Sweet Spot Control of 1:2 Array Antenna using A Modified Genetic Algorithm

Kyo-Hwan HYUN
Dept. of Electronic Engineering, Dongguk University
Soul, 100- 715, Korea

and

Kyung-Kwon JUNG
Dept. of Electronic Engineering, Dongguk University
Soul, 100- 715, Korea

and

Ki-Hwan EOM
Dept. of Electronic Engineering, Dongguk University
Soul, 100- 715, Korea

ABSTRACT

This paper presents a novel scheme that quickly searches for the sweet spot of 1:2 array antennas, and locks on to it for high-speed millimeter wavelength transmissions, when communications to another antenna array are disconnected. The proposed method utilizes a modified genetic algorithm, which selects a superior initial group through preprocessing in order to solve the local solution in a genetic algorithm. TDD (Time Division Duplex) is utilized as the transfer method and data controller for the antenna. Once the initial communication is completed for the specific number of individuals, no longer antenna's data will be transmitted until each station processes GA in order to produce the next generation. After reproduction, individuals of the next generation become the data, and communication between each station is made again. The simulation results of 1:1, 1:2 array antennas, and experiment results of 1:1 array antenna confirmed the efficiency of the proposed method. The bit of gene is each 8bit, 16bit and 16bit split gene. 16bit split has similar performance as 16bit gene, but the gene of antenna is 8bit.

Keywords: Sweet Spot, Modified Genetic Algorithm, 1:2 Array Antenna, Time Division Duplex, 16 bit split.

1. INTRODUCTION

Today electronic communication has an important position in society, and requires the transmission of substantial information. A few years ago, communication speeds reached the Kbps range but now communication speeds of Mbps are required. Current tools, i.e. IEEE802.11b/11a, Bluetooth, HomeRF, etc, which are band-limited in 100MHz, are already matured. In traditional bandwidth, there isn't sufficient space and costs are high for its use. Broad-spectrum space and free frequency bandwidth is 25GHz or more [2]. Therefore millimeter wave transmissions are embossed by an alternative idea of increasing the limited bandwidth, and enabling fast communication. In networks, beam connected array links are fixed in matched directions. Considering real situations that require adjustment of antenna arrays, fixing the beam is dangerous for SNR (Signal to noise ratio) reduction or unexpected disconnect. We think that, in communication, if an antenna beam could preserve sweet spot alignment, it is possible that Giga-bps transfer could be realized. And if communication is disconnected, quickly search for the sweet spot of the other antenna array and maintain communication. This system consists of 1:2 array antennas, which raises stability above a single array antenna.

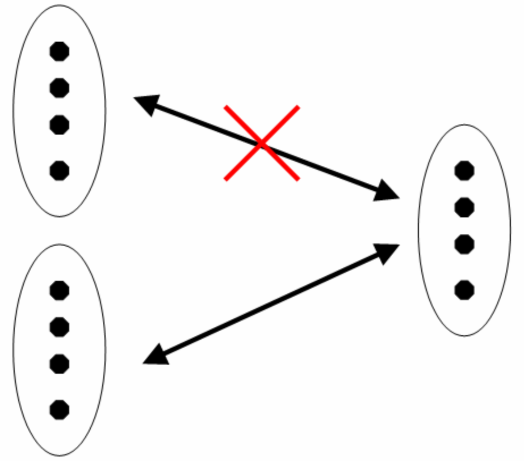
A Genetic Algorithm (GA) is suitable for sweet spot search because it is a more whole and sound method in comparison with other algorithms in optimization problems. A GA uses coding parameters directly and searches for an optimum value with the blind and the population method [1], [7]. Application fields of a GA consist of function optimization, signal and image processing, system recognition and control, design and learning of neural network, VLSI design, prediction and analysis in non-linear system, TSP (traveling salesman problem) and work scheduling [8], [4]. And it is also applied to the optimal control of laser beam. But a GA has a propensity to get stuck at local minima that is caused by the selection of an initial group.

This paper proposes an adaptive method that searches for a sweet spot between each station on 1:2 array antenna links, and keeps it. We use TDD (Time Division Duplex) as the transfer method and data controller for the antenna. The proposed method is a modified genetic algorithm (MGA), which selects a superior initial group through preprocessing in order to solve the local solution in a genetic algorithm. A proposed method finds a maximum angle by MGA. The individual of MGA represents intensity of the beam as a distance function. It is transferred on each station and MGA uses multiplication of the distance function to the fitness function. In order to verify the effectiveness of the proposed method, simulations and experiments were performed by 8 bit, 16 bit and 16 bit split gene. The proposed 16 bit split adds the gene of each station, operates crossover and mutation, and then splits genes.

2. SWEET SPOT

In beam networks, finding and preserving a beam's suitable direction is required to prevent SNR reduction and disconnect. But if communication is disconnected by power failure, breakdown antenna system, etc, then quickly search for the sweet spot of the other array antenna and maintain the link. Fig. 1 shows the single array antenna and the diversity of 1:2 array antennas.

(a) Relay line by single array antenna.



(b) Diversity by 1:2 array antennas
Fig. 1 Relay type.

Fig. 2 shows the Sweet Spot of antenna beam, and Fig. 3 is a case in which the beam failed to find sweet spot for both stations being swerved to all different direction.

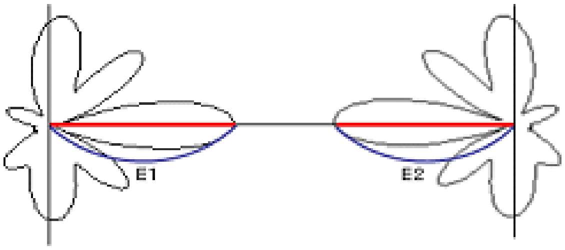


Fig. 2 The ideal situation.

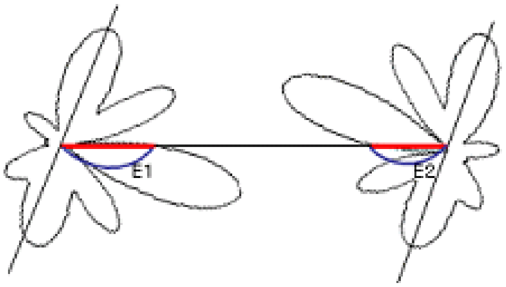


Fig. 3 Both stations turn around to wrong directions.

In this situation, $\boldsymbol{E_1}$ and $\boldsymbol{E_2}$ are values that represent the intensity of each station as distance values about an angle. If the angle from horizon between each station sets $\boldsymbol{\theta_1}$ and $\boldsymbol{\theta_2}$ then $\boldsymbol{E_1}$ and $\boldsymbol{E_2}$ are given like equation (1) and (2) [5], [6].

$$E_1 = \sum_{n=1}^{N/2} w_n \cos((2n-1)\frac{\pi d}{\lambda}(\sin\theta - \sin\theta_1)) \qquad (1)$$

$$E_2 = \sum_{n=1}^{N/2} w_n \cos((2n-1)\frac{\pi d}{\lambda}(\sin\theta - \sin\theta_2)) \qquad (2)$$

Where, w_n is array weight, $\boldsymbol{d}$, $\boldsymbol{\lambda}$ are distance and wavelength of each antenna and $\boldsymbol{N}$ is array number.

3. PROPOSED METHOD

Proposed MGA Method

The local minima problem of GA is resulted from the selection of the initial generation. In the proposed method, in order to resolve this problem MGA preprocesses initial generations which are based on a master / slave model [9]. MGA makes k - slave generation and each slave generation evaluates suitability. The master processor sets the most superior group (generation) to initial generation and weeds out the other group. The master processor executes GA by selecting a superior initial group.

A master processor, which stores whole slave group in its own memory, is in charge of selecting the initial group. And k - slave processors are in charge of evaluating the functions of initial groups [4], [9].

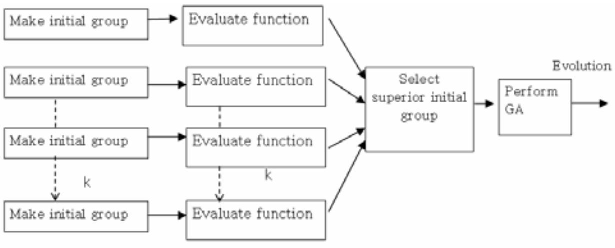


Fig. 4 Proposed MGA.

In GA process, a bubble sort algorithm is used at reproduction. It decides the ranking of individuals. The higher half ranks of the individuals are reproduced and new individuals are made by crossover by as many as half of the individuals. So reproduction produces new individuals by crossover and upper alive individuals reorganize new generation. Fig. 5 is the flow chart of proposed method.

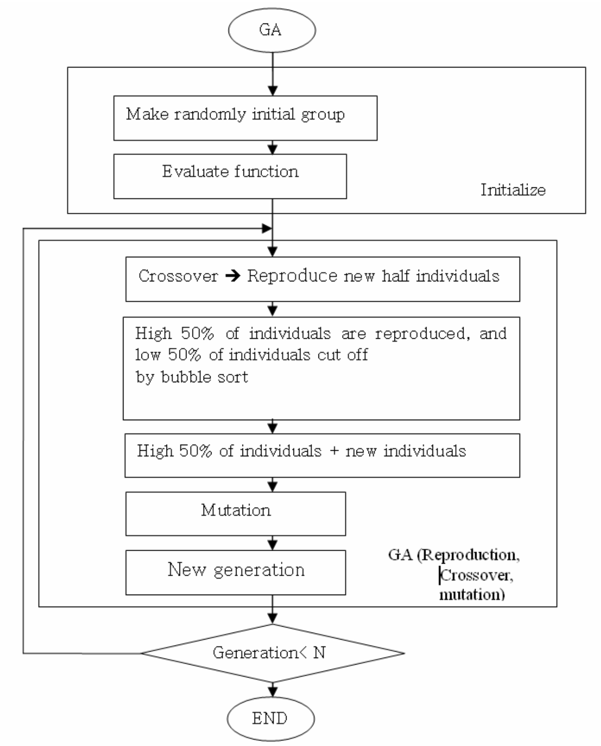


Fig. 5 Flow chart of the Proposed MGA.

The Gene of MGA

8 bit, 16bit and 16bit split genes are used in MGA, and the operation of 16bit split is as follows.

In Fig. 6, each antenna has an 8bit gene. We combine each gene as one. That is, 8bit (A) + 8bit (B) = 16bit. So, the crossover and mutation are processed for the 16-bit gene. After all operation is finished, the gene splits into each antenna.

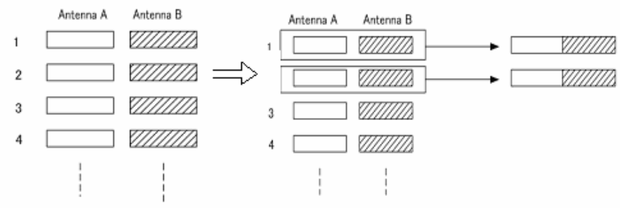


Fig. 6 The operation of 16bit split.

For example, if there are 40 individuals, 20 superior individuals are reproduced, and the other half is reproduced by flowing operation. About crossover, Fig. 7 shows that genes are selected randomly, e.g. No.2 and 7. If gene No2 and 7 are selected and cross point is antenna A side, the result means that antenna A only achieved crossover. There is the gene of No7 left in antenna B just as it is.

The crossover continues by the number of ¼ individual namely 10 individual. And the cross point is changed from antenna A side to B. So Fig. 8 shows new individual.

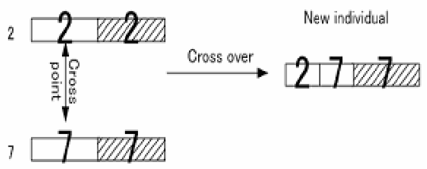


Fig. 7 The example of Crossover.

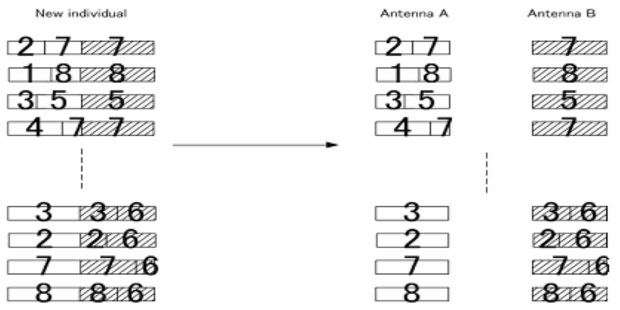


Fig. 8 New individual after Crossover.

This result shows that the genes in the half of new individuals are left without crossover. In this method, we may operate crossover of the 16 bit gene by A and B shift.

Application to Sweet spot search

RSSI(Received Signal Strength Indication) value is as follows

$$RSSI_1 = 20\log_{10}(E_1) \tag{3}$$

$$RSSI_2 = 20\log_{10}(E_2) \tag{4}$$

A sweet spot search is used to compute an optimized value for the direction of beams between two stations. Beam direction data for each station become gene for each generation, and we can find the sweet spot by using multiplication of $\boldsymbol{RSSI_1}$ and $\boldsymbol{RSSI_2}$ as equation (3) and (4). Suitable function '*z*' is illustrated as equation (5). A desired target value is a point when suitable functions reach a maximum value.

$$z = -1/(RSSI_1 + RSSI_2) \tag{5}$$

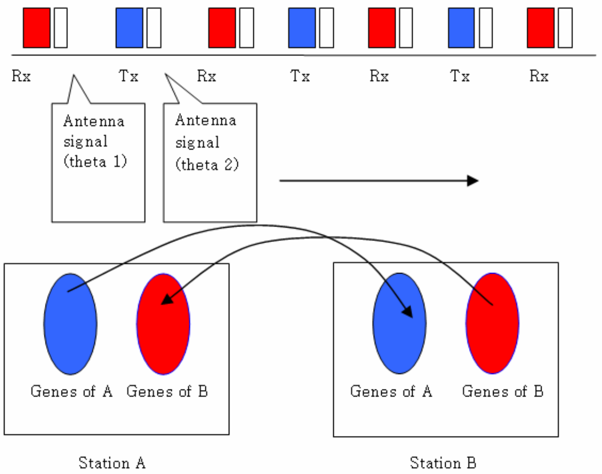


Fig. 9 Communication of antenna's data.

We use the TDD (Time Division Duplex) as a transfer method to control the data of antenna as Fig. 9. We can transfer and receive a large amount of data in the millimeter wave bandwidth. Because the antenna signal accounts for a few bits, influence on communication performance is small. Once the initial communication is completed for the specific number of individuals, no longer antenna's data will be transmitted until each station processes GA in order to produce the next generation. After reproduction, individuals of the next

generation become the data for the antenna, and communications between each other station is made again.
They transfer and receive the antenna's data for each other in each station, and each generation evaluates the function. So they process a GA from selected initial group, and the produced individuals of the next generation send the data to the opposite station again. A flow chart of this algorithm is illustrated as follows.

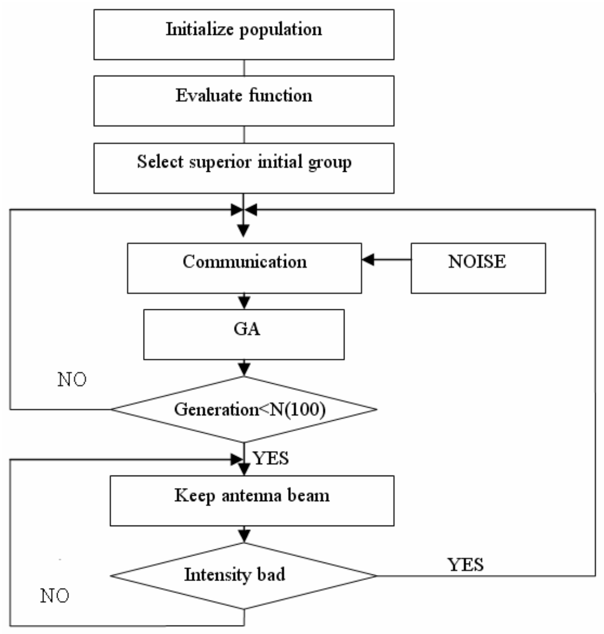


Fig. 10 Flow chart of the proposed sweet spot search.

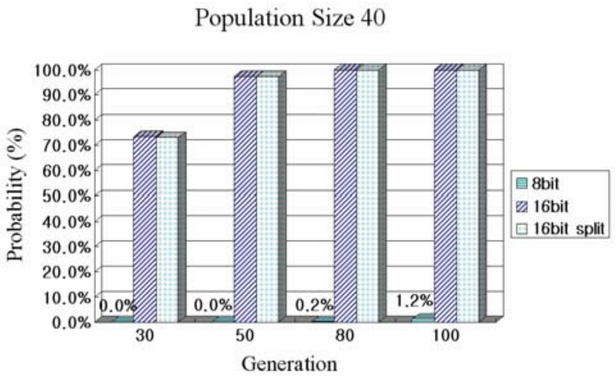
4. SIMULATION

We performed simulations with 8bit, 16bit and 16bit split genes. Simulations were performed using MATLAB 7. The parameters of the simulations are shown in Table I by trial and errors, and d = 0.001, λ = 0.004. In simulation assumes that noiseless, no loss and convergence range is -0.05dBm.

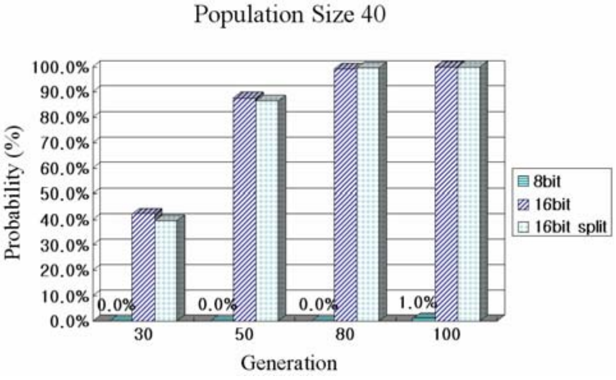
Table I Parameters

Parameters	value
Generation	30, 50, 80, 100
Population Size	20, 30, 40, 60, 80
Crossover Rate	0.9
Mutation Rate	0.04

Fig. 11 and 12 shows the convergence probability of MGA by 8bit, 16bit and 16bit split gene. Each simulation was performed 500 times.

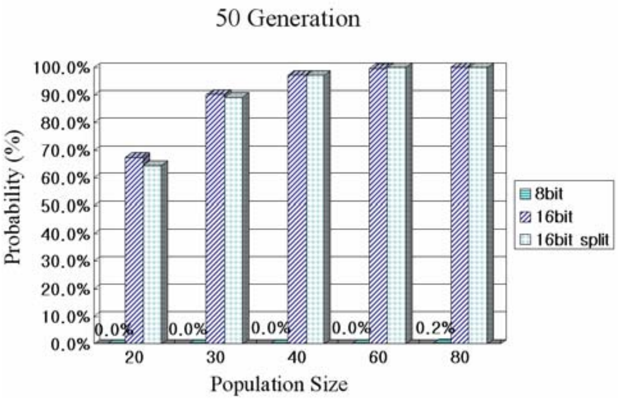


(a) Single array antenna

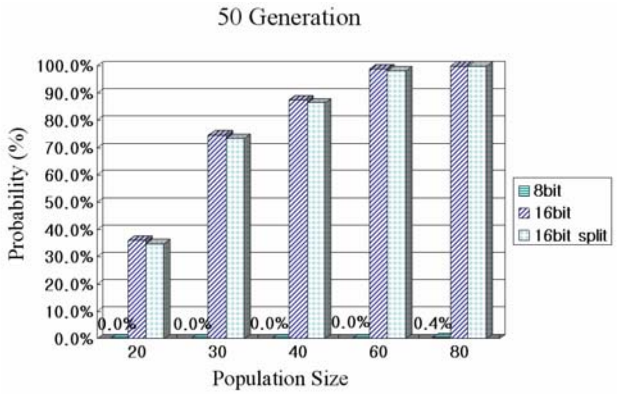


(b) 1:2 array antennas
Fig. 11 Convergence probability when population size is 40.

In Fig. 11 (a) the convergence probability of 16bit and 16bit split is near 100% at 50 generations. Therefore, 50 generations is the optimal generation when the population size is 40, and in Fig. 11 (b) the convergence probability of 16bit and 16bit split is near 100% at 80 generations. Therefore, 80 generations is the optimal generation when population size is 40. When we compare the single array antenna and the 1:2 array antennas at 40-population size, the convergence probability of a single array antenna is better than the convergence probability of 1:2 array antenna at 30 and 50 generations. But they are alike at 80 and 100 generation.



(a) Single array antenna



(b) 1:2 array antennas

Fig. 12 Convergence probability at 50 generation.

In Fig. 12 (a) the convergence probability of 16bit and 16bit split is near 100% when the population size is 40. Therefore, the optimal population size is 40 at 50 generations, and in Fig. 12 (b) the convergence probability of 16bit and 16bit split is near 100% when population size is 60. Therefore, the optimal population size is 60 at 50 generations. When we compare the single antenna array and the 1:2 array antennas at 50 generations, the convergence probability of a single antenna array is better than the convergence probability of a 1:2 array antenna when the population size is from 20 to 40. But they are alike when population size ranges from 60 to 80. In Fig. 11 and 12, the 8 bit gene can not converge to the sweet spot. But 16bit split has the 8bit gene, and it has same good performance as 16bit gene.

5. EXPERIMENT

Experiments were performed with 8bit, 16bit and 16bit split genes. Used directional antenna is PM-GR19, and used RF Board is CC2430DK. The parameters of the simulations are shown in table II by trial and errors. In experiment assumes that convergence range is -12dBm, considering noise and loss.

Table II Parameters

Parameters	value
Generation	30, 50, 80, 100
Population Size	20, 40, 60, 80
Crossover Rate	0.9
Mutation Rate	0.04

Fig. 13 and 14 are the photograph of PM-GR19 and CC2430DK respectively.

Fig. 13 A photograph of PM-GR19.

Fig. 14 A photograph of CC2430DK.

Fig. 15 and 16 shows the convergence probability of MGA by 8bit, 16bit and 16bit split gene. Each experiment was performed 50 times.

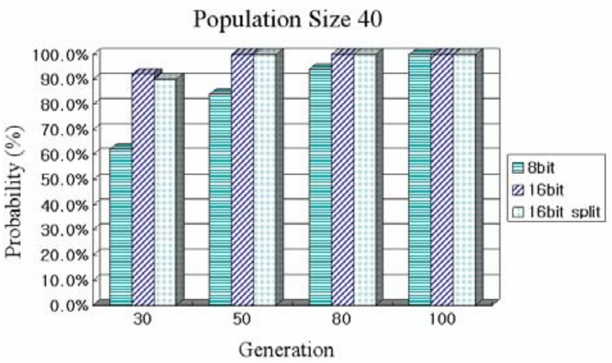


Fig. 15 Convergence probability when population size is fixed.

In Fig. 15 the convergence probability of 8bit is near 100% at 100 generations, and 16bit and 16bit split is near 100% at 50 generations.

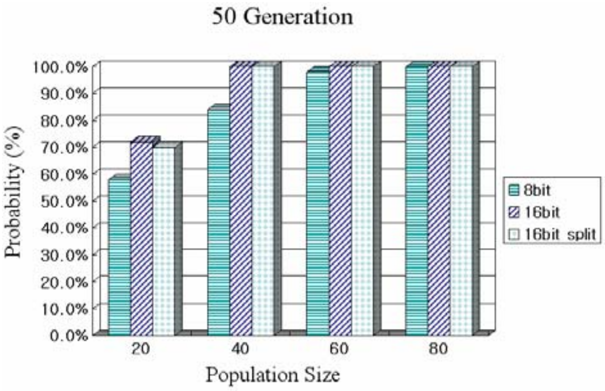


Fig. 16 Convergence probability when generation is fixed.

In Fig. 16 the convergence probability of 8bit is near 100% when the population size is 60, and 16bit and 16bit split is near 100% when the population size is 40.

6. CONCLUSION

This paper proposed a method that searches for the sweet spot of an antenna beam, and maintains it for high speed transmissions, and if communication disconnection occurs by means of a few special cases like power failure, breakdown antenna system, etc, and then quickly searches for the sweet spot of the other antenna array and keeps it in millimeter wave on 1:2 array antenna links. When each station transmits data by TDD, they send their antenna's information, and searches for the sweet spot using the information. The proposed method uses the modified genetic algorithm (MGA) which selects a superior initial group through preprocessing in order to resolve the local solution of genetic algorithm. 16bit split has the 8bit gene, and it has same good performance as 16bit gene. The proposed scheme is validated by simulation and experiment results. Proposed method can quickly searches for the sweet spot of 1:2 array antennas, and locks on to it. So it is possible that Giga-bps transfer could be realized.

Finally, the simulation and experiment results are summarized as follows:

- Convergence probability of 16bit and 16bit split of single array antenna is near 100% at 50 generations when the population size is 40.
- Convergence probability of 16bit and 16bit split of 1:2 array antennas is near 100% at 80 generations when the population size is 40.
- Convergence probability of 16bit and 16bit split of 1:2 array antennas is near 100% at 50 generations when the population size is 60.
- Genes of the antenna 16bit split is 8bit. But it has similar performance as 16bit gene.
- The Convergence probability of a single antenna array is better than the convergence probability of a 1:2 array antenna at 30 and 50 generations, but they are alike at 80 and 100 generations when population size is 40.
- The Convergence probability of a single array antenna is better than the convergence probability of a 1:2 array antennas when population size is from 20 to 40, but they are alike when population size is from 60 to 80 at 50 generations.

ACKNOWLEDGEMENTS

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7. REFERENCES

[1] D. E. Goldberg, **Genetic Algorithms in Search, Optimization and Machine Learning**, Addison-Wesley Publishing Co.Inc., N.Y., 1989

[2] R. Becher, M. Dillinger, M. Haardt, and W. Mohr, "Broad-band wireless access and future communication networks," *Proc. of the IEEE*, Vol.89, Jan. 2001, pp.58-75.

[3] Man, K., **Genetic algorithms for control and signal processing**, Springer, 1997

[4] Gang-gue Jin, **Genetic Algorithms and Their Applications**, Kyo Woo Sa, 2002

[5] John D. Kraus, **ANTENNAS**, McGraw-Hill, 2002

[6] F. Gross, **Smart Antenna for Wireless Communication**, McGraw-Hill, 2005

[7] M.Mitchell, **An Introduction to Genetic Algorithms**, MIT Press, 1966

[8] M.gen and R. Cheng, **Genetic Systems & Engineering Design**, John Wiley & Sons, Inc., N.Y., 1997

[9] H.Mühlenbein, M. Schomisch and J. Norn, "The Parallel Genetic Algorithm as Function Optimizer," **Parallel Computing**, Vol. 17, pp. 619-632,1991