On Meme Self-Adaptation in Spatially-Structured Multimemetic Algorithms

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Abstract. Multimemetic algorithms (MMAs) are memetic algorithms that explicitly exploit the evolution of memes, i.e., non-genetic expressions of problem-solving strategies. We consider a class of MMAs in which these memes are rewriting rules whose length can be fixed during the run of the algorithm or self-adapt during the search process. We analyze this self-adaptation in the context of spatially-structured MMAs, namely MMAs in which the population is endowed with a certain topology to which interactions (from the point of view of selection and variation operators) are constrained. For the problems considered, it is shown that panmictic (i.e., non-structured) MMAs are more sensitive to this self-adaptation, and that using variable-length memes seems to be a robust strategy throughout different population structures.

1 Introduction

Memetic algorithms [8] are a pragmatic integration of population-based global search techniques and trajectory-based local search techniques [6]. They rest on the notion of *meme* [2], which within this optimization context translates to computational problem-solving procedures. While different possibilities have been defined in the literature, such procedures are usually local-search techniques. Furthermore, they are often fixed or pre-defined and therefore the MA can be regarded as operating with static implicit memes. This fact notwithstanding, the explicit management of memes has been around for some time now –cf. [7]–, and can be found in, e.g., multimemetic algorithms (MMAs) [5]. Therein, each solution carries memes determining the way self-improvement is conducted. Such memes are themselves subject to evolution and hence conform a self-adaptive search approach.

While early population-based algorithms often used a panmictic approach, whereby any two solutions within the population could interact for reproductive purposes, more general population structures have been in use in the last decades – see e.g. [1, 4]. However, the deployment of such structures on MMAs has been less explored. Some steps to fill this gap were firstly taken in [9], in which an idealized model of spatially-structured MMAs was defined, hinting at the usefulness of spatial structures in this context (the slower convergence of the population buying time for good memes to express themselves). These findings have been also validated elsewhere on actual MMAs using fixed-length memes. Here we turn our attention to the use of memes of self-adaptive complexity in combination with spatially structured populations, analyzing comparatively their effectiveness in this context. To do so, let us firstly define the particular multimemetic scenario we have considered. This is done next.

2 Multimemetic Approach

As mentioned above, the core idea of MMAs is the explicit treatment of memes within the evolutionary process. Hence, we shall firstly describe the representation of memes, before getting into the deployment of spatial structure on MMAs.

2.1 Meme Representation and Self-Adaptation

Memes are taken to be non-genetic expressions of problem-solving strategies and as such can be represented in many ways depending on the level of abstraction and problem dependance considered. Following some ideas posed by Smith [10] in the context of pseudoboolean function optimization, we consider in this work memes expressed as pattern-based rewriting rules [*condition*→*action*] as follows: let $[C \rightarrow A]$ be a meme, where $C, A \in \Sigma^r$ with $\Sigma = \{0, 1, \#\}$ and $r \in \mathbb{N}$. In this ternary alphabet '#' represents a wildcard symbol; now, let $g_1 \cdots g_n$ be a genotype; a meme $[C \rightarrow A]$ could be applied on any genotypic substring into which the condition $C = c_1 \cdots c_r$ fits, i.e., for which $g_i \cdots g_{i+r-1} = c_1 \cdots c_r$ (for the purpose of this comparison, wildcard symbols in the condition match any symbol in the genotype). If the meme were to be applied on position i, its action would be to implant the action $A = a_1 \cdots a_r$ in that portion of the genotype, i.e., letting $g_i \cdots g_{i+r-1} \leftarrow a_1 \cdots a_r$ (in this case, the interpretation of wildcard symbols is as don't-change symbols, that is, keeping unchanged the corresponding symbol in the genotype). In order to avoid positional bias, the order in which the genotype is scanned to check for potential meme application sites is randomized. If a match is found the meme is applied and the resulting neighboring genotype is evaluated. A parameter w determining the maximal number of meme applications per individual is used to keep the total cost of the process under control. The best neighbor generated throughout the precess is kept if it is better than the current genotype.

The main advantage of having memes linked to individuals is giving the algorithm the ability to discover appropriate neighborhoods definitions for the corresponding solution, so as to effectively exploring neighboring points. Such neighborhoods can evolve alongside solutions, providing a self-adaptive means to boost the search by means of this dynamic definition of the local improvement mechanism. This self-adaptation is not limited to the actual definition of the neighborhood for a certain fixed *radius* (i.e., Hamming distance) but can also involve this radius itself. To do so, the length r of the meme is defined within a certain interval $\{l_{\min}, \cdots, l_{\max}\}$. Initially, each meme has a random length in that range. Subsequently, in each evolutionary step before a certain meme is going to be mutated and then applied, its length can be incremented or decremented by one much like in [10]. This is done with a certain probably p_r (in the case of increasing the meme length, a new random symbol is appended in the rightmost position; if the length is decreased the rightmost symbol in the meme is removed). By doing so, the length of the rewriting rule can be dynamically adjusted by evolutionary means, thus providing a self-adaptive control of its complexity: long memes are powerful tools for performing large jumps in the search space but, on the other hand, they are more specific and hence can have lower applicability. It is up to the algorithm to discover the appropriate meme complexity in each moment.

2.2 Spatial Structure

The spatial structure of the population can be regarded as a topological structure upon which individuals in the population are projected. More precisely, let T be this topological structure, comprising μ sites (μ being the population size), each of them identified by an index $i \in \{1, \cdots, \mu\}$. We can characterize this structure using a Boolean $\mu \times \mu$ matrix S. Each entry S_{ij} represents the interaction potential between two sites in the structure. More precisely, let S_{ij}= `true` if, and only if, the individual at the i-th site can interact with the individual at the j-th site.

In this work we consider interaction matrices induced by a particular spatial arrangement of individual sites in a grid: let $\mu = a \times b$; each site i can then be represented by a pair of coordinates $(i_x, i_y) \in \{1, \cdots, a\} \times \{1, \cdots, b\}$. Now, let $d : (\{1, \cdots, a\} \times \{1, \cdots, b\})^2 \to \mathbb{N}$ be a distance measure between sites. Given a certain neighborhood radius ρ, we take $S_{ij} \Leftrightarrow (d(i, j) \leqslant \rho)$, i.e., two sites can interact if they are within a certain distance threshold. Different spatial structures arise from the use of alternative distance measures. We have considered the following possibilities:

1. Panmixia: $d(\cdot, \cdot) = 0$.
2. Moore neighborhood: $d((i_x, i_y), (j_x, j_y)) = \max(|i_x - j_x|, |i_y - j_y|)$.
3. von Neumann neighborhood: $d((i_x, i_y), (j_x, j_y)) = |i_x - j_x| + |i_y - j_y|$.

The above operations are modulo coordinate ranges so as to make them toroidal. Fig. 1 illustrates these spatial structures.

3 Experimental Analysis

In order to analyze the impact of meme self-adaptation on the MMAs described in previous section we have considered two pseudoboolean optimization problems. These are described in Sect. 3.1; subsequently we shall analyze the results in Sect. 3.2.

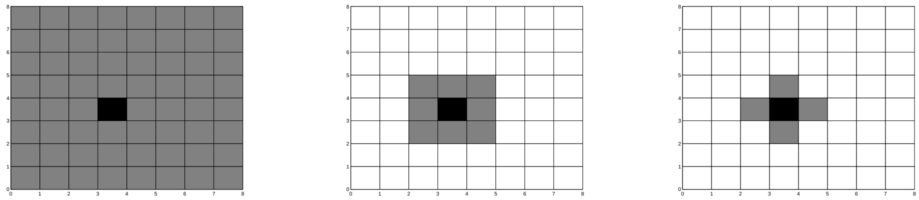

Fig. 1. Illustration of the different neighborhoods considered. The black cell indicates an arbitrary individual and the grey cells denotes its neighbors. From left to right: panmictic, Moore and von Neumann. In the last two cases, $\rho = 1$.

3.1 Benchmark and Settings

The functions considered in the test suite are Deb's trap function [3] (TRAP) and Watson et al.'s hierarchical if-and-only-if function [12] (HIFF). These are defined as follows. Consider firstly the TRAP function. A basic 4-bit trap is defined as

$$f_{trap}(b_1 \cdots b_4) = \begin{cases} 0.6 - 0.2 \cdot u(b_1 \cdots b_4) & \text{if } u(b_1 \cdots b_4) < 4 \\ 1 & \text{if } u(b_1 \cdots b_4) = 4 \end{cases} \tag{1}$$

where $u(s_1 \cdots s_i) = \sum_j s_j$ is the unitation (number of 1s in a binary string) function. A higher-order problem can be built by concatenating k such traps, and defining the fitness of a $4k$-bit string as the sum of the fitness contribution of each block. In our experiments we use $k = 32$ subproblems (i.e., 128-bit strings, $opt = 32$).

As to the HIFF function, it is a recursive epistatic function based of the interaction of increasingly large building blocks. It is defined for binary strings of 2^k bits by using two auxiliary functions $f : \{0, 1, \times\} \to \{0, 1\}$ (to score the contribution of building blocks), and $t : \{0, 1, \times\} \to \{0, 1, \times\}$ (to capture their interaction), where '$\bullet$' denotes a *null* value. These are defined as:

$$f(a, b) = \begin{cases} 1 & a = b \neq \bullet \\ 0 & \text{otherwise} \end{cases} \qquad t(a, b) = \begin{cases} a & a = b \\ \bullet & \text{otherwise} \end{cases}$$

These two functions are combined as follows:

$$\text{HIFF}_k(b_1 \cdots b_n) = \sum_{i=1}^{n/2} f(b_{2i-1}, b_{2i}) + 2 \cdot \text{HIFF}_{k-1}(b'_1, \cdots, b'_{n/2}) \tag{2}$$

where $b'_i = t(b_{2i-1}, b_{2i})$ and $\text{HIFF}_0(\cdot) = 1$. We have considered $k = 7$ (i.e., 128-bit strings, $opt = 576$)

We consider MMAs as described in Sect. 2, with a population size of $\mu = 100$ individuals. These MMAs follow a generational reproductive plan with binary tournament for parent selection, one-point crossover ($p_X = 1.0$), bit-flip mutation ($p_M = 1/\ell$, where $\ell = 128$ is the number of bits), local-search (conducted using the meme linked to the individual) and replacement of the worst parent (an inherently elitist strategy, following the model presented in [9]). Offspring inherit the meme of the best parent, which is subsequently subject to mutation with probability p_M. A run is terminated upon reaching 25,000 evaluations, and 20 runs are performed for each problem and algorithm. We consider meme lengths bounded by $l_{\min} = 3$ and $l_{\max} = 9$, and use $p_r = 1/l_{\max}$ for length self-adaptation. For comparison purposes we also consider fixed-length memes ($r \in \{3, 6, 9\}$). Spatially structured MMAs consider a 10×10 grid and a neighborhood radius $\rho = 1$.

3.2 Experimental Results

The numerical results of the different MMAs are shown in Table 1. Qualitatively, panmictic MMAs (regardless of meme lengths) seem to perform comparatively worse than the corresponding Moore/von Neumann versions, thus supporting the positive impact that the slower convergence induced by the latter spatial structures has on the final results. This is further supported by the slight superiority of the MMA with von Neumann topology over the MMA with Moore topology, which has a faster convergence rate, both at the genotypic and the memetic level – see Fig 2.

Let us now focus on the effect of meme lengths. If we firstly observe the results of using fixed-length memes, it seems that the intermediate value $r = 6$ offers the best tradeoff between memetic richness and meme specificity among the values considered. This offers a first gauge to the way meme lengths self-evolve. Indeed, if we take a look at Fig. 3 we can see that average meme lengths oscillate around values close to 6, indicating the fully self-adaptive MMA seems to be locating this area of memetic interest. This is further vindicated by the fitness results and the number of times the optimum is found by each algorithm: the

Table 1. Results (20 runs) of the different MMAs on the two problems considered. The number of time the optimum is found (n_{opt}), the median ($\tilde{x}$), the mean ($\bar{x}$) and the standard error of the mean (σ_x) are indicated.

		TRAP			HIFF		
topology	r	n_{opt}	$\tilde{x}$	$\bar{x} \pm \sigma_x$	n_{opt}	$\tilde{x}$	$\bar{x} \pm \sigma_x$
panmictic	3	5	30.4	29.5 ± 0.5	1	390.0	404.1 ± 14.9
	6	9	30.4	29.6 ± 0.5	4	382.0	420.3 ± 20.4
	9	3	28.4	28.7 ± 0.5	2	362.0	382.0 ± 16.6
	3 − 9	8	29.0	29.2 ± 0.6	8	456.0	475.3 ± 20.8
Moore	3	8	31.2	30.4 ± 0.4	5	444.0	460.0 ± 17.0
	6	10	31.2	30.0 ± 0.5	8	456.0	476.4 ± 19.7
	9	7	29.8	29.8 ± 0.4	6	456.0	449.0 ± 21.4
	3 − 9	11	32.0	30.8 ± 0.4	7	460.0	471.8 ± 19.5
von Neumann	3	6	30.8	30.1 ± 0.5	9	464.0	501.0 ± 16.9
	6	13	32.0	30.9 ± 0.4	12	576.0	518.4 ± 17.0
	9	10	31.8	30.4 ± 0.4	9	464.0	491.7 ± 18.6
	3 − 9	15	32.0	31.2 ± 0.3	12	576.0	515.6 ± 18.1

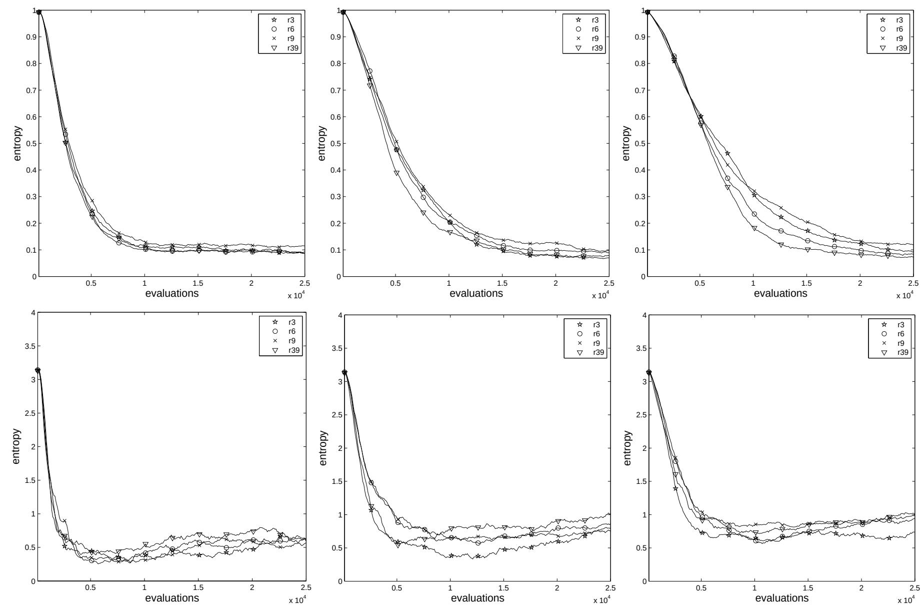

Fig. 2. Evolution of diversity of the different MMAs on the TRAP function. The top row corresponds to genetic diversity and the bottom row to memetic diversity. From left to right: panmictic, Moore, and von Neumann topology.

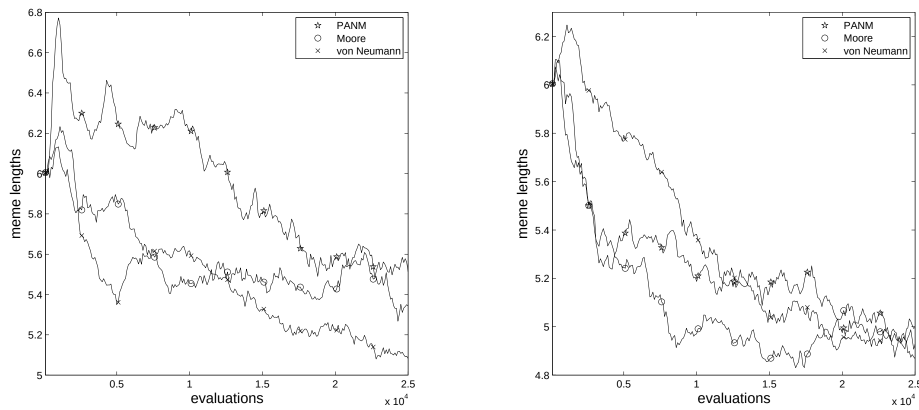

Fig. 3. Evolution of meme lengths in self-adaptive MMAs with different topology. (Left) TRAP. (Right) HIFF.

MMA_{3-9} performs analogously or better than the MMA_6 (the difference is more marked in favor of MMA_{3-9} in the case of panmictic population). The general decreasing trend of meme lengths in this MMA_{3-9} is an interesting phenomenon. We conjecture it is due to the fact that as evolution progresses, the algorithm

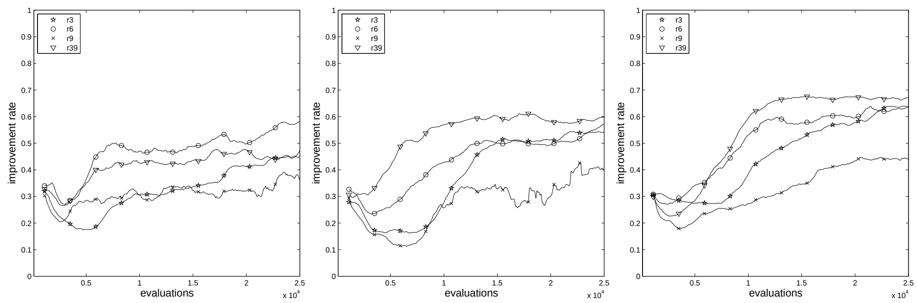

Fig. 4. Meme success ratio (percentage of meme applications resulting in an improvement) of the different MMAs on the TRAP function. From left to right: panmictic, Moore, and von Neumann topology.

starts to locate optimal or near-optimal solutions and the role of memes might be changing from being a search artifact (trying to find search directions to the optimal) to function as an error-correcting mechanism (correcting perturbations introduced by mutation on already (near-)optimal solutions), i.e., their role turns from exploratory to exploitative. This interpretation is consistent with the meme success rates (percentage of meme applications that result in an improvement) shown in Fig. 4. Notice that these follow an upwards trend (and that the values for MMA_{3-9} are normally superior to the remaining MMAs, in particular for non-panmictic populations), which may be indicating this active role as the result of error correction (fitness values are rather stable in those later evolution stages, and hence a high success rate would rather be interpreted as lower-quality solutions being repaired back to known optima than to the discovery of new better solutions). The evolution of diversity also fits nicely in this picture since –as seen in Fig. 2– the genetic diversity seems to decrease faster for the fully self-adaptive MMA (more clearly in the case of von Neumann topology), while memetic diversity stays comparatively higher.

4 Conclusions

It is well known that parameterization is a major issue in memetic algorithms [11], even more so if we consider MMAs which need additional parameters controlling meme representation. For this reason, the study of self-adaptation mechanisms alleviating this parameterization problem is of paramount interest. We have studied a class of spatially-structured MMAs featuring self-adaptation of meme lengths. The results obtained on two problems and three topologies (panmictic, Moore and von Neumann) indicate that the self-adaptation of meme lengths is not detrimental and sometimes even beneficial, although mainly in the case of panmictic population. We attribute this latter effect to the non-panmictic MMAs being more robust to suboptimal parameterization. At any rate, self-adaptation of meme lengths globally seems an adequate strategy for the problems considered, since it does not penalize performance and saves configuration time. Needless to say, further experimentation on other problems would be useful to confirm these findings. Work is underway in this direction. Another line for future development implies the use of other population structures, as well as analyzing the scalability of the approach.

Acknowledgements This work is partially supported by MICINN project ANYSELF (TIN2011-28627-C04-01), by Junta de Andalucía project DNEMESIS (P10-TIC-6083) and by Universidad de Málaga, Campus de Excelencia Internacional Andalucía Tech.

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