-solutions is not required and simple algorithms can out-perform the GA. In contrast, a decomposable problem has identifiable sub-problems, but they need not be separable: which one of several locally optimal solutions to a sub-problem is globally optimal may be strongly and non-linearly dependent on how other sub-problems are solved. The notion of ‘quasi-separable’ problems approaches this idea but has previously not been defined clearly. My work illustrating these concepts, and defining a new test problem

for GAs that has a principled recursive building-block structure, shows that even strong interdependencies do not preclude identifiable sub-problems [10], [11].

Using this problem we have verified that, when interdependent bits are adjacent on the genome (i.e. *linkage is tight* [3]) and diversity in the population can be maintained, the regular GA is able to search combinations of progressively higher-order schemata, as the BBH suggests, and out-perform the simpler algorithms. But, when linkage is poor the regular GA cannot combine schemata effectively [10].

Alternate Recombination Methods

Recombination in the Messy GA (MGA) [3], designed to operate on problems of poor linkage, is very different from recombination in standard crossover. By removing the moving-locus aspects of the algorithm my work shows that the advantage of the MGA is fundamentally due to the use of partially-specified genomes [12]. These enable individuals to specify for a fit schema without having to specify all the remaining genes. Thus recombination can combine good schemata from two individuals without ‘garbage’ genes causing conflicts with desirable genes. This works best when the two parents have no genes in common, which, interestingly, is a condition more similar to the combination of symbionts from different species than the sexual recombination of individuals from the same gene-pool.

Approaching Models of Symbiogenesis

We are still missing important parts of the natural symbiogenesis process. Specifically, there is no co-adaptation of the individuals concerned and we cannot properly call them symbionts when their interaction is purely competitive prior to being joined (as is the case in the MGA work). The formation of mutually beneficial relationships, that gradually increase dependence between symbionts, may provide a continuum between exploration and exploitation in building-block assembly. To begin investigation of this approach a simple model of symbiosis demonstrates a process of *scaffolding*—where organisms *fill-in* for one another’s unspecified genes during evaluation [13]. And, compounding associations with existing work, this begins to look very much like using co-adapted members of the evolving population as the

competitive template [3] of the MGA, and it has the advantage of resurrecting the *implicit parallelism* [5] of the regular GA.

Ongoing research extends this formal work into robust algorithms for decomposable problems and pursues further understanding of how the broad view of natural evolution and mechanisms like symbiogenesis can provide algorithmic advantage for artificial evolution.

details and related work can be found at:

http://www.cs.brandeis.edu/~richardw/#gecco99_wkshp

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