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# Modified Linkage Learning Genetic Algorithm for Difficult Non-Stationary problems

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## Abstract

The linkage learning genetic algorithm (LLGA) proposed by Harik (Harik 1997), evolved tight linkage in a bid to solve difficult problems. This paper extends this work to difficult *non-stationary* problems. The probabilistic expression mechanism of the LLGA is akin to the dominance and ploidy found in nature. This redundancy of gene expression found in the LLGA was found to benefit the adaptation of the solution to dynamic fitness landscapes. However as the LLGA converges to tight linkage the available diversity decreases considerably. In this study it was found that by allowing disruption of tightly linked structures (with low probability) through the crossover operator and introducing explicit mutation and diploidy, much improvement could be gained in solving non-stationary deceptive problems without relearning the linkage evolved over the run.

## 1 NON-STATIONARY OPTIMIZATION USING MODIFIED LLGA

Our non-stationary problem consisted of  $k$ -bit trap functions and TMMPs (truncated massively multimodal problems) (Harik, 1997). To introduce non-stationarity an intermediate, periodically changing, XOR mask was used to change the expression of the genotype, in effect changing the fitness landscape for a given genotype.

The original LLGA performed satisfactorily on this problem when the fitness change was rapid, however it converged to tightly linked building blocks when the change was slow. The diversity in the LLGA introduced through the redundancy in the extended probabilistic mechanism (EPE-2) (Harik, 1997) was useless as an adaptive memory because as the LLGA progressed, building blocks clustered together making it increasingly difficult to express alternate solutions when fitness changed. This was primarily due to the non-disruptive

crossover operator (that chose crossover points from non-coding regions) used by Harik. Allowing the crossover points to be within a ‘coding region’ allowed the shielded BBs to be expressed (analogous to the dominance change in traditional diploid GAs), and the new optima to emerge. This was at the cost of linkage, since every time crossover broke the linked structure the LLGA had to relearn the linkage. To tackle this an explicit diploidy scheme was introduced wherein each chromosome had a repressed partner (diploid) that could be expressed with a low rate. This significantly improved the performance of the LLGA (Figure 1), showing the importance of diploidy in non-stationary optimization.

The performance over concatenated traps and TMMPs was not as good. This was attributed to the sequential nature of linkage learning in LLGA, which caused a time scale problem with the fitness change due to which only partial BBs could be discovered in one epoch.

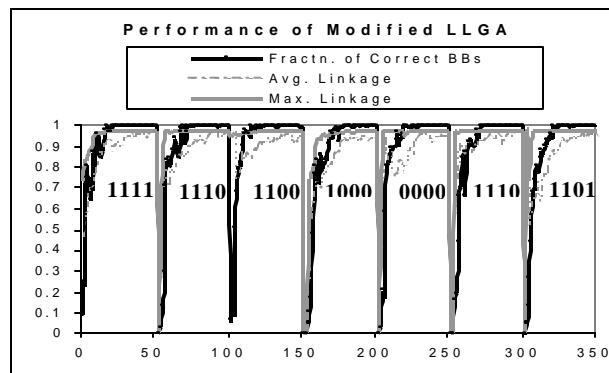


Fig 1. Performance of the modified LLGA (with changing optima in bold). The maximum linkage values are consistently high. In addition, the time for discovering the new optima decreases.

## Reference

Harik, G R. (1997). *Learning Gene Linkage to Efficiently Solve Problems of Bounded Difficulty Using Genetic Algorithms*. Doctoral dissertation, University of Illinois, Urbana-Champaign. IlliGAL Report Number 97005.