Selective Crossover in Genetic Algorithms

Kanta Vekaria and Chris Clack
Department of Computer Science
University College London
Gower Street
London WC1E 6BT
United Kingdom
Email: {K.Vekaria, C.Clack}@cs.ucl.ac.uk

ABSTRACT

This paper proposes a recombination operator, "selective crossover" for use in genetic algorithms.

1. Selective Crossover

Genetic Algorithms (GAs) have a vast parameter-space and our knowledge of which parameter settings are appropriate for which classes of problem is rudimentary, being based primarily on anecdotal evidence (case-based reasoning). If GAs are to become more effective, we need to improve our understanding (and control) of this parameter-space. As a first step, we are investigating just one such parameter: the recombination (crossover) operator. We restrict our investigation to epistatic problems and are exploring the design of a recombination technique which never gives bad performance yet exhibits similar best performance to traditional crossover operators.

We start with the observation that, partly, the unpredictable performance of traditional crossover operators is due to the way that they interact with the epistatic linkage inherent in the encoding of the chromosome. We focus on the gene as the unit of natural selection and develop a recombination technique that evolves knowledge about the contribution of groups of (one or more) genes to the fitness of the individual - these groups need not be contiguous in the chromosome and this technique is therefore independent of the representation of epistatic linkage in the chromosome. We call this technique "selective crossover".

Selective crossover associates a real-valued vector with each chromosome, such that each gene has an associated "dominance" value (see Figure 1). We use the term "dominance" to draw an analogy with the way that genes exert their influence in nature. However, we retain the traditional GA haploid characteristics.

On initialisation, the dominance values are randomly generated, as is the population, but are restricted to be in the range [0,1]. During crossover, the dominance values of each gene for both parents are compared linearly and two children are produced. The first child receives all the dominant alleles (and their dominance values), whereas the second child receives all the recessive alleles (and their dominance values). The subsequent fitness of both children is compared with that of their parents: where an increase in fitness occurs, we increase the dominance values in the fitter child of those genes that have changed:

Parent 1 – fitness = 0.36

0.4	0.3	0.01	0.9	0.1	0.2	Dominance values
1	0	0	1	0	0	Alleles

Parent 2 – fitness = 0.30

0.01	0.2	0.4	0.2	0.9	0.3
0	1	1	1	1	0

Child 1 – fitness = 0.46

0.4	0.3	0.4	0.9	0.9	0.3
1	0	1	1	1	0

Child 2 – fitness = 0.20

0.01	0.2	0.01	0.2	0.1	0.2
0	1	0	1	0	0

Figure 1: Reproduction with Selective Crossover

Child 1 – fitness = 0.46

0.4	0.3	0.5	0.9	1.0	0.3	New dominance values
1	0	1	1	1	0	

Child 2 – fitness = 0.20

0.01	0.2	0.01	0.2	0.1	0.2
0	1	0	1	0	0

Figure 2: Updating Dominance Values

Unlike one-point or two-point crossover, selective crossover is not biased against schema with high defining length. Selective crossover propagates good schema regardless of their defining length – for example, interacting genes at the two extremes of the chromosome can be propagated as easily as those located adjacent to each other.

Results

We have some encouraging initial experimental results: selective crossover was applied to the L-Sat problem generator [DePoSp97] where epistasis can be varied. In this experiment, selective crossover performed exceptionally better than two-point and uniform crossover.

Bibliography

[DePoSp97]   De Jong, K. A., Potter, M. A. and Spears, W. M. (1997) Using Problem Generators to Explore the Effects of Epistasis. In T. Bäck (editor), *Proceedings of the Seventh International Conference on Genetic Algorithms,* 338-345. Morgan Kauffman