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A New Approach to Genetic Based Machine Learning for Efficient Improvement of Local Portions of Chromosomes

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Abstracts:This paper presents a new approach to genetic based machine learning(GBML). The new approach is based on an imaginary mechanism of evolution. The authors call the new approach Nagoya approach. The Nagoya approach is efficient in improving local portions of chromosomes. A simulation of simple computer graphics using the new approach is done. An obstacle avoidance of mobile robot is also simulated using the Nagoya approach and complex fuzzy rules are found.

1. Introduction

The genetic algorithm (GA)[1] is one of the basic models of evolution and is one of the effective tools for constructing evolvable / adaptive complex systems. There are two distinct approaches to genetic based machine learning(GBML). These two approaches are called the Michigan approach[1] and the Pitt approach[2]. The Michigan approach uses a single set of production rules or classifiers. The production system with the set of rules senses the environment and outputs actions to the environment. Each individual rule has a strength which indicates the utility of the rules to the goal of the system. The apportionment of credit system obtains payoffs from the task environment for the actions and shifts strength of the rules in proportion to the amount of payoffs as well as to the contribution of the rules to the goal. Genetic operators are applied to the rules on the basis of strength. The individual in the Pitt approach comprises a set of rules. There are sets of rules in the population. Each set of rules is used in the production system and the payoffs from the environment are directly given to the set of rules. The fitness value of individual set of rules is assigned with the amount of payoffs. The Pitt approach does not need the apportionment of credit system which requires careful design with profound knowledge of the task environment. Although the Pitt approach needs extensive computational resources to evaluate many rule sets through generations, recent rapid progress in computer hardware makes this approach more promising for GBML paradigm.

Through some experiments using the Pitt approach, it is found that the improvement of individual rules of a chromosome is hard to achieve. This is because that the payoff from the environment combines all the information of the task level performance, the number of rules that fire, the degrees of contribution of rules, etc. into a scalar value. J. J. Grefenstette proposed a multilevel credit assignment[3] in the context of the Pitt approach to assign credit at the level of individual rules using the bucket brigade algorithm. The use of credit assignment system makes the construction of the GBML system difficult again.

This paper presents a new approach to the GBML. The new approach is based on an imaginary hypothesis of evolution and is simple and efficient in improving individual production rules in the set of rules. The authors call the new approach "Nagoya approach".The new algorithm is first applied to a simple problem of computer graphics to demonstrate the effectiveness of the new approach in improving the local portions of chromosomes. The problem is to allocate numerous polygons on the designated area. Then the new approach is applied to find complex fuzzy rules for obstacle avoidance of mobile robot. The simulation result show that the new GBML method is very efficient in finding control rules with the limited information from the payoffs provided by the task environment.

2. Pitt Approach

Figure 1 shows an example of flow of the Pitt approach applied to knowledge finding for obstacle avoidance. The initial population is randomly generated. There are n_{chr} chromosomes each of which consists of n_r rules. Each chromosome is used to steer the robot to avoid a moving obstacle. The payoffs are given to the chromosome for its performance. All the chromosomes are tested one by one and their fitness values are determined in proportion to their own payoffs. The stopping condition is, for example, the achievement of all the tasks by at least one chromosome. If the

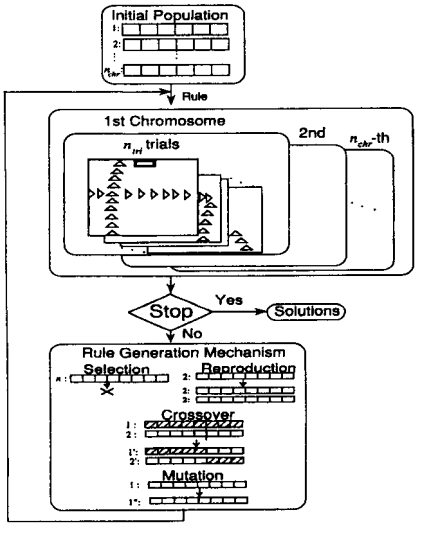


Fig.1 Flow of Pitt approach

stopping condition is not met, the rule generation mechanism is applied to the population. The genetic operators such as selection, reproduction, crossover and mutation are applied to the chromosomes to generate new rule sets. Through the iteration of the trials of obstacle avoidance by the chromosomes and the generation of new ones, the tasks will finally be achieved.

It is found through some experience that the individual rules in a chromosome is hard to be improved in the Pitt approach. Because the payoffs from the environment to a chromosome are scalar values for its performance. No indivual rule is evaluated. J. J. Grefensttete[3] proposed a method to assign credit to each rule of the chromosome using the bucket brigade, i.e. a kind of combination of the Michigan approach and the Pitt approach. This method loses the merit of the Pitt approach in that the Pitt does not need profound knowledge of the task environment for the credit assignment.

3. Hypothesis of Evolution

Let's imagine a mechanism of evolution. The authors call this hypothesis "Implantation of healthy cell (gene)". The hypothesis is an analogy of the implantation of a cancerous cell.

Figure 2 shows an example of adaptation of a fish to its carnivores. The mouths of the fishes are well adapted to their meal. The ancestors of the fishes ate insects. For some unknown change of its environment, some group of the fish changed their carnivores to other fishes or to shellfishes. Their lips and teeth were changed and well adapted to their carnivores. This kind of adaptation is found in anywhere in the natural world on this planet. What are the mechanisms of this evolution? If the mutation of DNA is the case, it is said that the probability of mutation should be very very higher than the natural rate.

Here, let's consider mutations in tissues of a body. The mutations should have occurred in tissues in every organ. Since there are numerous cells in an organ, the probability of mutation is high enough to generate mutants many times in the life of the organ as illustrated in Fig. 3. It is said that the probability of mutation is about 10^{-6} per a locus of genes. If 10^{6} cells in the tissue are reproduced, the probability of mutation in the tissue is 1. It is reasonable to think that mutations occur in the tissue many times. Most of the mutants will probably die immediately. If a mutant having a high adaptability to its environment is generated, the newly evolved cell will survive and produce many clones. When the clones dominate the organ, the new cells (or their genes) are assumed to be implanted into other organs like cancerous cells as in Fig. 4. The healthy cells (genes) will do nothing wrong in other organs, since other parts of genes will be activated in those organs. If the implantation reaches the sexual organ, the newly evolved genes will be inherited to the offsprings. This inheritance is illustrated in Fig. 5.

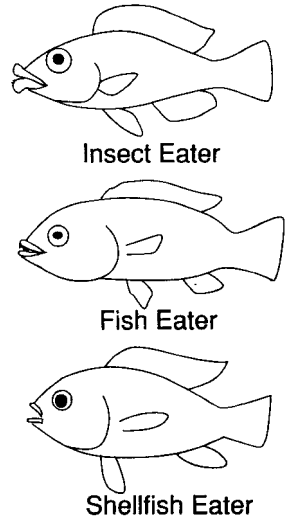


Fig.2 Adaptation of fish to its carnivores

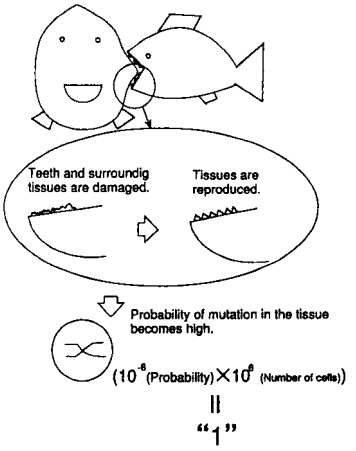


Fig.3 Mutations in tissues

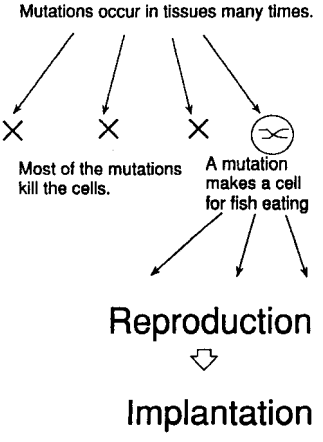


Fig.4 Implantation of adapted mutants

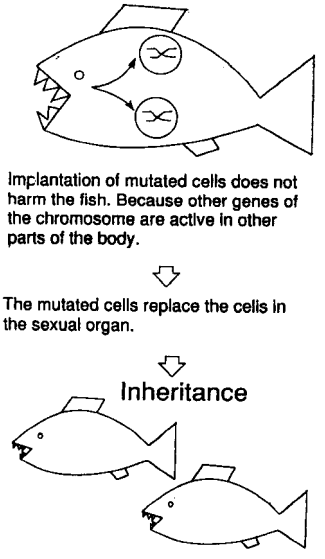


Fig.5 Implantation of healthy cells and inheritance

4. Nagoya Approach

The new GBML derived from the above hypothesis of evolution is given in this chapter.

Figure 6 shows the basic flow of the Nagoya approach.

(a)Generation of initial population

n individuals are generated randomly.

(b)Genetic operation

The following genetic operations are applied to individuals and new populations of chromosomes are generated:

(i) Mutation and selection of cells: Suppose there are Np parts (organs) in which Np portions of the chromosome are activated, respectively. One chromosome "1" is chosen and a portion(gene) of the chromosome is activated. m clones of the gene are reproduced and the newly generated clones are mutated. Each gene is evaluated in the environment where the cell is exposed. One gene with the highest fitness value is then selected. Np genes are selected from Np parts and are aggregated (implanted) into the new chromosome "1' ". This genetic operation is applied to all the n chromosomes.

(ii)Selection and reproduction of chromosomes: The selection and the reproduction are done to chromosomes. Each chromosome is evaluated in the environment where the individual lives. Those with lower fitness values are deleted. Some chromosomes are reproduced after, for example, the roulette wheel selection from the remaining chromosomes. In Figure 6, chromosome k' is deleted, since its fitness value is the least. The chromosomes i', j' are selected and reproduced.

(iii)Crossover: The crossover operation is applied to the newly generated chromosomes and the offsprings i'', j'' are generated.

The above genetic algorithm is efficient in local improvement of chromosomes, since the evolution is carried out on the level of each gene of the chromosomes.

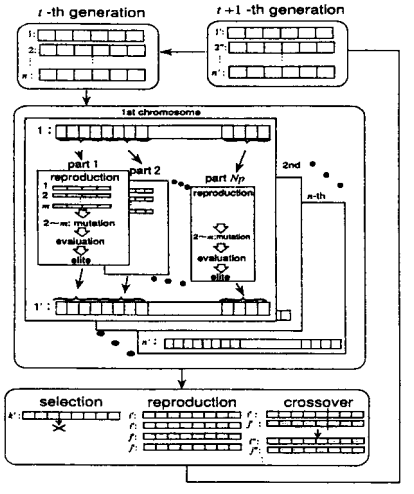


Fig.6 Flow of Nagoya approach

5. Computer Graphics

Nagoya approach is applied to a simple computer graphic problem. We chose a problem having many elements to evaluate and simple evaluation functions to demonstrate the effectiveness of the new approach in improving the local parts of the chromosomes.

5.1 Coding

Figure 7 shows the problem formulation. The problem is to allocate numerous polygons between the two circles in Fig.7(a) or (b). In the simulation, the area is changed from Fig.7(a) to (b) and vice versa at every 200th generation. The evaluation functions are shown in Fig.7(c) and (d). For the area in Fig.7(a), the polygons of which the centers are in between the two circles with radiuses r_1 and

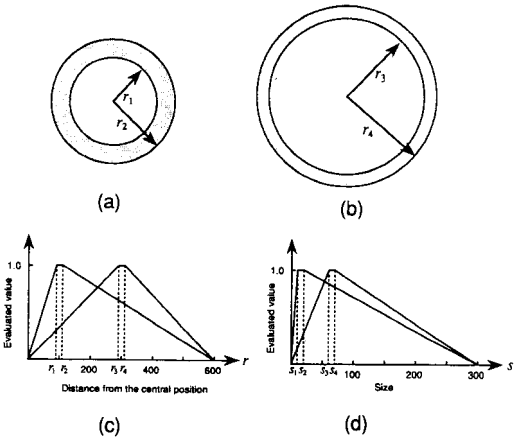


Fig.7 Problem formulation

r_2 have higher evaluated values. For the area surrounded by the two circles with radiuses r_3, r_4, the evaluation function is also set as a trapezoidal one. The unit of distance is a dot on the CRT screen. The size of each polygon is also evaluated by the functions in Fig.7(d). The sizes of polygons are defined as the radiuses of the circumscribed circles of the polygons. The evaluation functions are used alternately for every 200 generations. All the evaluated values of polygons are summed up for the fitness value of the chromosome.

The allocation of polygons is encoded into a chromosome as shown in Fig.8. The positions of each polygon on the x, y-coordinate and the size of each polygon are encoded into the chromosome. In this simulation, the number of polygons were set at 90. The loci of the chromosome were thus $90 \times 3 = 270$. The number of chromosomes was 30. Each chromosome was divided into 3 parts. Each portion was reproduced to 4. The newly generated genes were mutated with the ratio of 10%. The selection rate was 33.3%. One point crossover was applied.

For the comparison, conventional GA was also applied to the graphic problem. The number of chromosomes was 150. The selection rate was 33.3%. The chromosomes have less fitness values were deleted. The mutation rate was 10%. The elitist policy was employed.

Figure 9(a) and (b) show the simulation results at the 600th and 800th generations, respectively, using the Nagoya approach. Almost all of the polygons were on the designated areas. Figure 9(c) and (d) are the results at the corresponding generations to those in (a) and (b), respectively, with the conventional GA. It was not efficient with the conventional GA to improve the local portions of the chromosomes. Polygons were scattered over the 2-dimensional space. Figure 10 shows the fitness values of the elite chromosomes

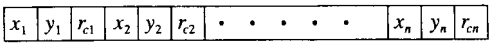
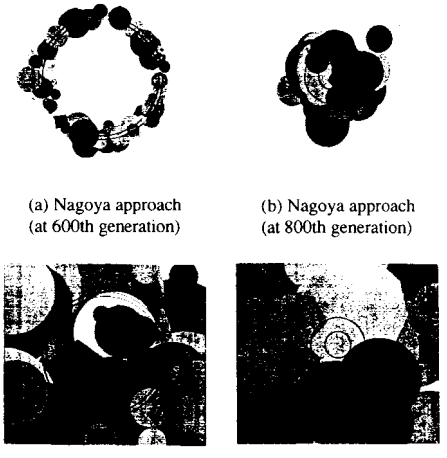


Fig.8 Coding of positions and sizes of polygones



(a) Nagoya approach (at 600th generation)

(b) Nagoya approach (at 800th generation)

(c) Pitt approach (at 600th generation)

(d) Pitt approach (at 800th generation)

Fig.9 Simulation results of graphic problem

obtained by the new approach and the conventional one. The fitness values were normalized with the possible maximum value. The figure shows that the new approach was efficient in adapting the chromosomes to the changing environment.

6. Finding of Fuzzy Rules

The new GBML derived in the chapter 4 is applied to a collision avoidance problem of a mobile robot. The avoidance rules are evolved with the new GA.

6.1 Coding

The authors propose a method of coding of knowledge into a gene as shown in Fig. 11. A kind of knowledge concerned with the input x_1 is expressed by

$$\mu = h \cdot \exp\left(-\frac{(x_1 - x_c)^2}{2\sigma^2}\right) \qquad (1)$$

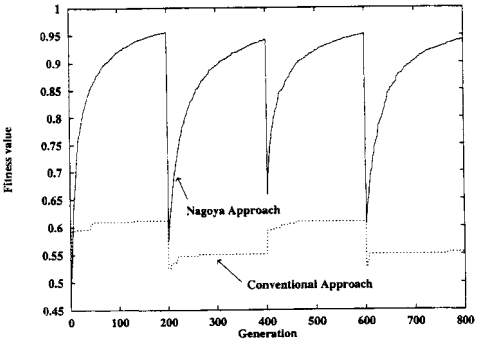


Fig.10 Fitness values of elite chromosome

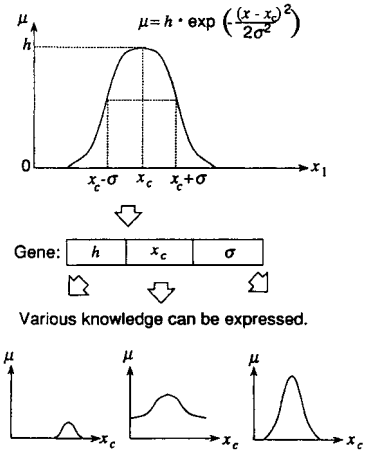


Fig.11 Example of coding of knowledge into a gene

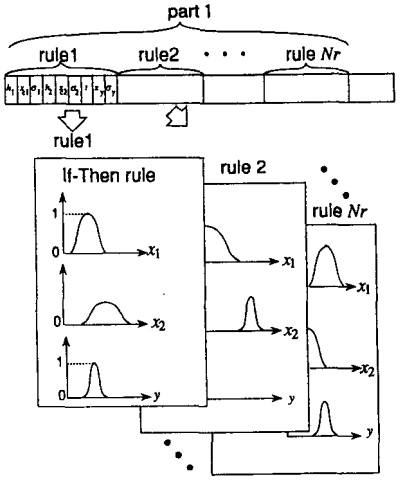


Fig.12 Example of if~ then~ rules encoded into chromosome

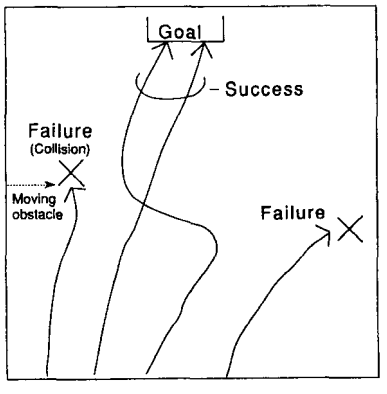


Fig.13 Problem formulation

where x_c is the central position, σ is the width (standard deviation) and h is the height of this function. Using these three parameters as shown in the figure, various types of knowledge can be expressed. The three parameters are encoded into the gene. This way of expression of knowledge has a feature in that when the shape of the function has a clear correspondence with a membership function of fuzzy logic, the knowledge with this function can be labeled and has a correspondence with a symbolic expression. When the function does not have any shape of membership functions, yet the knowledge can be handled and some inference can be carried out.

Figure 12 shows an example of if ~ then ~ rules encoded into a chromosome. The figure shows the case where there are two inputs x_1, x_2 and one output y and Nr rules in a part. Each rule

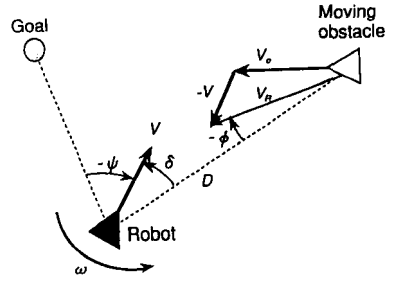


Fig.14 Denotations of parameters

has the parameters of eq. (1), i.e. the heights h_1, h_2, the central positions x_{c1}, x_{c2}, and the widths σ_1, σ_2, for the inputs x_1, x_2, respectively. For the output y, the central position x_y and the width σ_y are encoded. For the clarity and simplicity, the height h_y is fixed to be unity. The parameter $t \in [0\ 1]$ defines the truth value in the antecedent in between product-sum-center of gravity and sum-sum-center of gravity. The machine itself will find the inference method.

6.2 Simulation conditions

The robot is approximated as a first order system given by

$$T\,d\omega/dt + \omega = u \quad (2)$$
$$\theta = \int \omega\ dt + \theta_0 \quad (3)$$
$$dx/dt = |V| \sin\theta \quad (4)$$
$$dy/dt = |V| \cos\theta \quad (5)$$

where T is the time constant, $|V|$ is the speed of the robot, u is the steering angle, ω is the angular velocity, θ is the angle from the north, x, y are the coordinates of the robot.

Figure 13 shows the problem formulation. The robot starts from a line opposite to the goal. The initial angular velocity of the robot is 0 rad/s. It is a success when the robot reaches the goal, and a failure when the robot collides with a moving obstacle or goes off the screen. The faster the robot reaches the goal, the better the evaluation. The nearer the failed point, also the better the evaluation.

Figure 14 shows the denotations of relative distances and velocities between the robot and the moving obstacle as well as the goal. The speeds of the robot and the moving obstacle are $|V|$, $|V_0|$, respectively. The speed of robot will be changed by

$$|V| = |V_S| + \Delta V \quad (6)$$

where $|V_S|$ is a constant value and ΔV is the manipulated variable determined by the control rules. The speed of moving obstacle $|V_0|$ is set to be constant. The distance between the robot and the obstacle is denoted by D. The angle between the direction of the robot and the direction of the obstacle viewed from the robot is denoted by δ. In the same way, the angle between the direction of the robot and the goal is ψ. V_R is the relative velocity between the robot and the obstacle. The angle between the relative velocity V_R and the direction of the robot from the moving obstacle is ϕ. When ϕ is nearly zero, it means that the moving obstacle comes toward the robot. Each angle is set to be counterclockwise positive viewed from the reference line in Fig. 14.

The control rules used in this paper are expressed in Figure 15. The chromosome has three parts. Each part has five rules. The inputs of each rule are D, ϕ, δ, ψ, and the angular velocity of the robot ω. The output of the rule is the steering angle u and the change of speed Δv. The truth value in the antecedent of the rule is determined by t_{ij} (i = 1, •••, 5, j = 1,2,3). If t_{ij}= 0, then the product of grades in the antecedent is used. If t_{ij}= 1, then the sum is the truth value. The truth value is in between [0 1] in proportion to t_{ij}. Every parameter is randomly generated. The control rules are evolved by the new GA through the interaction with the environment. The new GA here has to determine $20 \times 5 \times 3$ = 300 parameters.

6.3 Application of new GA

The new GA is applied in the way as shown in Fig. 16. In this simulation, there are ten chromosomes in a population. Each gene is reproduced to (Np =) four. One of the 18 parameters of each newly generated gene is selected and changed using uniform random numbers as illustrated in Fig. 17. Each chromosome, of which one of the three parts are replaced with the new gene, controls the robot using all the rule s in the chromosome simultaneously and is evaluated under five different simulation conditions. The robot and the moving obstacle start from different positions under the different conditions. The definitions of payoffs are given as shown in Fig. 18. In case of success, the gene receives the following payoff:

$$1+\frac{100}{\text{No. of steps}}. \qquad (7)$$

In case of failure, the gene receives the payoff given by

$$\frac{10}{\text{Distance to the goal}}. \qquad (8)$$

It takes at least about 200 steps for the robot to reach the goal from the starting point. The width of the screen is 640 dots and the length is 750 dots. The unit of the distance is this dot on the screen. The elite with the highest payoff among the four genes is selected. The new chromosome is then evolved by aggregating the elite genes from the three parts. The fitness of the new chromosome is given by the

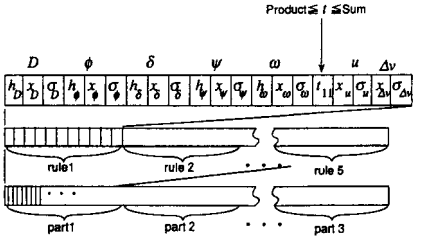


Fig.15 Coding of rules into a chromosome

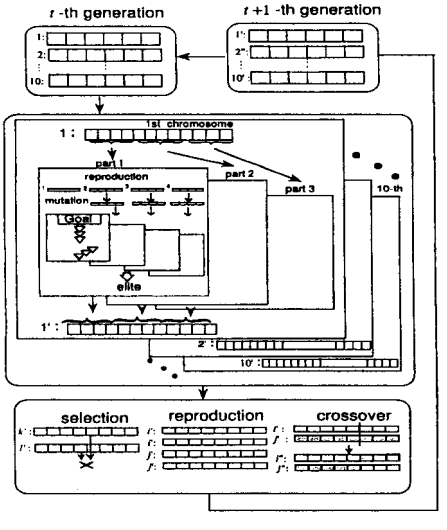


Fig.16 Application of new GA

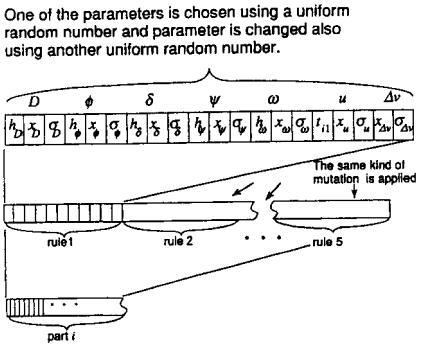


Fig.17 Mutations

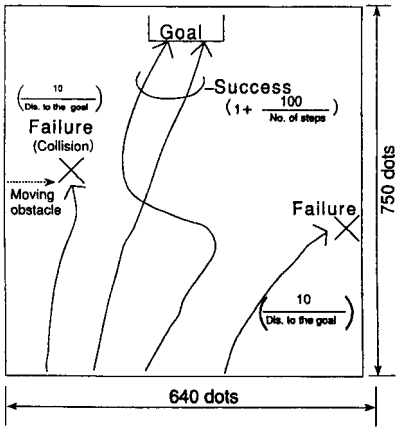


Fig.18 Definition of payoffs

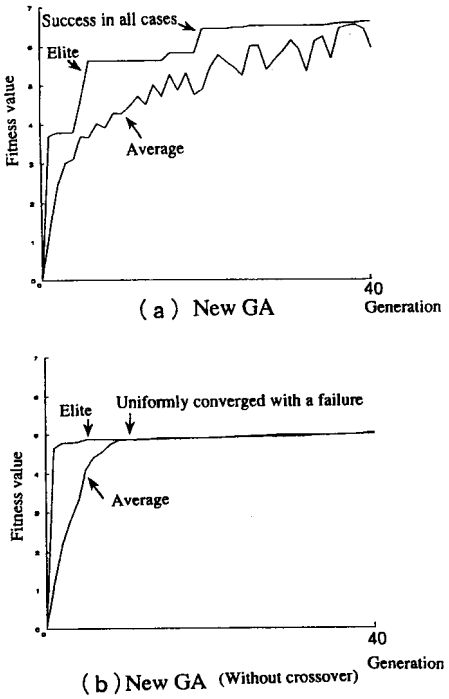


Fig.19 Fitness values with the new GA

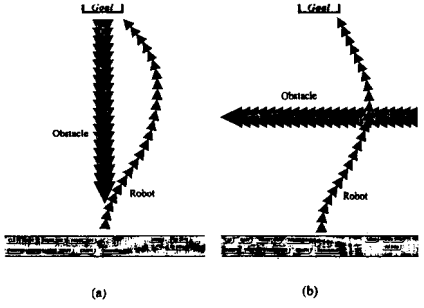


Fig.20 Tracks of robot with new GA

sum of the payoffs of the tree elite genes. This genetic operation is applied to the remaining nine chromosomes one by one.

The selection and reproduction operations are applied to the newly generated ten chromosomes. Two of the chromosomes with the least fitness values are deleted. Two out of the remaining eight chromosomes are reproduced and the new chromosomes are changed by the one point crossover operation.

6.4 Results

Figure 19 shows changes of fitness values with the Nagoya approach. The horizontal axis is the generation. The fitness value of the elite chromosome and the average fitness value of the ten chromosomes are shown in the figure. The top figure shows a case where the new GBML is applied. The elite chromosome obtained by the new approach succeeded in controlling the robot to reach the gaol under all the five conditions at around the 20-th generation. The bottom figure shows a case where the crossover operation is not used in the new GA . Without the crossover, the chromosomes are fast to converge uniformly to local minima.

Figure 20 shows examples of tracks of the robot and the moving obstacle. Figure 20 (a) shows the case where the obstacle comes from the fore and (b) is the case the obstacle goes from the right hand side to the left in front of the robot. The tracks of the robot were smooth.

Figure 21 shows an example of the acquired fuzzy rule used in the early stage of control in Fig. 20(a). The rule can be read as

> If the distance between the robot and the obstacle D is *Big*, the danger of collision is *Negative Small*(ϕ is *Negative Big*), the obstacle is in the right hand side (δ is *Positive Big*), the goal is on the left hand side (ψ is *Negative*), the robot is rotating clockwise a little (ω is *Negative small*),
> Then the robot is steered to the right a little (u is *Negative Small*) and the robot is not braked (ΔV is *Zero*).

The truth value of this rule is nearly the sum of the grades of the membership functions in the antecedent. It is known that the rule works simply to steer the robot to the right hand side while the obstacle is far.

Figure 22 shows the fitness value obtained with the Pitt approach. The number of chromosomes were twenty. The roulette wheel selection is applied to delete four chromosomes and reproduce

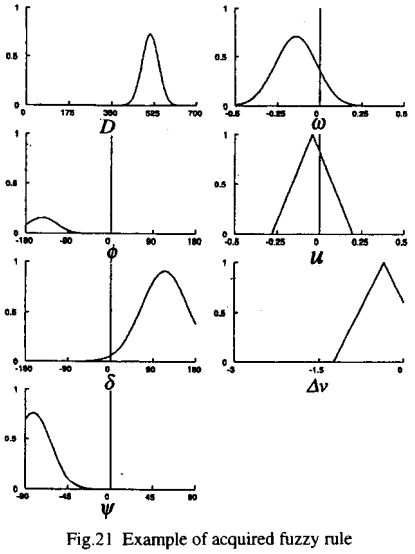


Fig.21 Example of acquired fuzzy rule

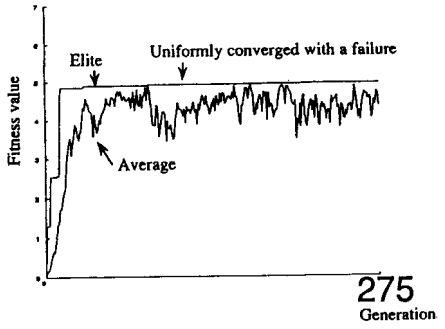


Fig.22 Fitness values with Pitt approach

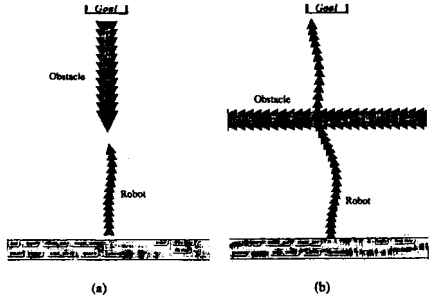


Fig. 23 Tracks of robot with Pitt approach

new chromosome. The one-point crossover is applied to the newly generated chromosomes. The mutation rate was set at 10%. It was difficult to find out a set of rules which succeed in all the five conditions with the conventional approach even after the 275-th generation. The computation time was more than two times larger than the case at the 20-th generation of the Nagoya approach. Figure 23 shows the tracks of the robot at 275-th generation obtained by the Pitt approach. Figure 23 (b) shows clearly that the local improvement of the chromosome is hardly done by the conventional approach.

Figure 24 shows another result of simulations. The simulation in Fig.19(a) (Nagoya approach) was repeated 10 times with different initial chromosomes. The averaged fitness values of elite and average are shown. The simulation in Fig. 22 (Pitt approach) was also

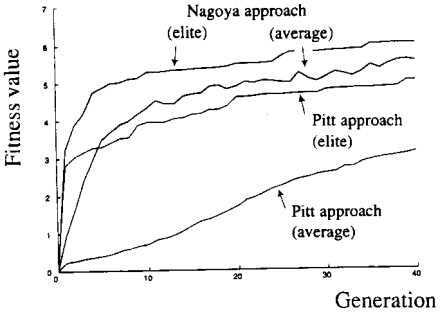


Fig.24 Fitness values with Nagoya/Pitt approach

repeated 10 times. The number of populations was increased to 100 for this simulation. The averaged fitness values of this simulation is also shown in the figure. The new approach showed a higher performance in achieving the goal.

7. Conclusions

This paper presented a new GBML called Nagoya approach. The new approach was based on a hypothesis of evolution. The new algorithm is efficient especially in local improvement ofchromosomes and is expected to be effective for the construction of evolvable / adaptive complex systems.

It should be noted that the proposed method is clearly different from Grefenstette's method called Lamarckian learning[4].

The authors is now doing further research on application of the new GA to a mass of rules and the emergence of collective behavior of the rules.

7. References

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