

Importance of Information Exchange in Quasi-Parallel Genetic Algorithms

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ABSTRACT

In this paper, we make a brief study on the effect of exchange rate in quasi-parallel genetic algorithms. The exchange rate is determined by two elements: the communication topology of the parallel populations and the communication capacity on each link. Here we formulate the communication capacity as the number of chromosomes one population exchanges with its neighbors. To study the effect of the two elements of exchange rate separately we did some tests on the minimization of the Weierstrass Function. Our results show that topology with a larger number of exchanged chromosomes generally yields better performance.

Categories and Subject Descriptors

G.1.6 [Optimization]: Global Optimization; I.6.8 [Types of Simulation]: Parallel; F.1.2 [Theory of Computation]: Computation by Abstract Devices – *Modes of Computation – interactive and reactive computation, parallelism and concurrency, probabilistic computation.*

General Terms

Algorithms, Design, Performance

Keywords

Parallel Genetic algorithms, Exchange Rate, Topology, Optimization, Weierstrass Function

1. INTRODUCTION

We consider parallel computing nodes as independent populations and run programs on each population before allowing their communication. This is all done in one computer to ensure the equality of computing resources. In this formulation, we archive an implementation of a real parallel genetic algorithm by a simulation on one computer, and we call this formulation “Quasi-Parallel Genetic algorithms” [1]-[4]. We study the information exchange by varying the topology and adjusting the information flow capacity on each link. The benchmark problem presented is the Weierstrass Function minimization problem. The 0-1 knapsack problem is also tested and the result is similar.

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2. QUASI-PARALLEL GENETIC ALGORITHMS AND EXCHANGE RATE

We focus on the coarse-grained parallel genetic algorithms, in which each node is an independent sub-population. We simplify the model by assuming that every sub-population runs Mutation Matrix Genetic Algorithms [5] and has the same number (N_c) of chromosomes. As to the communication between sub-populations, the only form of exchange allowed is the exchange of chromosomes between neighboring sub-populations connected in the communication network. One population gets the best M chromosomes from each of its K neighbors in the communication network to replace its worst $M \cdot K$ chromosomes. Both the topology of the communication network and the rule of communication contribute to the performance of the parallel genetic algorithms, so that the exchange rate (ER) depends on both of them:

$$ER = M \cdot K / N_c \quad (1)$$

Since it is reasonable to assume that the exchanged-in chromosomes are different from the exchanged-out chromosomes, we can deduce the limit:

$$M + M \cdot K = M(1 + K) \leq N_c \quad (2)$$

3. EXPERIMENT

Our algorithms will be performed on the Weierstrass Function. The definition of Weierstrass’s Function is:

$$f(x_1, \dots, x_D) = \sum_{i=1}^D \left\{ \sum_{k=0}^{k_{\max}} \left[a^k \cos(2\pi b^k (x_i + 0.5)) \right] \right\} - D \sum_{k=0}^{k_{\max}} \left[a^k \cos(2\pi b^k \cdot 0.5) \right] \quad (3)$$

where $a = 0.5$, $b = 3$, $k_{\max} = 20$, $x_i \in [-0.5, 0.5]$. D is the dimensionality of the function. The global minimum of the function is obtained when all $x_i = 0$, and $f_{\min} = 0$. This problem is different from the Knapsack Problem because its variables are continuous. Therefore, we do not expect to find the global optima exactly using discrete encoding. Here we employ a binary string to encode each $\{x_i\}$. Hence the binary string of length 15 can represent an integer I whose value ranges from 0 to $2^{15} - 1$ in decimal notation. For a chromosome s , its value after decoding is

$$C_s = I_s / (2^{15} - 1) - 0.5 \quad (4)$$

where I_s is the integer represented by chromosome s . Because the Weierstrass's Function have D variables, the total length of the chromosome is $L = D \times 15$.

3.1 Different Exchange Rates by Changing the Number of Links in the Topology

We focus on the test of the effect of ER on the performance of the algorithm by varying the average of degree K with the same M . We start from a fully connected network, so that K is at the maximum. We randomly cut links until the network becomes a ring, which is the topology of a connected network with minimum K . Every step after we cut one link we run our algorithm on the current topology for 30 times and obtain the average as well as the standard deviation of the results. Each time we run for 3 generations before one round of communication, and the results are collected after 5 rounds of communications. As the intermediate networks are generated by randomly cutting links in the initially fully connected network, the exchange rate for each population can be quite different. In order to illustrate the effect of exchange rate we define the Global Exchange Rate:

$$GER \equiv 2M \cdot N_{links} / \sum N_c \quad (5)$$

N_{links} is the total number of links in the topology. The exchange rate is normalized by the total number of chromosomes. The factor 2 in Equation (5) comes from the fact that the link is undirected so that the exchanged chromosomes will be doubled. Recall that the constraint on ER in Equation (2) requires that $K \leq N_c/M - 1$. We will use a topology with 16 computing nodes so that the maximum K for a fully connected network is 15. If we fix $M=1$, then the minimum size of our sub-population is $N_c = 16$. We perform numerical experiment on the optimization of the Weierstrass Function of $D=1$ for different exchange rates by changing the topology of the network from a fully connected one to a ring. The number of nodes is 16 and number of chromosomes in each node is 16. For each given exchange rate, we run for 30 times and take average. The results show that as the exchange rate decreases from 0.93 to 0.13 by decreasing K , the difference between the calculated and the actually minimum of the 1D Weierstrass function first decreases from 0.020 to 0.006 (when the exchange rate is 0.44) and then increases back to 0.021, indicating that the performance increases first and then decreases. A best performance plateau is achieved when the exchange rate is in the range of 0.4 to 0.7.

3.2 Different Exchange Rates by Changing the Number of Exchanged Chromosomes M

Now we focus on the information flow capacity on each link. We test the performance of the quasi-parallel genetic algorithms under the same topology with different M . We fix K to see the performance under different M . Because of the limit in Equation (2) we have $M_{max} = N_c/(K+1)$, with a corresponding maximum exchange rate $ER_{max} = M_{max} \cdot K / N_c = K/(K+1)$.

We now investigate the effect exchange rate induced by different numbers of exchanged chromosome M . We test this on the optimization of the 3D Weierstrass Function using the fully connected network. The total number of chromosomes N_c is 320 and the number of links is $K=15$. For this fully connected network, $M_{max}=320/16=20$ and $ER_{max}=15/16$. The results of our test show that as we increase the exchange rate increases from 0.047 to 0.938 by increasing M , the difference between the

calculated and the actually minimum of the 3D Weierstrass function decreases from 0.58 to 0.32, indicating an improved performance. In this investigation, we fixed the topology and adjust M to achieve different exchange rates. When M is large, each population receives quite a few middle-ranking and even low-ranking chromosomes from its neighbors to replace its own worst chromosomes. The difference between the members of the subpopulations before and after the exchange is not as large as the case when we only exchange a few good chromosomes from our neighbors. For large M , the sub-populations are spending most of the time in the exploration on the chromosomes that are of average fitness, rather than spending time in the exploitation of the best chromosomes. The increased exchange rate through increasing M for a fixed topology is not so efficient in the improvement of performance.

4. CONCLUSION AND DISCUSSION

Within the confine of numerical tests on two benchmark functions (0-1 Knapsack and Weierstrass function), we can say that there exists a basin for best performance in terms of communicating topologies. Our tests show that increasing M alone for improving performance is actually not very efficient. A good strategy for the optimization on these benchmark functions is to first choose a topology by selecting a value of K so that the global exchange rate is in the range of 0.4 to 0.7, and then increase M to obtain the best performance. In application, we should select a topology with the global rate around 0.4 since the cost of hardware can be reduced by using less links. We then assign a reasonable M to control the algorithm complexity to obtain the best performance.

5. ACKNOWLEDGMENTS

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