

Diversity Through Multiculturalism: Assessing Migrant Choice Policies in an Island Model

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Abstract—The natural mate-selection behavior of preferring individuals which are somewhat (but not too much) different has been proved to increase the resistance to infection of the resulting offspring, and thus fitness. Inspired by these results we have investigated the improvement obtained from diversity induced by differences between individuals sent and received and the resident population in an island model, by comparing different migration policies, including our proposed *multikulti* methods, which choose the individuals that are going to be sent to other nodes based on the principle of *multiculturalism*; the individual sent should be different enough to the target population, which will be represented through a proxy string (computed in several possible ways) in the emitting population. We have checked a set of policies following these principles on two discrete optimization problems of diverse difficulty for different sizes and number of nodes, and found that, in average or in median, *multikulti* policies outperform the usual policy of sending the best or a random individual; however, the size of this advantage changes with the number of nodes involved and the difficulty of the problem, tending to be greater as the number of nodes increases. The success of this kind of policies will be explained via the measurement of entropy as a representation of population diversity for the policies tested.

Index Terms—Distributed memory systems, diversity, genetic algorithms, island model, parallel algorithms.

I. INTRODUCTION

DIVERSITY is a key factor in the behavior of any evolutionary algorithm: without a minimum level of diversity evolution soon ends in stagnation and the algorithm is unable to use the current pool of solutions to find new areas of the search space holding a better or the best solution to the problem. In fact, the tradeoff between selective pressure and population diversity has already been discussed in several works [1], [2], and there also exist proposals [3], [4] which explicitly include measures of diversity in the selection process. In particular, diversity (or rather, its preservation) has been viewed as the cause of the advantages observed in the island models of evolutionary algorithms [5], since the exchange of

individuals after periods of isolated evolution usually provides new genetic material to the destination population, which increases diversity through mating with it; the mating restriction that is inherent to the isolation of the population in several islands avoids premature convergence of the population as a whole, while the increased diversity attained with the incorporation to the genetic pool of the incoming members of the other populations takes it closer to finding a solution.

However, diversity is not automatically increased in the long run by the incorporation of immigrants. According to the intermediate disturbance hypothesis [6], not all immigrants are the same: the closer (in phenotypic or genotypic terms) the immigrant is to the current state of the population, the smaller effect it will have on the overall performance; if its distance is too big, its disruptive effect (if it effectively enters the reproductive pool) will on one hand, be equivalent to hypermutation, and on the other, if its fitness differences are too high, will imply a fast takeover of the whole population.

These adverse effects on the genetic pool as a whole should be translated individually to a restrictions in the admission of new individuals in a genetic pool: not too similar, not too different, because, as these migrants are entered in the gene pool, they are eligible as possible mates; in fact, a study on natural systems performed by Milinski [7] has found evidence that a limited degree of difference is preferred in the selection of mates. Several studies cited by that one (e.g., [8]–[12]) have shown, for instance, that female mice prefer as mates those males that have alleles that differ from their own, in the immune genes of the major histocompatibility complex (MHC).¹ Studies on other vertebrates such as humans and fish have discovered that its MHC system is very similar to mice, so the finding above may be also valid for them and it might thus be a quite general natural mechanism, as mentioned in the abstract. The optimal complement from the partner should include those MHC alleles that provide resistance against parasites, which could be revealed by the expression of costly secondary sexual characters. This maximizes resistance to ever-changing infectious diseases.

¹When a cell of the body is infected by a pathogen, e.g., a virus, it contains virus-derived proteins, which are degraded into small peptides of a length of about nine amino acids. Outside the cell cytotoxic T lymphocytes (T cells) are waiting, which are able to tell whether such a peptide is derived from foreign or self-proteins. Because mature T cells are usually tolerant to uninfected cells, they kill infected cells thereby eliminating the virus. However, virus-derived peptides have to be picked up within the cell, taken to the cell surface and displayed to T cells. This is done by MHC molecules, i.e., glycoproteins encoded in the large cluster of genes known as the MHC.

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In this area of research, Milinski [13] has carried out another study on the degree of difference of the immune genes of the MHC which is observed in the selection of mate in different species. The study has revealed that preferring just MHC-dissimilar mates is not the option with the best payoff. Specifically, the author states, "Individuals should be optimally, not maximally, major histocompatibility complex heterozygous".

Taking these natural findings into account, and letting nature be our guide [14], our intention in this paper has been to explore a similar mate-choice methodology in an evolutionary algorithm following an island model. Intuitively, maximally different individuals should enhance diversity in the island they fall; however, this also implies a price to pay if they reduce the population average fitness or its fitness is so low that they are never selected for mating.

Accordingly, this paper investigates which degree of diversity induced via the introduction of sufficiently different new individuals in an island model can be algorithmically advantageous. Our starting hypothesis has been that there exists a particularly appropriate degree of induced diversity which provides the best performance for a particular problem and execution environment. In this paper, we make different tests on a new model, that selects as migrant an individual "relatively" different to the receiving subpopulation (to which we will refer to by p_2). In order to do this, the node choosing the migrant needs information on the composition of the receiving node. We have considered different ways of providing this information in a concise manner, since it is impossible (or at least impractical, due to bandwidth limits) for the emitting population to have information about *all* individuals in the receiving population. One of them is taking the best individual of subpopulation p_2 as a representative; the other, using a kind of average genotype, the so-called *consensus* sequence (which we will describe later on). Another important issue to investigate is the tradeoff between promoting diversity and favoring the best individuals. Sending the most different individual as immigrant can imply that if its fitness value is low compared to those of the destination subpopulation and the immigrant would probably disappear immediately from the pool.

In this paper, we will perform systematic experimentation of the different ways of performing the selection of immigrants to p_2 applying it to the optimization of one continuous and two discrete functions, and we will test it on real parallel environments with different number of nodes; the number of nodes has an impact on performance, but also on diversity, with more nodes usually (but not always) meaning better performance [in average number of evaluations to solution, (AESs)], but also a higher risk of premature convergence. Since the testing environment is a real multicomputer, it allows us to measure not only the number of evaluations, but also the running time of all policies tested, which in turn allows us to check whether the overhead incurred by them is offset by the algorithmical improvement achieved. The algorithmical efficiency of the methods will be measured on well-known combinatorial optimization problems, which are considered *deceptive* due to their structure; they are also multimodal,

making them harder for evolutionary algorithms; in any case, the three problem instances used represent three different degrees of difficulty. How well they perform will be measured using average evaluations to solution, as an indication of the fraction of the search space that has been explored to find a correct solution. More efficient algorithms are able to cut a shorter path to the solution, thus needing less AESs; worse algorithms will need, on average, more evaluations. We have also included a study of the entropy in order to check its correlation with the migration policy.

The rest of this paper is organized as follows. Section II reviews some related works, Section III describes the details of the model, Section IV is devoted to describing some implementation details and the problems tested. Finally, Section V presents and discusses the experimental results, and Section VI draws the main conclusions from the experiments performed.

II. STATE OF THE ART

The population to which an evolutionary algorithm is applied can be divided among computing nodes in many different ways: by farming out evaluation of members of the population to other computing nodes (in an approach usually called *farming* [15]), or by letting every node carry out its own evolutionary algorithm, with frequent interchange of information among them via *migration* of individuals from one node to the others; this is usually called an *island model* [16], [17].

The population structure designed for parallel evolutionary algorithms (EAs) can also be applied in sequential ones: in *diffusion EAs*, for instance [18]–[21], the population is endowed with a spatial structure that restricts selection, mating, and replacement; some early work on memetic algorithms was actually conducted following this approach [22], [23]. Even as this model lends itself naturally to parallelization on massively parallel systems—such as the island model—it can be also studied from an algorithmic point of view without relying on physical parallelization.

In fact, parallel evolutionary computation was from the beginning found advantageous over the sequential version; in the initial papers, linear speedups² with the number of nodes (islands) were easily achieved [24]; in some case super-linear speedups were reported [25]. There is a reason for this: since the prevention of inbreeding (mating among similar individuals, which will not increase diversity) is one of the keys in maintaining a healthily diverse population that can efficiently explore the search space, and distribution in islands (physical or otherwise) partially isolates populations from each other leading them to explore different portions of the search space, it has been frequently proved that distributed evolutionary algorithms can improve the results of the sequential version at the same computational effort measured in number of fitness evaluations (see [26]).

Besides reproductive isolation, there is an additional factor that contributes to this increased performance: the effect that incoming immigrants have on the population they are

²Ratio of the sequential execution time to the parallel one.

incorporated to, which means that different choices for the immigrant selection method will enhance or blur this effect. This is why migration policies have frequently been the subject of study, looking at its different facets, such as the number of migrant individuals, the frequency of the migration, the policy for selecting the individuals sent to other nodes and to be replaced by the received ones, the network topology or the synchronous or asynchronous nature of the communications.

Those different facets of the selection of immigrants and the way they are sent have been partially tackled by several researcher teams. For instance, Alba *et al.* [27] have compared synchronous and asynchronous policies, concluding that asynchrony does not have a negative effect on performance, and can even outperform synchronous ones; one of the authors of this paper [28] also looked at what would be the degree of asynchrony that would achieve the best algorithmic performance, applying also the above mentioned theory of intermediate disturbances.

However, one of the most complete research on the selection of outgoing immigrants and their incorporation into the population has been done by Cantú-Paz [5], [29]. This paper studied the four possible combinations of random and fitness-based emigration and replacement of existing individuals. Cantú-Paz found that the migration policy that causes the greatest reduction in work (measured as *takeover time*)³ is to choose both the immigrants and the replacements according to their fitness, because this policy increases the selection pressure and may cause the algorithm to converge significantly faster. However, if convergence is too fast it can lead to algorithm failure, as Cantú-Paz [5] states the following referring to parallel EAs:

Rapid convergence is desirable, but an excessively fast convergence may cause the EA to converge prematurely to a suboptimal solution.

This is due to the fact that the effect of this high-fitness immigrant in the population will usually be, as has already been mentioned above, to reduce diversity via combination with other (probably similar) high-fitness individuals, which will eventually lead to a diversity collapse, as high-fitness individuals are circulated from one node to others, as stated by Denzinger and Kidney in [30]. In fact, it is usually observed that after a few rounds of immigration, populations no longer behave as isolated islands, their composition being very similar. And, curiously enough, this effect is explained by the already mentioned *intermediate disturbance hypothesis*, [6], which states that the effect of a disturbance on diversity depends on its magnitude: a perturbation will produce a collapse if it is too big, no effect if it is too small, and a maximum increase in diversity if it is in the intermediate region. In fact, this hypothesis explains some results [28] found in evolutionary algorithms. Several results in evolutionary computation are explained by this hypothesis: some authors such as Alba and Troya [31] found that in the island model the migration of a random string prevents the “conquest” effect

in the target island for small or medium sized subpopulations; this could be explained by the random immigrant individual behaving as an *intermediate* disturbance, as opposed to the strong disturbance initially provoked by the high-fitness individual.

Even without considering this hypothesis, some authors have researched different immigrant selection policies: after selecting the best and a random individual, other researchers have sought other modes of selection: Noda *et al.* [32] propose an adaptive policy for choosing the individuals to migrate and/or replace based on some knowledge-oriented rules. To do this, each agent receives information about the fitness function from its peers. Moreover, in one of the policies considered in Noda’s paper the individuals sent are chosen to be quite different from others previously sent. The tested adaptive policies were proved useful, providing better solutions than the sequential execution. A later paper by Yang *et al.* [33] proposes selecting immigrants from an *elite* set, instead of random ones, and using them and their bit-wise complements as a pool for creating a set of immigrants; this yields good results in dynamic environments, which are known to need a high population diversity. A similar contextual approach was also considered in the area of dynamic optimization problems (DOP) by Yu and co-authors [34]: to preserve diversity, new random *immigrants* were created by using the allele distribution and its complementary; new population individuals (so-called immigrants) were generated from this allele distribution substituting the worst in the population. This approach was found advantageous over a canonical GA and other DOP-oriented GAs such as self-organizing random-immigrants genetic algorithm.

Outside the island model, there are several ways of designing distributed evolutionary algorithms so that diversity is preserved, if not enhanced. Affenzeller and Wagner [35] have proposed a model that differs from the island model, and which follows an approach of segregation and reunification. In this case, subpopulations evolve independently until detecting local premature convergence, which is indicated by a selection pressure value computed in each one. If stagnation is detected the operations for this subpopulation are stopped until the next reunification phase is reached. Such a reunification phase is initiated also if all subpopulations have converged prematurely.

In spite of some of the policies mentioned above having the effect of increasing diversity and thus performance, diversity, by itself, is not acknowledged as one of the factors that should be dealt with explicitly. One of the first papers following this research line is the one mentioned above by Denzinger and Kidney in [30]. Their approach derives from sequential evolutionary algorithms that take into account diversity (in the form of difference from each individual to the rest of the members of the population) explicitly when selecting an individual. Other approach in this line is the algorithm proposed by de Jong and co-authors in [36], which converts a single-objective evolutionary algorithm in a multiobjective one that considers diversity as the second objective to optimize; or the *diversity-guided evolutionary algorithm* [37], which alternates phases of exploration and exploitation depending on the *concentration* of individuals around a single point in

³Takeover time is the number of generations required to converge to the best individual from the initial population, by applying the selection operator alone; this is roughly equivalent to the average evaluations to solution used in this paper.

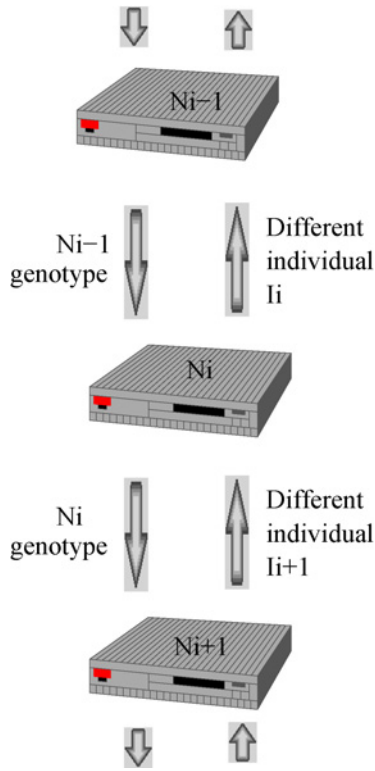


Fig. 1. Scheme of the multikulti algorithms.

search space. Denzinger *et al.* aggregate the difference of every individual to the average chromosome in every island for a *quality* value that is then used to select the individuals that are going to be sent to other nodes. They test different weights for fitness and quality, concluding that a 70:30 proportion (fitness: difference) or 50:50 is a better choice than just fitness by itself, or using the difference in a larger proportion.

Besides, although some of the papers above study policies for selecting immigrants, very few of them offer adaptive policies that, at the same time, try to enhance diversity via sending individuals that are as different as possible (but, as per the intermediate disturbance hypothesis and the biological studies mentioned above, not *too* different). In a preliminary work the authors proposed the multikulti algorithm [38] and tested it on a simulated parallel environment, finding that it yielded better results than random or best-individual migration policies in most cases. Now we have developed an exhaustive study on a real parallel environment, which will be presented after the model explanation on the next section.

III. MODEL DESCRIPTION

For the island model we have adopted a ring topology (Fig. 1), in which each node can only send or receive information from the next and previous nodes in the ring. Nodes communicate in an asynchronous manner. The node N_i receives from node N_{i+1} a message with a genotype that *represents* the population. We have considered two different ways of doing this in a concise manner: the best individual and the consensus sequence, which are described subsequently.

Once the node N_i has received this information, it sends an individual different enough from the individual representing subpopulation N_{i+1} to node N_{i+1} . The mechanism we have adopted to control the degree of difference of the migrant individual consists of selecting the individual with the most different genotype from the receiving population among an elite of the fittest individuals. The size of this elite controls the degree of difference. Other policies have been explored in previous works [38], where we have also studied the use of an elite (a set of individuals with the highest fitness), though in a simulated parallel environment. In this paper, the elite size was a constant, half of the population. The results obtained indicate that the use of an elite improves the results of choosing the most different individual as migrant; however this finding needs to be confirmed in a parallel implementation which allows the measurement and comparison of actual execution times. At the same time, we have also carried out an exhaustive study of the effect of the elite size, which was initially found to have great influence on the outcome.

As done in the previous papers, we have represented the receiving population in two different ways: using the best individual or a consensus sequence. We can expect that after a number of generations without exchanging individuals each subpopulation is close enough to convergence for the best individual being a fair representation of the whole population. Obviously, this is not true in the first generations, but, in any case, it is impossible to be different from *all* individuals in the population, and what matters is that the immigrant sent is different enough from those individuals with which it is most likely to mate. We called it the *mk_best* approach.

On the other hand, the consensus sequence is a concept taken from biology [39] where it is defined as the sequence that reflects the most common base (in the case of DNA/RNA strings) or amino acid (in the case of protein strings) found at each position in a genome. The consensus sequence is a compact formulation to represent all possible alignments for any given numbers of sequences. In biology sometimes it is necessary for certain positions in a sequence to be represented as ambiguous symbols because some residues cannot be resolved during laboratory experiments. A sequence with ambiguity codes is actually a mix of sequences, each having one of the nucleotides defined by the ambiguity at that position. The consensus sequence in essence is a condensed sequence with ambiguity codes that shows which nucleotides are allowed in each column. In our case it is composed of the most frequent allele for each position of the genotype. Policies using this approach will be labeled *mk_cons* from now on.

Next, we will explain how we set up the experimental environment to test the implementation of the model explained in this section.

IV. EXPERIMENTAL SETUP

For our experiments we use chromosomes that are fixed-length binary strings. The selection mechanism to choose individuals for the new population uses a generational algorithm, with single one-point crossover operator (preliminary experiments showed that the results are similar with a two-point

TABLE I
EVOLUTIONARY ALGORITHM PARAMETERS USED IN THE 100-PEAKS
EXPERIMENTS

Parameter	Value
Chromosome length	100
Total population	512
Crossover rate	40%
Mutation rate	1%
Generations to migration	20
Max number of iterations	3000

crossover) and multiple-point bitflip mutation. The parallel implementation details and the problems considered for the experiments are explained below.

The system has been implemented in C++ and it is available from <http://code.google.com/p/multikulti/>. The considered problems have been run in parallel using the PVM 3.4.5 software package⁴ on a 8 nodes Hypercat cluster from the University of Granada, Spain, running under Linux. Parallel virtual machine allows a heterogeneous network of parallel and serial computers to appear as a single concurrent computational resource.

Tests have been made for 2, 4, and 8 nodes, to see how the different migration methods fared under different initial diversity conditions. The total population was kept constant, dividing it among the nodes.

In our parallel scenario, at the end of a preset number of generations, each node sends a single individual to the next node according to the policy being tested.

A. Problems Tested

The functions we have selected for testing are **P-Peaks** and the massively multimodal deceptive problem (MMDP), two of the three discrete optimization problems presented by Giacobini *et al.* in [40]. These problems, while being both multimodal, represent different degrees of difficulty for parallel evolutionary optimization; both together are sufficiently representative of a wide range of problems, and results obtained here can be extrapolated to others of the same degree of difficulty. They have been previously used [41], [42] to evaluate parallel evolutionary systems.

The **P-Peaks** problem is a multimodal problem generator proposed by De Jong in [43], and is created by generating P random N -bit strings where the fitness value of a string \vec{x} is the number of bits that \vec{x} has in common with the nearest peak divided by N

$$f_{P-Peaks}(\vec{x}) = \frac{1}{N} \max_{1 \leq i \leq p} \{N - \text{HammingDistance}(\vec{x}, \text{Peak}_i)\}. \quad (1)$$

We consider an instance of $P = 100$ and 100 bits where the optimum fitness is 1.0 (1). The parameters used in the EA are shown in Table I.

On the other hand, the MMDP [44] is a deceptive problem composed of k subproblems of 6 bits each one (s_i). Depending on the number of ones (unitation) s_i takes the values depicted

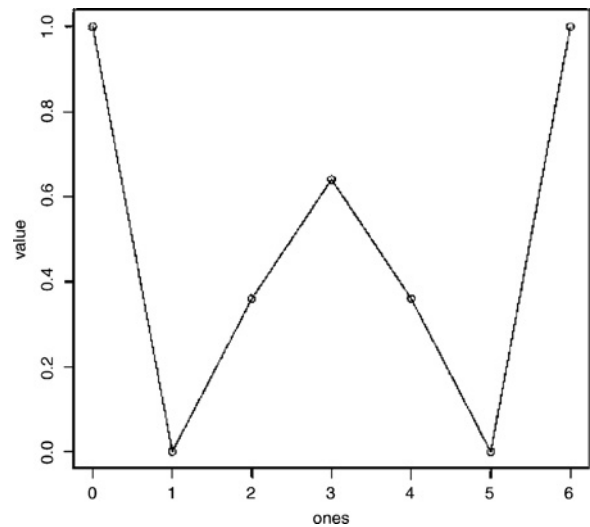


Fig. 2. Representation of one of the variables of the MMDP problem.

TABLE II
EVOLUTIONARY ALGORITHM PARAMETERS USED IN THE MMDP
EXPERIMENTS FOR TEN VARIABLES (LEFT) AND 15 (RIGHT)

Parameter	Value	
Chromosome length	60 (10 var.)	90 (15 var.)
Total population	512	
Crossover rate	40%	
Mutation rate	1%	
Generations to migration	20	
Max number of iterations per node	20 000	50 000

The only change is the chromosome length and the maximum number of iterations allowed per node.

next

$$\begin{aligned} \text{fitness}_{s_i}(0) &= 1.0 & \text{fitness}_{s_i}(1) &= 0.0 \\ \text{fitness}_{s_i}(2) &= 0.360384 & \text{fitness}_{s_i}(3) &= 0.640576 \\ \text{fitness}_{s_i}(4) &= 0.360384 & \text{fitness}_{s_i}(5) &= 0.0 \\ \text{fitness}_{s_i}(6) &= 1.0. \end{aligned}$$

The fitness value is defined as the sum of the s_i subproblems with an optimum of k (2). Fig. 2 represents one of the variables of the function. The number of local optima is quite large (22^k), while there are only 2^k global solutions

$$f_{MMDP}(\vec{s}) = \sum_{i=1}^k \text{fitness}_{s_i}. \quad (2)$$

For this problem, we have considered instances with $k = 10, 15$ subproblems, whose maximum is then $f_{MMDP}(\vec{s}) = 10, 15$; this will be represented in a chromosome of length 60/90. The parameters used in the EA for this problem are shown in Table II.

B. Genetic Algorithm

The genetic algorithm running in every island is a canonical evolutionary algorithm, following the implementation described in [45], that is, a generational algorithm, which uses roulette wheel selection, one-point crossover and multiple-bit

⁴<http://www.epm.ornl.gov/pvm/>.

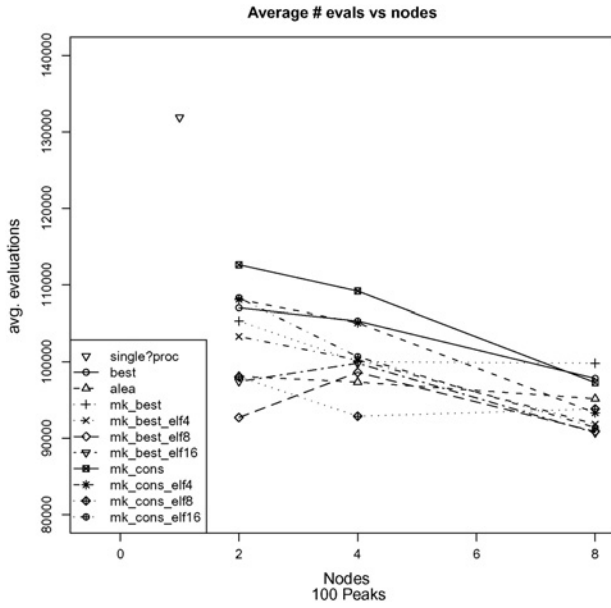


Fig. 3. Number of evaluations needed to find the solution for 100-Peaks from 1 to 8 nodes, for the different migration policies. **best** stands for sending the best individual, **rand** for sending a randomly selected one, **mk_best** for the multikulti policy using the best individual as the population representation, **mk_best_elfN** for the same but using an elite of N individuals to select the individual, **mk_cons** for the multikulti policy using the consensus sequence as population representation, and **mk_cons_elfN** for the same but using an elite of N individuals to select the individual. The number of evaluations is the sum of the evaluations of each node.

mutation. These operators are canonical, and chosen to be general enough and not designed specifically for this type of migration policies, namely, we do not include any provision to make immigrants actually mate with the receiving population. After the pool is generated using roulette wheel selection, individuals are randomly chosen in group of two, changed using crossover and mutation.

The algorithm has been extended with parallel instructions. Every node, after a fixed number of generations, sends an individual representing the population, the best individual or the consensus sequence, to the previous node in the ring. The implementation also includes sentences to check the reception of a population representation from the next node in the ring. After receiving it the node selects an appropriately different individual and sends it to the next node. All nodes thus run asynchronously.

V. EXPERIMENTAL RESULTS

In order to evaluate the model we need to settle different aspects, such as the best way of presenting the population in a concise manner (so as not to take too much bandwidth and processing power), whether using or not an elite from which the individuals to migrate will be chosen, and which is the best size of that elite set. The next subsection studies these issues by comparing the performance of the different policies tested. Each combination was run 30 times, with termination condition being success or a maximum of generations. Results correspond to successful executions. Then, we also compare the execution time of classical migration policies and the

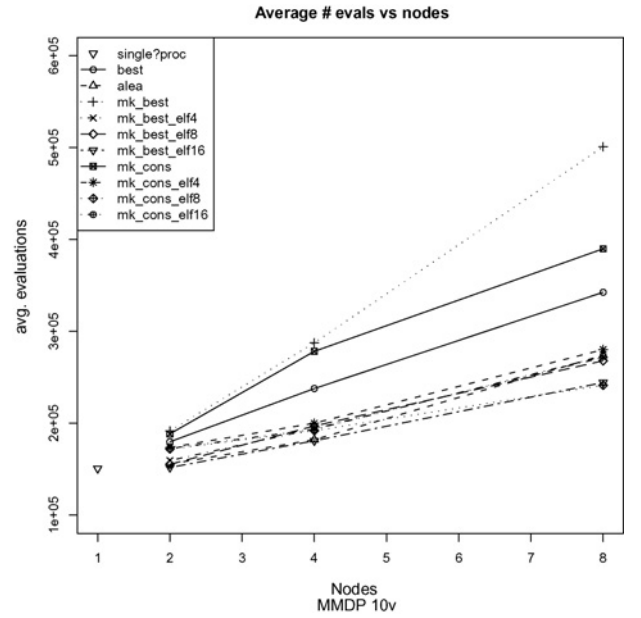


Fig. 4. Number of evaluations needed to find the solution for MMDP with 10 variables and from 1 to 8 nodes, for the different migration policies. **best** stands for sending the best individual, **rand** for sending a randomly selected one, **mk_best** for the multikulti policy using the best individual as the population representation, **mk_best_elfN** for the same but using an elite of N individuals to select the individual, **mk_cons** for the multikulti policy using the consensus sequence as population representation, and **mk_cons_elfN** for the same but using an elite of N individuals to select the individual. The number of evaluations is the sum of the evaluations of each node.

multikulti policy selected as the most representative. In all cases, we compare the results obtained to the sequential version of the same GA. Finally, we have also measured the entropy in order to check whether the quality of the solutions found is truly correlated with it.

A. Performance Comparison

Figs. 3–5 show the average number of evaluations required to reach the solution (successful runs) for the different problems considered and for each representation with different numbers of nodes. Tables III–V show the corresponding numerical values. The parameter corresponding to the maximum number of evaluations for each problem has been chosen to ensure all runs are successful.

We can observe that the results obtained with the classical policies, *best* and *random*, have a wide range of variation. Sometimes they are far from the best result, and sometimes they are closer to it. But neither the *best* nor the *random* policy reach the best average result for any number of nodes in any problem. The differences between the classical policies and the multikulti one tend to increase with the number of nodes, since the population per node becomes smaller and the diversity enhanced by the multikulti policies becomes more relevant.

Another observation is that in all the cases the use of the elite is advantageous, for both representations, *best* and *consensus*. For the 100-Peaks problem with 2 and 4 nodes and using the best individual as the population representation, the best result is obtained with an elite of 4 individuals, while for 8 nodes the best result for this policy is obtained with an elite of

TABLE III

COMPARISON OF MEDIAN, MEAN, AND STANDARD DEVIATION (SD) OF THE TOTAL NUMBER OF EVALUATIONS FOR DIFFERENT POLICIES AND NUMBER OF NODES IN THE 100-Peaks PROBLEM

	2 Nodes			4 Nodes			8 Nodes		
	Median	Mean	SD	Median	Mean	SD	Median	Mean	SD
Best	96924.5	98105.87	17824.85	97 716	97344.47	15828.22	94848.5	95172.67	10512.8
Rand	108981.5	106993.7	19361.77	101 990	105309.5	18231.52	97071.5	97822.7	11733.03
MKB	107326.5	105324.67	21556.67	97547	100009.47	21671.48	99 514	99814.2	12899.24
MKC	109 010	112609.97	28050.55	105 616	109186.17	22017.7	91622.5	97282.63	16613.17
MKB4	93326.5	92713.43	12650.53	95141.5	98627.67	16975.44	91319.5	90865.67	13486.06
MKC4	95641.5	98049.1	17787.62	92 569	92884.83	12080.3	90 844	93830.37	12865.52
MKB8	95 135	97426.7	14573.67	99 541	99817.2	13993.97	88473.5	90724.6	12566.45
MKC8	106079.5	108297.27	21179.13	99243.5	100662.5	17813.82	91 590	91405.97	8282.85
MKB16	103 868	103302.4	16534.54	95 521	100248.9	14482.89	90737.5	91842.4	12641.89
MKC16	108 190	108 086	20444.83	102322.5	105084.33	20398.64	91085.5	93333.83	14392.44

MKB stands for the multikulti policy representing the population with the best individual, MKC, for multikulti representing the population with the consensus sequence, MKBN, for multikulti-best using an elite of N individuals, and MKCN, for multikulti-consensus with elite of the N individuals. Best values appear in boldface.

TABLE IV

COMPARISON OF MEDIAN, MEAN, AND STANDARD DEVIATION (SD) OF THE TOTAL NUMBER OF EVALUATIONS FOR DIFFERENT POLICIES AND NUMBER OF NODES IN THE MMDP PROBLEM WITH TEN VARIABLES

	2 Nodes			4 Nodes			8 Nodes		
	Median	Mean	SD	Median	Mean	SD	Median	Mean	SD
Best	149060.5	155537.63	49237.24	183260.5	182 047	53409.41	269 460	273890.43	77819.2
Rand	169 123	179724.9	51206.6	237 790	237687.6	69392.33	320648.5	342511.13	91096.04
MKB	187789.5	191504.67	50971.79	255702.5	287506.63	105213.25	489 495	500995.67	135902.79
MKC	183 724	188349.83	43450.76	270 729	278197.07	73423.41	408297.5	389865.2	123275.03
MKB4	150009.5	155114.3	42143.73	184476.5	196927.33	46438.72	261608.5	267921.77	64547.91
MKC4	168 132	171803.77	44036.09	177368.5	191838.17	57030.98	227583	241308.47	55012.64
MKB8	152683.5	151752.3	36322.57	177 309	180794.53	41358.96	238407.5	244246.87	54150.05
MKC8	154 703	172513.9	51737.54	187 621	193246.87	57742.43	247908.5	272755.63	77676.21
MKB16	147371.5	159278.53	41676.53	184394.5	193893.23	54842.35	243662	271616.3	92420.69
MKC16	164 486	173508.7	47782.02	184535.5	199946.8	49 038	264 876	280 123	85598.41

MKB stands for the multikulti policy representing the population with the best individual, MKC, for multikulti representing the population with the consensus sequence, MKBN, for multikulti-best using an elite of N individuals, and MKCN, for multikulti-consensus with elite of the N individuals. Best values appear in boldface.

TABLE V

COMPARISON OF MEDIAN, MEAN, AND STANDARD DEVIATION (SD) OF THE TOTAL NUMBER OF EVALUATIONS FOR DIFFERENT POLICIES AND NUMBER OF NODES IN THE MMDP PROBLEM WITH 15 VARIABLES

	2 Nodes			4 Nodes			8 Nodes		
	Median	Mean	SD	Median	Mean	SD	Median	Mean	SD
best	794667.5	938 328	501242.94	969 191	1058849.57	399410.37	1 167 855	1203659.17	299642.98
rand	1049953.5	1139739.1	406117.81	1222458.5	1268339.13	419397.59	1565413.5	1622745.87	593822.8
MKB	1 303 143	1301492.27	397765.78	1 589 259	1829996.03	686372.12	2497095.5	2454792.23	694284.21
MKC	1197690.5	1265176.4	379353.79	1819872.5	1922086.27	555959.6	3 007 514	2967528.8	960376.9
MKB4	879812.5	939949.8	353516.72	980 455	1018048.7	388815.33	924558.5	1054506.33	367731.59
MKC4	825 289	918957.97	438783.73	906518.5	990503.2	359069.46	1 214 125	1184510.67	303949.94
MKB8	873 590	937391.17	442380.83	859414.5	931306.73	278 118.27	1017394.5	1104681.87	428080.19
MKC8	789584.5	842215.47	264369.77	850807.5	997 860	518566.15	1 137 170	1191909.47	462464.59
MKB16	960279.5	960058.33	361354.21	1100143.5	1087952.8	339926.35	1 470 018	1563973.37	436592.34
MKC16	874543.5	1018206.17	524575.22	1129779.5	1129193.57	435669.69	1 405 006	1464780.7	381161.91

MKB stands for the multikulti policy representing the population with the best individual, MKC, for multikulti representing the population with the consensus sequence, MKBN, for multikulti-best using an elite of N individuals, and MKCN, for multikulti-consensus with elite of the N individuals. Best values appear in boldface.

TABLE VI

WILCOXON TEST OF THE NUMBER OF EVALUATIONS RESULTS FOR 100-Peaks WITH 2, 4, AND 8 NODES FOR DIFFERENT MIGRATION POLICIES

	R	B	MKB	MKC	MKB4	MKC4	MKB8	MKC8	MKB16	MKC16
R	1									
B	+0.01307	1								
MKB	0.3257	0.1701	1							
MKC	0.8357	+0.001594	0.2590	1						
MKB4	+0.0001285	+0.01291	+0.004963	+0.0001582	1					
MKC4	+0.0002434	+0.01291	+0.01093	+0.0007551	0.6298	1				
MKB8	+0.002913	+0.0572	+0.05053	+0.002301	0.3215	0.6277	1			
MKC8	+0.002913	+0.04223	0.5585	0.1166	+0.02056	+0.03586	0.1588	1		
MKB16	+0.03462	+0.0726	0.2713	+0.03341	+0.054	0.1227	0.3257	0.64	1	
MKC16	0.3517	+0.01563	0.9464	0.2713	+0.004704	+0.01473	+0.04854	0.547	0.2676	1

B stands for sending the best individual, R, for a random one, MKB, for the multikulti policy representing the population with the best individual, MKC, for multikulti representing the population with the consensus sequence, MKBN, for multikulti-best using an elite of N individuals, and MKCN, for multikulti-consensus with elite of N individuals. Statistically significant differences with a confidence above 90% are marked with +.

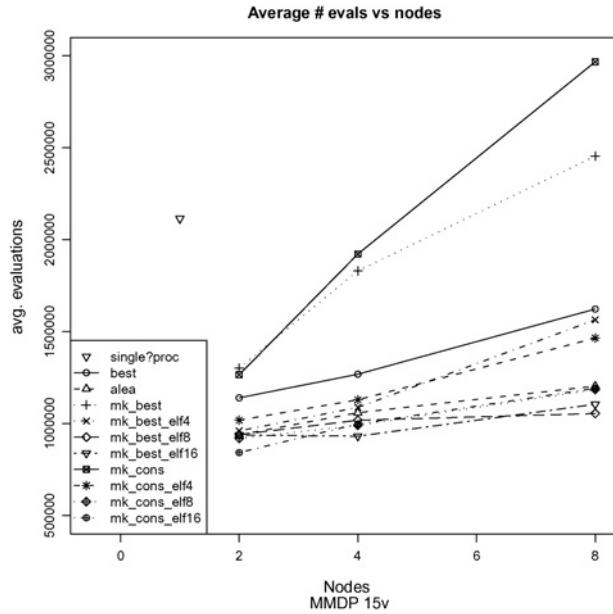


Fig. 5. Number of evaluations needed to find the solution for MMDP with 15 variables and from 1 to 8 nodes, for the different migration policies. **best** stands for sending the best individual, **rand** for sending a randomly selected one, **mk_best** for the multikulti policy using the best individual as the population representation, **mk_best_elfN** for the same but using an elite of N individuals to select the individual, **mk_cons** for the multikulti policy using the consensus sequence as population representation, and **mk_cons_elfN** for the same but using an elite of N individuals to select the individual. The number of evaluations is the sum of the evaluations of each node.

8 individuals. Using the consensus sequence as representation, the best result is for an elite of 8 individuals for 2 nodes and of 4 individuals for 4 and 8 nodes. For the MMDP problem with 10 variables and for the best representation, the best result for 2 nodes is reached using an elite of 4 individuals, and of 8 individuals for 4 and 8 nodes. For the consensus representation the best result for 2 nodes corresponds to an elite of 8 individuals, and for 4 and 8 nodes of 4 individuals. For MMDP with 15 variables the best results for the best representation are obtained with an elite of 8 individuals for 2 and 4 nodes, and of 4 individuals for 8 nodes. For the consensus sequence the best result corresponds to an elite of 8 individuals for 2 nodes and of 4 for 4 and 8 nodes. Although

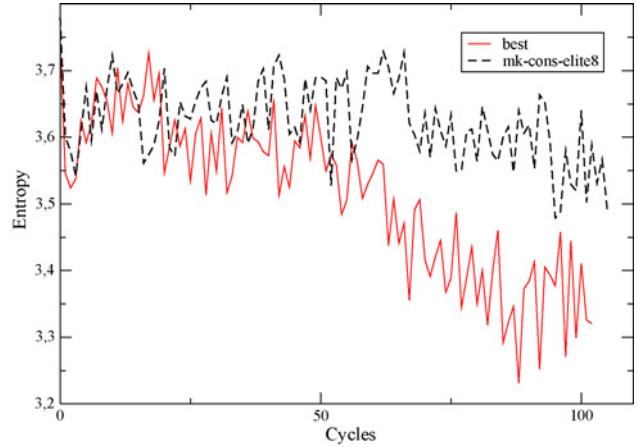


Fig. 6. Entropy (computed using the Shannon formula $H(P) = -\sum_{g \in P} p(f(g)) \log_b p(f(g))$, where g is a member of the population, $f(g)$ its fitness, and $p(f(g))$ the frequency of that fitness across the whole population) in a typical run of the MMDP problem, with the multikulti-cons-elite8 migration policy (mk-cons-elite8) and the best migration policy (best). Measures are taken after each migration cycle of 20 generations. The figure compares average values of eight runs in parallel.

the optimal size of the elite set depends on the problem and the number of nodes, we think that an elite of 8 individuals is a good choice in average, specially looking at the significance tables that are presented below.

Comparing the two representations of the population, the best individual and the consensus sequence, we can see that both of them are able to improve the results of the classical migrations policies, being the differences among them very small.

Tables VI–VIII present the results of a Wilcoxon test to assess the statistical significance of the differences among the different migration policies tested. Each table presents the data corresponding to each policy for the different numbers of nodes considered, normalizing the values with respect to the average of the random policy. We can observe in the three problems that the results of the Wilcoxon test are less than 0.1 among the multikulti policy using the consensus sequence as representation and an elite of eight individuals and the classical policies. In fact, in most cases it is less than 0.1. The statistical significance is smaller in some cases among different

TABLE VII

WILCOXON TEST OF THE NUMBER OF EVALUATION RESULTS FOR MMDP WITH TEN VARIABLES (60 BITS) AND 2, 4, AND 8 NODES FOR DIFFERENT MIGRATION POLICIES

	R	B	MKB	MKC	MKB4	MKC4	MKB8	MKC8	MKB16	MKC16
R	1									
B	+1.047e-05	1								
MKB	+6.231e-05	+3.772e-14	1							
MKC	+0.01557	+6.448e-11	+0.06904	1						
MKB4	+1.361e-05	+0.06096	+1.910e-14	+4.566e-11	1					
MKC4	+9.17e-06	+0.09055	+4.907e-14	+1.098e-10	0.64	1				
MKB8	+1.938e-08	+0.03078	+2.2e-16	+2.220e-14	+0.0879	0.2701	1			
MKC8	+0.0004798	+0.02892	+1.186e-11	+1.726e-08	0.5897	0.3286	+0.03955	1		
MKB16	+2.827e-05	+0.07825	+1.654e-13	+3.422e-10	0.741	0.8896	0.2015	0.4272	1	
MKC16	+0.001563	+0.01032	+1.831e-11	+2.105e-08	0.2128	0.1026	+0.004438	0.6196	0.1403	1

B stands for sending the best individual, R, for a random one, MKB, for the multikulti policy representing the population with the best individual, MKC for multikulti representing the population with the consensus sequence, MKBN, for multikulti-best using an elite of N individuals, and MKCN, for multikulti-consensus with elite of 4 individuals. Statistically significant differences with a confidence above 90% are marked with +.

TABLE VIII

WILCOXON OF THE NUMBER OF EVALUATION RESULTS FOR MMDP WITH 15 VARIABLES (90 BITS) AND 2, 4, AND 8 NODES FOR DIFFERENT MIGRATION POLICIES

	R	B	MKB	MKC	MKB4	MKC4	MKB8	MKC8	MKB16	MKC16
R	1									
B	+1.570e-05	1								
MKB	+2.565e-08	+2.2e-16	1							
MKC	+1.429e-10	+2.2e-16	0.1614	1						
MKB4	+6.282e-07	+0.03667	+2.2e-16	+2.2e-16	1					
MKC4	+1.212e-06	+0.06036	+2.2e-16	+2.2e-16	0.644	1				
MKB8	+9.445e-08	+0.01546	+2.2e-16	+2.2e-16	0.644	0.3532	1			
MKC8	+6.454e-08	+0.01925	+2.2e-16	+2.2e-16	0.7628	0.3343	0.8424	1		
MKB16	+0.02979	+0.001235	+1.665e-14	+2.2e-16	+0.0005008	+0.002173	+0.0001117	+0.0001734	1	
MKC16	+0.03201	+0.003663	+2.184e-12	+1.621e-14	+0.004810	+0.009742	+0.001269	+0.001563	0.8874	1

B stands for sending the best individual, R, for a random one, MKB, for the multikulti policy representing the population with the best individual, MKC, for multikulti representing the population with the consensus sequence, MKBN, for multikulti-best using an elite of N individuals, and MKCN, for multikulti-consensus with elite of the N individuals. Statistically significant differences with a confidence above 90% are marked with +.

multikulti policies, which indicates that the other alternatives, such as the best individual as population representation can also be valid. We can also observe that statistical significance becomes greater for the MMDP problem with 15 variables, that is the more difficult one.

B. Running Time Comparison

Though we have shown the comparison for the number of evaluations, which is less dependent on the network features, we also want to present the execution times in order to show the equivalence of both measures. Tables IX–XI compare the median, mean and standard deviation of different migrations policies for different numbers of nodes. We can see that in all the problems and numbers of nodes the best results correspond to a multikulti policy, sometimes with the best representation, sometimes with the consensus sequence, and using an elite of 4 or 8 individuals. Furthermore, the differences among both policies and elite of 4 or 8 individuals are very small. We can also observe that the deviation associated with these cases is smaller than for other policies.

This proves that, even if multikulti policies are computationally more complex than the simple method of sending a random or the best individual, it does not increase running time so much as to offset the improvements in the number of evaluations.

Concerning the number of nodes, we can see that a quite steady behavior is found for the three problems, which leads to expect an improvement of the system performance as more nodes are added. Nevertheless it will be interesting to test the system in a larger cluster to be able to measure speedups more accurately; however, that lies beyond the scope of this paper.

We have also computed the statistical significance for the execution times. Tables XII–XIV present the results. We can observe that in this case the statistical significance for all the tested problems and number of nodes is even higher than for the number of evaluations.

C. Evolution of Entropy

In order to investigate whether the quality of the solutions found is truly correlated with entropy, we have measured the entropy for some MMDP-15 experiments, chosen for being the hardest problem of the set. Results are presented in Fig. 6, which shows the evolution of the phenotypic entropy (computed using the Shannon formula) with the multikulti migration policy using the consensus sequence as representation and an elite of 8 individuals (mk-cons-elite8) and the best migration policy (best); this policy was chosen since it consistently shows the best or close to the best results. The graph shows the averages of the entropy registered at each node in a typical run for every considered policy. The multikulti

TABLE IX

 COMPARISON OF MEDIAN, MEAN, AND STANDARD DEVIATION (SD) OF THE EXECUTION TIME (μ s) FOR DIFFERENT POLICIES AND NUMBER OF NODES IN THE 100-Peaks PROBLEM

	2 Nodes			4 Nodes			8 Nodes		
	Median	Mean	SD	Median	Mean	SD	Median	Mean	SD
best	118 700 177	121 808 945	21388033.1	59 059 993	59 558 923	9 576 572	28 812 665	29 175 866	3 456 335
rand	126 048 527	130 332 421	25463856.5	63 856 660	63 629 417	11 031 999	29 870 856	30 137 087	3 547 751
MKB	130 394 466	126 351 652	26609594.9	57 564 069	60 145 552	14 112 773	29 984 230	30 102 950	3 866 451
MKC	130 459 459	132 494 362	33481700.2	65 466 755	65 174 299	13 075 805	27 161 196	28 973 321	5 034 809
MKB4	109 387 655	110 053 452	16 524 933	58 426 694	58 804 544	9952928	27 309 920	27 068 552	3 985 523
MKC4	112 843 042	117 993 644	22 282 106	55 787 321	55 806 730	7249975	27 427 799	28 226 452	3 804 144
MKB8	117 484 724	117 833 608	18 513 371	58 721 301	59 192 035	8 208 652	26 729 806	27 263 827	3 787 503
MKC8	127 704 618	130 177 084	25 788 646	61 165 717	60 460 861	10 292 872	27 166 656	27 378 560	2 476 568
MKB16	122 175 655	124 425 945	20 831 869	58 575 339	59 563 690	8 521 579	27 448 283	27 561 457	3 844 003
MKC16	127 311 181	129 263 693	25 181 349	60 516 374	63 402 167	12 832 919	27 101 809	28 007 323	4 384 046

MKB stands for the multikulti policy representing the population with the best individual, MKC for multikulti representing the population with the consensus sequence, MKBN for multikulti-best using an elite of N individuals, and MKCN for multikulti-consensus with elite of the N individuals. Best values appear in boldface.

TABLE X

 COMPARISON OF MEDIAN, MEAN, AND STANDARD DEVIATION (SD) OF THE EXECUTION TIME (μ s) FOR DIFFERENT POLICIES AND NUMBER OF NODES IN THE MMDP PROBLEM WITH TEN VARIABLES

	2 Nodes			4 Nodes			8 Nodes		
	Median	Mean	SD	Median	Mean	SD	Median	Mean	SD
best	8373855.5	9058809.4	2971080.2	4799193.5	4843402.7	1325557.5	3464928.5	3407118.6	961254.8
rand	9 783 591	10428427.2	3191766.6	6285375.5	6266700.4	1757245.6	4143075.5	4313334.6	1134305.2
MKB	11 200 815	11145211.6	2925 950	6 834 502	7586509.1	2758314.3	6171374	6290105.4	1691440.9
MKC	11008534.5	11243309.5	2639374.1	7 030 303	7475108.77	1889004.4	5248880	5025058.1	1560147.1
MKB4	8951518.5	8995488.8	2484969.7	4 917 713	5241330.3	1190245.1	3336116.5	3352991.4	777724.9
MKC4	9562002.5	10024332.6	2681897.4	4732385.5	5153904.8	1492323.3	2972865.5	3091278.4	690843.1
MKB8	8 495 346	8755510.6	2023456.3	4687995	4836601.4	1089773.8	3035680.5	3080224.8	669723.7
MKC8	9486890.5	10 096 388	2905025.7	4961798.5	5160975.3	1487588.2	3 160 592	3468843.6	945729.6
MKB16	8832084.5	9289677.7	2376310.7	4 971 878	5169300.6	1407504.1	3 120 183	3416939.6	1130878
MKC16	9491635.5	10166771.4	3001534.1	4 872 894	5355426.6	1269353.4	3 311 469	3534043.1	1056027.5

MKB stands for the multikulti policy representing the population with the best individual, MKC for multikulti representing the population with the consensus sequence, MKBN for multikulti-best using an elite of N individuals, and MKCN for multikulti-consensus with elite of the N individuals. Best values appear in boldface.

TABLE XI

 COMPARISON OF MEDIAN, MEAN AND STANDARD DEVIATION (SD) OF THE EXECUTION TIME (μ s) FOR DIFFERENT POLICIES AND NUMBER OF NODES IN THE MMDP PROBLEM WITH 15 VARIABLES

	2 Nodes			4 Nodes			8 Nodes		
	Median	Mean	SD	Median	Mean	SD	Median	Mean	SD
best	57373019.5	66184912.1	34159128.2	31146116.5	34 129 942	12760687.9	18540502.5	19331182.1	4731796.5
rand	75051094.5	81290964.3	28782373.4	39 506 947	42315293.5	13966964.4	25 338 818	26273564.9	9541044.1
MKB	89720224.5	93201556.4	30037523.1	52 933 182	61100311.4	22728627.8	40543916.5	40086146.3	11 267 529
MKC	87753405.5	92740347.4	27762597.8	62 368 363	66136062.3	19686919.6	50448613.5	49238153.9	15778389.1
MKB4	63 783 927	67303342.6	24773288.1	32 043 157	33933764.1	13583564.1	14 959 929	17087749.5	5920531.5
MKC4	56 221 249	65743701.7	31637653.9	30 240 931	33065569.9	11755805.9	19838598.5	19306482.9	4891593.4
MKB8	61432039.5	65752695.1	28824873.3	28 508 856	30918720.2	9364492.3	16649714.5	17864782.4	6876657.9
MKC8	54 611 366	60274541.2	19431863.3	28 660 214	33243353.5	17034204.2	18 799 917	19536330.6	7567293.2
MKB16	63654388.5	67537074.8	24704829.6	36 404 881	36273815.2	11157919.1	23636278.5	25216740.8	6987955.7
MKC16	62 631 764	73428940.6	38602713.6	36118820.5	37 997 933	14689245.9	23 117 150	24129072.4	6315158.5

MKB stands for the multikulti policy representing the population with the best individual, MKC for multikulti representing the population with the consensus sequence, MKBN for multikulti-best using an elite of N individuals, and MKCN for multikulti-consensus with elite of the N individuals. Best values appear in boldface.

TABLE XII

WILCOXON TEST OF THE EXECUTION-TIME RESULTS FOR 100-Peaks WITH 2, 4, AND 8 NODES FOR DIFFERENT MIGRATION POLICIES

	R	B	MKB	MKC	MKB4	MKC4	MKB8	MKC8	MKB16	MKC16
R	1									
B	+0.03846	1								
MKB	0.1133	0.6379	1							
MKC	0.4596	0.2801	0.4492	1						
MKB4	+7.608e-06	+0.007009	+0.003226	+0.0004597	1					
MKC4	+2.722e-05	+0.02462	+0.01606	+0.005893	0.3458	1				
MKB8	+0.0005008	+0.01206	+0.06154	+0.01076	0.2246	0.64	1			
MKC8	+0.03413	+0.08626	0.5624	0.2290	+0.009267	+0.06075	0.1571	1		
MKB16	+0.004985	+0.04124	0.2402	+0.0822	+0.03927	0.2076	0.4011	0.5023	1	
MKC16	0.1153	+0.07303	0.96	0.4289	+0.003537	+0.02873	+0.06562	0.7153	0.2944	1

B stands for sending the best individual, R for a random one, MKB, for the multikulti policy representing the population with the best individual, MKC for multikulti representing the population with the consensus sequence, MKBN for multikulti-best using an elite of N individuals, and MKCN for multikulti-consensus with elite of N individuals. Statistically significant differences with a confidence above 90% are marked with +.

TABLE XIII

WILCOXON TEST OF THE EXECUTION-TIME RESULTS FOR MMDP WITH TEN VARIABLES (60 BITS) AND 2, 4, AND 8 NODES FOR DIFFERENT MIGRATION POLICIES

	R	B	MKB	MKC	MKB4	MKC4	MKB8	MKC8	MKB16	MKC16
R	1									
B	+6.134e-06	1								
MKB	+3.961e-05	+1.358e-14	1							
MKC	+0.002677	+2.184e-12	0.2004	1						
MKB4	+2.398e-05	0.5624	+1.399e-14	+3.154e-12	1					
MKC4	+2.368e-05	0.644	+7.283e-14	+1.284e-11	0.8536	1				
MKB8	+3.278e-08	+0.03652	+2.2e-16	+8.882e-16	0.08528	0.1877	1			
MKC8	+0.000779	+0.01546	+1.21e-11	+2.938e-09	0.3386	0.2827	+0.01619	1		
MKB16	+4.266e-05	+0.06016	+1.519e-13	+3.224e-11	0.8806	0.9078	0.1622	0.3343	1	
MKC16	+0.002323	+0.005729	+1.659e-11	+2.99e-09	0.1514	0.1291	+0.002506	0.7346	0.1522	1

B stands for sending the best individual, R for a random one, MKB, for the multikulti policy representing the population with the best individual, MKC for multikulti representing the population with the consensus sequence, MKBN for multikulti-best using an elite of N individuals, and MKCN for multikulti-consensus with elite of 4 individuals. Statistically significant differences with a confidence above 90% are marked with +.

TABLE XIV

WILCOXON TEST OF EXECUTION-TIME RESULTS FOR MMDP WITH 15 VARIABLES (90 BITS) AND 2, 4, AND 8 NODES FOR DIFFERENT MIGRATION POLICIES

	R	B	MKB	MKC	MKB4	MKC4	MKB8	MKC8	MKB16	MKC16
R	1									
B	+4.485e-06	1								
MKB	+2.248e-08	+2.2e-16	1							
MKC	+1.140e-11	+2.2e-16	+0.07307	1						
MKB4	+4.202e-07	+0.05413	+2.2e-16	+2.2e-16	1					
MKC4	+1.711e-06	+0.09282	+2.2e-16	+2.2e-16	0.572	1				
MKB8	+5.241e-08	+0.02448	+2.2e-16	+2.2e-16	0.6056	0.2997	1			
MKC8	+1.159e-07	+0.03577	+2.2e-16	+2.2e-16	0.8023	0.3995	0.829	1		
MKB16	+0.01920	+0.0006485	+1.243e-14	+2.2e-16	+0.0006804	+0.003636	+9.471e-05	+0.0002056	1	
MKC16	+0.04789	+0.001328	+3.421e-12	+3.775e-15	+0.002677	+0.00824	+0.0005935	+0.001257	0.9214	1

B stands for sending the best individual, R for a random one, MKB, for the multikulti policy representing the population with the best individual, MKC for multikulti representing the population with the consensus sequence, MKBN for multikulti-best using an elite of N individuals, and MKCN for multikulti-consensus with elite of the N individuals. Statistically significant differences with a confidence above 90% are marked with +.

policy keeps the entropy high along the evolution while the policy of migrating the best provides quite much lower levels of entropy, with an almost continuous decreasing trend. This proves the utility of the multikulti policy to maintain diversity, and supports the result that the improvement in the number of evaluations is due precisely to this diversity-enhancing effect brought by the *multikulti* policies.

D. A Numerical Optimization Problem

In order to confirm the previous findings for other kind of problems we have also tested the system for a numerical

optimization problem, the Rastrigin's function

$$f(x_i|i = 1..n) = 10n + \sum_{i=1}^n x_i^2 - 10\cos(2\pi x_i) : x_i \in [-5.12, 5.12]$$

which presents a global minimum in 0 for $x = (0, \dots, 0)$. It is a linearly separable test function previously used in the study of the behavior of the island model [16]. We have taken $n = 10$ and 10 bits per argument.

Fig. 7 shows the average number of evaluations required to reach the solution (successful runs) to this problem for each representation and with different numbers of nodes. We can

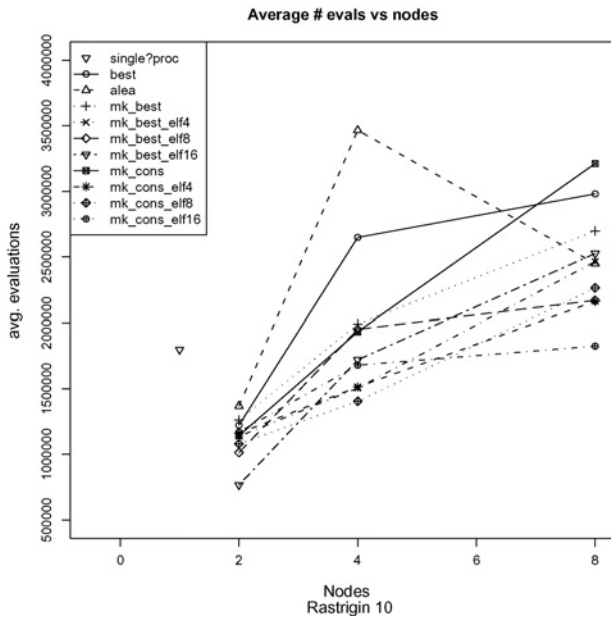


Fig. 7. Number of evaluations needed to find the solution to the Rastrigin's function from 1 to 8 nodes, for the different migration policies. As usual, **best** stands for sending the best individual, **rand** for sending a randomly selected one, **mk_best** for the multikulti policy using the best individual as the population representation, **mk_best_elfN** for the same but using an elite of N individuals to select the individual, **mk_cons** for the multikulti policy using the consensus sequence as population representation, and **mk_cons_elfN** for the same but using an elite of N individuals to select the individual. The number of evaluations is the sum of the evaluations of each node.

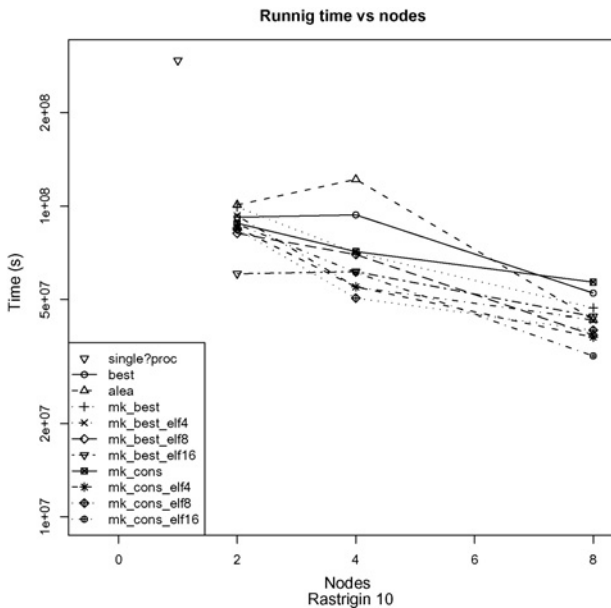


Fig. 8. Execution time required to find the solution to the Rastrigin's function from 1 to 8 nodes, for the different migration policies. The number of evaluations is the sum of the evaluations of each node.

observe that for 2 and 4 nodes all multikulti policies perform better than the classical ones. For 8 nodes the multikulti policies using elite are also better than the classical ones.

In Fig. 8 we can also observe the execution times for the different policies and numbers of nodes. We can observe that again the best results are obtained with the multikulti policies,

specially for those using an elite: for 2 nodes the best result corresponds to *mk_best_elf16*, for 4 nodes to *mk_cons_elf8* and for 8 nodes to *mk_cons_elf16*. Thus the results for this problem confirm results shown above for other kind of problems.

VI. CONCLUSION

In this paper, we have investigated on a real (as opposed to the simulations we used in our previous papers [38]) parallel setup a new mechanism to improve diversity in an island model. This mechanism affects the migrant selection phase of a genetic algorithm, and is based on genotypic differences of the immigrant individual which is included in a destination subpopulation. According to the tradeoff between promoting diversity and favoring the best individuals, we have also considered the individual quality in the selection mechanism, carrying out experiments to discover the best policy for both, representing the destination subpopulation in a concise manner, and selecting the immigrant.

The results obtained prove the usefulness of the multikulti policies, which in most cases outperform non-adaptive random and best-individual migration policies, especially when the number of processors increases and the size of each subpopulation becomes smaller. Results have also shown the usefulness of using an elite from which to select the most different individual. These results support our initial hypothesis according to which, as it happens in nature, there is an optimal degree of difference in the exchanged genetic material to improve evolution. In our case this degree depends on the appropriate level of quality of the associated phenotype, which is given by the size of the elite from which migrants are taken.

Concerning the best manner of representing the target population, results indicate that using the consensus sequence is slightly better in most cases but the best individual is also a valid representation. The consensus sequence might be a better representative (being closer on average to all the population) at the beginning of the run, while the best chromosome might be better at the end of the run. In any case, adaptively selecting a population representative might yield better, or at least more consistent, results.

We have also performed an entropy study which has revealed that multikulti policies effectively increase diversity, which explain why these policies outperform best or random policies. Nevertheless, there are several issues that deserve further studies: first, it is difficult to characterize a population using a single string, second, it is also hard to send an individual that is different enough and, at the same time, is not immediately selected out of the population by its selection policy. Consensus is maybe too drastic a way of representing the population; even if there is just a small difference between allele frequency, one of them will always be the winner. That is why we intend to investigate the representation of the population using *rough* consensus, which only sets an allele value when its frequency is over a threshold, say 70%. We also plan to investigate the application of the ideas presented herein to other types of evolutionary algorithm, and search for the appropriate manner of representing the population for them.

Other possible avenues of research will be to investigate the influence of the topology on the performance, in relation with the average path length from one node to another and in the sense of the general connectivity.

The ideas described herein can also be applied to other GAs when they are run in parallel following an island model, though the effect can be something different depending on the optimal degree of diversity required by each GA. Therefore, it would be interesting to investigate this issue.

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