MultiKulti Algorithm: Migrating the Most Different Genotypes in an Island Model

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Abstract. Migration policies in distributed evolutionary algorithms has not been an active research area until recently. However, in the same way as operators have an impact on performance, the choice of migrants is due to have an impact too. In this paper we propose a new policy (named multikulti) for choosing the individuals that are going to be sent to other nodes, based on multiculturality: the individual sent should be as different as possible to the receiving population (represented in several possible ways). We have checked this policy on different discrete optimization problems, and found that, in average or in median, this policy outperforms classical ones like sending the best or a random individual.

1 Introduction and state of the art

Evolutionary algorithms (EAs) make individuals in the population evolve in parallel, which suggests that the exploitation of parallelism can be quite natural in these algorithms. This has led to many efforts to parallelize them with the intention of reducing the execution time and improving the quality of the solutions. There have been several attempts to classify the numerous works devoted to parallel EAs \cite{1,2}, with island or coarse grained models being one of the most popular approach of parallelization of EAs. This approach is usually implemented on distributed systems, since it does not require a high cost in communications: nodes only exchange a few individuals after several generations. The population is divided in subpopulations, which usually evolve isolatedly except for migrations, that is, the exchange of some individuals after a number of generations. The behavior of the island model differs from the sequential EA, since the composition, and thus the dynamics, of every subpopulation is different: since subpopulations are smaller than the whole population, the parallel EA will converge faster. Furthermore, migrations among subpopulations usually improve the quality of the sequential solutions \cite{3}, which makes the parallel model
interesting even for sequential executions. Not only does this apply to genetic algorithms; similar results have been found for Genetic Programming: Tomassini et al. [4] have analyzed diversity in multipopulation genetic programming (GP) finding a correlation between diversity and the better convergence properties of distributed GP.

These results have inspired this work. Diversity in the subpopulation is so important that it leads to improvement in quality and efficiency at the same time. Accordingly, we have looked for the way of enhancing the diversity induced by the usual migration policies, by using the notion of *multiculturality*: migrants should be chosen on the basis of genotypic difference to the receiving population; we have called this new migrant-selection policy *multikulti*.

Let us then look at how these diversity enhancement could be realized through migration policies, which include several issues:

– the number of individuals undergoing migration,
– the frequency of migration, i.e. the number of generations or evaluations between migrations,
– the policy for selecting migrants,
– the migration replacement policy,
– the topology of the communication among subpopulations,
– the synchronous or asynchronous nature of the communications.

These issues have been investigated in different papers: Alba et al. [5] compare synchronous and asynchronous migration policies, Herrera et al. [6] studied some of the aforementioned issues in a hierarchical configuration of subpopulations, and Cantú-Paz [7,8], Alba and Troya [9], and Noda et al. [10] have analyzed different migration policies. Several results presented in these mentioned works indicate that diversity is a fundamental key in the success of the island model. For example, works comparing synchronous versus asynchronous models [5], have found that the asynchronous algorithms outperformed the synchronous ones in all the experiments. Cantú-Paz [7,8] has studied the four possible combinations of random and fitness-based emigration and replacement of existing individuals. He found that the migration policy that causes the greatest reduction in work (takeover time\(^2\)) is to choose both the migrants 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 [8] states referring to parallel EAs:

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

So, other policies must also be considered. In fact, Alba and Troya [9] found that migration of a random string prevents the “conquest” effect in the target

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1. *Multikulti*, as defined by the wikipedia entry [http://en.wikipedia.org/wiki/Multikulti](http://en.wikipedia.org/wiki/Multikulti), is an slogan for a multicultural approach to public policy.

2. Number of generations required to converge to the best individual from the initial population, by applying selection only.
island for small or medium sized sub-populations. Noda et al. [10] have proposed choosing which individuals to migrate and/or replace adaptively depending on some knowledge-oriented rules. To do this, each agent receives information about the fitness function from its peers. The tested adaptive policies have proved useful providing best solutions than the sequential execution.

In spite of the results shown above, there is still a number of issues that have not been investigated yet. In this work we also focus on the policy for migrants selection. Previous works dealing with this aspect have studied the use of any of the selection operators usually applied in evolutionary algorithms: proportional selection, tournament, random, etc. Only the work by Noda et al. [10] considers, among other policies, one in which the individuals sent are chosen to be quite different from others previously sent.

The aim of this work is to exploit differences in the various subpopulation. To do this, we focus on the selection of the individuals to be sent to other subpopulation. Our thesis is that migrating individuals different enough to the destination subpopulation instead of the best individuals can result in a better performance through the diversity enhancement it produces. Consider the Figure 1 with two subpopulations. The black points represent the distribution of the population along the function to optimize. Individual \( a \) in subpopulation P1 has the highest fitness, and thus it would be sent to subpopulation P2 following the most common migration policies. We propose to send individual \( b \), whose genotype is quite different from those of subpopulation P2. In the example it would lead to exploration of a new area of the search space where the global optimum is placed. In order to achieve this, the process corresponding to subpopulation P1 needs to receive information on the composition of the individuals in subpopulation P2. We have considered different ways of providing this information in a concise manner. One of them is taken the best individual of subpopulation P2 as representative. The other one is using a kind of average genotype, the consensus sequence described later, as representative of subpopulation P2. Another important issue to investigate if the trade-off between promoting diversity and favoring the best individuals. The risk of sending the most different individual as migrant is that if its fitness value is low compared to those of the destination subpopulation, the migrant would probably disappear immediately. Therefore, another question tested in the experiments has been if the most different individual is fit enough to survive when migrating, or if it is best to select the most different from an elite.

The rest of the paper proceeds as follows: section 2 describes the model details; section 3 is devoted to describe the evolutionary algorithm and its implementation; section 4 presents and discusses the experimental results, and section 5 draws the main conclusions of this work.

2 Model Description

We have considered a ring topology (Figure 2), in which each node can send one or more individuals to the next node in the ring. To perform the choice of the
migrants, the node $P_i$ receives from node $P_{i+1}$ information about the genotype of its subpopulation. We have considered two different ways of representing this information in a concise manner:

1. With the best individual of the subpopulation. After a number of generations without exchanging individuals we can expect that each subpopulation is close enough to converge for the best individual being a fair representation of the whole population.
2. With the consensus sequence of the population. This is a concept taken from biology where it is defined as the sequence that reflects the most common choice of base or amino acid at each position of a genome. Areas of particularly good agreement often represent conserved functional domains. In our case it is composed of the most frequent allele for each position of the genotype.

Once the node $P_i$ has got this information, it sends to node $P_{i+1}$ an individual different enough from the subpopulation $P_{i+1}$ representative. Here we have considered two approaches:

- **Base**: Selecting the most different from the subpopulation $P_i$.
- **Elite**: Selecting the most different among the best half of subpopulation $P_i$.
3 Implementation

Chromosomes of our GA are fixed-length binary strings. The selection mechanism to choose individuals for the new population uses a steady state algorithm, with two-point crossover operator and single-bit-flip mutation. The rest of the parameters are shown in tables (a) and (b).

| Parameter                  | Value |
|----------------------------|-------|
| Population                 | 32    |
| Selection rate             | 60%   |
| Generations to migration   | 20    |
| Mutation priority          | 2     |
| 2-point crossover priority | 3     |

| Parameter                  | Value |
|----------------------------|-------|
| Chromosome length          | 120   |
| Population                 | 256   |
| Selection rate             | 20%   |
| Generations to migration   | 20    |
| Mutation priority          | 2     |
| 2-point crossover priority | 3     |
| Max number of evaluations  | 200000|

Table 1. Evolutionary algorithm parameters used in the P-Peaks (a) and in the MMDP (b) experiments.

P-Peaks and the massively multimodal deceptive problem (MMDP), two of the three discrete optimization problems presented in [12] have been selected for testing. These problems, while being both multimodal, represent different degrees of difficulty for parallel evolutionary optimization. They will be described below.

These two problems have been implemented and integrated in the Algorithm::Evolutionary library, which is freely available under the GPL license from http://opeal.cvs.sourceforge.net/opeal/Algorithm-Evolutionary/. In order to simulate a parallel algorithm, the cooperative multitasking Perl module POE has been used; each node is represented by a POE session. The rest of the evolutionary algorithm has been implemented using the same Algorithm::Evolutionary Perl module [13]. The program, along with the parameter sets used, is also available under an open source license from the same site.

In this simulated parallel scenario, each node runs a rank-based substitution, steady state algorithm. At the end of a preset number of generations, each node sends a single individual to the other node according to the policy being tested.

3.1 Problems tested

Two functions have been used for testing: P-Peaks and MMDP, two of the three discrete optimization problems presented in [12]: The massively multimodal deceptive problem (MMDP) and the problem generator P-Peaks. These problems, while being both multimodal, represent different degrees of difficulty for parallel evolutionary optimization. They will be described next.
The MMDP [14] 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 next:

\[
\begin{align*}
\text{fitness}_{s_i}(0) &= 1.0, \\
\text{fitness}_{s_i}(1) &= 0.0, \\
\text{fitness}_{s_i}(2) &= 0.360384, \\
\text{fitness}_{s_i}(3) &= 0.640576, \\
\text{fitness}_{s_i}(4) &= 0.360384, \\
\text{fitness}_{s_i}(5) &= 0.0, \\
\text{fitness}_{s_i}(6) &= 1.0
\end{align*}
\]

The fitness value is defined as the summatory of the $s_i$ subproblems with an optimum of $k$ (equation 1). The number of local optima is quite large ($2^k$), while there are only $2^k$ global solutions. In this paper, we consider a single instance with $k = 20$.

\[
\text{fitness}_{s_i} = \sum_{i=1}^{k} \text{fitness}_{s_i}
\]

The P-Peaks problems is a multimodal problem generator proposed by De Jong in [15], and is created by generating $P$ random $N$-bit strings where the fitness value of a string $x$ is the number of bits that $x$ has in common with the nearest peak divided by $N$. In the experiments made in this paper we will consider $P = 100$; the optimum fitness is 1.0.

\[
f_{P-Peaks}(x) = \frac{1}{N} \max_{1 \leq i \leq P} \{N - \text{HammingDistance}(x, Peak_i)\}
\]

We consider an instance of $P = 100$ and 64 bits where the optimum fitness is 1.0 (Equation 2).

These two problems have been also implemented and integrated in the Algorithm::Evolutionary library.

4 Experimental results

First, we tested several parameter configurations for the P-Peaks problem. In general, when diversity conditions are not too harsh, the performance difference between different migration policies is not too high. Eventually, when the going gets tough, differences such as those shown in Figure 3 do appear. In that graph, taken for a 8-node, population = 32 experiment, results are quite different depending on the migration policy. For starters, sending the best individual yields the worst results. If we consider the median, the multikulti is similar to the random policy, but its behavior is better if we consider the average and the worst case, as shown in table 2.

The MMDP was also tested with a similar setup; results are shown in figure 4 where three new versions of the algorithm, named multikulti-elite, consensus-multikulti and multikulti-elite-consensus, have been tested. Multikulti-elite chooses the individual most different to the receiving population best individual, but only among the 50% best. In this case, not surprisingly, this strategy beats the multikulti by far as well as the random strategy, but more closely. This is probably due to the nature of the MMDP: it is a deceptive problem, where increasing diversity might not have the desired result, since competing conventions for the
best mk random
1000 2000 5000 10000 20000 50000
Policies comparison, P−Peaks problem

Fig. 3. Boxplot (with logarithmic y axis) of the number of evaluations needed to find the solution in the P−Peaks problem. best represents the behavior of the experiment when the best individual in the population is sent, random with a random individual, and finally mk, in the middle, stands for multikulti, the algorithm we are testing in this paper which sends the individual in the population most different to the best in the receiving population.

same 6-bits portion can lead in each population. This why, instead of sending the most different as the multikulti policy does, doing it with one that is different enough, but at the same time, fit enough, produces the best results.

The second strategy tested, consensus-multikulti, achieves an intermediate performance among the two, beating the multikulti, but achieving worse results than multikulti-elite. This strategy sends the individual that is most different to the consensus string, that is, the string whose every bit represents the majority value for that position among the population. The result is probably due to the same reason: a value that is too different represents a high disturbance, and thus is bad for diversity. In fact, the third strategy, multikulti-elite-consensus, which sends the individual most different to the consensus string which is among the
| Policy       | Median | Average |
|--------------|--------|---------|
| Best         | 25820  | 25310   |
| Random       | 1545   | 6410    |
| Multikulti   | 1544   | 1252    |

Table 2. Statistics for number of evaluations of different migration policies for the P-Peaks problem.

50% best, achieves results similar to Multikulti-elite, although, in general, a bit better.

In order to investigate what is going on, we have measured the entropy for the MMDP. The results are shown in Figure 5, which shows the different evolution paths of phenotypic entropy (computed using the Shannon formula) with the multikulti-elite migration policy (left) and the best migration policy (center). The behavior es quite different. The multikulti policy, not only keeps the entropy high, but considerably increases it in some populations during evolution. The policy of migrating the best provides quite much lower levels of entropy; with a decreasing trend that never changes, leading to a collapse of entropy from cycle 12. 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.

5 Conclusions

This paper has explored new alternatives to promote diversity in an island model. This is achieved by selecting as migrant individuals with a genotype different enough to the destination population. Because there is a trade-off between promoting diversity and favoring the best individuals, we have performed experiments to find out the degree of difference which produces the best results. These experiments have shown that results only improve substantially if the migrant is chosen from the elite; that is, those with an above-average fitness, which indicates that diversity only improves the results if the incoming migrant has a minimum level of quality. We have compared two different ways of characterizing the destination population: the best individual and the consensus sequence. Results have shown that both of them represent appropriately the population, with the consensus sequence performing only slightly better. Studying the phenotypic entropy of the population we have found that our method effectively improves entropy by avoiding entropy to fall too fast and also creating an entropy differential among populations, and thus diversity.

In the future we intend to develop a parallel implementation of the system, which will allow us to measure also execution times. We are also working on alternative mechanisms to characterize the destination population, and thus select the more appropriate migrants. We will also test results obtained by changing other algorithm parameter such as number of migrants or the number of nodes.
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Fig. 4. Boxplot (with logarithmic $y$ axis) of the number of evaluations needed to find the solution for MMDP. Three different versions of the multikulti migration policy have been tested here: mk, in which the most different individual is sent; mk-cons, that sends the most different to the target’s consensus string, multikulti-elite (mke) which chooses the most different among the 50% most fit, and mke-cons which sends the most different to the target’s consensus string among the 50% most fit. The rightmost result corresponds to random migration.
Fig. 5. Entropy (computed using the Shannon formula $H(P) = -\sum_{g \in P} p(f(g)) \log p(f(g))$, 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-elite migration policy (left) and the best migration policy (center). Every line corresponds to a different population, of the eight running in parallel. The figure on the right compares average values, with the dashed line corresponding to the multikulti-elite experiment and the other to the experiment that sends the best individual.