

A multipopulation genetic algorithm aimed at multimodal optimization

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Abstract

This paper considers a new method that enables a genetic algorithm (GA) to identify and maintain multiple optima of a multimodal function, by creating subpopulations within the niches defined by the multiple optima, thus warranting a good 'diversity'. The algorithm is based on a splitting of the traditional GA into a sequence of two processes. Since the GA behavior is determined by the exploration/exploitation balance, during the first step (*Exploration*), the multipopulation GA coupled with a speciation method detects the potential niches by classifying 'similar' individuals in the same population. Once the niches are detected, the algorithm achieves an intensification (*Exploitation*), by allocating a separate portion of the search space to each population. These two steps are alternately performed at a given frequency. Empirical results obtained with F6 Schaffer's function are then presented to show the reliability of the algorithm. © 2002 Elsevier Science Ltd. All rights reserved.

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1. Introduction

Genetic algorithms (GAs) are stochastic optimization techniques that mimic the Darwinian evolution by modeling the natural selection process and genetic modifications [1]. They act on a population of individuals that evolve under the effect of three basic operators: selection, crossover and mutation. The parents with high 'fitness' survive and reproduce in order to create individuals again more adapted. In the case of standard unimodal GAs, the population quickly converges towards a promising zone of the search space.

However, this attractive feature is not of use for many problems. Indeed, in the case of multimodal functions, the algorithm risks converging on a sub-optimum: this feature is known as the premature convergence. It is mainly due to a loss of diversity in the population. In particular, this issue is worrying in the case of some practical optimization problems, in which one searches for a set of minima, instead of only one. This type of multimodal optimization especially occurs when the working out of the objective function requires the modeling of a difficult problem.

To overcome this problem, some diversity must be main-

tained during the generations in the population, by preventing its individuals of being 'clones' of the current best one. The speciation/niching techniques aim at maintaining an appropriate diversity to find several optima. However, even with a speciation method, possible promising regions found late will not be able to be exploited because of the high selection pressure generated by previously discovered peaks. To avoid this harmful behavior, it is desirable that the selection pressure in regions of the search space far from the previously discovered peaks does not depend on these peaks. This objective led us to consider a multi-population model, or island model, to improve the robustness of existing speciation methods. The use of island models to perform speciation has been studied by some authors with different motivations or techniques [2–4]. In this paper, we propose a new algorithm aimed at multimodal optimization. It handles an island model cooperating with a classification tree speciation [5]. In Section 2, we describe in detail the algorithm. Our experiments are presented in Section 3 and some results relating to F6 Schaffer's function are discussed in Section 4. Section 5 contains the conclusions.

2. A multipopulation genetic algorithm aimed at multimodal optimization

The algorithm that we propose identifies and maintains

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the best optima of an objective function, by generating subpopulations around these optima. In several recent ‘metaheuristics’, the search for the optima of an objective function is performed as suggested by Glover [6], by using two processes, namely ‘exploration’ and ‘exploitation’. Roughly speaking, exploration aims at locating promising zones within the search domain and exploitation allows a descent to the bottom of detected valleys. The proposed algorithm tries to find a compromise between both processes. It comprises two steps alternating at a given frequency. During the first one, namely diversification (Exploration), a multipopulation algorithm associated with a speciation module detects the potential niches, first by combining the genetic material available, then by gathering the individuals in different subpopulations, in function of their similarities. In the second step, the algorithm performs an intensification (Exploitation), during a given number of generations, by allocating to each subpopulation a portion of the search space, the size of which is determined by a speciation module. This two-steps process is reiterated until a stopping condition is reached. The switching frequency between the two steps constitutes a parameter of the algorithm.

2.1. Diversification

The exploration is performed through the coupling between a multipopulation GA and a speciation method. It aims at keeping diversity among the subpopulations, by gathering individuals representing a same region inside one subpopulation.

2.1.1. Multipopulation genetic algorithm

Generally, GA’s handle a single population, randomly generated within the search space of the problem at hand. However another model, called an ‘island model’, based on the use of several subpopulations, has been proposed [8,9]. To keep diversity in the course of the optimization process, a splitting of the population into separated subpopulations was performed. However, to favor the proliferation of good individuals through the set of subpopulations, an exchange of individuals between subpopulations is periodically performed. In addition, the exchange of individuals coming from different regions allows the algorithm to generate, through the crossover operator, individuals belonging to regions not already explored. That exchange, uses the migration operator.

A symbolic representation of the migration stage used by a multipopulation GA is shown in Fig. 1. The diversification allows an exploration of several areas of the search domain at the same time. For instance, we consider the Schwefel’s 2-variable function:

$$SH(x) = \sum_{i=1}^2 -x_i \sin(\sqrt{|x_i|})$$

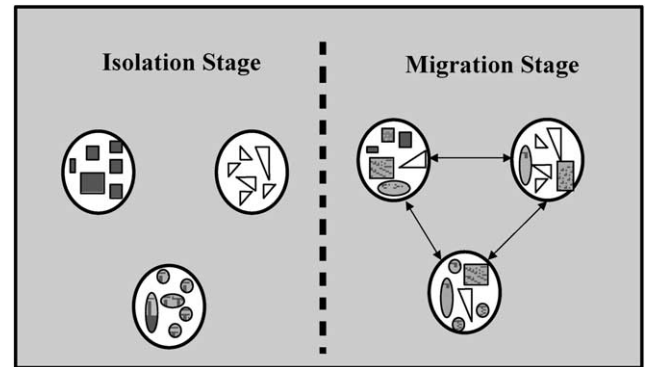


Fig. 1. Symbolic representation of the migration stage used by a multipopulation GA.

search domain: $-500 \leq x_i \leq 500$, $i = 1, 2$; 1 global minimum: $x^* = (420.9687, 420.9687)$; $SH(x^*) = -837.9658$.

We represent in Fig. 2 the search space for that function, and its exploration by the algorithm, during the diversification phase. The results shown in Fig. 2 were obtained with the following settings: 15 subpopulations and 15 individuals per subpopulation. That distribution of solutions was achieved at the end of the diversification stage. We can see that most of the valleys are explored.

In the case of the diversification operator in our algorithm the GAs shown in Fig. 3 are operated with only one generation, for each subpopulation.

2.1.2. Migration

It consists in an exchange of individuals between subpopulations [10], allowing the population to better cover the search space and avoid a premature convergence. Migration of individuals between the different subpopulations, followed by application of genetic operators, achieves generation of new individuals representing still unexplored regions. The selection of individuals to be migrated and individuals to be replaced is performed at random, to the exclusion of the best individual in each subpopulation. The rate of migration (which determines, for a given subpopulation, the number of individuals to be replaced) allows the algorithm to control the level of diversity to be maintained inside the subpopulation.

2.1.3. Speciation

Speciation consists in the gathering of individuals according to their genetic likeness. With a multipopulation GA the request for that mechanism is fruitful to avoid the accumulation of several subpopulations around a same peak of the fitness function. In consequence, a high diversity will be maintained inside subpopulations. Several techniques have been proposed in the literature, such as clustering based methods [11], neighboring techniques [10] and the speciation tree [5]. We used this last method, because its algorithmic complexity is $O(n \log n)$ and it does not require lot of individuals (two for each peak) to achieve a good classification. In addition it needs no problem-dependent

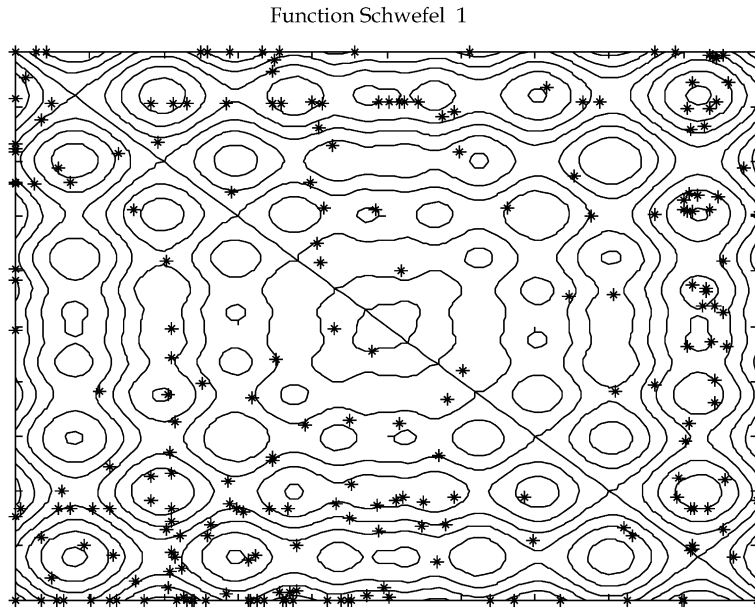


Fig. 2. Exploration of the search space of Schwefel's function by a multipopulation GA.

information, on the contrary to neighboring methods, which use a problem-dependent parameter, namely the niche radius [5].

The speciation module is coupled with the multipopulation GA (see Fig. 3), so that at the end of the diversification each subpopulation gathers individuals both similar and exploiting the same peak of the fitness function. For that purpose, at each generation, all individuals from different subpopulations are gathered inside a common 'speciation pool', which is subsequently processed by the speciation module. The number k of subpopulations returned depends on the pool diversity and particularly on the landscape of the fitness. Therefore, it is a variable function of the problem at hand. Practically, a maximal number, P_{\max} , of subpopulations that can be returned is specified. It must be chosen so that the diversity is sufficient.

$$k \leq P_{\max} \quad (1)$$

In case of multimodal optimization, P_{\max} must be higher than the desirable number of peaks to be determined. At the end of the speciation step, one keeps only the subpopu-

lations for which the best individual is better than the average one.

2.1.4. Distance

Speciation uses a distance to evaluate the similarity between the individuals, thus clustering them into subpopulations formed with individuals having the same genotypic features. The method implemented is the normalized Euclidean distance: let there be two individuals X and Y of dimension n ; each of the n parameters has max and min values (the search space being bounded). The distance $\text{dist}(X, Y)$ between X and Y is:

$$\text{dist}(X, Y) = \sqrt{\frac{1}{n} \sum_{i=1}^n \frac{(X_i - Y_i)^2}{(\max_i - \min_i)^2}} \quad (2)$$

2.2. Intensification

Intensification is used in Tabu Search [6], in conjunction with diversification, to explore the neighborhood of promising points of the search space. In the scope of the present

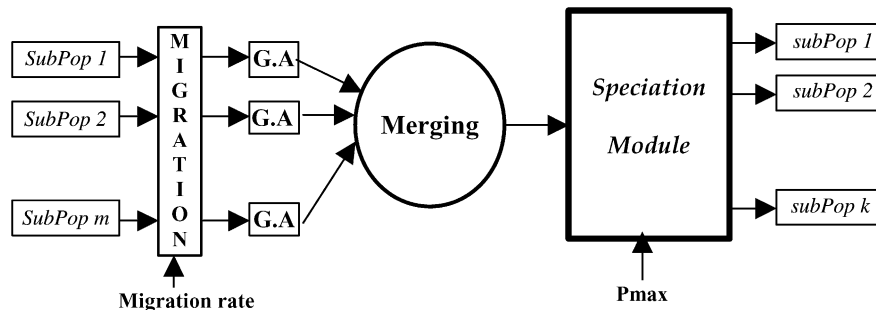


Fig. 3. Synoptic diagram of the diversification step.

algorithm, each population determined during the diversification step should be located in the neighborhood of the peaks of the fitness function, because these neighborhoods are determined by the speciation operator. So, it is natural to perform an intensification on each of these neighborhoods, to approach the optima accurately. The intensification consists in applying a genetic algorithm independently on each population during a fixed small number of generations, identical for all the populations.

The size of the populations is set to N , identical for all the populations issued from the diversification. However, the diversification provides variable population sizes. The size N is obtained from the first intensification generation by selecting only N individuals for the reproduction. If there is only one individual in a population after the diversification, this individual will be selected N times. If there are more than N , the best ones will be reproduced to obtain exactly N individuals, according to the selection algorithm of the GA.

The intensification domain, which is the search space associated with each population i , is centered on the best individual x_d^i determined just after the diversification step. Let x_{dj}^i be the j th coordinate of this individual, let x_{kj}^i be the j th coordinate of an individual k belonging to this population, then:

$$x_{kj}^i \in [x_{dj}^i - \Delta_j^i, x_{dj}^i + \Delta_j^i],$$

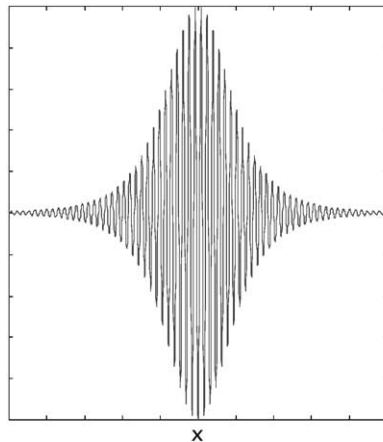
with

$$\Delta_j^i = \max\left(10^{-3}|x_j^{\max} - x_j^{\min}|, \max_{l=1, \dots, N} |x_{dj}^i - x_{lj}^i|\right),$$

where x_j^{\max} is the upper bound of x_j in the global search domain, and x_j^{\min} is its lower bound. The term $10^{-3}|x_j^{\max} - x_j^{\min}|$ guarantees that Δ_j^i is not null.

3. Experiments

The behavior of the algorithm was studied with success



by using several functions. We describe in this paper only the results obtained with the F6 Schaffer's function [12], shown in Fig. 4. That function was selected to illustrate the algorithm efficiency because it is known as one of the most 'difficult' standard test functions.

It possesses one global optimum at $(0,0)$ ($F6(0,0) = 0$) and a large number of local optima. The global optimum is difficult to find because the value at the best local optimum differs from only about 10^{-3} . In addition, that local optimum is not well defined, as it forms a crown around the global optimum which behaves like a trap. This feature will allow us to test the ability of our algorithm to isolate the region of the global optimum, by assigning to that optimum a specific subpopulation. Indeed, to efficiently deal with this function by using a GA, some authors advocate a hybridization with some local descent algorithm [7].

$$F_6(x_1, x_2) = 0.5 + \frac{\sin^2\left(\sqrt{x_1^2 + x_2^2}\right) - 0.5}{(1 + 0.001(x_1^2 + x_2^2))^2} \quad (3)$$

with $x_i \in [-100, 100]$, $i = 1, 2$.

3.1. Experimental conditions

The configuration of the genetic algorithm handling each subpopulation is the following one:

- Linear ranking selection.
- Elitism.
- Stochastic Universal Sampling (SUS) [13].
- Real coding.
- Extended intermediate recombination [14]. Let P_1 and P_2 be the two parents; the two offspring C_1 and C_2 are generated in the following way:

$$C_1 = P_1 + \alpha(P_2 - P_1), \quad C_2 = P_2 + \alpha(P_1 - P_2) \quad (4)$$

where α is a uniform random number in $[-0.25; 1.25]$. The crossover rate is 0.9.

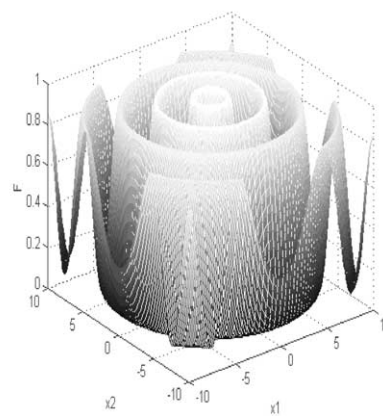


Fig. 4. Representation of F6: (a) in one dimension in $[-100, 100]$, (b) in two dimensions in $[-10, 10]$.

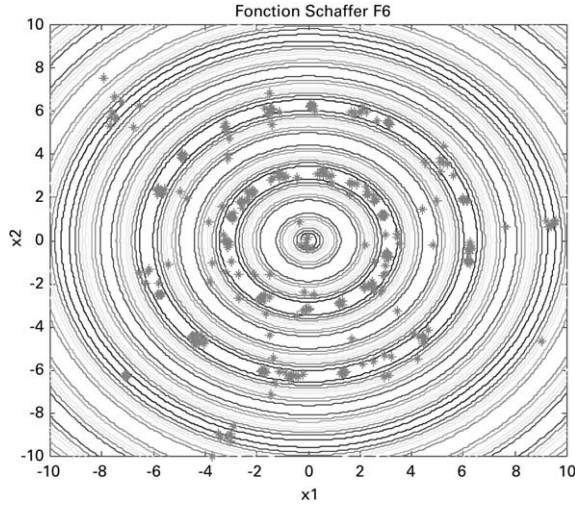


Fig. 5. Final distribution of the subpopulations for $P_{\max} = 40$ and $N = 10$.

- BGA Mutation [14]

$$x' = x \pm 0.2(x_{\max} - x_{\min})\delta, \quad \delta = \sum_{i=0}^{k-1} \alpha_i 2^{-i} \quad (5)$$

with $k = 16$ and $\alpha_i = 1$ with probability equal to $1/k$, otherwise $\alpha_i = 0$; the mutation rate is 0.9.

- Periodicity of diversification = 5 (one diversification generation after 4 intensification generations).
- The communication graph for migration is complete.

3.2. Criteria retained to validate the algorithm

We adopted the following criteria:

- Number of objective function evaluations $NbEval$ (in case of convergence) necessary to reach the global optimum with an accuracy relating to its position equal

to 10^{-3} . The maximal number of generations is equal to 100.

- Success rate: the genetic algorithm being of stochastic nature, we must proceed to several executions: 30, for all results discussed later. *Success rate* represents the ratio of the number of successful executions (global optimum reached) to the total number of executions.

4. Results

We present the evolution of the algorithm versus two parameters: the number of individuals of each subpopulation (N) and the maximal number of subpopulations (P_{\max}). Fig. 5 shows the final distribution of the subpopulations for one execution of the program, with $P_{\max} = 40$ and $N = 10$. We see that the algorithm reduces the search space drastically: all individuals are now within the domain $[-10, 10]^2$, to be compared to the F6 initial search domain $[-100, 100]^2$.

4.1. Study of the migration rate

The migration rate was varied from 0 to 100%, in the case: $P_{\max} = 40$ and $N = 10$. The results are shown in Fig. 6. For each diagram, three curves are represented: the evolution of the average and the evolutions of the upper and lower bounds of the 95% confidence interval.

It can be pointed out that when the migration rate increases, the number of evaluations slightly diminishes, and the success rate increases. Results shown in Fig. 6 indicate that the migration rate is best set between 80 and 100%. We advocate that the migration rate must be advantageously tuned at a high value, about 100%, thus maximizing diversification.

The dependence of the algorithm upon N and P_{\max} is represented in Figs. 7 and 8, for respective migration rates

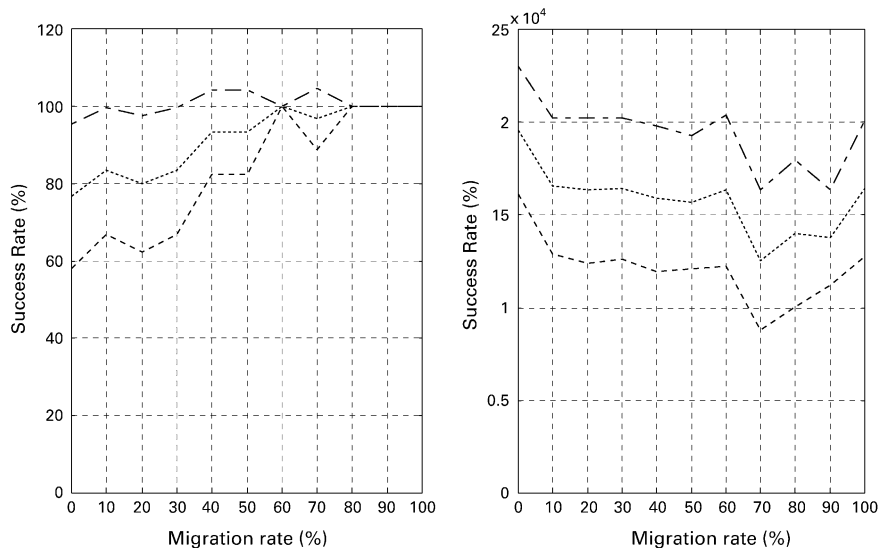


Fig. 6. Evolution of the optimization process versus the migration rate.

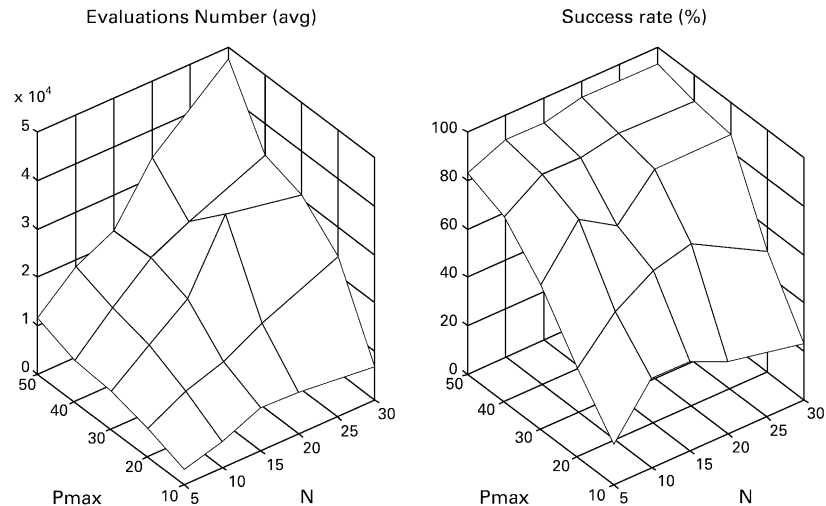


Fig. 7. Evolution of the algorithm versus N and P_{\max} with a 10% migration rate.

of 10 and 80%. Figs. 7 and 8 show that the algorithm is robust from the viewpoint of the success rate: an abrupt fall is observed only for $N < 10$. The evaluations number being increased when the number of individuals is increased, we propose to fix that parameter N around 10.

However the maximal number of subpopulations must be high enough to keep a high success rate: a good compromise seems around $P_{\max} = 30$ –40. Results displayed in Fig. 8 are better than those in Fig. 7, which confirms the interest of choosing a high migration rate, as shown in Fig. 6.

Finally, we compared the results provided by our algorithm with that achieved by a standard GA (one single population), with or without speciation:

	N	NbEval (Avg)	Success rate (%)
Speciation + clearing	400	16,100	27
Without speciation	400	24,800	4

The rate of success is evaluated after 30 executions: thus, the convergence is observed only once for GA without speciation and 8 times for GA with speciation and clearing. Clearly, the results provided by our algorithm for F6 Schaffer's function are notably better.

5. Conclusion

We have proposed a new algorithm comprising an island model cooperating with speciation for multimodal optimization. The concepts of diversification and intensification, assumed from Tabu Search, warrant a good diversity of the search process. The diversification steps allow the algorithm to explore the global search space to find new promising regions. The intensification steps prevent the algorithm from losing these regions because of the strong selection pressure generated by the peaks already found.

Compared to a standard real-coded GA, we have

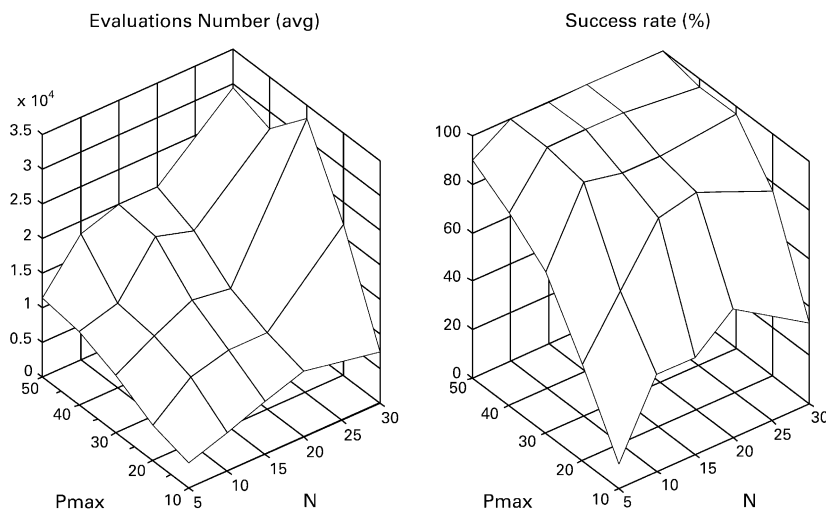


Fig. 8. Evolution of the algorithm versus N and P_{\max} with a 80% migration rate.

empirically shown that F6 Schaffer's function can be optimized with an outstanding rate of success, especially when one selects high migration rates. Two tasks are in progress to improve more the efficiency of the algorithm: first, we empirically search for an optimal tuning of the parameters of the method; secondly we are systematically validating the algorithm over a large set of difficult test problems.

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