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Theory of evolutionary algorithms: a bird's eye view

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EAs are adaptive systems having a ‘basic instinct’ to increase the average and maximum fitness of a population, thus optimizing, but are not optimizers in the strict sense. From this perspective, population dynamics is a typical issue for theoretical investigations. For instance, the development of the populations gene distribution over time is an important issue. In GAs, where typically bit-strings of fixed length are evolved, it frequently occurs that the population converges<sup>1</sup> to a relatively good bit-string before having approached the actual solution sufficiently. Analysis of such premature convergence is essential in the genetic algorithm field.

Additionally to the question whether, and if yes, how fast and by what kind of population dynamics a solution can be reached, there are important issues regarding the means to desired goals. An answer to this question in ES is self-adaptation, meaning that the algorithm adjusts itself (its own technical parameters, called strategy parameters) to the problem while running on the same problem. Practice indicates that self-adaptation is indeed a powerful tool, but only little theoretical work has been devoted to analyzing this phenomenon. In GAs the emphasis traditionally lies on the search operators: mutation and recombination (crossover). The notion of schemata, later generalized to formae, and the effects of search operators in preserving, respectively destroying schemata is one of the key issues in GA theory.

There are of course further theoretical questions (especially in future) but it is certainly feasible to say that the limit behavior, running time, and dynamical behavior of evolutionary algorithms are the key topics of evolutionary computation theory in its current stage.

### 3. Tools and methods

The above overview of theoretical questions showed a variety of issues. Accordingly, the technical/theoretical tools that are used, or can be used, for answering the arising questions are also diverse. Without claiming to be complete, the following methods are relevant.

#### 3.1. Schema theory

The so-called schema theory represents an early attempt to explain the behavior of a specific evolutionary algorithm named the simple genetic algorithm [25]. First published in 1975, this theory was considered fundamental to the understanding of GAs until the early 1990s. The reasons for this change of opinion were as follows: First, schema theory cannot explain the dynamical or limit behavior of EAs. Second, it is implicitly assumed that the problem is separable to some extent. The ignorance of this assumption has led to the “building block hypothesis” which allegedly explains the

<sup>1</sup> The term ‘convergence’ in GAs mostly denotes the phenomenon that the population approaches a state where it consists of multiple copies of the same bit-string. This differs from the traditional use of the word, standing for the approximation of a solution.

working mechanism of GAs. Alternative explanations do exist [14]. Third, the advent of Markov chain theory in the field of evolutionary computation.

### 3.2. *Markov chains theory*

Since the population of an EA only depends on the state of the previous population in a probabilistic manner, it is clear that Markov chains are appropriate to model and analyze evolutionary algorithms. First theoretical results, basing on qualitative models, concerning the limit behavior of EAs were available in 1991 [19]. About the same time there appeared the first papers presenting the exact transition matrices of the Markov chains associated with certain evolutionary algorithms [17, 31]. Although the entire information about the evolutionary process is contained in these transition matrices, the degree of aggregation is too high to allow a simple derivation of detailed answers to particular questions (like the expected time of visiting the optimum for the first time). As a consequence, only simple versions of evolutionary algorithms have been successfully examined in this manner by now (see [35] for a summary of the results).

### 3.3. *Dimensional analysis*

The observation that the exact Markov model is isomorphic to the associated EA but offers only little chances to extract important aspects has led to the idea of approaching EAs via dimensional analysis [24, 38]. This methodology is borrowed from engineering sciences [26]. Dimensional analysis tries to identify the important dimensions or key features of a complex system and establishes a functional relationship between them. When applied to evolutionary algorithms, isolated measures for iterated selection, crossover, and mutation operators (like takeover time, mixing time and others) are put into some functional relationship which choice is validated (or not) by simulations. Needless to say, these functional relationships are a result of “good guessing”. But these descriptive models may give some clues for a more detailed theoretical study – an avenue that has apparently not been entered yet.

### 3.4. *Order statistics*

The theory of order statistics [2, 16] has proved useful in determining the convergence rates of ESs for convex fitness functions [11–13, 34, 36]. Moreover, if the population size is infinitely large there is a close theoretical relationship to the theory of quantitative genetics.

### 3.5. *Quantitative genetics*

At a first glance, it seems obvious that an analysis of biologically inspired dynamical systems should exploit the results developed in theoretical biology. The problem, however, is that the theoretical questions raised in evolutionary computation usually differ from those raised in theoretical genetics. An exception was detected by Mühlenbein and Schlierkamp-Voosen [30], who presented a specific evolutionary algorithm that can be

analyzed via a theory originally developed for quantitative genetics [15, 20]. Although this approach is limited to additively separable fitness functions and infinitely large populations, it contributes a piece to the mosaic of evolutionary computation theory that is under constant development.

### 3.6. *Orthogonal functions analysis*

Orthogonal functions like Fourier, Walsh, and Haar functions [9] have been used as a tool for constructing fitness functions that are either hard or easy for a specific evolutionary algorithm [10]. Occasionally, Walsh transforms played an important role in the analysis of evolutionary algorithms that were modeled by quadratical dynamical systems.

### 3.7. *Quadratical dynamical systems*

The quadratical dynamical systems (QDS) model has been classically used to model various natural phenomena in physics and biology [3]. As shown in [39] and subsequent papers, the simple genetic algorithm can be cast into a QDS, provided the population size is infinitely large. Since the simulation of a QDS is PSPACE-complete [3], this approach does not lead to an efficient method of analysis. As a consequence, most work in this field is devoted to the determination of the systems' eigenvalues and their stability. Moreover, it can be shown [3] that, in general, the predictions of the QDS approach are only sufficiently accurate for extremely large populations.

### 3.8. *Statistical physics*

Physicists have developed various tools to cope with stochastic systems they encounter in statistical physics. Not surprisingly, there is some work of casting biological and EA models into their theoretical framework (see e.g. [1, 32]).

## 4. **Concluding remarks**

This paper has provided a road map to evolutionary computation theory. Rather than producing an immense list of references, we have outlined the most important questions, research topics and technical tools used in various branches of EAs. Hereby we hope to facilitate the readers' orientation in a field that for a long time had the reputation of "childish games" among theoretical computer scientists. We are convinced that this survey and those works in the corresponding bibliography sufficiently demonstrate that evolutionary computation does have a theory with many important results and even more interesting challenges.

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