WS model based Massively Parallel Genetic Algorithm and its Various Applications

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Abstract: Abstract
Genetic algorithms are widely used method as solutions for optimization problems. On the other hand, some researchers report the limitations of GA, that is, it is difficult to obtain solutions that satisfy constraints of optimization problems. To solve this problem, we propose the GA with diversity that using WS-model for Massively Parallel model of Genetic Algorithm to overcome the constrains problem. Experiment this system at Function optimizations and classroom layout optimization. We confirmed that the results of proposed method is better than other method.

Keywords—**Genetic Algorithm, Funciton optimization, Graph theory, WS-model**

1. Background and Motivation

Genetic algorithms[1] (GA for short) are widely used method as solutions for optimization problems. On the other hand, some researchers report the limitations of GA, that is, it is difficult to obtain solutions that satisfy constraints of optimization problems. In [2], the GA is applied for the classroom optimization based on multi-agents simulation, and the obtained solutions are mainly composed of the solution candidates that do not satisfy the constraints of optimization problems. The reason why the genes that do not satisfy the constrains are generated, because the constrains of the optimization problem are too complex.

To solve this problem, we propose the GA with diversity to overcome the constrains problem. That is, the proposed method increase the number of genes that can satisfy complex constraint. We use the Massively Parallel model of Genetic Algorithm [3] (MPGA for short) that is a form of Parallel Distributed Genetic Algorithm[4] (PDGA for short). The MPGA has a problem that slow calculation speed. To solve this problem, we use Watts and Strogatz Model[7](WS-Model for short) for MPGA. The MPGA can consider kind of graph. WS Model is the real network model that possess certain properties of small-world. In this report, we discuss this property is able to solve the problem of MPGA.

In previous researches, Perego et al.[**?**] proposed that the MPGA of cubic lattice type. They extend the MPGA in a three-dimensional. In this research they do not apply to complex problems. And if have made constrains, it may be considered that making it difficult to reach optimal solutions.

Section 2 introduces the proposed system. Section 3 shows the experimental comparisons of Standard GA, MPGA and the proposed method (MPGA+WS-Model). Using these GA for Function optimization and classroom layout optimization(fig. 1). Section 4 presents conclusions.

2. Proposed Method

In order to propose such the GA with diversity, we employ the massively parallel genetic algorithm. The overview
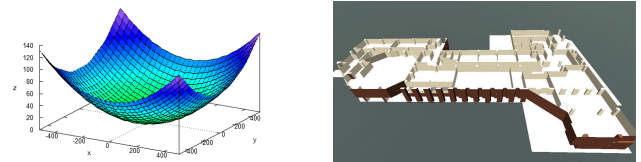

Figure 1. Function optimization(left) and Classroom layout optimization (right)
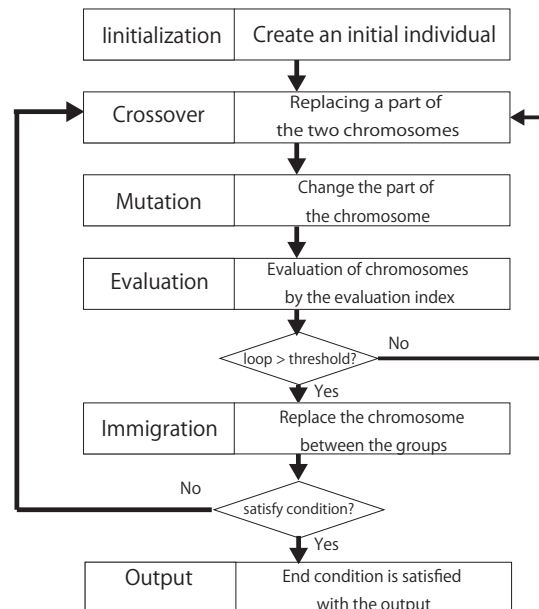
of MPGA is shown in Fig. 2.

Figure 2. Overviewt of MPGA

As can be seen from Fig. 2, the initialization, crossover, mutation, evaluation processes are same as the standard GA (SGA for Short) [6]. The difference between MPGA and the SGA is the immigration part. Fig .3 represents the immigration part of MPGA, and the followings are overview of the immigration process.

1). Divide the chromosomes into n groups
2). The chromosome in the group evolve over predefined generations
3). Exchange the chromosomes between selected groups based on the transition probability
4). Repeat (1), (2), (3) until the defined condition

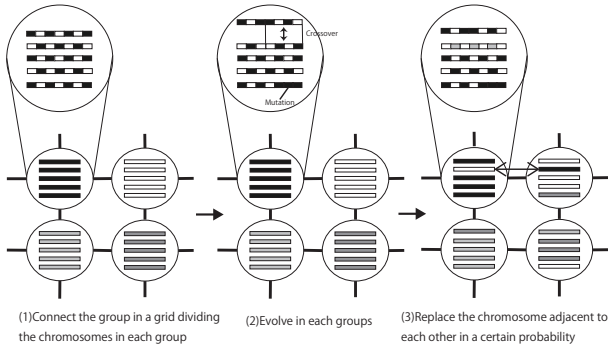### 2.1 Improvements of MPGA

MPGA has the following features,

Figure 3. State of MPGA chromosome replacement

1). Because evolve unique to each group, it can create chromosome having various properties

2). Because the crossover of chromosomes is not performed at high speed, it has less susceptible to local optimal solution

Chromosome have various properties, it is possible to optimize complex problem that simple GA can't solve. However it has slow optimization speed that can not converge to the optimal solution. As a view of graph theory, MPGA has long average path length, and make more groups, it is necessary to has the more long average path length. Long path length induce the slow calculating speed.

2.2 WS model

The problem of MPGA is slow optimization speed, because of long average path length. We have concluded that can solve this with WS model. Fig.4 shows how to make WS model.
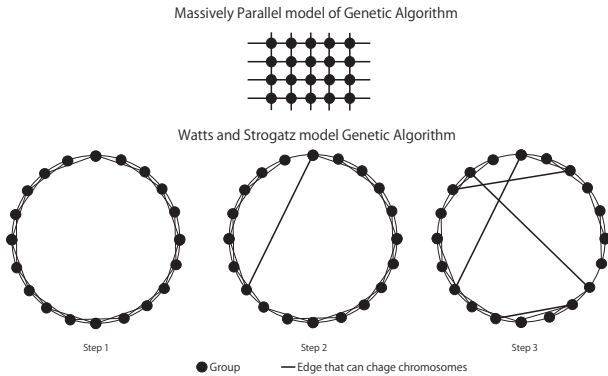

Figure 4. How to make WS mode

step1 Connect all of the vertices in the neighboring two of the vertices and edges

step2 To create a new route to a vertex

step3 The route created for vertex at a certain probability

WS model is a kind of real world network that has the small-world property. small-world property that connected any two

vertices through less vertices. In the case of n vertices, MPGA has $\sqrt{n/2}$ of average path length, WS-Model has $\log n$ of average path length. For example in the case of 16 vertices, average path length on MPGA will be 2.8, WSGA will be 1.2. We consider this property can solve the problem at MPGA.

The proposed GA is based on the MPGA, and we extend the network structure of chromosome group (Fig. 10, left) of MPGA to WS-Model (Fig. 10, right). The extension is to decrease the average of path length of the network structure, and it increase the activities of immigration. It can control the trade-off between the diversity and convergence.

3. Experimental Comparison

In order to show the effectiveness of the proposed method, we perform two experiments.

3.1 Function optimization

The first experiment is function optimizations, where Rastring function, Rosenbrock function and Griewank function are used.

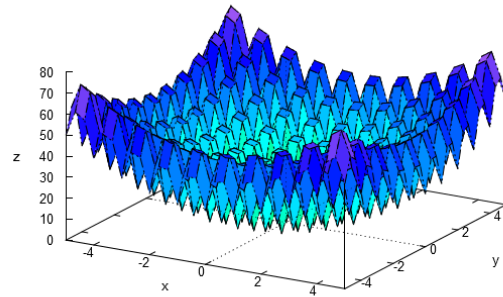Fig. 5 is shown Rastrign function overview Rastrign func-

Figure 5. Rastrign function

tion represented by flowing equation

$$F_{Rastrigin}(x) \quad = \quad 10n + \sum_{i=1}^{n} \left(x_i^2 - 10\cos(2\pi x_i) \right) \quad (1)$$

$$(-5.12 \leq x_i < 5.12) \tag{2}$$

There exists independently solutions rather dependencies between variables.

Fig. 6 is shown Rosenbrock function overview
Rosenbrock function is represented

$$F_{Rosenbrock}(x) \quad = \quad \sum_{i=1}^{n-1} \left(100(x_{i+1} - x_i^2)^2 + (1 - x_i)^2 \right) \tag{3}$$

$$(4)$$

$$(-2.048 \leq x_i < 2.048) \tag{5}$$

There are interdependent variable, sometime solution of the overall greatly changes due to one solution. It is a function
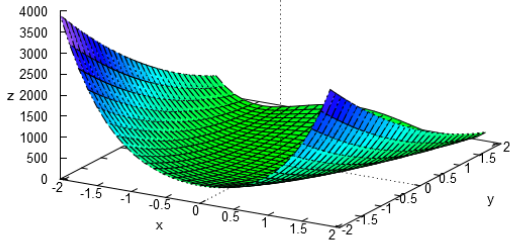
Figure 6. Rosenbrock function

Griewank function is reperesented

$$F_{Griewank}(x) \quad = \quad 1 + \sum_{i=1}^{n} \frac{x_i^2}{4000} - \prod_{i=1}^{n} \Big(\cos \big(\frac{x_i}{\sqrt{i}} \big) \Big) \quad (6)$$

$$(-512 \le x_i < 512)$$

$$(7)$$

As well as the Rosenbrock function a relationship of inter-dependence between the variables, but function is the multimodal.

All function make $min(F_{(x)}) = F(0, 0, \ldots, 0) = 0$. In this experiment, apply SGA, MPGA and WSGA for three functions. Chromosome correspond numbers to binary number. In this experiment, the chromosome length is set to 20, it means split the set range 2^{20}. The variable to set 20,Chromosome number is 256 that are divided into 16 groups, 70 % crossover rate, mutation rate of 3 %, the experiment with the number of 3000 generations.

The results obtained by SGA, MPGA, and WSGA are shown in Table 1.

of the unimodal It is difficult as an optimization problem by dependencies between variables described above.

Fig. 7 & 8 is shown Griewank function overview and enlarged view at vicinity 0.
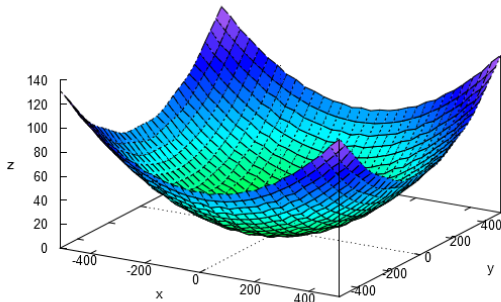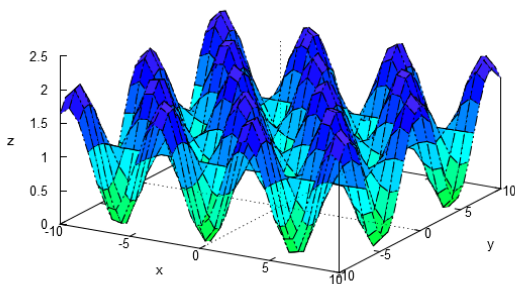
Table 1. average of final result

	SGA	MPGA	WSGA
Rastrign	169.54	169.20	169.42
Rosenbrock	303.45	303.17	299.48
Griewank	86.21	91.42	79.56

It is difficult to recognize the effectiveness of the WS model GA in the results of Rastrign function, however, in the case of Griewank function and Rosenbrock results, we can see the effectiveness of the proposed WS model GA.
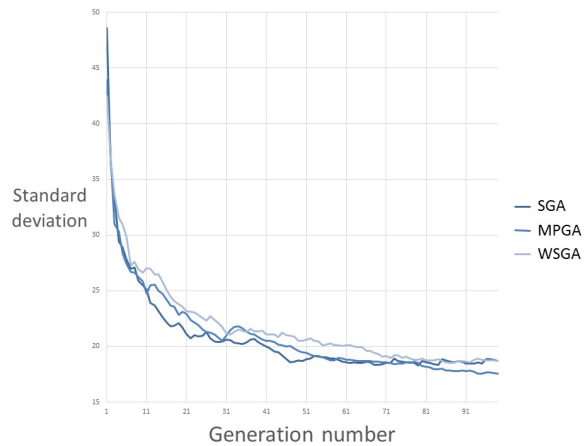

Figure 7. Griewank function overview

Figure 9. Changes in the standard deviation

Form Fig. 9, that represents the standard deviation of chromosomes of each methods, and it can be seen that the standard deviation of WSGA is partially bigger than those of other method.

Fig. 10, presents the network structure of group of chromosomes, and left is MPGA and right figure is WSGA, respectively.
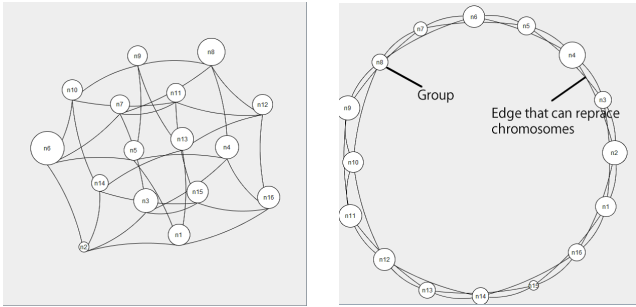

Figure 8. Griewank function enlarged view of around 0

Figure 10. The average value of each group of MPGA(left) and WS model GA(right)（3000 th generation）
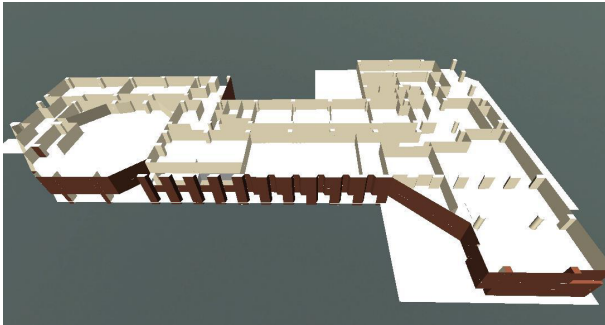

Figure 11. Part of the map to be used in the classroom layout optimization problem

3.2 classroom layout optimization

The second experiment is applied to the classroom layout optimization problem having a complex constraints. Shows the map and the state of classroom placement optimization problem Fig. 11&12.

Figure 12. Appearance of the classroom placement optimization experiment

In this issue, it aims to create a classroom layout that students moving time becomes smaller. As the experimental conditions, 30 lectures are offered in one day, using 160 classrooms that exist in 1300 square meters of floor, 300 students set up a situation where move on the basis of the course data.

The Chromosome number is 256 , 80 % crossover rate, 5 % mutation rate , the experiment with the number of 200 generations.

Results are shown Table2.

In this case, WS model also has the best results in average and considering standard deviation, it has better result than

Table 2. Classroom placement optimization problem results

	SGA	MPGA	WSGA
average	5930.8	5931.3	5734.0
standard deviation	496.2	320.0	334.3
minimum value	5218.0	5515.4	5300.3

MPGA.

4. Conclusions

Based on the MPGA, the GA with diversity has been proposed by using the WS network structure in chromosome groups.

MPGA has slow propagation of the solution because of the average path length become too large. To solve this probrem, using WS model that has small average path length.

Through the experimental comparison between the proposed WS model GA and MPGA, SGA, using two problems (function optimizations, classroom optimization problems), it has been confirmed that the results of proposed method is better than those of MPGA and SGA.

References

[1] Chua, Alvin L-S., et al. "A genetic algorithm for predicting the structures of interfaces in multicomponent systems." Nature materials 9.5 (2010): 418-422.

[2] K. Maekawa, K. Sawase, and H. Nobuhara, "Multi-Resolution Dijkstra Method Based on Multi-Agent Simulation and its Application to Genetic Algorithm for Classroom Optimization," Journal of Advanced Computational Intelligence and Intelligent Informatics, Vol. 18, No. 2, pp. 113-120 (2014).

[3] SPIESSENS, Piet; MANDERICK, Bernard. "A massively parallel genetic algorithm: Implementation and first analysis. In: Proceedings of the Fourth International Conference on Genetic Algorithms," Morgan Kaufmann San Mateo, CA, 1991. p. 279-286.

[4] SHONKWILER Ron,"Parallel Genetic Algorithms,"ICGA. 1993. p. 199-205.

[5] Baraglia, Ranieri, and Raffaele Perego "Parallel Genetic Algorithms for Hypercube Machines.", Third International Conference, Porto, Portugal, June 21-23, 1998. Selected Papers and Invited Talks

[6] GKOUTIOUDI, Kyriaki; KARATZA, Helen D. A "simulation study of multi-criteria scheduling in grid based on genetic algorithms." Parallel and Distributed Processing with Applications (ISPA), 2012 IEEE 10th International Symposium on. IEEE, 2012. p. 317-324.

[7] Watts, Duncan J., and Steven H. Strogatz.., "Collective dynamics of〝small-world〞networks.", . nature 393.6684, 440-442, 1998