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ORIGINAL ARTICLE

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PID controller design using double helix structured DNA algorithms with a recovery function

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Abstract PID controllers have been widely used in industrial fields. Since the PID parameters have a great influence on the stability and performance of the control system, many approaches have been proposed to determine them. In this article, we propose double helix structured DNA algorithms to design the type of PID controller and optimize the PID parameters. The double helix structured DNA algorithms employ a DNA encoding method based on a base-64 notational system to represent the PID parameters, define various mutation methods, and have a recovery function to preserve a DNA strand that has good fitness value. A computer simulation shows that we can get satisfactory results with the proposed method.

Key words DNA algorithms · PID controller

1 Introduction

It is a well known fact that proportional integral derivative (PID) controllers have been widely used in industrial fields because, despite their simplicity, they can ensure an adequate and satisfactory performance for a wide range of processes. Since the PID parameters have a great influence on the stability and performance of the control system, many approaches have been proposed to determine them.

One of the approaches that can obtain a global optimization solution is GAs. Although this approach can get optimal PID parameters, it has some disadvantages. As the size of the chromosomes and the populations in the GAs increase, their computation time also increases, and a chromosome that has a good fitness value can be lost by a mutation.

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Deoxyribonucleic acid (DNA) is a nucleic acid that contains the genetic instructions for the biological development of a cellular form of life. That is, DNA is a blueprint of living things, because DNA makes RNA which makes proteins. If we implement DNA into a computer, we can mimic the process that occurs in organic life and can overcome the limitations of traditional GAs. Some studies have been conducted to design a controller inspired by DNA. Lin et al.[1] suggested a self-organizing PID control design based on a DNA computing method, Ding and Ren[2] designed the generalized memberhip-type Takagi–Sugeno fuzzy control system using DNA algorithms, and Yourui et al.[3] proposed optimization for the parameters of a PID based on the DNA genetic algorithm.

Here, we present a new way to design a type of PID controller and optimize the PID parameters by using double helix structured DNA algorithms. More specifically, we use a DNA encoding method based on a base-64 notational system to represent the PID parameters, define various mutation methods, and suggest a recovery function to preserve a good DNA strand that has a good fitness value. This article is organized as follows. In Sect. 2, the biological basis and implementation are given. The simulation results are shown in Sect. 3, and the conclusion is given in Sect. 4.

2 Biological basis and implementation

The nucleic acid DNA (deoxyribonucleic acid) serves as the genetic material in all living organisms, and makes the RNA that makes proteins. Base on biological information about DNA,[4] we implemented DNA in a computer to design a type of PID controller and optimize the PID parameters.

2.1 DNA encoding method

The DNA molecule exists in cells as a long, coiled ladder-like structure described as a double helix. Each strand of the helix consists of a linear polymer made up of genetic building blocks called nucleotides, of which there are four

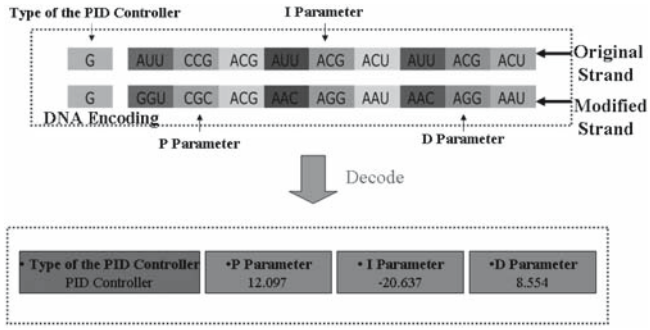

Fig. 1. The encoding of stands corresponding to the type of PID controller and the PID parameters

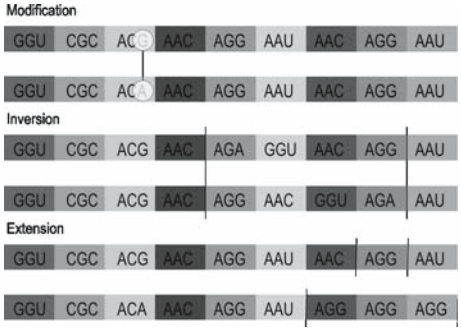

Fig. 2. Description of each mutation

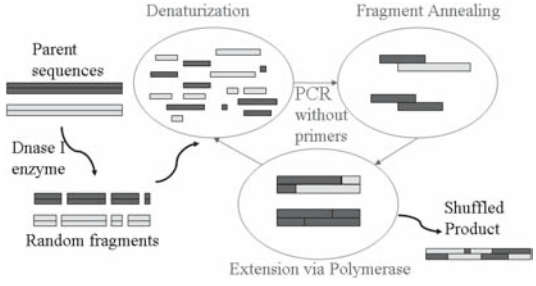

Fig. 3. A PCR process

types. Nucleotides vary, depending upon which of the four nitrogenous bases is part of the molecule: A (adenine), G (guanine), T (thymine), or C (cytosine). A triplet code of nucleotide bases specifies the codon, which in turn contains a specific anticodon on transfer RNA (tRNA) and assists the subsequent transmission of genetic information in the formation of a specific amino acid. A chromosome consists of combinations of the four bases and can represent different genes.

A single strand of DNA can be likened to a string consisting of a combination of four different symbols, A, G, C, T. Mathematically, this means we have a four-letter alphabet to encode information, which is more than enough, considering that an electronic computer needs only two digits, 0 and 1, for the same purpose. In Fig. 1, the first part of the DNA strand is the type of PID controller, and the second part is the PID parameters. The type of PID controller is determined by a nucleotide only, while each PID parameter is determined by three codons that use a base-64 notational system. Because each parameter is composed of three codons, the maximum decimal value is 262144 ($64 \times 64 \times 64$). The length of the DNA strand and the maximum value can be modified to meet a specification.

Double helix structured DNA is used to preserve a good DNA strand. Each DNA strand is a template for synthesizing a new strand which is nearly identical to the previous strand. When one strand is modified by a mutation operation, the modified strand is evaluated. If the modified strand is better than the original strand, the original strand is changed to the modified strand. Otherwise, the modified strand is recovered from the original strand.

A further description about the usage of double helix structured DNA is given in Sect. 2.5.

2.2 Genetic operators

Two genetic operators, DNA mutation operations and a PCR operation, are developed to modify our DNA.

Errors that occur in the synthesis are called mutations. Mutations are the results of the cells' attempts to repair chemical imperfections in this process, where a base is accidentally skipped, inserted, or incorrectly copied, or the chain is trimmed, or added to. Only three mutations, "modification," "inversion," "extension," are used to mutate DNA. One of the mutation methods is selected randomly. A description of each mutation is shown Fig. 2. The modification mutation is a point mutation that changes in one base of the DNA sequence. A randomly selected point is changed among A, G, T, and C. In inversion mutation, a section determined by a randomly selected start point and an end point is inverted. After inversion, the order of the strand in the inversion region is reserved. An extension, last mutation method, is a kind of infection that influences adjacent codons.

2.3 DNA shuffling

The polymerase chain reaction (PCR) is a rapid method of DNA cloning that has extended the power of recombinant DNA research and eliminated the need for host cells in DNA cloning. PCR generates many copies of a specific DNA sequence through a series of in vitro reactions, and can amplify the target DNA sequences present in infinitesimally small quantities in a population of other DNA molecules. The PCR is implemented in a computer to shuffle DNA. A PCR process is shown Fig. 3. It is a process of exchange of genetic information. All individuals are shuffled with the best DNA by saving the previous best individual.

2.4 Fitness function

After decoding the type of PID controller and PID parameters that were encoded in a DNA strand, the PID control-

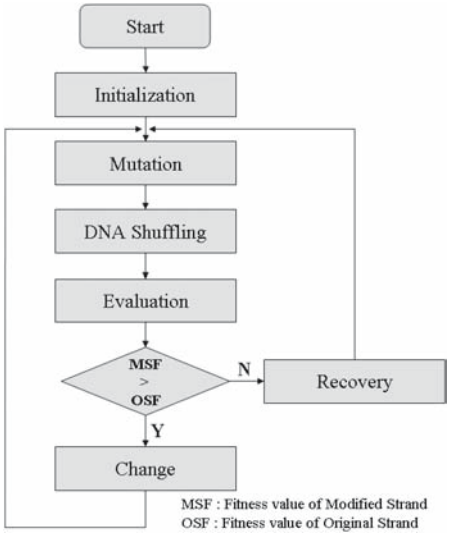

Fig. 4. Overall process of the double helix structured DNA algorithms

ler design can be evaluated. A fitness function that minimizes the rise time to 15 steps, the overshoot to 5%, and the settling time to 50 steps is set. The fitness function is defined as Eq. 1 to evaluate the decoded parameters. C_1, C_2, and C_3 are determined by their priority.

$$f_{fit} = C_1 \times RTGap + C_2 \times OSGap + C_3 \times STGap \quad (1)$$

where RTGap represents the gap between the real rise time and 15 steps, OSGap represents the gap between the real overshoot and 5%, and STGap represents the gap between the real settling time and 50 steps.

2.5 Overall process

The overall process of the double helix structured DNA algorithms is shown in Fig. 4. The process first initializes each individual, and then they mutate, and do DNA shuffling, evaluation, recovery, or change until a maximum generation is reached. An individual is the same as the DNA, and has two strands. When one of the strands is modified by a mutation operation, the modified strand is evaluated. If the modified strand is better than the original strand, the original strand is changed to the modified strand. Otherwise, the modified strand is recovered from the original strand. This process is possible because the double helix structured DNA was used.

3 Simulation

To verify the PID controller design method given in Sect. 2, a motor model, Eq. 2, is used as a simulation.

$$G(z) = \frac{0.02937z^2 + 0.0153205z + 4.64302 \times 10^{-5}}{z^3 - 1.03869z^2 + 0.0386917z - 8.99251 \times 10^{-8}} \quad (2)$$

Table 1. Simulation parameters

Parameter	Value
Maximum number of shuffles	10
Mutation rate for PID parameters	0.1
Mutation rate for PID-type controller	0.005
Number of individuals	500
Maximum generations	1000

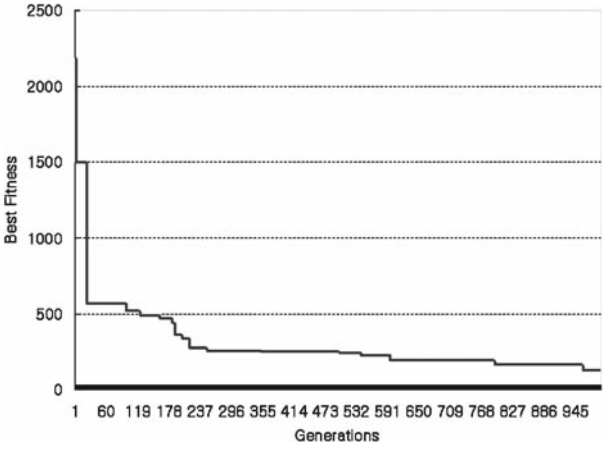

Fig. 5. Convergence of the fitness function

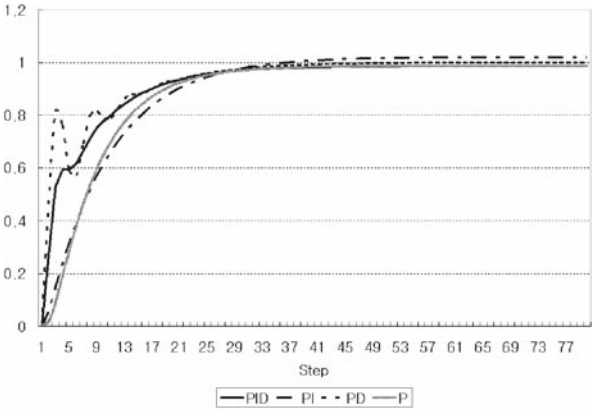

Fig. 6. Unit step response of each PID controller design

The fitness function means that the rise time has high priority, the overshoot has medium priority, and the settling time has a lower priority. The maximum fitness value is set to 10000.

The maximum number of shuffles for each process is 10, the mutation rate of the PID parameters is 0.1, and the mutation rate of the PID-type controller is 0.005. Furthermore the number of individuals is set to 500, and the maximum is 1000. The specified parameter values that we use are given in Table 1. The convergence behavior of the fitness function is shown in Fig. 5. The initial fitness value is 10000, but it converges into 124 at the 1000 generation.

Some unit step responses of the each PID controller design are shown in Fig. 6, and the PID parameters and specifications of the PID controller are given in Table 2.

Table 2. Some of the PID parameters and specifications of PID controllers

	PID	PI	PD	P
Kp	3.0337	1.9688	3.2827	2.1724
Ki	–0.0059	0.0039		
Kd	6.5205		12.3657	
Rise time	15	18	15	15
Overshoot	0	1.945	0	0
Settling time	36	29	30	35

Computer simulations show that after the convergence of the double helix structured DNA algorithms, we can always find a group of parameter values for the type of PID controller and PID parameters that obtain a satisfactory control performance.

4 Conclusions

This article uses double helix structured DNA algorithms to design a type of PID controller and optimize the PID parameters. The double helix structured DNA algorithms use a DNA encoding method based on a base-64 notational system to represent the PID parameters, define various mutation methods, and suggest a recovery function to preserve a DNA strand that has a good fitness value.

The proposed method is well demonstrated and verified by simulations. The double helix structured DNA algorithms can be used not only to design a PID controller, but also to design other controllers.

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