# Initial Results with Coevolving Dominance Mapping

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## Abstract

Chromosomes are diploid in nature. The advantage of having a diploid representation is that the inferior alleles are protected from the adverse conditions and they may become prominent when a favorable environment comes. Previous attempts to diploid representation largely used a pre-determined mapping scheme to resolve the allelic conflict in the same locus from different strands. This paper argues that an *à priori* and constant dominance mapping is not always desirable, but an evolving scheme is a more appropriate choice. This is especially true when the organism is left in a highly fluctuating environment. A coevolving algorithm is used which allows the dominance mapping and the solutions to evolve at the same time. A 17-object knapsack problem is used in the experiment. The coevolving scheme is found to adapt and produce better results in non-stationery environments.

## 1 INTRODUCTION

Chromosomes in typical evolutionary algorithms are in haploid representation because this is sufficient and efficient enough for most of the problems. However, the performance degrades rapidly once the environment starts to fluctuate and becomes non-stationery.

There were previous attempts in using diploid representation. In the knapsack problem experiment, Smith and Goldberg (1992) shown that the results from a diploid representation outperformed those using haploid representation in a non-stationery environment. They resolved the conflict of alleles in the corresponding locus from different strands with a mapping scheme determined in advance. However, there is a hidden intention behind each pre-determined dominance scheme, the designer of the algorithm has prior knowledge about the problem as well as the solution. This leads to the formulation of a dominance scheme biased for that purpose. Experiments have been conducted to highlight this fallacy. In the context of a diploid representation, in order to work out an effective (homologous) chromosome from multiple strands of chromosomes, we to find a right configuration of alleles as well as a suitable dominance mapping scheme.

A coevolving algorithm (Maher and Poon 1996) is used to model the interaction between the dominance mapping and the solution genes. This coevolving algorithm was applied to a 17-object knapsack problem. Two scenarios were tested: stationery and non-stationery environments.

In the stationery environments, two weight constraints $W$ were tried; they were 104 and 30 respectively. The evolving mapping was found to be slightly inferior to the haploid representation, but it performed better than the tri-allelic scheme (Smith and Goldberg, 1992). In the non-stationery environment, the weight changed between 104 and 30 in every 15 generations. Results were compared among four different dominance mapping schemes: 1-always-dominates-0, 0-always-dominates-1, tri-allelic scheme and evolving dominance scheme. The evolving dominance mapping was the champion in the non-stationery environment. It maintained a good performance in both constraints. In terms of the best fitness, the evolving dominance was comparable with the 1-always-dominates-0 and the tri-allelic scheme when $W$=104. It was always the winner when $W$=30. This indicates the evolving scheme is sensitive to the environment and adjusts itself quickly to any changes. This behavior makes the evolving dominance mapping scheme a very good candidate to be deployed in a non-stationery environment.

### References

Maher, M. L. and Poon, J. (1996). Modelling Design Exploration as Co-evolution. *Microcomputers in Civil Engineering* **11**(3): 195-209.

Smith, R. E. and Goldberg, D. E. (1992). Diploidy and Dominance in Artificial Genetic Search. *Complex Systems* **6**(3): 251-285.