GENERATION OF SIGNALS FOR MULTIPLE SONARS BY THE GA

M. Ohki, S. Tabuchi and M. Ohkita

Department of Electrical and Electronic Engineering
Faculty of Engineering, Tottori University
101, 4 Koyama-Minami, Tottori, Tottori 680-8552 Japan

Abstract: We propose to apply the genetic algorithm (GA) to generation of pulse pattern for the multiple supersonic sensors to measure distance. Such the supersonic sensors are, for example, to be devised on a autonomous mobile robot. Those supersonic sensors actually yield crosstalk themselves on a real robot. The pulse pattern has to satisfy some conditions to keep probability of erroneous measurement caused by the crosstalk low. While A problem to generate such pulse pattern is difficult, it should be solved by using the GA as a combinatorial optimization problem. In this paper, we propose two ways of genotype coding which yield different results respectively.

Keywords: supersonic sonar, genetic algorithm, pulse modulation

1   INTRODUCTION

Supersonic sonars are, for example, used to be devised on an autonomous mobile robot traveling indoor/outdoor environment, because they can be easily and cheaply implemented [1,2]. In general, many sonars are devised on the robot to accurately measure distance. Then the signal is required to be modulated by a pulse pattern which is different for each sensor to avoid crosstalk among multiple sonars [3,4]. The pulse pattern has to satisfy those complex demands and numerical conditions to minimize the erroneous probability. However, a probability of erroneous measurement caused by the crosstalk does not become zero when the number of pulses for each sonar's signal is less than the number of sonars. When the pulse pattern is decided, the erroneous probability can be numerically computed [5]. On the other hand, the term of the signal that each sensor sends should be short to implement quick measurement.

We are studying on application of the genetic algorithm (GA). The GA is applied to many optimization problems. By means of multiple and probabilistic search capabilities of the GA, a global optimum is able to be obtained in various problems. The GA is also able to solve a combinatorial optimization problems, even in a case of obtaining the pulse pattern as above mentioned. When the GA is applied to such a combinatorial optimization problem, an effective genotype coding technique is required. In this paper, we first dedicate a genotype code including pulse intervals between pulses forming a modulation signal for a sensor. To improve a problem of the first technique, the second genotype code is dedicated. Finally, the effectiveness of the second one is shown by comparing these two techniques.

2 CROSSTALK AMONG MULTIPLE SONARS

An example of the autonomous mobile robot traveling through a course with recognizing its environment is shown in Fig. 1 (a). In general, multiple sonars are used to be devised on such the robot. Each sonar has to receive signal sent itself to measure a distance between the robot and obstacles or walls, while some receivers of sonar receive signal given as a summation of signals which have been sent from other sonars and have been propagated on different acoustic paths, The multiple sonars devised

(a) example of cross talk

(b) pulse-modulated signal

Figure 1. An example of an autonomous mobile robot recognizing its environment.

on the autonomous mobile robot yield crosstalk each other, and then fail to measure distances between the robot and an obstacles as shown in Fig. 1 (a). To avoid such a crosstalk, a pulse-modulated signal shown in Fig.1 (b) are used handled the sonar. Now we define S, T_s, R_s and r_{qs} as the number of sonars, a signal sent from the s-th sonar, where we call it a source signal, a signal received at the s-th sonar and a signal sent from q-th

sonar, propagated on an acoustic path and received at s-th sonar respectively. The term of the signal is divided by L intervals, or time slots, whose length equals the length of one pulse. The modulation pulses for each sonar are formed by giving 0 or 1 at some time slots. In other words, the source signal T_s is defined by 0 or 1. The signal R_s is given by a summation, $ó_q \, r_{qs}$, as shown in Fig.2 and organized as the following equation:

$$R_s(i) = 1 \quad for \quad \left(\sum_{j=1}^{S} r_{js} \geq 1 \right) \quad or \quad 0 \quad for \quad \left(\sum_{j=1}^{S} r_{js} = 0 \right) \tag{1}$$

A correlation between the source signal T_s and the received signal R_s given by the following equation is

$$C(T_s, R_s, i) = \sum_{j=0}^{L} R_s(j) T_s(j+i) \quad (i = 0,1,2,\cdots) \tag{2}$$

computed for each sonar to measure distance.

The distance is given according to time delay i giving the highest value of the correlation C for all i or a value larger than a threshold $á$.

To completely detect the time delay between the source signal and the received signal, the following conditions have to be satisfied.

$$\sum_{j=0}^{L-1} T_s(i) T_q(i+j) \leq 1 \quad (0 \leq j < L) \tag{3}$$

$$\sum_{j=0}^{L-1} T_s(i) T_s(i+j) \begin{cases} = P & (j = 0), \\ \leq 1 & (0 < j < L), \end{cases} \tag{4}$$

These conditions are able to be changed in other words that any pair of interval lengths arbitrarily choosen from the whole source signals are different each other. In Fig.2, time of flight of the signal r_{ss} should be detected while an erroneous signal formed by other sonars' pulses are detected in the received signal R_s.

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Figure 2. Signals received at the s-th sonar.

In cases using a set of signals satisfying Eqs.(3) and (4), the value of the correlation C between different signals is less than or equal to one. Then P different signals are required to form pulses with same form to T_s. Therefor if the number of the sensors, are less than the number of the pulses, P, such a signal having same form to T_s can not be formed. In other words, if the condition, P $S+1$, is satisfied, erroneous measurement caused by the crosstlk is completely avoided. However, such a set of signals or pulse pattern is difficult to obtain. We propose a technique to automatically form such a pulse pattern to avoid or restrain erroneous measurement and to minimize its length of the signals at the same time by using the GA.

3   SIGNAL GENERATION USING THE GA

In order to automatically generate a pulse pattern satisfying Eqs.(3) and (4) by using the GA, the pulse patter is coded as a genotype as shown in Fig.3. The row means a sonar's number and the column means a pulse interval's number. Each number in those boxes denotes length of interval between pulses which neighbor each other. Since those numbers at each locus of the genotype are randomly given, a gene without any procedures does not satisfy Eqs.(3) and (4). Then the following procedures, shown in Fig.4, are derived for changing the gene so as to satisfy these equations. In the following procedures and Fig.4, g_{sp} denotes the number at the locus of the p-th interval of the s-th sonar.

(0) Prepare a check list as shown in Fig.4. The check list can be composed as an array in the C language.

(1) Check the intervals for the first sonar.

   (1-1) Refer q_{11} which equals 3. Since the ($q_{11}=3$) -th position of the check list is vacant, check this position and fix q_{11} at 3.
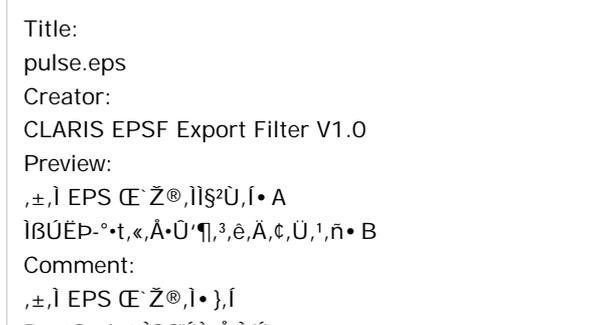
(1-2) Refer q_{12} which equals *13*. Since the (q_{12}=*13*)-th and ($q_{12}+q_{11}$=*16*)-th positions of the check list are vacant respectively, check these positions and fix q_{12} at *13*.

(1-3) Refer q_{13} which equals *8*. Since the (q_{13}=*8*)-th, ($q_{13}+q_{12}$=*21*)-th and ($q_{13}+q_{13}+q_{13}$=*24*)-th positions of the check list are vacant respectively, check these positions and fix q_{13} at *8*.

Then all the intervals for the first sonar are checked and fixed.

(2) By means of the same manner, the intervals for the following sonar can be checked and fixed. When a position which would be checked has already checked or is not vacant, increase the number at locus by one and repeatedly refer the number.

(3) Note when the intervals for the third sonar are processed.

(3-1) Refer q_{31} which equals *2*. Since the (q_{31}=*2*)-th position of the check list is vacant, check this position and fix q_{31} at *2*.

(3-2) Refer q_{32} which equals *7*. While the (q_{32}=*7*) -th positions of the check list is vacant, ($q_{32}+q_{31}$=*9*)-th positions is not vacant. Then increase q_{32} by one, refer q_{32} which equals *8* with same manner. However *8*-th and *9*-th position are not vacant neither. Finally, q_{32} can be taken at *10*. Since the (q_{32}=*10*)-th and the ($q_{32}+q_{31}$=*12*)-th positions of the check list are vacant respectively, check these positions and fix q_{32} at *10*.

(3-3) Refer q_{33} which equals *14*. By means of the same manner, it is finally fixed at *18* and checked the *18*-th, the *28*-th and the *30*-th positions are checked.

Then all the intervals for the third sonar are checked and fixed.

(4) Apply the same manner to the following sonars' intervals.

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Figure 3. genotype coding. **Figure 4.** Procedures to change a gene so as to satisfy Eqs.(3) and (4).

The population which includes twenty-seven individuals is defined as shown in Table 1. In the Table 1, e denotes an elite individual giving the best performance through the whole generation, s_1 and s_2 denote parent individuals giving the minimum number of the signal length except for the elite and the minimum difference between the maximum and minimum lengths of the signal given by the decoded pulse pattern respectively. The operator (...)' denotes a mutation operator which randomly changes the numbers at some loci selected according to mutation probability P_m. The operators and $\times_p$ denote crossover operators. The crossover operator $\times_s$, to be applied to two individuals, changes some pulse intervals defined for the sonars selected according to crossover probability P_{cs} and provides multi-points crossover. The crossover operator $\times_p$, also to be applied to two individuals, changes sets of locus divided by a interval boundary selected according to crossover probability P_{cs} and provides one-point crossover.

Table 1. Composition of the population.

e'	s_1'	s_2'
$e\times_s s_1$	$e\times_s s_2$	$s_2\times_s s_1$
$s_1\times_s e$	$s_2\times_s e$	$s_1\times_s s_2$
$e\times_p s_1$	$e\times_p s_2$	$s_2\times_p s_1$
$s_1\times_p e$	$s_2\times_p e$	$s_1\times_p s_2$
$(e\times_s s_1)'$	$(e\times_s s_2)'$	$(s_2\times_s s_1)'$
$(s_1\times_s e)'$	$(s_2\times_s e)'$	$(s_1\times_s s_2)'$
$(e\times_p s_1)'$	$(e\times_p s_2)'$	$(s_2\times_p s_1)'$
$(s_1\times_p e)'$	$(s_2\times_p e)'$	$(s_1\times_p s_2)'$

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The GA searches for a good solution which provides a pulse pattern satisfying Eqs. (3) and (4) and having shorter length of the pulse pattern. In the initial stage of the GA, the initial population including 27 individuals is randomly generated. In the performing stage, all the individuals of the population are transformed into the phenotype by means of the above procedures and performed by the length of the pulse pattern. In the selection stage, one elite individual and two parent individuals are selected from the population. The elite individual provides the shortest length of the pulse pattern through whole generation. One of those parent individuals provides the second shortest length of its pulse pattern except for the elite individual among the current population. Another of those parent individuals provides the smallest difference between the maximum and minimum lengths of the signal defined for each sonar in its phenotype. In the reproduction stage, new population is reproduced as shown in Table 1. The search is repeated for thousand generations.

One of results for an example of the sonar system composed by eight sonars and nine pulses, are shown in Table 2. In this table, these values are given in a values of interval length between pulses neighboring each other. And its length of the pulse pattern is 740.

Table 2. One of results for a case composed by eight sonars and nine pulses.

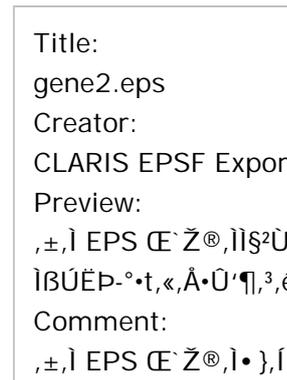| S	interval length							
1	1	60	94	76	24	135	2	55
2	41	21	54	50	72	101	102	73
3	3	66	11	35	74	119	52	56
4	14	70	43	16	67	157	86	91
5	9	96	42	64	140	124	81	144
6	4	40	38	130	111	178	160	47
7	5	85	89	92	128	141	93	107
8	13	110	99	134	131	153	19	79

4　IMPROVEMENT ON GENOTYPE CODING

We have considered on the method to code the genotype. By using the genotype coding provided in the previous section, there are some cases that differences of a part of the gene do not appear in difference of phenotype code or difference of the pulse pattern. This is caused by the transformation to make the gene satisfy the Eqs. (3) and (4). In the procedures of the transformation, some values at locus are increased to check vacant position of the check list. This means that such value has been able to be less than or equal to a value which is repeatedly increased by one and finally obtained. This situation yields futile searches in the GA. Therefor, the genotype coding leaves much room for improvement.

To avoid the futile searches and to improve the efficiency of the GA process, we propose a new technique of genotype based on the conventional technique. In the new genotype coding, a number at each locus of the gene dedicates a selection number as shown in Fig. 5. The selection number denotes the number of vacant position of the check list while the interval number in the previous genotype coding denotes the interval length between pulses which neighbor each other. The check list dedicates the same meaning what its position number denotes the interval length. When a position of the check list pointed by the selection number is invalid as shown in the previous procedures, the next position is selected and tried to be checked. The example of the gene shown in Fig. 5 dedicates a same pulse pattern given from the gene shown in Fig. 3.

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Figure 5. new genotype coding.

One of results for an example of the sonar system composed by eight sonars and nine pulses, are shown in Table 3. In this table, these values are given in a values of interval length between pulses neighboring each other. And its length of the pulse pattern is 616.

To compare the results given by those two ways of genotype coding, the ratios, I_p/I_r, E_p/E_r, A_p/A_r, I_p/I_r, E_p/E_r and A_p/A_r, are held and illustrated in Fig.6 (a)-(c) where I_p and I_p denote the minimum value among the results by using the previous and the new genotype coding respectively, E_p and E_r denote the average value among the results by using the previous and the new genotype coding respectively,

A_p and A_r denote the maximum value among the results by using the previous and the new genotype coding respectively. The previous genotype coding is advantage in the cases when the size of the problem is small, in other words, the numbers of sonars and pulses are small. On the other hand, when the size of the problem become larger, or the numbers of sonars and pulses become larger, results using the new genotype coding provide smaller values of result, where the smaller value is held, the result gives the shorter length of the signal which is considered as the better one.

Table 3. One of results using the new genotype coding for a case composed by eight sonars and nine pulses.

S	interval length							
1	3	208	63	7	1	52	67	42
2	36	44	32	118	45	61	69	62
3	77	17	115	33	88	34	74	90
4	47	28	79	92	78	89	95	41
5	22	24	57	30	110	100	135	125
6	2	56	68	91	142	85	31	141
7	4	19	82	149	73	66	102	117
8	14	25	152	27	147	98	128	18

By using the new genotype coding, change of the individual by the genetic operator certainly appears in its phenotype code or the pulse pattern. Then individuals even which subtly changed tried to performed. Therefor, such the futile search is avoided and the GA is efficiently executed through whole generations.
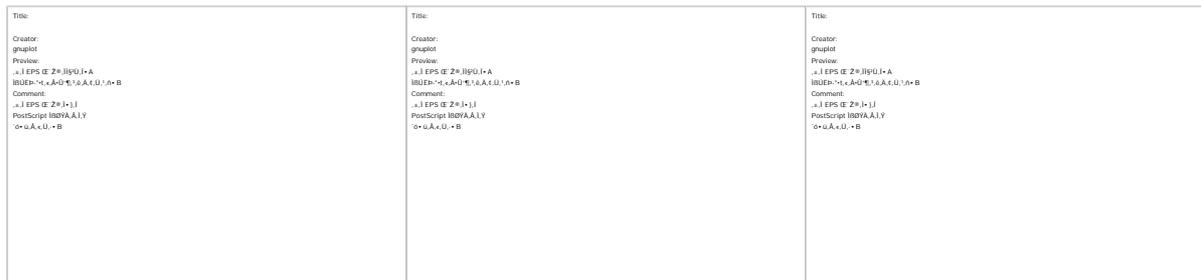
(a) I_p/I_r **(b)** E_p/E_r **(c)** A_p/A_r

Figure 6. The valus of I_p/I_r, E_p/E_r and A_p/A_r.

5   CONCLUSION

We have discussed on automatic generation of pulse pattern using the GA. To obtain a valid pulse pattern, constraint have to be satisfied. This constraint is able to be changed in other words that any pair of interval lengths arbitrarily chosen from the whole source signals are different each other.

To satisfy this constraint, we have first produced a genotype coding and procedures to transform from an individual in genotype to a valid pulse pattern. This genotype coding yields futile search in the GA and leaves much room for improvement. Then we have second proposed a new genotype coding to avoid such the futile search. By means of the new genotype coding, the GA is efficiently executed without futile search.

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AUTHORS: Ass. Dr. M. OHKI, Student-MC. S. TABUCI, Prof. Dr. M. OHKITA, Dept. of Electrical and Electronic Eng., Faculty of Eng., Tottori Univ., 101, 4 Koyama-Minami, Tottori, Tottori 680-8552 Japan, Phone: +81-857-31-6701, Fax.:+81-857-31-0880, E-mail: mohki@ele.tottori-u.ac.jp