

PID Controller Design Using Double Helix Structured DNA Algorithms with Recovery Function

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Abstract

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

Keywords : *DNA Algorithms, PID Controller.*

1 Introduction

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

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

The DNA(deoxyribonucleic acid) 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 that makes proteins. If we implement DNA into a computer, we can mimic the process that occurred in organic life and can overcome the limitations of the traditional GAs. Some studies have been conducted to design controller inspired from the DNA. Yongsheng Ding et al.[1] designed the generalized membership-type Takagi-Sugeno fuzzy control system using DNA algorithms, Chu-Liang Lin et al.[2] suggested self-organizing PID control design based on DNA computing method and Huang Yourui et al.[3] proposed optimization for parameter of PID based on DNA Genetic Algorithm.

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

2 Biological Basis and Implementation

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

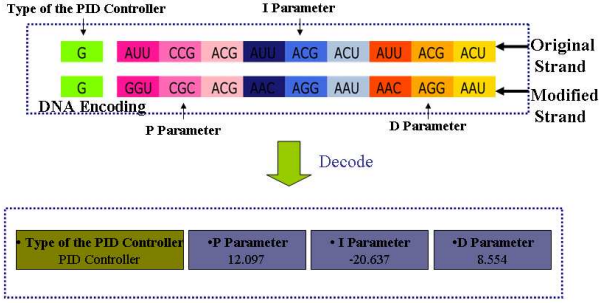


Figure 1: The encoding of stands corresponding to the type of the PID controller and PID parameters

strand of the helix consists of a linear polymer made up of genetic building blocks called nucleotides, of which there are four types. Nucleotides vary, depending upon which of four nitrogenous base 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 subsequent transmission of genetic information in the formation of a specific amino acid. A chromosome consists of combinations of the above 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 the Fig.1, the first part of the DNA strand is the type of PID controller, and the second part is PID parameters. The type of PID controller is determined by only a nucleotide, while each PID Parameter is determined by three codons that use a base-64 notational system. Because each parameter is composed with three codons, a maximum decimal value is 262144($64 \times 64 \times 64$). The length of DNA strand and maximum value are can be modified to meet a specification.

The double helix structured DNA is used to preserve good DNA strand. Each DNA strand is a template for synthesizing a new strand which is nearly identical to the previous strand. When one of 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 modified strand. Otherwise, the modified strand is recovered from the original strand.

Further description about usage of double helix

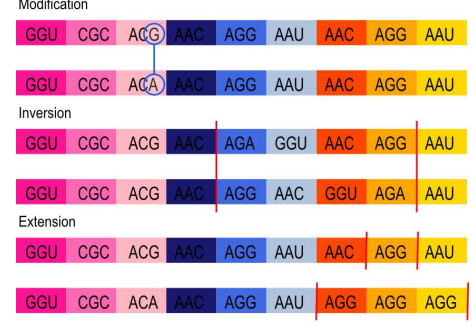


Figure 2: Description of each mutation

structured DNA is shown in section 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. 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, 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 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 a vitro reaction and can amplify 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 process of PCR is shown Fig.3. It is a process of the exchange of genetic information. All individuals are shuffled with best DNA by saving previous best individual.

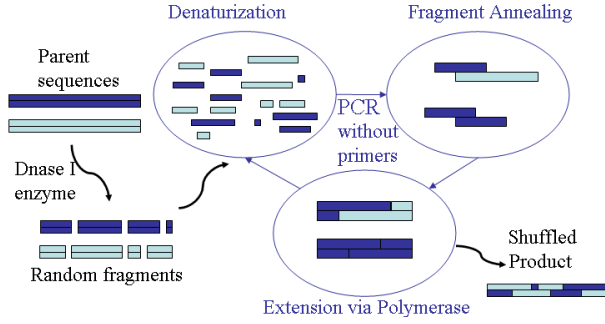


Figure 3: A process of PCR

2.4 Fitness Function

After decoding the type of PID controller and PID parameters that was encoded in a DNA strand, the PID controller design can be evaluated. A fitness function that minimizes rise time 15 steps, overshoot 5 percent, and settling time 50 steps is set. The fitness function is defined as (1) to evaluate decoded parameters. C_1 , C_2 and C_3 are determined by their priority.

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

RTGap represents gap between real rise time and 15steps, OSGap represents gap between real Overshoot and 5 percent and STGap represents gap between real Settling Time and 50 steps.

2.5 Overall Process

An overall process of the double helix structured DNA algorithms is shown in Fig.4. The process first initialize each individual, and do mutation, DNA shuffling, evaluation, and recovery or change until maximum generation. An individual is the same as DNA, and has two strands. When one of 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 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 that is designed in section 2, a motor model (2) is used to simulate.

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

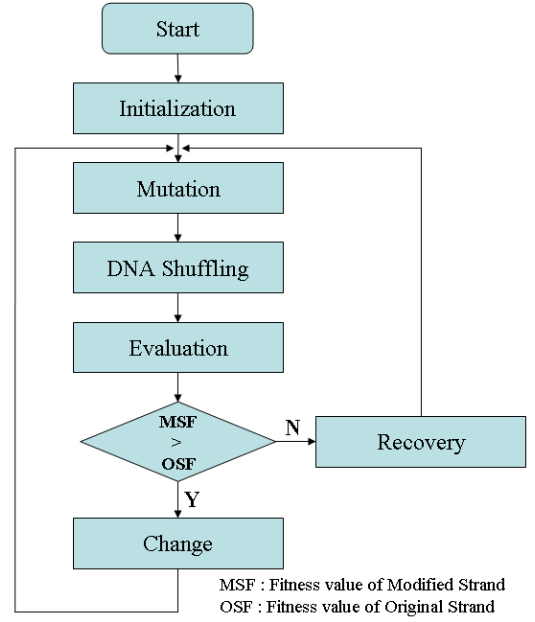


Figure 4: Overall process of the double helix structured DNA algorithms

Table 1: Simulation parameters

Parameter	Value
Maximum number of shuffling	10
Mutation rate for PID parameters	0.1
Mutation rate for type of PID controller	0.005
Number of individual	500
Maximum generation	1000

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

The maximum number of shuffling for each process is 10, mutation rate of PID parameters is 0.1, mutation rate of PID controller type is 0.005. Furthermore the number of individual is set to 500, and Maximum is 1000. The specified parameter value that we use is given in Table1. Convergence behavior of the fitness function is shown in Fig.5. Initial fitness value is 10000, but it converges into 124 at the 1000 generation.

Some unit step response of the each PID controller designs are shown in Fig.6, and the PID parameters and specifications of PID controller are given in Table2.

Computer simulations show that after convergence

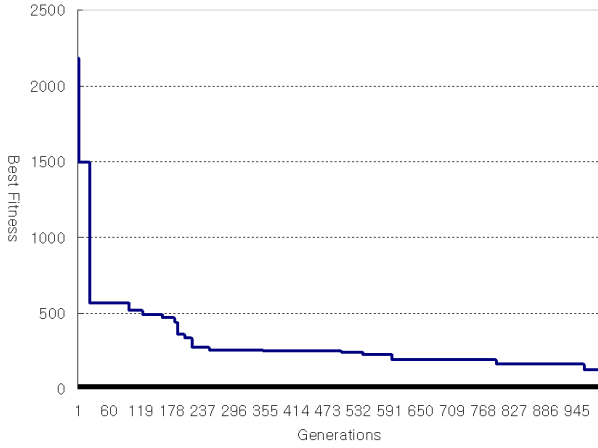


Figure 5: Convergence of the fitness function

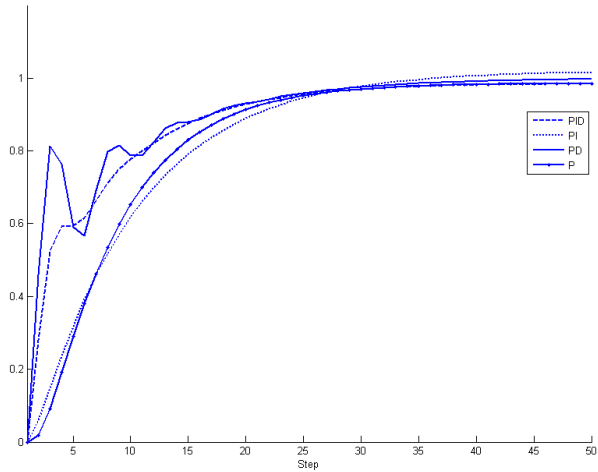


Figure 6: Unit step response of the each PID controller design

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

	PID	PI	PD	P
Kp	3.0337	1.9688	3.2827	2.1724
Ki	-0.0059	0.00391		
Kd	6.5205		12.3657	
Rise Time	15	18	15	15
Overshoot	0.000	1.945	0.000	0.000
Settling Time	36	29	30	35

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 satisfactory control performance.

4 Conclusions

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

The proposed method is well demonstrated and verified by simulations.

The Double helix structured DNA algorithms can be used for not only to design PID controller but also to design other controllers.

References

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