

An Analysis of Migration Strategies in Island-Based Multimemetic Algorithms

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Abstract. Multimemetic algorithms (MMAs) are memetic algorithms that explicitly represent and evolve memes (computational representations of problem solving methods) as a part of solutions. We consider an island-based model of MMAs and provide a comparative analysis of six migrant selection strategies and two migrant replacement operators. We use a test suite of four hard pseudoboolean functions to examine qualitative behavioral differences at the genetic and memetic level, and provide a sound statistical analysis of performance. The results indicate the choice of migrant selection operator is more important than that of migrant replacement, and that policies based on fitness or pure genetic diversity do not compare favorably to more holistic strategies.

1 Introduction

Memetic optimization [11] is a long standing search paradigm conceived as a pragmatic combination of population-based global search techniques and trajectory-based local search techniques. The notion of *meme* as unit of imitation (ultimately translating to local-improvement procedures in this computational context) is central to this paradigm. While many simple memetic approaches rely on predefined local-search procedures (i.e., static memes), the idea of explicitly exploiting the computational evolution of memes has been around for some time [10] and is now the central tenet of memetic computing [13] defined as “...a paradigm that uses the notion of meme(s) as units of information encoded in computational representations for the purpose of problem solving”. Such an explicit treatment of memes can be found in multimemetic algorithms (MMAs) [9], in which solutions carry memes indicating how they are going to self-improve.

An important issue in such MMAs is the way in which memes propagate throughout the population. In this sense, meme propagation dynamics is more complex than that of their genetic counterparts, if only because memes are only indirectly evaluated according to the effect they exert on the solutions they are attached to (hence, mismatches between genes and memes may cause potentially good memes become extinct or poor memes proliferate [12]). These issues are specifically relevant to multi-population models of MMAs, in which in addition to internal population dynamics one also has to consider the effect of the communication among populations. Although the influence of the migration policy

has been well-studied in the context of evolutionary algorithms –e.g., [1, 3, 14]; see also [5, 17]– to the best of our knowledge it has not been attempted on this family of MMAs. Notice that in addition to the role that the migration policy can have on properties such as population diversity, in this family of techniques individuals are also responsible for conducting actively part of the search in a self-adaptive way, and carry information for this purpose. Hence design decisions regarding migration do not just affect implicitly the search process via gene diffusion but do it explicitly by means of meme propagation. In this work we take some steps in this direction and provide a comparative analysis of migration policies on a class of MMAs.

2 Island-Based Multimemetic Model

To analyze the impact that the choice of migration strategies has on island-based MMAs, let us firstly describe the basic underlying model and then go to detail the migration policies considered in the experimentation.

2.1 Basic Algorithmic Model

Our MMA is close in spirit to the model defined by Smith [15] in which each individual in the population carries a binary genotype and a single meme. The latter represents a rewriting rule expressed as a pair $\langle \textit{condition}, \textit{action} \rangle$ as follows: let $\langle C, A \rangle$ be a rule, with $C, A \in \Sigma^r$ where $\Sigma = \{0, 1, \#\}$ is a ternary alphabet in which ‘#’ represent a wildcard symbol; now, given a genotype $b_1 b_2 \cdots b_n$, a rule $\langle c_1 \cdots c_r, a_1 \cdots a_r \rangle$ could be potentially applied on any part of the genotype into which the condition fits, i.e., $b_i b_{i+1} \cdots b_{i+r-1} = c_1 \cdots c_r$ (wildcard symbols in the right hand side are assumed to match any symbol in the left hand side). Were the rule applied on a site i , its action would be to implant the action $A = a_1 \cdots a_r$ in that part of the genotype, i.e., letting $b_i b_{i+1} \cdots b_{i+r-1} \leftarrow a_1 \cdots a_r$ (here, wildcard symbols in the right hand side are interpreted as don’t-change symbols, leaving the corresponding symbol in the left hand side unchanged). To avoid positional bias, the order in which the genotype is scanned is randomized. Once a match is found the rule is applied and the resulting neighboring genotype is evaluated. In order to keep the total cost of the process under control, a parameter w which determines the maximal number of rule applications per individual is used. The best neighbor generated (if better than the current genotype) is kept.

Besides the use of memes embedded within individuals, our MMA otherwise resembles a standard memetic algorithm in which parents are selected using binary tournament, and in which recombination, mutation and local-search (conducted using the meme linked to the individual) are used to generate the offspring, which replaces the worst parent following the model presented in [12].

2.2 Migration Strategies Considered

In order to deploy the MMA described before on a multi-island model it is necessary to define a interconnection topology (e.g., a ring, a grid, a hypercube,

etc.) and a migration policy. Such a policy encompasses determining parameters such as the number m of individuals undergoing migration, the frequency ζ of such events, the procedure ω_S used to select the individuals to be migrated from the emitting island, the procedure ω_R used to handle migrants in the receiving island, and the synchronous/asynchronous character of the interaction – see [1]. In this work we are going to consider synchronous interaction and we will be specifically concerned about ω_S and ω_R , whose nature is qualitative as opposed to the quantitative nature of the numerical parameters m and ζ , and whose study cannot therefore be approached using a numerical tuning approach.

Regarding the migrant selection operator ω_S , we have considered the following six possibilities:

- **best**: the best m individuals in the emitting population are selected for migration. This strategy could be seen as an attempt to provide the maximal immediate boost in fitness in the receiving island, probably inducing the latter to re-focus the search if the migrants start to takeover the population.
- **random**: migrants are selected by random sampling (without replacement) of the emitting population. In this case, the goal is injecting diversity in the target population by providing a random sample of the genetic/memetic material of the emitting island.
- **probabilistic**: this strategy borrows inspiration from estimation of distribution algorithms and is related in spirit to the previous strategy. Here, a probabilistic model of the emitting population is created and used to produce the migrants. Hence, these provide a sample of the information contained in the emitting island but do not necessarily correspond to existing individuals in the latter. It can thus be seen as more exploratory than random selection. In this work we consider a simple univariate model in which migrants are generated so that the probability of each symbol in a given position matches the relative frequency of that symbol in that position in the population.
- **diverse-gene**: in the line of the multikulty algorithm [2], migrants are here selected so as to introduce as much diversity as possible in the target population, cf. [4]. To this end, individuals whose genotypic distance (in a Hamming sense) to individuals in the receiving population is maximal are selected.
- **diverse-meme**: this is the natural extension of the previous strategy to the memetic realm. In this case, migrants are individuals carrying memes whose distance (again in a Hamming sense) to memes in the receiving island is maximal. The goal is thus not introducing explicit genetic diversity but do this implicitly by introducing diversity in the way solutions are improved.
- **random-immigrants**: this strategy generates the migrants completely at random whenever they are needed [7]. Since it does not take into account the emitting island at all, this strategy represents an attempt to measure the raw effect of introducing new individuals in the target population, decoupling it from the effects attributed to the actual information exchange between islands. In some sense, it thus provides a performance baseline above which the performance of the other strategies could be assessed.

As to the migrant replacement operator ω_R , we have considered the following two possibilities:

- **replace-worst**: the worst individuals in the population are replaced by the incoming migrants.
- **replace-random**: the migrants replace randomly selected individuals.

In either case we choose to perform the replacement unconditionally (i.e., the migrants are always accepted in the target population) for two reasons: firstly, we aim to maximize the effects (positive or negative) of the migration operation, and secondly we promote diversity over immediate fitness loss (recall that in MMAs, solutions are subject to local improvement and hence such losses can be relieved via meme application; furthermore, exploring the basins of attraction of other optima may be a more valuable asset than a good quality solution in a well-represented –by other solutions in the population– basin of attraction).

3 Experimental Analysis

The migration strategies introduced in the previous section have been subject to experimental scrutiny. Before presenting the actual results, next section describes the experimental setting and test suite considered in the experimentation.

3.1 Benchmark and Settings

The MMA has been tested using the following four different problems defined on binary strings:

- Deb’s 4-bit fully deceptive function (TRAP henceforth) [6]. In our experiments we have considered the concatenation of $k = 32$ 4-bit traps (i.e., 128-bit strings, $opt = 32$).
- Watson et al.’s hierarchically consistent test problems (HIFF and HXOR) [16]. These are recursive epistatic problems defined on 2^k -bit strings which force the algorithm to search for combinations of increasingly larger building blocks. We have considered $k = 7$ (i.e., 128-bit strings, $opt = 576$).
- Boolean satisfiability: a classical NP-complete problem in which a truth assignment to n variables has to be found in order to satisfy a certain Boolean formula Φ . We consider this formula is expressed in conjunctive normal form with $n = 128$ variables and $k = 3$ variables per clause. We use a problem generator approach, generating a different satisfiable instance with the critical clauses/variable ratio ($opt = m = 4.3n = 550$) in each run of the MMA.

We consider an island-based MMA (iMMA) as described in Sect. 2.1, with a population size of $\mu = 128$ individuals, recombination probability $p_X = 1.0$ and mutation probability $p_M = 1/\ell$ ($\ell = 128$, the genome length). This population is arranged in $n_i \in \{1, 2, 4, 8\}$ islands, each of them comprising μ/n_i individuals. The case $n_i = 1$ (denoted as sMMA) corresponds to panmixia and involves

no migration whatsoever. In the remaining scenarios, the islands are arranged in a unidirectional ring and migration takes place every $\zeta = 20$ generations, thus allowing a reasonable lapse of isolated evolution in each deme, cf. [1]. One migrant is selected using ω_S and inserted in the receiving population using ω_R , where both ω_S, ω_R are the strategies described in Sect. 2.2. The memes are expressed as rules of length $r = 3$ and we consider $w = 1$. In all cases the cost of applying a meme is accounted as a fractional evaluation (i.e., as the fraction of the fitness function that needs being reevaluated as a result of a genotypic change) and added to the total number of evaluations. A run is terminated upon reaching 50,000 evaluations, and 20 runs are performed for each combination of problem, number of islands, ω_S and ω_R .

3.2 Experimental Results

First of all, full numerical results are provided in Table 1. As expected, the quality of results does globally improve when the number of islands is increased (note that all problems considered are maximization problems, and hence higher values are better). This is a well-known consequence of the use of decentralized evolutionary algorithms which naturally manifests itself in the multimemetic context as well. The main focus of this analysis is not how better results can get by increasing the number of islands though (an admittedly interesting issue that can be tackled in subsequent research), but the relative effect that design decisions regarding migrant selection and replacement have on the performance of the algorithm. To this end, we have conducted a systematic statistical analysis to ascertain the relative impact that each migration policy exerts on the iMMA.

We firstly consider results of all migrant selection strategies for either $\omega_R = \text{replace-worst}$ or $\omega_R = \text{replace-random}$. We perform a rank-based comparison by computing the relative ordering of each ω_S operator for a given problem and number of islands n_i : the selection strategy with the best mean is given rank 1 and the worst one is given rank 6 (recall there are six ω_S operators). In case of ties, the mean rank of the tied positions is awarded. Fig. 2 shows the distribution of ranks for each ω_S operator. Notice that these ranks are mostly consistent for both migrant replacement strategies. The fact that **random-immigrants** ranks consistently in the last positions is compatible with the fact that the iMMA is actually benefiting from the information exchange among islands beyond pure random diversity (hence the better results for a increasing number of islands – see Table 1). Also, **best** ranks in a poor position in both cases. This is often attributed to the premature convergence induced by this more intensive strategy. Indeed, this effect is illustrated in Fig. 1 (left). Note in any case that higher global diversity per se does not equate to better performance: MMAs also require that memes sustainedly support the search process and strategies such as **random** and **diverse-meme** are better at this, see Fig. 1 (right). In fact, another interesting observation is that migrant selection strategies based on memetic diversity perform better than their genetic counterparts. This indicates that injecting new diverse memetic material can have a larger influence in the behavior of the algorithm than just new genetic material, in line with the active role that the former

Table 1. Results (20 runs) of the different iMMAs on TRAP, HIFF, HXOR and SAT, using the **replace-worst** strategy (upper half) and the **replace-random** strategy (lower half). The median (\tilde{x}), mean (\bar{x}) and standard error of the mean ($\sigma_{\bar{x}}$) are shown.

	TRAP		HIFF		HXOR		SAT	
	\tilde{x}	$\bar{x} \pm \sigma_{\bar{x}}$						
replace-worst								
sMMA	$n_i = 1$	31.4 30.0 \pm 0.5	408.0	427.6 \pm 13.9	360.0	360.2 \pm 4.4	547.0	546.6 \pm 0.4
	$n_i = 2$	30.6 30.3 \pm 0.3	456.0	471.1 \pm 17.2	380.0	382.4 \pm 6.2	547.0	547.3 \pm 0.3
random	$n_i = 4$	31.2 30.6 \pm 0.4	520.0	509.2 \pm 15.7	408.0	416.0 \pm 10.5	548.0	547.5 \pm 0.4
	$n_i = 8$	31.6 30.7 \pm 0.4	576.0	564.0 \pm 8.3	412.0	415.1 \pm 7.3	547.0	547.5 \pm 0.3
best	$n_i = 2$	29.6 30.0 \pm 0.3	436.0	470.0 \pm 20.4	372.0	379.4 \pm 7.6	547.0	547.1 \pm 0.4
	$n_i = 4$	30.8 30.3 \pm 0.4	456.0	469.4 \pm 17.2	380.0	385.8 \pm 5.4	546.0	546.5 \pm 0.4
	$n_i = 8$	31.4 30.3 \pm 0.4	576.0	519.6 \pm 14.5	374.0	378.2 \pm 6.9	547.0	546.9 \pm 0.4
diverse-gene	$n_i = 2$	29.6 29.6 \pm 0.4	456.0	473.8 \pm 16.5	384.0	384.0 \pm 4.7	548.0	547.4 \pm 0.3
	$n_i = 4$	30.2 30.0 \pm 0.4	528.0	499.7 \pm 18.3	395.0	404.6 \pm 10.7	547.0	546.9 \pm 0.4
	$n_i = 8$	30.4 30.1 \pm 0.4	576.0	543.6 \pm 11.8	394.0	404.8 \pm 8.5	547.0	547.3 \pm 0.4
diverse-meme	$n_i = 2$	30.6 30.1 \pm 0.4	456.0	475.8 \pm 16.0	380.0	381.4 \pm 4.4	548.0	547.4 \pm 0.4
	$n_i = 4$	31.0 30.5 \pm 0.4	472.0	501.2 \pm 16.1	404.0	411.2 \pm 11.4	548.0	547.5 \pm 0.3
	$n_i = 8$	31.2 30.7 \pm 0.3	576.0	553.2 \pm 10.5	402.0	418.2 \pm 11.9	548.0	547.5 \pm 0.3
random-immigrants	$n_i = 2$	29.4 29.4 \pm 0.5	436.0	451.0 \pm 15.7	352.0	356.4 \pm 5.0	547.0	547.5 \pm 0.3
	$n_i = 4$	28.6 28.7 \pm 0.5	454.0	453.2 \pm 16.0	348.0	351.6 \pm 3.6	547.0	546.9 \pm 0.3
	$n_i = 8$	30.4 29.3 \pm 0.5	454.0	471.1 \pm 14.8	331.0	336.9 \pm 4.3	547.0	546.8 \pm 0.3
probabilistic	$n_i = 2$	31.4 30.5 \pm 0.4	456.0	493.6 \pm 17.6	374.0	386.2 \pm 7.2	547.0	547.0 \pm 0.3
	$n_i = 4$	32.0 30.8 \pm 0.4	464.0	500.0 \pm 13.6	394.0	387.6 \pm 5.0	548.0	547.4 \pm 0.3
	$n_i = 8$	32.0 30.4 \pm 0.5	576.0	551.6 \pm 11.3	390.0	390.2 \pm 3.9	547.0	547.4 \pm 0.3
replace-random								
sMMA	$n_i = 1$	31.4 30.0 \pm 0.5	408.0	427.6 \pm 13.9	360.0	360.2 \pm 4.4	547.0	546.6 \pm 0.4
	$n_i = 2$	30.4 30.1 \pm 0.3	456.0	480.0 \pm 18.9	380.0	390.4 \pm 7.5	547.0	547.0 \pm 0.4
random	$n_i = 4$	30.8 30.2 \pm 0.4	520.0	506.8 \pm 16.5	412.0	426.6 \pm 10.0	547.0	547.2 \pm 0.3
	$n_i = 8$	31.4 30.7 \pm 0.3	576.0	543.2 \pm 11.6	408.0	414.9 \pm 6.4	548.0	547.5 \pm 0.3
best	$n_i = 2$	29.6 30.0 \pm 0.4	440.0	457.2 \pm 19.3	378.0	379.2 \pm 5.8	547.0	547.1 \pm 0.3
	$n_i = 4$	31.0 30.3 \pm 0.4	468.0	482.8 \pm 20.5	378.0	390.6 \pm 7.8	547.5	547.0 \pm 0.5
	$n_i = 8$	31.4 30.2 \pm 0.5	576.0	518.8 \pm 14.8	384.5	384.6 \pm 6.6	547.0	547.1 \pm 0.3
diverse-gene	$n_i = 2$	30.6 30.2 \pm 0.4	456.0	471.0 \pm 17.4	384.0	385.7 \pm 8.1	547.0	546.7 \pm 0.3
	$n_i = 4$	30.0 29.7 \pm 0.4	520.0	503.8 \pm 17.1	385.0	391.9 \pm 7.7	547.0	546.8 \pm 0.4
	$n_i = 8$	31.6 30.4 \pm 0.4	576.0	546.8 \pm 11.6	382.0	388.5 \pm 5.7	547.0	546.6 \pm 0.3
diverse-meme	$n_i = 2$	31.0 30.2 \pm 0.4	464.0	490.6 \pm 18.6	388.0	386.0 \pm 6.6	547.0	547.2 \pm 0.3
	$n_i = 4$	30.6 30.5 \pm 0.3	472.0	503.2 \pm 14.1	396.0	405.1 \pm 5.9	548.0	547.6 \pm 0.3
	$n_i = 8$	32.0 31.1 \pm 0.3	576.0	535.0 \pm 12.8	408.0	411.9 \pm 9.4	547.0	547.3 \pm 0.3
random-immigrants	$n_i = 2$	30.6 29.8 \pm 0.5	432.0	442.4 \pm 15.1	352.0	355.6 \pm 3.9	546.5	546.9 \pm 0.4
	$n_i = 4$	28.4 28.8 \pm 0.5	456.0	446.3 \pm 19.6	352.0	353.9 \pm 2.9	548.0	547.3 \pm 0.4
	$n_i = 8$	28.6 29.1 \pm 0.5	456.0	475.8 \pm 16.4	338.0	337.8 \pm 4.1	547.0	547.0 \pm 0.4
probabilistic	$n_i = 2$	30.9 30.5 \pm 0.4	464.0	482.4 \pm 16.8	370.0	372.4 \pm 5.1	547.0	546.7 \pm 0.4
	$n_i = 4$	31.6 30.9 \pm 0.3	576.0	518.6 \pm 15.5	384.0	384.6 \pm 4.9	547.0	547.3 \pm 0.3
	$n_i = 8$	31.0 30.3 \pm 0.5	576.0	548.4 \pm 13.1	394.0	400.9 \pm 5.8	547.0	547.3 \pm 0.3

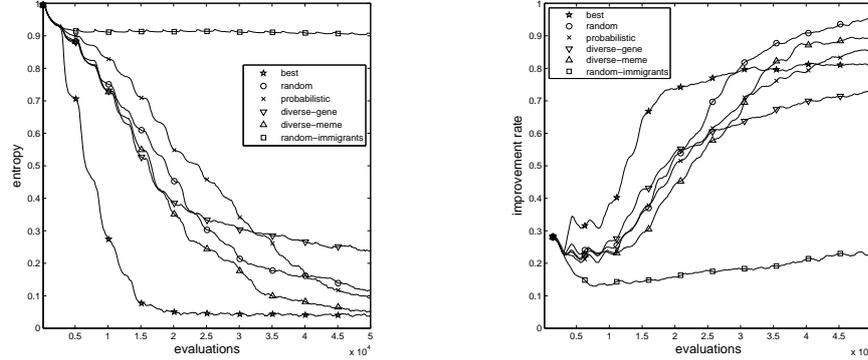


Fig. 1. (Left) Global population entropy (Right) Meme success rate (percentage of meme applications that result in an improvement). In both cases the data corresponds to HIFF, $n_i = 8$, $\omega_R = \text{replace-worst}$.

Table 2. Statistical tests for the migration selection strategies ($\alpha = 0.05$).

	Critical value	replace-worst	replace-random
Friedman	11.070498	35.416667	28.238095
Quade	2.382823	14.811603	9.189948

actually has on the search process itself. The **random** strategy provides high performance as well, which could be attributed to its constituting a good tradeoff between genetic and memetic diversity. Along this line, note that this selection strategy performs slightly better in a relative sense when used in conjunction with **replace-worst** due to its more exploratory nature being compensated by the more intensive character of the latter replacement strategy. Note finally how the probabilistic generation of migrants sits comfortably in the third position in either case, not far from **random** selection. Obviously, a simple univariate model cannot adequately grasp the interdependencies among variables and hence this strategy behaves as a more exploratory variation of the **random** strategy.

To determine the extent to which rank differences are significant we use two well-known non-parametric statistical tests, namely Friedman and Quade tests. The results, at the standard level of $\alpha = 0.05$, are shown in Table 2. The statistic values obtained are clearly higher than the critical ones, thus indicating significant differences in their ranks. Hence, we have performed a post-hoc analysis using Holm test to determine whether the differences are significant with respect to a control strategy (in this case the strategy which provided the best average rank as shown in Fig. 2). Table 3 shows the results of this test. Notice that the test is passed in either case for **random-immigrants**, **best** and **diverse-gene**, hence indicating the control algorithm is significantly better than these. No statistical differences can be shown between **diverse-meme**, **random** and **probabilistic**.

If an analysis is conducted along the replacement dimension, i.e., by keeping fixed the selection strategy and comparing both replacement strategies, we can

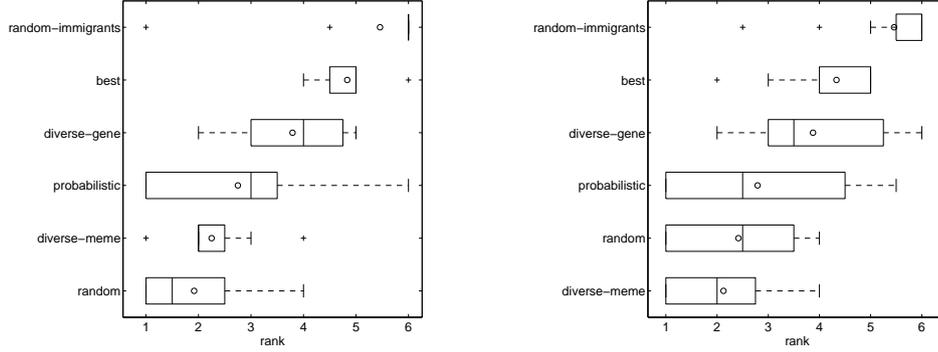


Fig. 2. Rank distribution of migration selection strategies. Each box comprises from the first to the third quartile of the distribution, the median (2nd quartile) is marked with a vertical line, the mean with a circle, whiskers span 1.5 times the inter-quartile range, and outliers are indicated with a plus sign. (Left) Results for $\omega_R = \text{replace-worst}$ (Right) Results for $\omega_R = \text{replace-random}$.

Table 3. Results of Holm test. (Top) $\omega_R = \text{replace-worst}$ using $\omega_S = \text{random}$ as control strategy (Bottom) $\omega_R = \text{replace-random}$ using $\omega_S = \text{diverse-meme}$ as control strategy.

	i	strategy	z -statistic	p -value	α/i
replace-worst	1	diverse-meme	0.436436	0.331260	0.050000
	2	probabilistic	1.091089	0.137617	0.025000
	3	diverse-gene	2.454951	0.007045	0.016667
	4	best	3.818813	0.000067	0.012500
	5	random-immigrants	4.637130	0.000002	0.010000
replace-random	1	random	0.381881	0.351275	0.050000
	2	probabilistic	0.872872	0.191367	0.025000
	3	diverse-gene	2.291288	0.010973	0.016667
	4	best	2.891387	0.001918	0.012500
	5	random-immigrants	4.364358	0.000006	0.010000

observe that **replace-worst** performs slightly better than **replace-random** but the difference does not reach significance at 0.05 level in any case, using a Wilcoxon ranksum test to perform head-to-head comparisons between both replacement strategies in each (problem, ω_S , n_i) combination. If we analyze specific (ω_S , ω_R) pairs, we find that there are statistically significant differences in the rank distribution of the 12 combinations (using Friedman and Quade test: values of 71.317308 and 11.251898 are respectively obtained, much larger than the critical values 19.675138 and 1.868615). Holm test is subsequently performed as shown in Table 4. Consistently with the previous results, the test is passed for all pairs involving **random-immigrants**, **best** and **diverse-gene** using **random+replace-worst** as control algorithm. No statistical differences can be shown between pairs involving **diverse-meme**, **random** and **probabilistic**.

Table 4. Results of Holm Test for all combinations of selection/replacement strategies, using random+replace-worst as control strategy.

i	strategy	z -statistic	p -value	α/i
1	diverse-meme+replace-worst	0.651059	0.257504	0.050000
2	diverse-meme+replace-random	0.735980	0.230871	0.025000
3	probabilistic+replace-worst	1.075663	0.141039	0.016667
4	random+replace-random	1.103970	0.134803	0.012500
5	probabilistic+replace-random	1.755029	0.039627	0.010000
6	diverse-gene+replace-worst	2.745772	0.003018	0.008333
7	diverse-gene+replace-random	3.085455	0.001016	0.007143
8	best+replace-random	3.623287	0.000145	0.006250
9	best+replace-worst	4.132811	0.000018	0.005556
10	random-immigrants+replace-worst	5.123554	0.000000	0.005000
11	random-immigrants+replace-random	5.180167	0.000000	0.004545

4 Conclusions

The choice of migrant selection and migrant replacement operators is acknowledged as having a crucial impact on the performance of island-based GAs. In this work we have conducted an analysis of the influence of these two operators in the context of MMAs, in which individuals are not just points in the search space but also carry information on how to perform the search. Besides confirming some results which had been previously reported in the context of GAs (such as, e.g., the fact a migrating the best individual leads to a quick degradation of diversity and diminished performance), we have found that the replacement strategy (at least in the two incarnations considered) has less impact than the selection strategy, and that a selection strategy purely aimed at maintaining genotypic diversity does not compare favorably to other strategies based on memetic diversity (although the former still provides better results than a single-island panmictic model or a strategy based on random immigrants). The latter performs statistically similar to two other strategies aimed at randomly sampling the emitting population. It is specifically interesting to note that a probabilistic modeling of the population (even an arguably simple one such as the univariate model considered here) is still competitive with other migration operators. This suggest a potential line of future developments focusing on more complex probabilistic models capturing bivariate or multivariate dependencies [8]. Confirming these findings on problem instances of higher dimensionality and on other self-adaptive memetic models [15] are other interesting lines of future work.

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