

Research Article

The Displacement of Base Station in Mobile Communication with Genetic Approach

Yong Seouk Choi,¹ Kyung Soo Kim,¹ and Nam Kim²

¹Wireless system research group, Electronics and Telecommunications Research Institute, (ETRI), 161 Gajeong-Dong, Yuseong-Gu, Daejeon 305-700, South Korea

²The school of Electrical and Computer Engineering, Chungbuk National University, 12 Gaeshin-Dong, Heungduk-Gu, Chungju 361-763, South Korea

Correspondence should be addressed to Nam Kim, cys@empal.com

Received 5 July 2007; Revised 18 January 2008; Accepted 2 March 2008

Recommended by Vincent Lau

This paper addresses the displacement of a base station with optimization approach. A genetic algorithm is used as optimization approach. A new representation that describes base station placement, transmitted power with real numbers, and new genetic operators is proposed and introduced. In addition, this new representation can describe the number of base stations. For the positioning of the base station, both coverage and economy efficiency factors were considered. Using the weighted objective function, it is possible to specify the location of the base station, the cell coverage, and its economy efficiency. The economy efficiency indicates a reduction in the number of base stations for cost effectiveness. To test the proposed algorithm, the proposed algorithm was applied to homogeneous traffic environment. Following this, the proposed algorithm was applied to an inhomogeneous traffic density environment in order to test it in actual conditions. The simulation results show that the algorithm enables the finding of a near optimal solution of base station placement, and it determines the efficient number of base stations. Moreover, it can offer a proper solution by adjusting the weighted objective function.

Copyright © 2008 Yong Seouk Choi et al. This is an open access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

1. INTRODUCTION

Base station placement is a highly important issue in achieving high cell planning efficiency. It is a parameter optimization problem which has a set of variables, such as traffic density, channel condition, interference scenario, the number of base stations, and other network planning parameters. The objective is to set the various parameters so as to optimize base station placement and transmit power. Due to the combined effects of the parameters, this type of problem is a nonlinear one that is not able to treat each parameter as an independent. As a result, it is very complex problem in which we will not be able to find a polynomial time algorithm in the theory of computational complexity [1]. A genetic algorithm is useful for solving this type of NP-hard problem.

This algorithm is often described as a global search method, and is performed as an optimization tool. This method is a computational model inspired by evolution. It represents feasible solutions in terms of individuals with

genomes, and determines which individuals could survive in a certain criterion formulated to maximize (or minimize) a given objective function. Some research has been reported on methods for automatically determining the best possible base station placement [2, 3]. References [2, 3] utilized genetic approaches for the network planning. In [2], a binary string representation, the classic representation method of genetic algorithm, is applied. That is, candidate solutions are encoded as chromosome-like bit strings. In order to reduce the computational complexity, a hierarchical approach is considered in [3]. It divides the service area into several pixels, which are taken as potential base stations. Since the above approaches represent base station positions as discrete points, it is not possible to consider all of the potential base stations. In this paper, we present the genetic approach to automatically determine base station positions and obtain the transmit power. A real-valued representation describing base station placement and corresponding genetic operators are proposed. Candidate sites are defined based on site-specific traffic distribution. Each candidate site is

represented by real-valued coordinates, and can be located at an arbitrary position. Therefore, all the possible base station positions can be considered, and there is no restriction on representing potential solutions. According to an objective function, the proposed algorithm determines the best-fitted set of base stations from predefined candidate sites. To increase both coverage and economy efficiency, we establish a simple weighted objective function. To verify the proposed algorithm, a situation in which the optimum positions and number of base stations are obvious is utilized. The transmitted power of base station is considered as a factor of the proposed algorithm. The proposed algorithm is verified by applying it to homogeneous traffic density case as an obvious optimization problem. In addition, the approach is tested in an inhomogeneous traffic density environment.

2. OVERVIEW OF GENETIC ALGORITHM

Like other computational systems inspired by natural systems, genetic algorithms have been used in two ways: as techniques for solving technology problems, and as simplified scientific models that can answer questions about nature [3]. Genetic algorithms (GA) are evolutionary optimization approaches which are an alternative to traditional optimization methods. GA approaches are most appropriate for complex nonlinear models where location of the global optimum is a difficult task. It may be possible to use GA techniques to consider problems which may not be modeled as accurately using other approaches. Therefore, GA appears to be a potentially useful approach. GA performance will depend very much on details such as the method for encoding candidate solutions, the operator, the parameter setting, and the particular criterion for success. As for any search, the way in which candidate solutions are encoded is very important. Many genetic algorithm applications use fixed-length, fixed-order bit strings to encode candidate solution. However, the algorithm proposed in this paper uses real-valued encoding schema to represent solutions. In GA, feasible solutions are modeled as individuals described by genomes. A genome is an arrangement of several chromosomes, which symbolize characteristics of the individual. Population is the total amount of individuals. Some of them can survive and others will die in the next generation by their own fitness and a given selection rule. Fitness is evaluated by a given objective function. Genetic operations such as crossover and mutation are performed to produce new individuals in subsequent generations. The crossover operator defines the procedure of generating a child from its parent's genomes. The mutation is carried out chromosome by chromosome, and its exploration and exploitation help the algorithm to avoid local optimum. If the current population accepts the given termination condition, new generation is no longer produced. Otherwise, dominant individuals are selected and genetic operators reproduce new individuals from them. The best individual of each generation is transferred over to the next generation if elitism is adopted.

The theoretical basis of GA relies on the concept of schema. A schema is defined as the similarity of templates describing a subset of genomes with similarities in cer-

tain chromosomes. Schemata are available to measure the similarity of individuals. John Holland's schema theorem and building-block hypothesis [4] have often been used to explain how the GA works. According to the schema theorem, short, low-order, and above-average schemata receive exponentially increasing trials in subsequent generations. This proves that the individuals with high fitness will have a high survival probability when a suitable representation is applied. The building-block hypothesis suggests that the GA will perform well when it is able to identify above-average-fitness and low-order schemata and recombine them to produce higher-order schemata of higher fitness. In sum, individuals with similar characteristics must be represented by a similar genotype.

3. PROPOSED ALGORITHM FOR BASE STATION PLACEMENT

The processing of the proposed algorithm is implemented in a two-dimensional map; therefore, representation in binary form is difficult to present for the genome which describes the number of base stations and the location of the base stations. For a good approximation, it is necessary to have a longer genotype. A real value representation is more efficient than the representation of a binary genome in this case. Consequently, in this paper the genotypes that have real value representations for the optimization algorithm were chosen. Given the allowable transmitted power of a cell site in a traffic map, this chapter introduces GA that optimizes the cell site location, the number of cell sites, and the transmitted power. A GA that works well in terms of the base station placement problem is proposed. The main characteristics considered for the development of the proposed algorithm are

- (i) the genome must represent all of the base station locations, and the genotype can describe the number of base stations as well as the position of the base station,
- (ii) a chromosome expresses one base station position,
- (iii) the number of possible base station locations must be unlimited; therefore, there are infinite candidates of base station locations,
- (iv) similar genotypes represent the genomes of the closely located base stations.

An algorithm satisfying the above factors is consistent with the building-block hypothesis and schema theorem.

The three things that must be defined in order to solve a problem through genetic algorithms are as follows:

- (i) define a representation,
- (ii) define the genetic operators,
- (iii) define the objective function.

How one defines a representation, genetic operators, and objective function determines the algorithm. It is essential to design the genetic algorithm by considering (i)–(iv). The following chapters explain the proposed algorithm in detail.

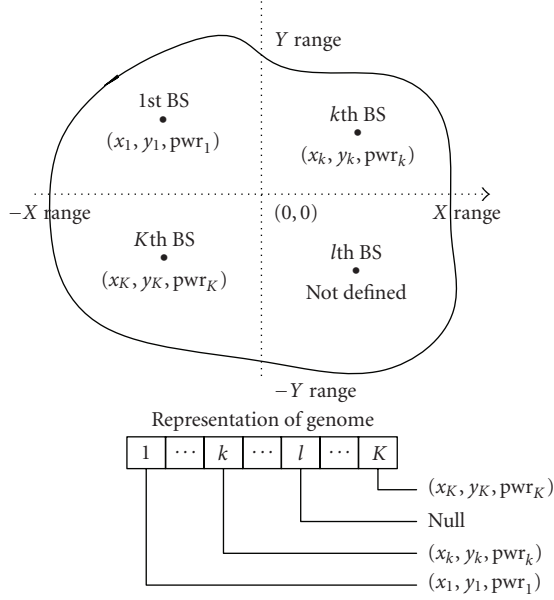


FIGURE 1: Representation of the genome for the placement of the base station.

3.1. Representation

Figure 1 illustrates the representation of the genomes. A genome is denoted as a vector $g = (c_1, \dots, c_k)$, where $c_k = (x_k, y_k)$ is the chromosome for the k th base station position. This method fulfills (i) and (ii). K is the maximum number of base stations, and all of these can be located in the x -range $[-X_{\max}, X_{\max}]$ and y -range $[-Y_{\max}, Y_{\max}]$ with origin $(0, 0)$.

If the position of a base station is not defined, it is expressed as NULL. This method applies for a case in which there are fewer base stations than in K , so that it fulfills (i). $n(g)$ is defined as the number of EXISTENCE in g . In order to satisfy (iii) and (iv), x_k and y_k must be real numbers. M is assumed as population size.

3.2. Genetic operators (crossover and mutation)

It is necessary to design an initialization and a termination method, a crossover and mutation operator, and a selection strategy in order to define the reproduction procedure.

A proper initial population can provide a fast convergence to the optimum point. It is desirable for a user to define initial positions of base stations intuitively. The first individual, $c_{1k} = (x_{1k}, y_{1k})$ for $k = 1, \dots, K$, is determined by a user and other individuals (for $m = 2, \dots, M$) are determined by the following rule: if $c_{1k} = \text{NULL}$, then $c_{mk} = \text{NULL}$ with probability P_n^I or $c_{mk} = (v_1, v_2)$ with probability $1 - P_n^I$, where $v_1 = U(-X_{\max}, X_{\max})$ and $v_2 = U(-Y_{\max}, Y_{\max})$. If c_{1k} is defined ($c_{1k} \neq \text{NULL}$), then $c_{mk} = \text{NULL}$ with probability $1 - P_v^I$ or $c_{mk} = (x_{1k} + \xi_1, y_{1k} + \xi_2)$ with probability P_v^I , where $\xi_1, \xi_2 = N(0, \sigma_\xi^2)$. $U(a, b)$ is a uniformly distributed random variable between a and b . $N(\bar{x}, \sigma^2)$ denotes a Gaussian distributed random variable with mean \bar{x} and variance σ^2 . P_n^I and P_v^I indicate the probability of producing NULL from NULL and that

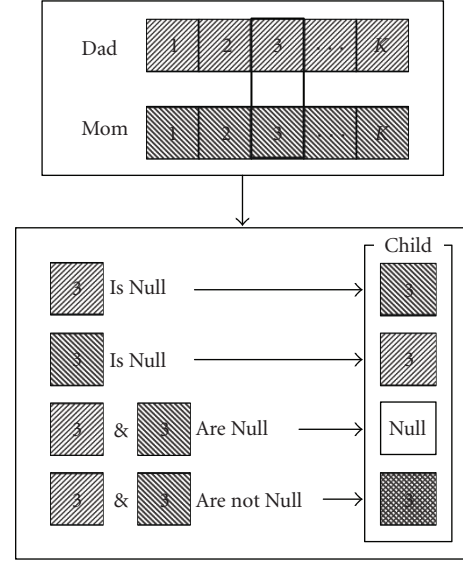


FIGURE 2: One child crossover operation.

of producing EXISTENCE from EXISTENCE, respectively. However, it may require further trials in order to determine the global optimum if the initial value, as user defined, is close to the local optimum. When the user does not define any initial positions, it is decided that $c_{mk} = \text{NULL}$ with \tilde{P}_n^I or $c_{mk} = (v_1, v_2)$ with probability $1 - \tilde{P}_n^I$ for $m = 1, \dots, M$, where \tilde{P}_n^I denotes the probability of producing NULL.

A termination criterion is used to determine whether or not a GA is finished. Generation, convergence, or population convergence can terminate the procedure of genetic algorithm. The easiest scheme is termination upon generation. When the number of current generations is larger than the specified number of generations, the algorithm is finished. Termination upon convergence compares the previous best-of-generation to the current best-of-generation. If the current convergence is less than the requested convergence, the reproduction procedure is ceased. Termination upon population convergence compares the population average to the score of the best individual in the population.

In the proposed application, one child crossover operator is used. A single child c_k^{child} is born from its father and mother, c_k^{dad} and c_k^{mom} . Figure 2 shows the procedure of one child crossover operation in the proposed algorithm. If one of the parents is NULL, the child receives the other parent's attributes. Otherwise, the child is generated by (1), where σ_C is the parameter of the crossover operation. $|x_k^{\text{dad}} - x_k^{\text{mom}}|$ and $|y_k^{\text{dad}} - y_k^{\text{mom}}|$ can be used as a measure of closeness. This method is based on the fact that if the attributions of both parents are similar, the child's attributions are also similar to its parents.

Mutation is performed chromosome by chromosome with probability P_{mut} . Figure 3 shows the procedure of the mutation operation in the proposed algorithm. The mutation is very close to the initialization scheme with the user-defined base station position. If $c_{mk} = \text{NULL}$, redefine

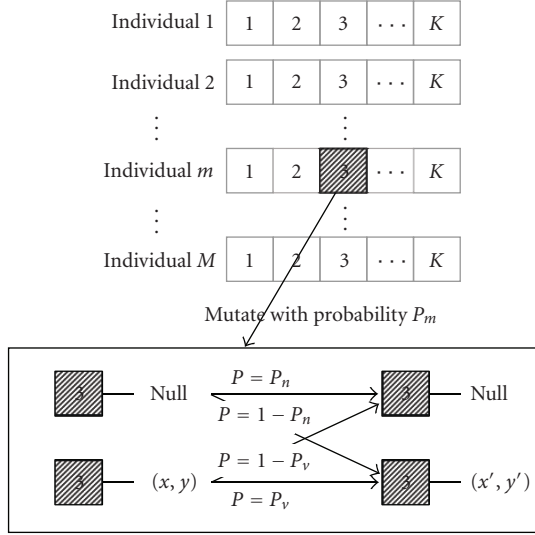


FIGURE 3: Mutation operation.

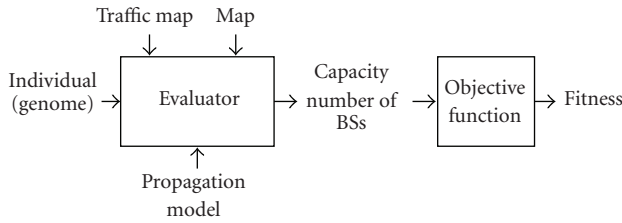


FIGURE 4: Fitness evaluation.

$c_{mk} = \text{NULL}$ with probability P_n or $c_{mk} = (v_1, v_2)$ with probability $1 - P_n$. If $c_{mk} \neq \text{NULL}$, redefine $c_{mk} = (x_{mk} + \chi_1, y_{mk} + \chi_2)$ with probability P_v or $c_{mk} = \text{NULL}$ with probability $1 - P_v$, where χ_1 and χ_2 are Gaussian distributed random variables with zero mean and variance σ_m^2 . P_{mut} and σ_m^2 are the parameters of the mutation operation.

A roulette wheel method is applied for the selection scheme. This selection method chooses an individual based on the magnitude of the fitness score relative to the rest of the population. The higher the score, the more selective an individual will be. Any individual has a probability p of the choice, where p is equal to the fitness of the individual divided by the sum of the fitness of each individual in the population. Therefore, the individual with a high fitness level can survive with high probability:

$$\begin{aligned} x_k^{\text{child}} &= \frac{x_k^{\text{dad}} + x_k^{\text{mom}}}{2} + \zeta_1, \\ \zeta_1 &= N\left(0, \left(\frac{(x_k^{\text{dad}} - x_k^{\text{mom}})\sigma_C}{2}\right)^2\right), \\ y_k^{\text{child}} &= \frac{y_k^{\text{dad}} + y_k^{\text{mom}}}{2} + \zeta_2, \\ \zeta_2 &= N\left(0, \left(\frac{(y_k^{\text{dad}} - y_k^{\text{mom}})\sigma_C}{2}\right)^2\right). \end{aligned} \quad (1)$$

3.3. Fitness evaluation

Figure 4 illustrates the fitness evaluation procedure composed of an evaluator and an objective function. The evaluator calculates the covered traffic by using a propagation model, traffic map, and map for a path loss prediction. Cell area covered by the base stations is evaluated, and the covered traffic is then obtained. Considering coverage, power, and economy efficiency, the objective function is defined as

$$f(G) = \omega_t \cdot f_t(G) + \omega_p \cdot f_p(G) + \omega_e \cdot f_e(G), \quad (2)$$

where f_t , f_p , and f_e are the objective functions for coverage, power, and economy respectively, and these are defined as:

$$\begin{aligned} f_t(G) &= \text{traffic coverage rate} \\ &= \frac{\text{covered traffic}}{\text{total traffic}}, \\ f_p(G) &= \text{BS power fitness} \\ &= \frac{\text{Available Maximum BS power} - \text{Used BS power}}{\text{Available Maximum BS power}}, \\ f_e(G) &= \text{economic fitness} \\ &= \frac{\text{Available Maximum BSs} - \text{Used BSs}}{\text{Available Maximum BSs}}. \end{aligned} \quad (3)$$

As the covered traffic area widens corresponding to the given propagation model, $f_t(G)$ increases. Conversely, $f_e(G)$ increases when fewer base stations are placed. Total fitness is calculated with w_t , w_p , and w_e subject to $w_t + w_p + w_e = 1$. The weights are determined by the user's preference. If coverage is more important, then one may choose a large w_t . Otherwise, a large w_e may be chosen to be more desirable using fewer base stations. Therefore, the purpose of optimization in this paper is to determine the maximum traffic coverage with the minimum number of base stations and minimum amount of power.

This paper uses Hata's model to obtain the coverage of the base station. It is possible that each individual can have K (the maximum number of base stations). To achieve the cell coverage, it is necessary to compute the path loss K times. If the population is large, the computing power required becomes very large. In this paper, to reduce processing time, Hata's model was used, which is fast for computing the path loss with height information.

3.4. Scaling

After the fitness is decided, this value is not directly applied for selection. The appropriate function is used to adjust the fitness value. This function is termed "scaling" and there are three general scaling methods.

The new fitness value f' is defined in Table 1.

3.5. Selection

The purpose of the selection is to emphasize the fit individuals in the population with the hopes that their offspring will in turn have an even higher fitness value. Selection has

TABLE 1: Scaling methods.

Scaling model	General form
Linear scaling	$f' = a \cdot f + b$
Sigma scaling	$f' = f - (\bar{f} - c \cdot \sigma)$
Power law scaling	$f' = f^k$



FIGURE 5: Homogenous traffic density for verification.

to be controlled in balance with crossover and mutation. Too strong a selection signifies that suboptimal highly fit individuals will take over the population, reducing the diversity needed for further change and progress. Too weak a selection will result in too slow an evolution. In this paper, the common selection method of tournament selection, rank selection, roulette-wheel selection, and uniform selection were employed.

4. TESTIFY ALGORITHM

To test the proposed algorithm, a one-tiered hexagonal cellular environment is considered, where traffic is distributed uniformly in each hexagonal cell whose radius is 2.5 km. In this case, the optimum position of the base station is in the center of hexagon, and the optimum number of base stations is obviously seven. A path loss prediction is carried out using the equation $L = L_0 \times (d/d_0)^{-4}$, where $L_0 = 140$ dB and $d_0 = 2.5$ km. As the generation increases, the base stations tend to be placed where they are optimum, and the number of base stations is also converged automatically. After the 1000th generation, a base station placement that guarantees 99.78% coverage can be determined.

The input parameter for the proposed algorithm is listed in Table 2. The maximum number of base stations depends on the width of the target area. The wider the target area, the more likely a greater amount of computing time for convergence is needed. Population size is the solution set. If the population size is large, the convergence of the solution can be quicker. However, in this case the total computing time is larger, as a processing of the propagation model will be needed for each individual in the population. As the individuals with low fitness values are removed, the initial values of base station's maximum number and location are not related to the entire performance. Therefore, a null-to-null probability and pos-to-pos probability is loosely coupled

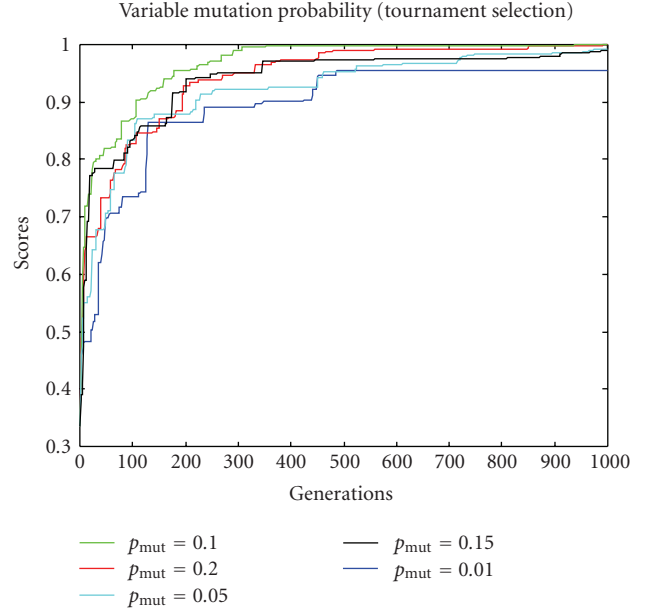


FIGURE 6: Fitness in various mutation probabilities.

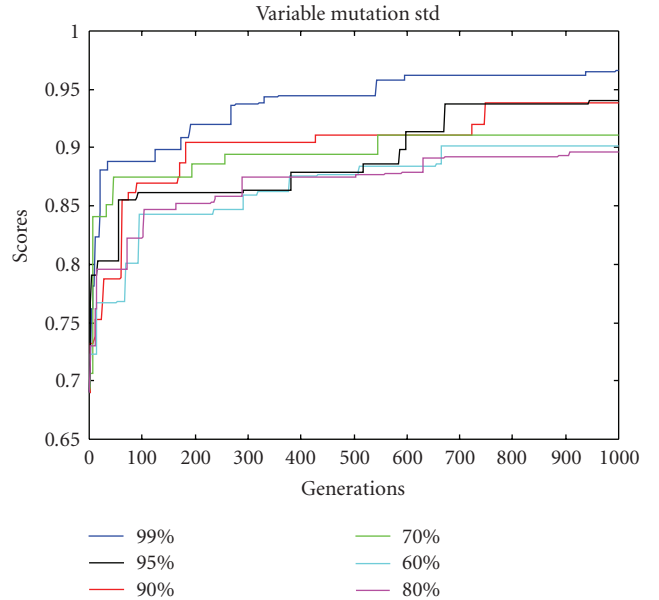


FIGURE 7: Fitness in various mutation deviations.

with the fitness relationship, and the mutation probability in a real value representation is the main factor in speeding the convergence.

Fitness with various mutation probabilities in each generation is shown in Figure 6. The higher the mutation probability, the better the fitness. However, too high a mutation probability has a tendency to downgrade the performance, as it has a frequently changing possible solutions set. In the given homogenous traffic in Figure 5, it is known that the best performance is shown when the mutation probability is 0.1 (Figure 6).

Figure 7 shows that a high deviation of mutation will be good for performance. From Figures 8 to 10, the changing of fitness with various scaling methods becomes clear.

TABLE 2: Input parameters list.

Parameter	Basic value	Range
The maximum number of BS	Depend on width of area	Variable
Population size	20	Variable
Crossover probability	1.0	Variable
Mutation probability	0.1	Variable
Init null-to-null probability	0.2	Variable
Init pos-to-pos probability	0.95	Variable
Null-to-null probability	0.5	Variable
Pos-to-pos probability	0.5	Variable
Standard deviation in mutation	3062.2 (95% in 6 Km)	Variable
Minimum BS power	20 dBm	Variable
Maximum BS power	40 dBm	Variable
Allowable traffic per BS	50 Erlang	Variable
Receiver sensitivity	-80 dBm	Variable
Selection	Tournament	Roulette wheel, rank, tournament, uniform
Scaling	No scaling	No scale, linear, power law, sigma truncation

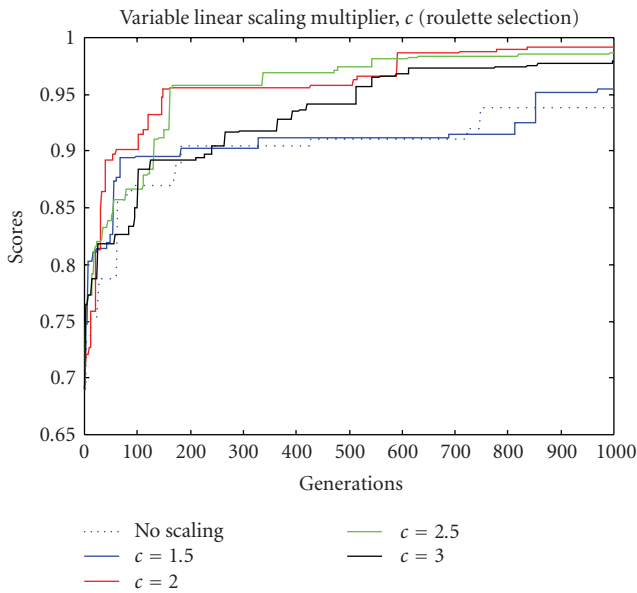


FIGURE 8: Fitness with linear scaling.

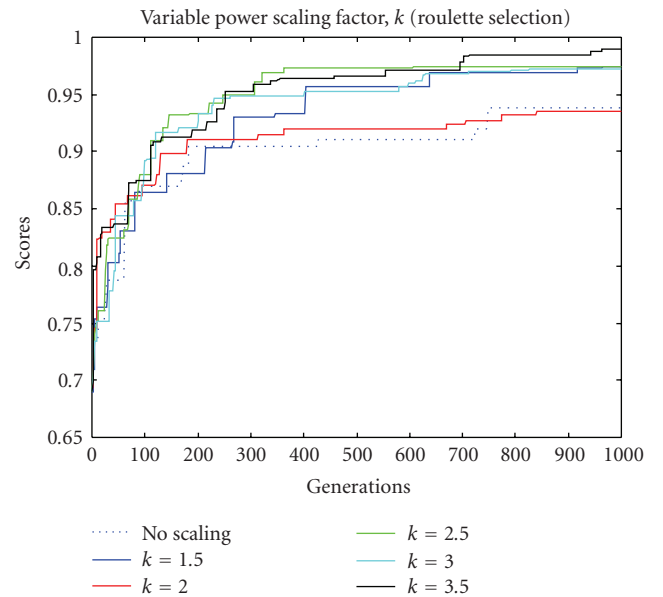


FIGURE 9: Fitness with power law scaling.

Selection is the operation by which chromosomes are selected for the reproduction of the next generation. The function of selection is that chromosomes corresponding to individuals with a higher fitness have a higher probability of being selected. There are a number of possible selection schemes. In this paper, several selection schemes were verified as mentioned in Chapter 3.5. Good results cannot be expected with the selections that do not have balanced crossover and mutation.

In Figure 11, it is clear that the fitness changes with the selection schemes, and the result shows the fitness order; tournament selection > rank selection > roulette-wheel selection > uniform selection.

Figures 12 to 16 show the optimization processing of base station displacements. Figure 12 shows the initial random location of the base stations, and in this case five base stations have covered 69% of the target area. In Figure 13, seven base stations have covered 92% of target area with uniform selection, but it is still not optimized. Figure 14 is the result of a roulette-wheel selection, and this is an improvement over the uniform selection. It covers 93.85% of the target area. The rank selection covers 97.90%; this is a very good result. The tournament selection offers 99.78% coverage. This is approximately at the optimization level. As fitness is sensitive in terms of selection schemes, optimization processing needs appropriate selection schemes.

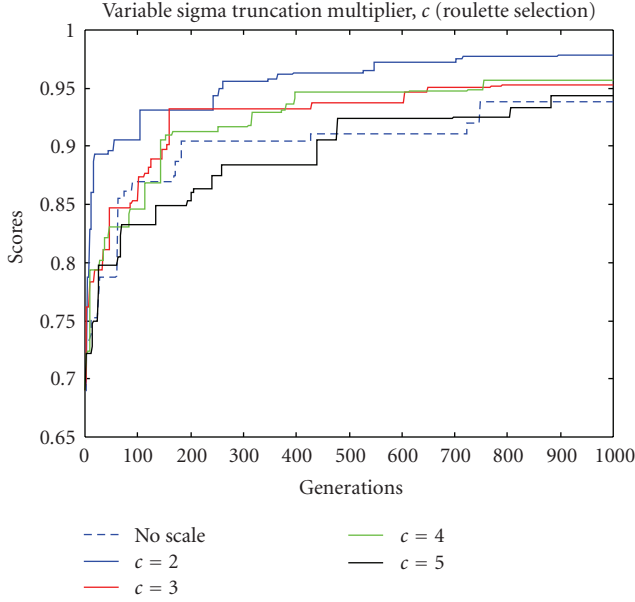


FIGURE 10: Fitness with sigma truncation.

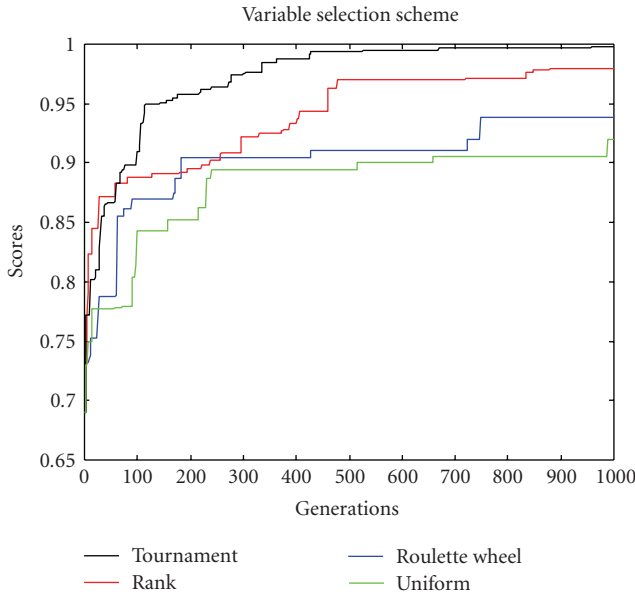


FIGURE 11: Fitness with selection schemes.

5. SIMULATION RESULTS

To demonstrate if the proposed algorithm determines which positions match optimum location, a simulation was conducted on areas similar to that in Figures 17 and 18 (inhomogeneous traffic). The actual-valued representations in this paper, as mentioned above, consist of the candidate location of the base station's transmit power. Figure 17 shows the altitude map of the target areas, and Figure 18 shows the traffic density map. The traffic density is inhomogeneous and the target area for simulation is an urban pattern. The width of the area for simulation is 12 Km \times 12 Km and the size of the bin is 120 m \times 120 m. Therefore, the total number of

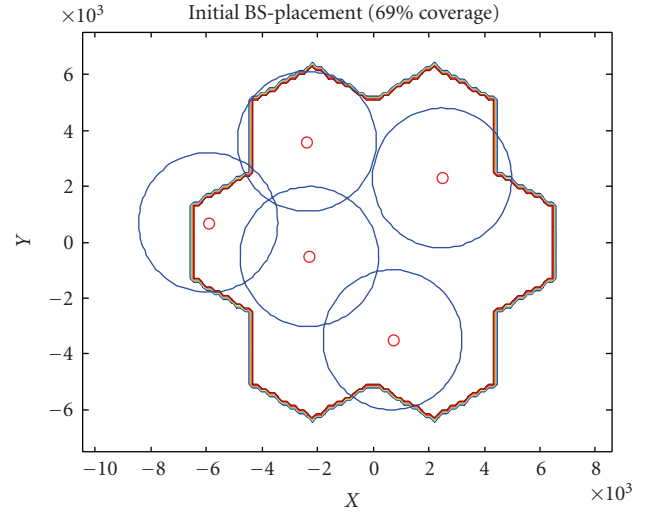


FIGURE 12: Initial base station location.

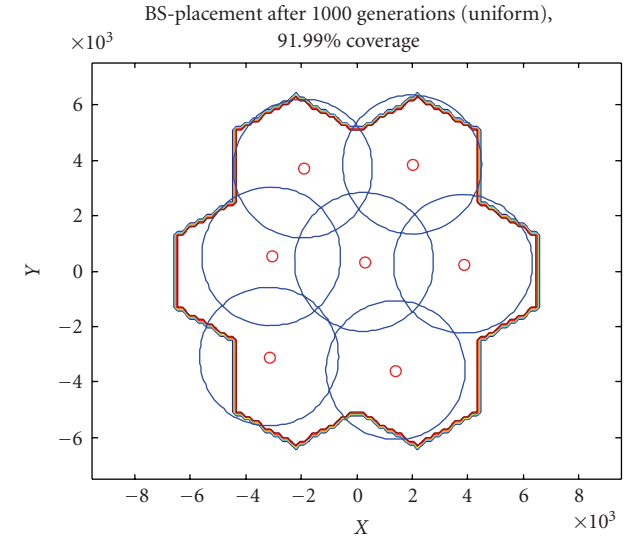


FIGURE 13: After the 1000th generation, base station location with uniform selection.

bins is 10 000. The parameters for the simulation are listed in Table 3.

Figures 19 and 20 show the location of the base station from one generation to 500 generations, when the weighting condition of their object function is $(\omega_t, \omega_p, \omega_e) = (0.9, 0.0, 0.1)$. The assigned transmit power range of each base station is from 22.63 dBm to 33.84 dBm, and its mean value is 33.84 dBm. In this case, the coverage rate is 82.62% and the fitness value is 0.74258.

In the case where the condition of object function is $(\omega_t, \omega_p, \omega_e) = (0.8, 0.1, 0.1)$, the results are shown in Figures 21 and 22. The coverage rate is 77.47%, and the fitness value is 0.663181. The assigned transmit power range of each base station is from 211 752 dBm to 3 857 794 dBm, and its mean value is 323 230 dBm. As the traffic capacity is limited, the cell boundaries of the high-traffic density are

TABLE 3: Simulation parameters.

Population size	30	Maximum BS power	40 dBm
Mutation probability	0.2	Receiver sensitivity	-85 dBm
Mutation std.	3062.2	Allowable traffic per BS	50 Erlang
Init null-to-null probability	0.2	Selection scheme	Tournament
Init pos-to-pos probability	0.95	Scaling scheme	No scaling
null-to-null probability	0.5	Termination criterion	Generation
Pos-to-pos probability	0.5	Eliticism	Used
Minimum BS power	20 dBm	Propagation model	Hata model (SU)

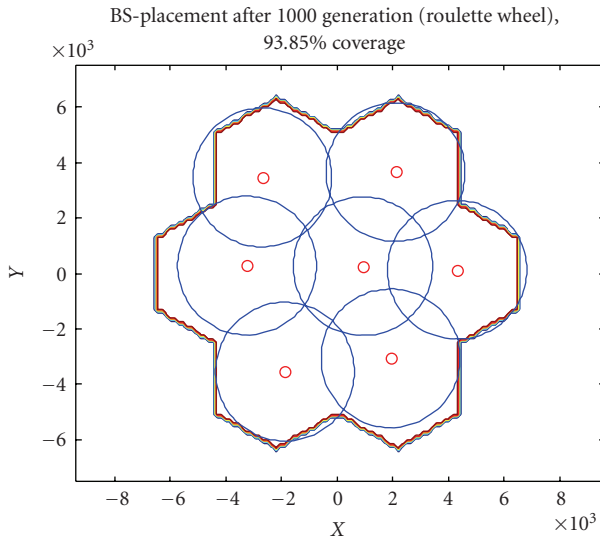


FIGURE 14: After the 1000th generation, base station location with roulette-wheel selection.

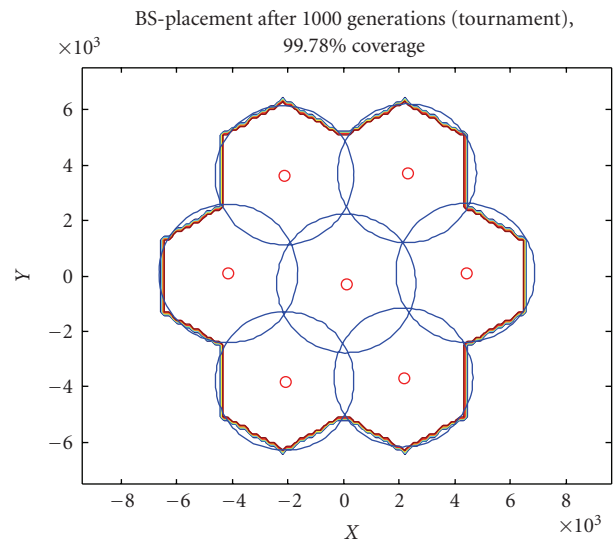


FIGURE 16: After the 1000th generation, base station location with tournament selection.

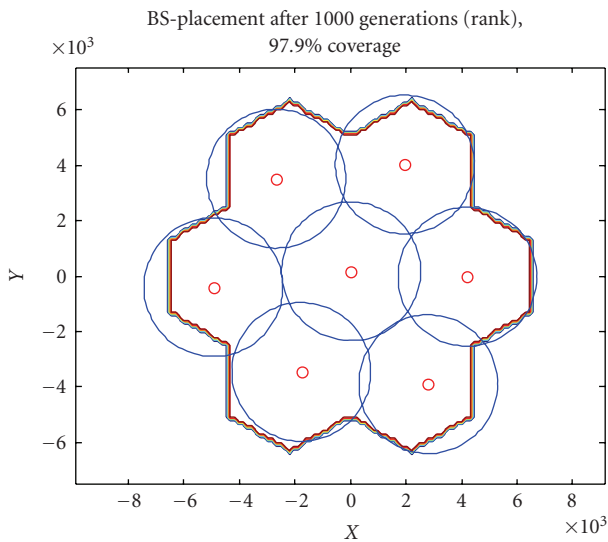


FIGURE 15: After the 1000th generation, base station location with rank selection.

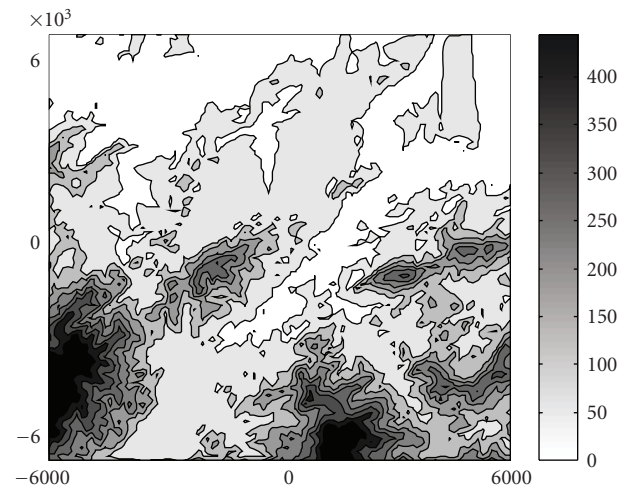


FIGURE 17: Altitude map.

less than those of the low-traffic density. The coverage rate is decreased according to the changing weight of the traffic factor, from 0.9 to 0.8. As the weight of the power factor increases, the actual assigned transmit power value decreases.

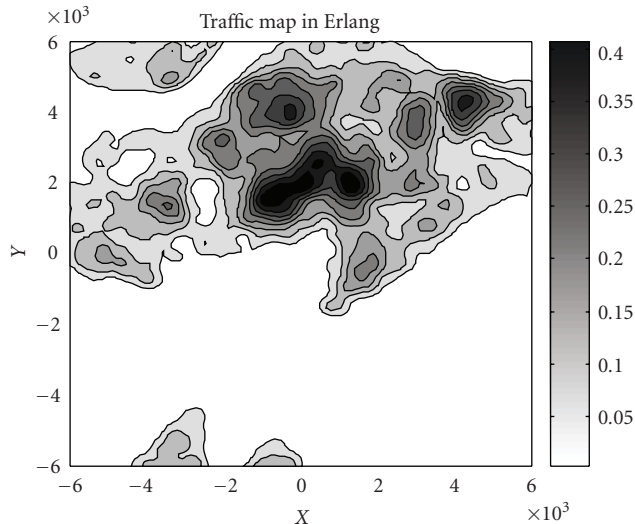


FIGURE 18: Traffic density map.

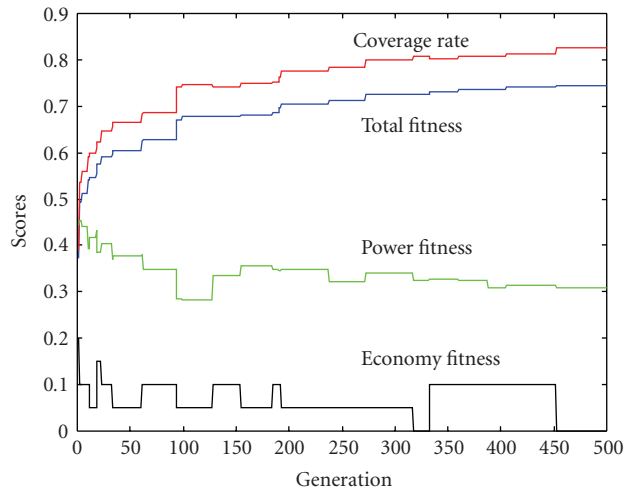


FIGURE 20: Fitness value, $(\omega_t, \omega_p, \omega_e) = (0.9, 0.0, 0.1)$.

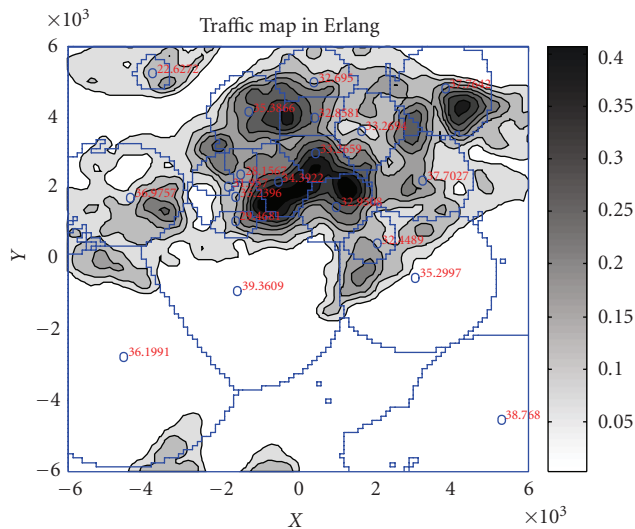


FIGURE 19: After 500 generations, the location of the base stations, $(\omega_t, \omega_p, \omega_e) = (0.9, 0.0, 0.1)$.

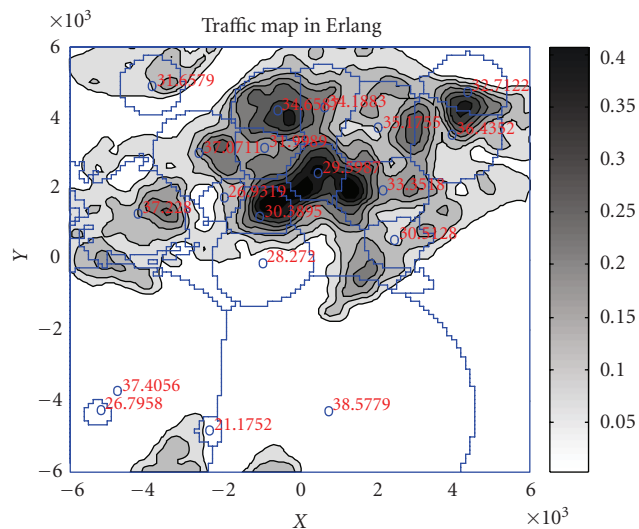


FIGURE 21: After 500 generations, the location of the base stations, $(\omega_t, \omega_p, \omega_e) = (0.8, 0.1, 0.1)$.

In the results shown in Figure 21, the overlapped base station is clearly shown. The cause of this is the decrease of the weighted economy factor. The traffic map that was used for the simulation consisted of high-traffic density areas and very low-traffic density areas such as mountains and rivers. Therefore, traffic is scattered in all directions on the map; consequently, the search space becomes larger. To obtain a better coverage rate, the population size can be enlarged or the mutation probability can be increased. Additionally, it is necessary to process more generations.

6. CONCLUSION

In this paper, given inhomogeneous traffic information and the map for the propagation model, a new algorithm was proposed that enables the optimization of the locations

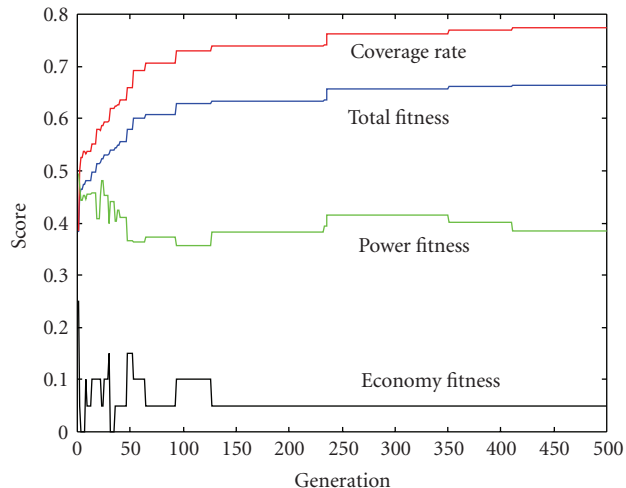


FIGURE 22: Fitness values, $(\omega_t, \omega_p, \omega_e) = (0.8, 0.1, 0.1)$.

and transmitted power of a base station. In addition, this algorithm includes an economic factor (the number of base stations). Good use was made of the genetic algorithm and, it was excellent for obtaining a solution of complex problems. Genetic operators using the real-valued representation are also suggested, and the objective function is defined in consideration of the coverage, the transmitted power of base station and the economy efficiency through an adjustment of crossover and mutation. The selection, input parameters, and scaling are shown to be tightly coupled with the algorithm performance. Therefore, there is a need for these to be harmonized. From a simulation, the proposed algorithm was verified.

REFERENCES

- [1] J. R. Evans and E. Minieka, *Optimization Algorithms for Networks and Graphs*, Marcel Dekker, New York, NY, USA, 1992.
- [2] P. Calegari, F. Guidic, P. Kuonen, and D. Wagner, "Genetic approach to radio network optimization for mobile systems," in *Proceedings of the 47th IEEE Vehicular Technology Conference (VTC '97)*, vol. 2, pp. 755–759, Phoenix, Ariz, USA, May 1997.
- [3] X. Huang, U. Behr, and W. Wiesbeck, "Automatic base station placement and dimensioning for mobile network planning," in *Proceedings of the 52nd IEEE Vehicular Technology Conference (VTC '00)*, vol. 4, pp. 1544–1549, Boston, Mass, USA, September 2000.
- [4] J. H. Holland, *Adaptation in Natural and Artificial Systems*, University of Michigan Press, Ann Arbor, Mich, USA, 1975.