Investigation on Parameterless Schemes for DSMGA-II

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ABSTRACT

The only parameter that dependency structure matrix genetic algorithm II (DSMGA-II) requires is the population size, and the practicability of DSMGA-II would be further enhanced by removing the parameter. Existing parameterless schemes cannot be directly applied to DSMGA-II due to the confliction with the back mixing—one of the major operators of DSMGA-II. This paper focused on developing such parameterless schemes for DSMGA-II. Empirically these scheme yields promising results.

Keywords

Evolutionary Algorithms; Population Sizing; Number of Function Evaluations

1. INTRODUCTION

The recently proposed dependency structure matrix genetic algorithm (DSMGA-II) has shown its superior performance to other existing evolutionary algorithms [4]. Nevertheless, the performance comparison was based on optimum population sizes, which are empirically decided. To make DSMGA-II parameterless, one may think of combining parameterless scheme work of Lobo and Harik [3] or P3 [2] with DSMGA-II in similar ways that the former is combined with hBOA [5] and the later is combined with LT-GOMEA [1]. However, these two schemes separate the population into subpopulations or layer, and hence contradicts with the idea behind the back mixing operator, one of the key to DSMGA-II's performance. As a result, directly applying them to DSMGA-II impairs the performance. The purpose of this paper is to introduce a parameterless scheme for DSMGA-II. Similar to the idea of parameterless hBOA and P3, we start with an extremely small population, and dynamically increases the population as needed. Unlike Lobo and Harik's parameterless scheme and P3, we view the population as a whole to ensure back mixing can work as the way it does. As a result, parameterless DSMGA-II can be expected to perform similarly to the original DSMGA-II with optimal population size.

2. DSMGA-II

DSMGA-II randomly chooses a chromosome as a receiver of restricted mixing. If the restricted mixing succeeds, it use the receiver as the donor of back mixing. The pseudo-code is given in Algorithm 1, and details of each operator are described below.

Algorithm 1: DSMGA-II

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$\mathcal{P}$: population, $n$: population size, $\ell$: problem size, $R$: constant, $s$: selection pressure $\mathcal{D}$: dependency structure matrix, $L$: chosen mask from incremental linkage sat,
Randomly initialize population $\mathcal{P}$
$\mathcal{P} \leftarrow$ GreedyHillClimbing $(\mathcal{P})$
while $\neg$ShouldTerminate $(\mathcal{P})$ do
    $\mathcal{P}_S \leftarrow$ TouramentSelection $(\mathcal{P}, s)$
    $\mathcal{D} \leftarrow$ UpdateMatrix $(\mathcal{P}_S)$
    for $k = 1$ to $R$ do
        $\mathcal{I} \leftarrow$ random shuffle $|\mathcal{P}|$
        for $i = 1$ to $n$ do
            $(P_{I_i}, L) \leftarrow$ RestrictedMixing $(P_{I_i})$
            $\mathcal{P} \leftarrow$ BackMixing $(P_{I_i}, L)$
return best instance in $\mathcal{P}$
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2.1 Dependency Structure Matrix (DSM)

DSM use mutual information as the dependency measure, which is the same as that of DSMGA. For every bit in chromosome, it use series of order set to build masks set which is latter used by other operators. For example, a chromosome consists of five bits, and for bit at position 3, the order of dependency from the most relevant to the least is is $(5, 1, 4, 2)$, so the masks set is $\langle(3), (3, 5), (3, 5, 1), (3, 5, 1, 4), (3, 5, 1, 4, 2)\rangle$, and this linkage model is called incremental linkage set (ILS).

2.2 Restricted Mixing

For the receiver chromosome, randomly choose a bit to start building ILS. From the smallest mask to the largest mask in ILS, consider the pattern of this mask in receiver. If its complementary pattern exists in the current population, evaluate this receiver chromosome with flipping segmentation according to the mask. The change is preserved and the restricted mixing process terminate if the fitness of receiver does not decrease.

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2.3 Back Mixing

After the changing of receiver by restricted mixing succeeds, launch back mixing. It takes the receiver of restricted mixing as donor chromosome. The successful flipping pattern of restricted mixing mixes to all chromosome in the current population. The changing keeps on only if the fitness is improved.

3. PARAMETERLESS SCHEME

We need proper initial size to collect enough information to build model. Because we use the binary decoder, the initial problem size is set to four times of $log(problem\ size)$. There are two schemes proposed. The first is incrementally increasing population size. The second is double scheme.

3.1 Incrementally Increasing Scheme

First, implement original DSMGA-II on the current population, when we detect the population's lack of model information, we introduce a randomly generated chromosome after local search and expect it to be carrying fragments of the global optimum. We perform crossover, which is restricted mixing and back mixing in DSMGA-II, on the f chromosome. When doing restricted mixing, we build mask starting from every bit to make sure the new chromosome is as good as current population. After that, we build new models, so the new models will carry the new chromosome's information and do whole DSMGA-II to the entire population. Taking advantage of the property of restricted mixing, the new chromosome will have the information we already got from the previous generation.

3.2 Double Scheme

Other than incrementally increasing population size, we double the population size when needed, and when the current population need new information, it is determined by the number of successful restricted mixing operation on the current population. If all restricted mixings failed, add new population; if not, perform restricted mixing to the whole population again. After adding new chromosomes, we do not perform model building immediately after each new chromosome generated. Because after many generations of DSMGA-II, the old population is much better than new ones. So the model built by the old population is better. We refine the nearly convergent population with new information by using a correct model and new subsolutions segmentation contributing to the old population.

4. EXPERIMENTS AND RESULTS

We consider four classic linkage-underlying problems and two real-world problems. They are concatenated trap, cyclic trap, folded trap, NK-landscape function, the maximum satisfiability problem and the Ising spin-glass benchmark. The result of NK-landscape problems with different degree of overlapping is shown in Figure 1, and s is the step size.

When compared with P3, our schemes outperformed P3 with hBOA on the NK landscape problems with non-overlapping and various degrees of overlapping structures. On the folded trap, our schemes led by a factor of more than 10, which indicated that our schemes with DSMGA-II handled plateaus well. On the concatenated trap, our scheme did not outperform P3 in terms of function evaluations on smaller problems, but scaled better, and hence outperformed P3 on larger problems. On other problems, our schemes performed similarly to P3 except for the Ising spin glass problem. We believe that our schemes currently do not handle cross competition as nicely as P3, and that leaves an important task for us to accomplish in the near future. To conclude, both doubling and increasing-by-one scheme work well with DSMGA-II. They both respect the nature of back mixing in DSMGA-II, and hence preserve the most of its performance while in a parameterless manner. For an unknown problem, we would suggest the doubling scheme because it appeared more stable, while both should work well enough on most problems.

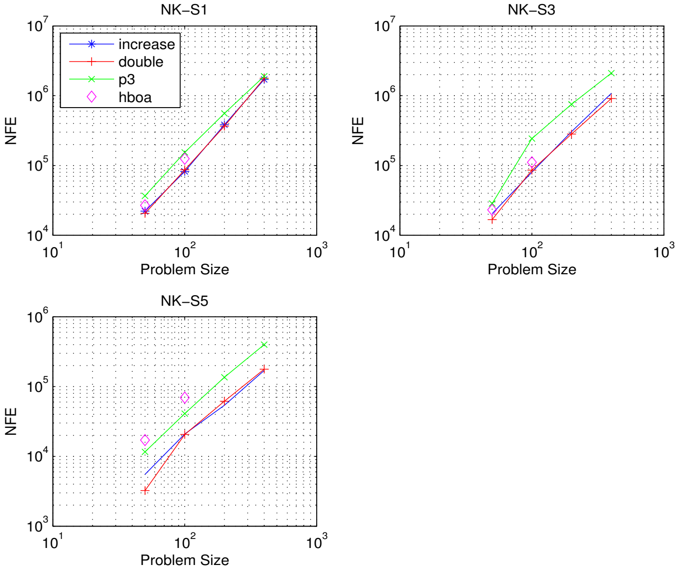

Figure 1: Scalability of incrementally-increasing, double-scheme DSMGA-II, P3 and hBOA on NK-landscape problems with various degree of overlapping

5. REFERENCES

[1] P. A. Bosman and D. Thierens. Linkage neighbors, optimal mixing and forced improvements in genetic algorithms. In *Proceedings of the 14th annual conference on Genetic and evolutionary computation*, pages 585–592. ACM, 2012.

[2] B. W. Goldman and W. F. Punch. Parameter-less population pyramid. In *Proceedings of the 2014 conference on Genetic and evolutionary computation*, pages 785–792. ACM, 2014.

[3] G. R. Harik and F. G. Lobo. A parameter-less genetic algorithm. In *GECCO*, volume 99, pages 258–267, 1999.

[4] S.-H. Hsu and T.-L. Yu. Optimization by pairwise linkage detection, incremental linkage set, and restricted/back mixing: Dsmga-ii. In *Proceedings of the 2015 on Genetic and Evolutionary Computation Conference*, pages 519–526. ACM, 2015.

[5] M. Pelikan and T.-K. Lin. Parameter-less hierarchical boa. In *Genetic and Evolutionary Computation–GECCO 2004*, pages 24–35. Springer, 2004.