

Species Adaptation Genetic Algorithms:

Species Adaptation Genetic Algorithms: A Basis for a Continuing SAGA.*

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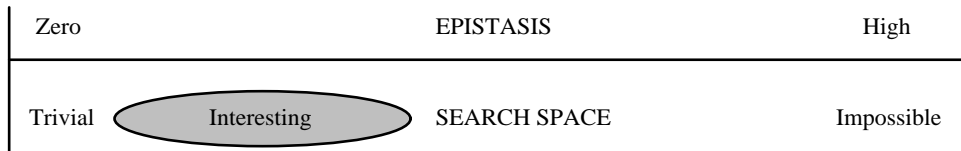


Figure 1: *Low, but non-zero, epistasis is associated with a search space that is possible, but non-trivial.*

ended if the environment itself alters over time, perhaps in response to the evolution of the animat itself. The classic case is the *Red Queen* (or *Arms Race*) phenomenon of coevolution of different species interacting with each other, where one can expect over time both the phenotype complexity and the genotype length to increase.

The notion of a search space is a metaphor which is usually a useful one. It does, however, imply a space of pre-defined extent, with a pre-defined or recognizable goal. In the natural world, tempting though it may be for any one species to think of evolution as a 4 billion year search for a goal of something very like them, it is evident that any such notion of a goal can only be *a posteriori*. So in order to distinguish the space of possibilities that a species can move in from that of a conventional search space, I shall use the term *SAGA space*². This corresponds to the acronym for Species Adaptation Genetic Algorithms, the altered and extended version of GAs necessary to deal with such a space.

2 Variable lengths in GAs

Variable length genotypes have been used in GAs in, for instance, Messy GAs (Goldberg *et al.* 1990), LS-1 classifiers (Smith 1980), Koza's genetic programming (Koza 1990). The first of these in fact uses an underlying fixed-length representation. The analyses offered in the other two examples do not satisfactorily extend the notion of a schema such that schemata are preserved by the genetic operators.

For instance, Koza's genetic programming (Koza 1990) uses populations of programs which are given in the form of LISP S-expressions, the word definition has rooted point-labeled trees with ordered branches. The primary genetic operator of crossover, or recombination, swaps complete sub-trees between the parents, and if these sub-trees are of different size then the offspring will have genotypes of different lengths from their parents.

Koza suggests that the equivalent of a schema in the search space of such programs can be specified initially by any one specific sub-tree. Since the set of all potential programs containing that sub-tree is infinite, Koza finds it necessary to partition it into finite subsets indexed

by the length of the program, and it is these subsets that are considered as schemata. The number of occurrences in the reproductive pool of examples of a particular schema which, as sampled in the parental pool, shows above-average fitness, will indeed tend to increase. But this does not cater for the fact that the crossover operator will in general turn the offspring into programs of different lengths, and hence disrupt the schema which has been defined by program length. A possible way to minimize this disruption would be to restrict the possible variations in length to only minimal changes, and indeed this will be echoed in the conclusions reached further on in this paper.

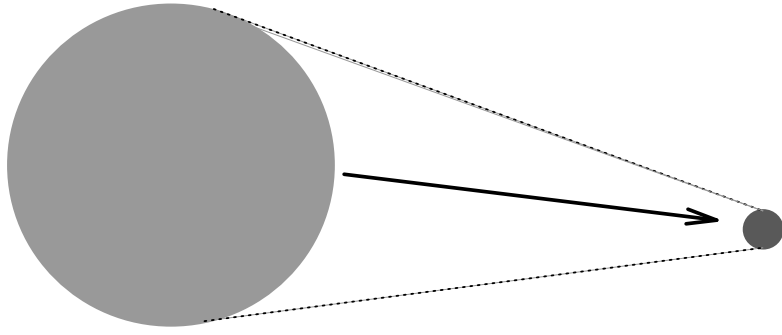
The obvious way to extend the crossover operator from fixed-length to variable-length genotypes is by randomly choosing different crossover positions for each of the two parents; an offspring may then inherit two short portions, or two long portions, and in general will have a genotype of significantly different length. It will be shown that this approach is flawed.

3 Epistasis

A gene is the unit of analysis in determining the phenotype, and hence its fitness, from the genotype; it is coded for by a small subsection of the genotype. The term epistasis refers to the linkage between genes on the genotype, such that the expression of one gene modifies or over-rules the expression of another gene.

If there is no epistasis, in other words if the fitness contribution of each element on the genotype is unaffected by the values of any of the others, then optimization can be carried out independently on each element;

²“Saga . . . story of heroic achievement or adventure; series of connected books giving the history of a family etc. [Old Norse = narrative].” Concise Oxford Dictionary.



is a large population of fixed size simultaneously sampling different mutants, and the population then moves as a whole to the fittest of any improved variant encountered. It is shown that the above result on waiting times remains almost unchanged.

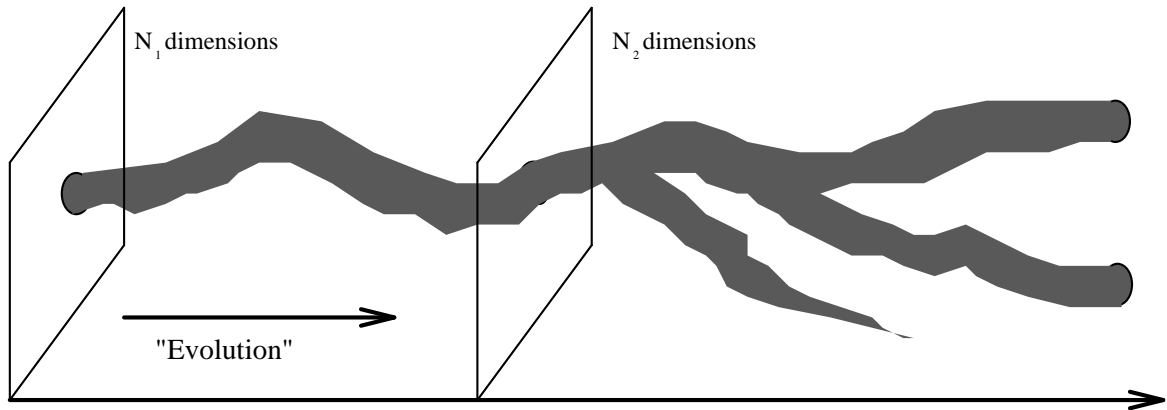
This search process is of course very different from that analysed in conventional GAs, where a population of points effectively spans the search space, and recombination allows effective moves to predominate. The distinction between these two types of search process must be kept in mind when we turn to looking at variable length genotypes.

6 Variable length genotypes

Let us spell out some assumptions about a genetic system with variation in the length of genotypes, within which many different types of representation, or mapping from genotype to phenotype to fitness, could be allowed.

- Firstly, it is assumed that the genotype can be analysed in terms of a number of small building blocks, or genes, that are coded for individually on it; possibly by a single symbol, or a sequence of symbols. These genes can be uniquely identified, either by their position by reference to an identified end of the genotype, as in conventional GAs; or by an attached tag or template, such as those used in messy GAs (Goldberg *et al.* 1990). Longer genotypes will code for genes that are not present at all on shorter ones.
- Secondly, it is assumed that each gene makes a separate additive contribution to the fitness of the whole; but that the contribution of any one gene can be modified by epistatic interactions with a number K of the other genes. This number K is less than the total number of genes available, otherwise the fitness landscape would be uncorrelated.
- Thirdly it is assumed that the total of all these additive contributions is then normalized in some way such that the final fitness remains within some pre-defined bound regardless of how many genes there are.

This last condition reflects the fact that any fitness function is only relevant in so far as it affects the selection process. On average in the long term each member of a viable population will be replaced by just one offspring. Less than one and the population is heading for extinction, more than one implies exponential growth. But there are always finite physical landscapes



Saga Space

no. of dimensions / time in aeons

Figure 3: *The progress of the always compact course of a species; the z axis indicates both time and the (loosely correlated) number of dimensions of the current search space. The x and y axes represent just two of the current number of dimensions.*

The possibility of splitting into separate species, and of extinction, are indicated in the sketch, although not here discussed.

- Thereupon the traditional GA operators of crossover and mutation will take over, and Holland's Schema Theorem will be applicable to this phase of the search.
- Those applications of the change-length operator which result in minimal changes of length will be moves on a correlated landscape, and therefore are feasible even if major changes are increasingly unlikely.
- If there are selectionary pressures which encourage the genotype lengths to increase, the population will become a nearly-converged 'species', with an almost uniform length that increase in small steps.⁴

7 SAGA and the Schema Theorem

A schema defines a subset of possible genotypes which share the same values at a specified number of genes. If there is no upper limit to the possible length of the genotype, these subsets will be infinite in size, and estimates of the 'average fitness' of a schema based on any finite sample become problematical.

We might be tempted to avoid this by saying, in this

0	1	1	0	1	1	0
---	---	---	---	---	---	---

i' i i''
 A: $i, i', i'' = 011$

0	1	1	0	1	1	0
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i'' i i'
 B: $i, i', i'' = 001$

Figure 4: *At the top, gene i ours0.Tf.09.Ti*

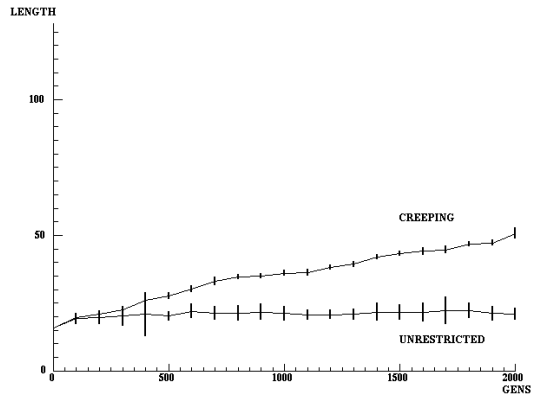
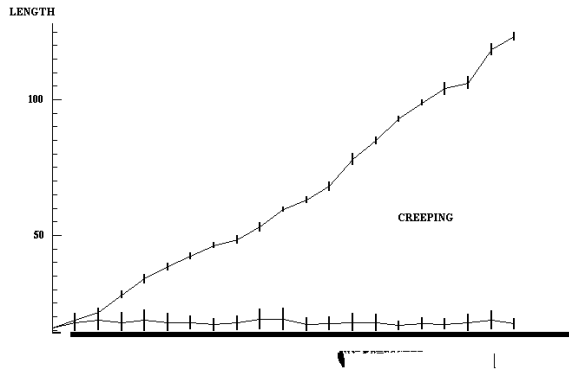


Figure 6:

model simulation above is the most trivial such operator, and depends on the identity of any gene being given by its position relative to one end of the genotype. Lindgren's (Lindgren 1991) doubling operator uses a representation which has this same dependency on position.

If the identity of a gene is given by a tag, or by template-matching as seems to happen in the real world of DNA, then absolute positions of genes on the genotype need not be maintained. This allows for duplication of a section of the genotype, after which mutations can differentiate the duplicated parts. The crossover operator can still be used in a fairly homogeneous population with slight variations in genotype length, although given any random crossover point in one parent, a 'sensible' corresponding crossover point in the other parent must be chosen. This can be uniquely defined as that point (or in some cases, any of a contiguous group of points) which maximises the longest common subsequences on both sides of the crossover. A version of the Needleman and Wunsch algorithm makes this computationally feasible (Needleman and Wunsch 1970, Sankoff 1972).

12 Conclusions

With fixed-length genotypes one can afford to think in terms of a fixed, pre-defined search space with a finite number of dimensions which, even if it is immense, is at least theoretically knowable by God or Laplace.

When one allows genotypes to vary in length the search space is potentially infinite and it stops making sense to think of it as predefined. Nevertheless, in the real world, evolution has taken place in such a fashion that we have very distant ancestors whose genotypes were much shorter than ours; the problems we face are not the problems the02(ary)]Tnsc.nbe.

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