Paper:

Robust Tuning of PID Controller Using Bacterial-Foraging-Based Optimization

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We propose a design approach to PID controllers with resistance to external disturbance in motor-controlled systems using a bacterial foraging-based optimal algorithm. PID controllers are used to operate AC motor drives because of their practical implementation and simple structure. Inexperienced personnel find it difficult, however, to achieve optimal PID gain because this is manually tuned by trial and error in industrial environments full of disturbances. To design disturbance-resistance tuning, we use disturbance-resistance conditions based on H_∞ and calculcate response the performance based on bacterial foraging for the PID controller as an integral of time-weighted squared error. Hence, parameters for the PID controller are selected by our bacterial foraging-based optimal algorithm to obtain the required response.

Keywords: PID control, disturbance control, bacterial algorithm, optimal algorithm, motor control

1. Introduction

The proportional-integral-derivative (PID) controller is widely used in most industrial processes despite continual advances in control theory because of its simple structure, which is theoretically easy to understand, and because andthe tuning technique provides adequate performance in the vast majority of applications. It cannot effectively control complicated or fast system such as motor-controlled systems, however, because the response of a plant depends on three parameters (P, I, and D) and gain must be manually tuned by trial and error. Most PID tuning rules use conventional methods such as frequency response [1]. This requires considerable technical experience to apply tuning formulas to determine PID controller parameters. In Ziegler-Nichols rule tuning, this often leads to a rather oscillatory response to set-point changes as in the following system [2]:

(a) Plants which the system has nonlinearities such as directionally dependent actuator and plant dynamics.

(b) Systems having uncertainties such as modeling error and external disturbance.

Due to these difficulties, PID controllers are rarely tuned optimally and engineers must search for highly tuning technology.

To improve PID controller tuning performance for processes with changing dynamic properties, proposed tuning strategies include automatic tuning PID, adaptive PID, and intelligent controllers. These controllers have recalibration to cope with little a priori knowledge and significant changes in process dynamics [4].

PID controller parameters are still calculated using classic tuning formulas and, as noted above, these do not provide good control performance in all situations, for example, for instable systems with time delay. De Paor used modified Smith predictors to cope with instable and integrating processes with long time delays.

To provide a consistent, reliable, safe, optimal solution to such industrial control problems, approaches to PID control and tuning have generally consisted of four basics: model estimation, desired system specifications, optimal tuning, and an online PID controller.

Over the last 50 years, many ways have been developed to determine PID controller parameters for stable processes suitable for autotuning and adaptive control [1–10]. Some use information about open-loop step response such as the Coon-Cohen reaction curve, while others use knowledge of the Nyquist curve, the Ziegler-Nichols frequency response, etc. [3]. Such tuning uses only a small amount of information about the system's dynamic behavior and often does not provide good tuning. Gain and phase margins (GPM) have served as important measures of robustness [3, 7, 8]. The phase margin is related to the damping of the system from classical control theories, and also serves as a performance measurement. Solutions are usually obtained numerically or graphically by trial-and-error Bode plots.

The many types of PID tuning for achieving the specified GPM are divided into two categories. First, approximation of the $\tan^{-1}$ function simplifies the problem, but is only applicable to simple models [4, 9]. Second, inverse function mapping is done by fuzzy neural networks (FNN) that identify the relationship between GPM and PID controllers, which is used for general linear systems [5]. To solve a problem, the first obstacle is the difficulty in finding the stabilizing region of PID controllers. The solution is a necessary first step to any rational design of PID controllers based on GPM.

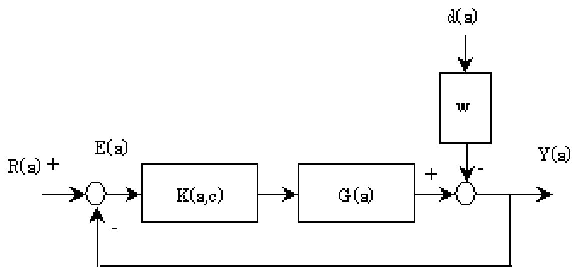


Fig. 1. Control system with disturbance.

Because the natural selection of bacterial foraging tends to eliminate entities with poor foraging strategies for locating, capturing, and ingesting food, optimization models are provided for social foraging where groups of parameters communicate to forage cooperatively.

We propose intelligent tuning of PID controllers by a bacterial foraging-based optimal algorithm for robust control with disturbance resistance in control of a motor control loop.

2. PID Controller Tuning with Disturbance Resistance

2.1. Conditions for Disturbance-Resistance

In **Fig.1**, the disturbance-resistance constraint is given by [7, 8]

$$\max_{d(t)\in D}\frac{\|Y\|}{\|d\|}=\left\|\frac{w(s)}{1+K(s,c)G(s)}\right\|_\infty<\delta \quad . . . \quad (1)$$

Here, $\delta<1$ is constant defining by the desired rejection level and $\|\bullet\|_\infty$ denotes the H_∞-norm, which is defined as

$$\|G(s)\|_\infty=\max_{\omega\in[0,\infty)}|G(j\omega)|. \quad . . . . \quad (2)$$

The disturbance-resistance constraint becomes

$$\left\|\frac{w(s)}{1+K(s,c)G(s)}\right\|_\infty=$$
$$\max_{\omega\in[0.\infty)}\left(\frac{w(j\omega)w(-j\omega)}{1+K(j\omega,c)G(j\omega,c)K(-j\omega,c)G(-j\omega,c)}\right)^{0.5}$$
$$=\max_{\omega\in[0.\infty)}(\sigma(\omega,c))^{0.5} \quad . . . . \quad (3)$$

Controller $K(s,c)$ is written as

$$K(s,c)=c_1+\frac{c_2}{s}+c_3s \quad . . . . \quad (4)$$

Vector c of the controller parameter is given by

$$c=[c_1,c_2,c_3]^T \quad . . . . \quad (5)$$

Hence, the condition for disturbance resistance is given as

$$\max_{\omega\in[0.\infty)}(\sigma(\omega,c))^{0.5}<\delta.$$

2.2. Performance Index for Disturbance-Resistance Controller Design

The performance index defined as an integral of the time-weighted square of the error (ITSE) is written by

$$PI=\int_0^\infty t(E(t))^2dt \quad . . . . \quad (6a)$$

$$E(s)=\frac{B(s)}{A(s)}=\frac{\sum_{j=0}^{m}b_js^{m-1}}{\sum_{i=0}^{n}a_is^{n-1}}. \quad . . . . \quad (6b)$$

Because $E(s)$ contains parameters of the controller (c) and plant, the value of the performance index, PI for a system of an nth order in minimized by adjusting vector c as follows [7]:

$$\min_c PI(c) \quad . . . . \quad (7)$$

Optimal tuning proposed is to find vector c, such that ITSE performance index $PI(c)$ is a minimum using the bacterial algorithm and constraint $\max_{\omega\in[0.\infty)}(\sigma(\omega,c))^{0.5}<\delta$ is satisfied through actual coded bacterial algorithms.

3. Behavior and Modeling of Bacteria Foraging

Since the selection behavior of bacteria tends to eliminate entities with poor foraging strategies and favor the propagation of genes of those that have successful foraging strategies, they are applied to an optimal solution through methods for locating, capturing, and ingesting food. After many generations, a foraging entity maximizes the energy obtained per unit time spent foraging. That is, poor foraging strategies are either eliminated or shaped into good ones. Optimization models are also valid for social foraging where groups of entities communicate to forage cooperatively in the face of constraints presented by physiology such as sensing and cognitive capabilities and environment.

As stated, foraging is modeled as optimization that may operate in groups and the relevance of these areas to optimization.

Foraging theory is described in Refs. [5–7]. The foraging behavior of bacteria is found using dynamic programming. Search and optimal foraging decision-making of entities is used in engineering. Selection behavior or bacteria forage as individuals and others forage as groups. In social foraging, an entity needs communication, it gains advantages in exploiting the sensing of the group, so the group can gang up on larger prey, individuals obtain protection from predators while in a group, and in a sense, the group forages with collective intelligence. We discuss optimal parameter selection of a PID controller using bacteria foraging.

3.1. Overview of Chemotactic Behavior of *E. coli*.

We start by outlining the research in foraging theory, foraging by communicating organisms (social foraging) which sometimes operate in swarms, and the relevance of these areas to optimization. We also provide a brief overview of the literature on bacterial foraging as the biological basis for this paper.

Foraging theory and its ecological validity is discussed in Refs. [1–3]

Natural selection tends to eliminate entities with poor foraging strategies through methods for locating, capturing, and ingesting food and favor the propagation of genes of those entities that have successful foraging strategies, so they are more likely to apply reproductive success to have an optimal solution. After many generations, poor foraging strategies are either eliminated or shaped into good ones. Logically, such evolutionary principles have led scientists in foraging theory to hypothesize that it is appropriate to model the activity of foraging as an optimization process: a foraging entity acts to maximize the energy obtained per unit time spent foraging in the face of constraints presented by its own physiology such as sensing and cognitive and environment, e.g., availability of prey, risks from predators, and the physical conditions of the search environment.

We consider the foraging behavior of *E. coli*, a common bacteria [4, 5] whose movement depends on up to six rigid 100–200 rps spinning flagella, each driven as a biological motor. An *E. coli* bacterium alternates between running and tumbling. Running is 10–20μm/sec, but it cannot swim straight. We summarize chemotactic actions of bacteria as follows:

- If in a neutral medium, alternate tumbles and runs involve searching.
- If swimming up a nutrient gradient (or out of noxious substances) or swimming longer (up a nutrient gradient or down a noxious gradient) sgt seeks an increasingly favorable environment.
- If swimming down a nutrient gradient (or up a noxious substance gradient), it searches to avoid unfavorable environments.

It climbs nutrient hills and avoids noxious substances. The sensors it needs for optimal resolution are receptor proteins very sensitive and high gain. That is, a small change in the concentration of nutrients may significantly change behavior. This is probably the best-understood sensory and decision-making system in biology.

Mutations in *E. coli* affect reproductive efficiency at different temperatures and occur at about 10^{-7} per gene and per generation. *E. coli* occasionally engages in a conjugation that affects the characteristics of a population of bacteria. Since there are many types of taxis used by bacteria, such as aerotaxis (it are attracted to oxygen), light (phototaxis), temperature (thermotaxis), and magnetotaxis (it it is affected by magnetic lines of flux. Some bacteria change their shape and number of flagella based on the medium to reconfigure and ensure efficient foraging in a variety of media. Bacteria form intricate stable spatiotemporal patterns in certain semisolid nutrient substances. They eat their way radially through a medium if placed together initially at its center. Under certain conditions, they secrete cell-to-cell attractant signals to group and protect each other. These bacteria swarm.

3.2. Optimization of Bacterial Swarm Foraging

The main goal based on bacterial foraging is to find the minimum of $P(\phi)$, $\phi \in R^n$, not in the gradient $\nabla P(\phi)$. ϕ is the position of a bacterium and $J(\phi)$ is an attractant-repellant profile, i.e., where nutrients and noxious substances are located, so $P < 0, P = 0, P > 0$ represents the presence of nutrients. A neutral medium and the presence of noxious substances is shown by

$$H(j,k,l) = \{\phi^{\,i}(j,k,l) \,\big|\, i = 1,2,\ldots,N\}. \quad . \quad . \quad . \quad (8)$$

This equation represents the position of each member in the population of N bacteria at the jth chemotactic step, kth reproduction step, and lth elimination-dispersal event. Let $P(i,j,k,l)$ denote the cost at the location of the ith bacterium $\phi^i(j,k,l) \in R^n$ [20, 21]. Let

$$\phi^i = (j+1,k,l) = \phi^i(j,k,l) + C((i)\varphi(j) \quad . \quad . \quad (9)$$

so $C(i) > 0$ is the size of the step taken in a random direction specified by a tumble. If at $\phi^i(j+1,k,l)$, cost $J(i,j+1,k,l)$ is better (lower) than at $\phi^i(j,k,l)$, then another chemotactic step of size $C(i)$ in this same direction is taken and repeated up to maximum steps N_s. N_s is the length of the lifetime of the bacteria measured by the number of chemotactic steps. Functions $P_c^i(\phi)$, $i = 1,2,\ldots,S$, to model cell-to-cell signaling via an attractant and a repellant is represented by [20, 21]

$$\begin{aligned}
P_c(\phi) &= \sum_{i=1}^{N} P_{cc}^i \\
&= \sum_{i=1}^{N} \left[-L_{attract} \exp\left(-\delta_{attract} \sum_{j=1}^{n} (\phi_j - \phi_j^i)^2 \right) \right] \\
&\quad + \sum_{i=1}^{N} \left[-K_{repellant} \exp\left(-\delta_{attract} \sum_{j=1}^{n} (\phi_j - \phi_j^i)^2 \right) \right] \\
&\quad . \; . \; . \; . \; . \; . \; . \; . \; . \; . \; . \; . \; . \; . \; . \; . \; . \; . \; . \quad (10)
\end{aligned}$$

Some bacteria change their shape and number of flagella based on the medium to reconfigure and ensure efficient foraging in a variety of media. *E. coli* and *S. typhimurium* form intricate stable spatiotemporal patterns in certain semisolid nutrient media. They eat their way radially through a medium if placed together initially at its center. Under certain conditions, they secrete cell-to-cell attractant signals to group and protect each other. These bacteria swarm.

Where $\phi = [\phi_1,\ldots,\phi_p]^T$ is a point on the optimization domain, $L_{attract}$ is the depth of the attractant released by the cell and $\delta_{attract}$ is a measure of the width of the attractant signal. $K_{repellant} = L_{attract}$ is the height of the repellant effect magnitude), and $\delta_{attract}$ is the width of the repellant. The expression $P_c(\phi)$ means that its value does not depend on nutrient concentration at position ϕ. That is, a bacterium with a high nutrient concentration secretes stronger attractant than one with a low nutrient concentration. The model use function $P_{ar}(\phi)$ to represent environment-dependent cell-to-cell signaling as

$$P_{ar}(\phi) = \exp(T - P(\phi)) P_c(\phi) \quad . \ . \ . \ . \ . \ . \ (11)$$

where T is a tunable parameter. The model considers minimization of $P(i,j,k,l) + P_{ar}\left(\phi^i(j,k,l)\right)$, so cells try to find nutrients, avoid noxious substances, and at the same time try to move toward other cells, but not too close to them. Function $P_{ar}\left(\phi^i(j,k,l)\right)$ implies that, with M being constant, the smaller $P(\phi)$, the larger $P_{ar}(\phi)$ and thus the stronger the attraction, which is intuitively reasonable. In tuning parameter M, when M is very large, $P_{ar}(\phi)$ is much larger than $J(\phi)$, and the profile of the search space is dominated by the chemical attractant secreted by *E. coli*. If T is very small, $P_{ar}(\phi)$ is much smaller than $P(\phi)$, and it is the effect of nutrients that dominates. In $P_{ar}(\phi)$, the scaling factor of $P_c(\phi)$ is given exponentially.

We describe the method in the form of an algorithm to search for the optimal PID parameter value.

[Step 1] : Initialize parameters $n, N, N_C, N_S, N_{re}, N_{ed}$, $P_{ed}, C(i)(i = 1,2,\ldots,N), \phi^i$, and random values of PID parameter where
n: Dimension of search space (each parameter of aPID controller),
N: Number of bacteria in the population,
N_C: Chemotactic steps,
N_{re}: Number of reproductive steps,
N_{ed}: Number of elimination-dispersal events,
P_{ed}: Elimination dispersal with probability,
$C(i)$: Size of the step taken in the random direction specified by a tumble.
The controller parameter is searched for in the range of $Kp = [0,30], Ti = [0,30]$, and $Td = [0,30]$.

[Step 2] : Elimination-dispersal loop: $l = l+1$

[Step 3] : Reproduction loop: $k = k+1$

[Step 4] : Chemotaxis loop: $j = j+1$

[Substep a] : For $i = 1,2,\ldots,N$, take a chemotactic step for bacterium i as follows:

[Substep b] : Calculate ITSE (i,j,k,l).

[Substep c] : Let ITSE$_{last}$ = ITSE (i,j,k,l) to save this value because we may find a better cost via a run.

[Substep d] : Tumble: generate a random vector $\Delta(i) \in R^n$ with each element $\Delta_m(i), m = 1,2,\ldots,p$, a randonumber on $[-1,1]$.

[Substep e] : Move: Let

$$\phi^i(j+1,k,l) = \phi^i(j,k,l) + C(i)\frac{\Delta(i)}{\sqrt{\Delta^T(i)\Delta(i)}}$$

This results in a step of size $C(i)$ in the direction of the tumble for bacterium i.

[Substep f] : Calculate ITSE $(i,j+1,k,l)$.

[Substep g] : Swim
i) Let $m = 0$ (counter for swim length).
ii) While $m < N_s$ (if have not climbed down too long).
Let $m = m+1$.
If ITSE $(i,j+1,k,l) <$ ITSE$_{last}$ (if doing better), let ITSE$_{last}$ = ITSE $(i,j+1,k,l)$ and let

$$\phi^i(j+1,k,l) = \phi^i(j+1,k,l) + C(i)\frac{\Delta(i)}{\sqrt{\Delta^T(i)\Delta(i)}}$$

and use this $\phi^i(j+1,k,l)$ to calculate the new ITSE $(i,j+1,k,l)$ as we did in [Substep f].
Else, let $m = N_s$. This is the end of the while statement.

[Substep h] : Go to next bacterium $(i,1)$ if $i \neq N$ (i.e., go to Substep b to process the next bacterium).

[Step 5] : If $j < N_C$, go to [step 3]. In this case, continue chemotaxis, since the life of the bacteria is not over.

[Step 6] : Reproduction:

[Substep a] : For given k and l, and for each $i = 1,2,\ldots,N$, let

$$ITSE^i_{health} = \sum_{j=1}^{N_c+1} ITSE(i,j,k,l)$$

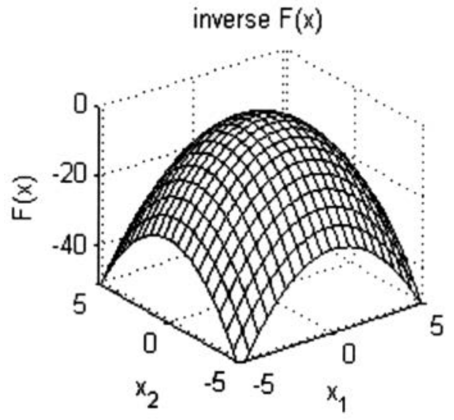
be the health of bacterium i (a measure of how many nutrients it got over its lifetime and how successful it was at avoiding noxious substances). Sort bacteria and chemotactic parameters $C(i)$ in order of ascending cost $ITSE_{health}$ (higher cost means lower health).

[Substep b] : S_r bacteria with the highest $ITSE_{health}$ values die and S_r bacteria with the best values split (and copies that are made are placed at the same location as their parent).

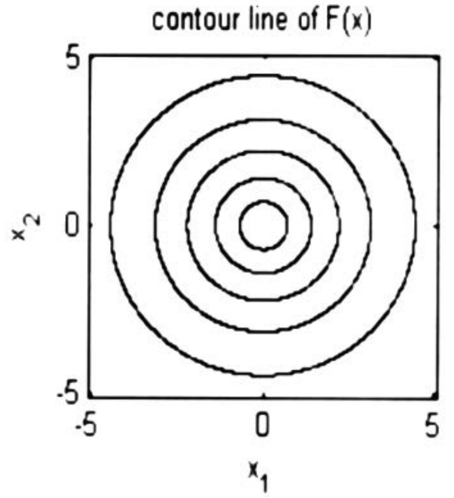
[Step 7] : If $k < N_{re}$, go to [step 3]. In this case, we have not reached the number of specified reproduction steps, so we start the next generation in the chemotactic loop.

[Step 8] : Elimination dispersal: For $i = 1,2\ldots,N$, with probability P_{ed}, eliminate and disperse each bacterium (this keeps the number of bacteria in the population constant).

To do this, if you eliminate a bacterium, simply disperse one to a random location on the optimization domain. If $l < N_{ed}$, then go to [step 2]; otherwise end.

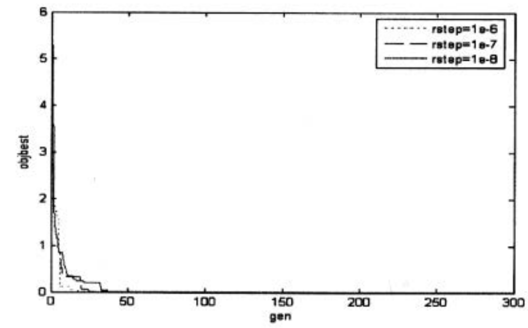


(a)



(b)

Fig. 2. (a) Contour of test function F_1. (b) Contour of test function F_1.



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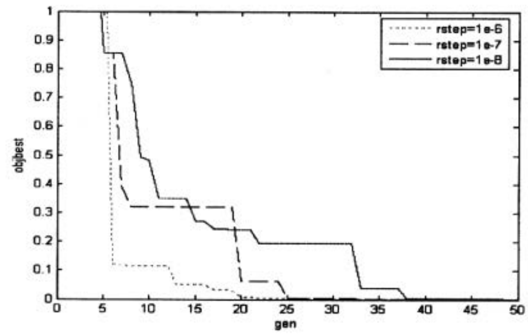

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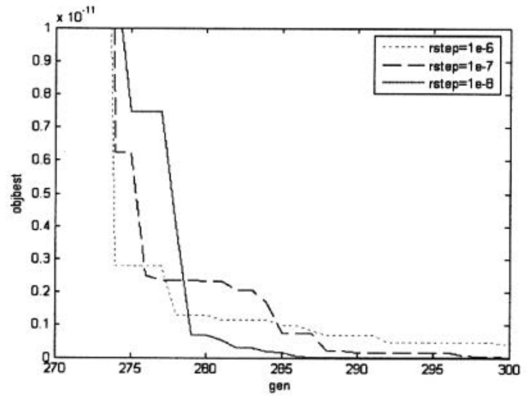

(c)

Fig. 3. (a) Variables versus variation of step size (generations=1−30). (b) Variables versus variation of step size (generations=1−50). (c) Variables versus variation of step size (generations=270−300).

Table 1. Parameter values versus step size of bacteria.

Step size	$x1$	$x2$	$x3$	Optimal objective function	Average objective function
1.0e−5	3.87E−13	6.60E−13	2.92E−07	−5.43E−07	−8.98E−08
1.0e−6	2.85E−14	2.34E−13	−5.52E−08	1.50E−07	−5.45E−08
1.0e−7	5.01E−16	1.43E−15	−1.70E−08	−1.44E−08	−2.31E−09

4. Simulation and Discussion

4.1. Performance in Variation of Step Size in Bacteria

To compare performance to variations of step size in bacterial foraging, test function F_1 is used as follows:

$$F_1(x) = \sum_{i=1}^{3} x_i^2. \qquad (12)$$

The test range is $-5.12 \le x_1, x_2, x_3 \le 5.11$. Step size means the distance moved per step by bacteria.

4.2. Simulation for Disturbance in Motor

Figure 3(a) is characteristic of variations in step size. **Figs.3(b)(c)** show characteristics to variation in step size for generations from 1 to 50 and from 270 to 300. From **Fig.2**, the bigger step size, the convergence is faster.

Figure 5 shows the step response to variation of chemotactic size. The response in which step size is 0.15 is the best. **Fig.6** compares results by GA , immune algorithm, and bacterial foraging. **Fig.7** shows the search for performance index (ITSE) by bacteria foraging and **Fig.6** is a search for have optimal PID parameters by bacteria foraging. **Fig.8** shows step response to a type of sine wave disturbance.

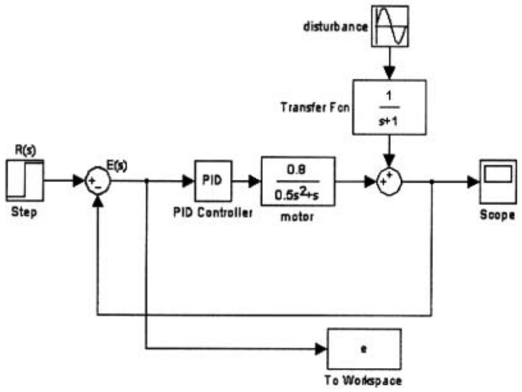

Fig. 4. Simulink block diagram for simulation of bacterial based optimization.

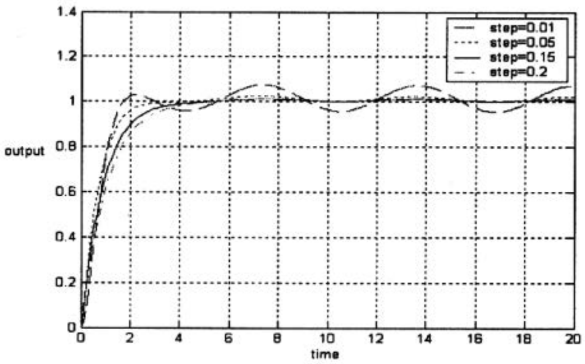

Fig. 5. Step response by variation in chemotactic step size.

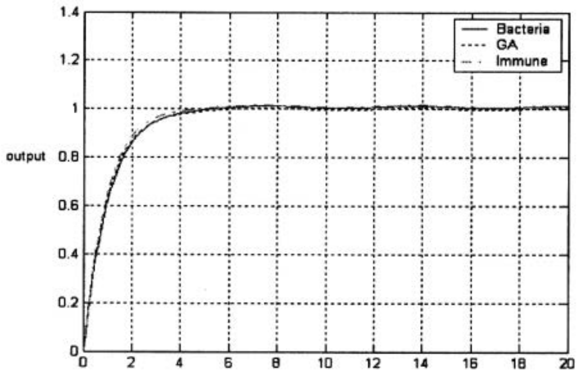

Fig. 6. Comparison of optimal algorithms. (GA, Immune algorithm, Bacteria Foraging).

5. Conclusions

PID controllers are conventionally used to operate process loops including motor control.Achieving optimal PID gain is very difficult for control loops with disturbances. Since the gain of the PID controller has to be tuned manually by trial and error. Tuning of the PID controller may not cover a plant with complex dynamics, such

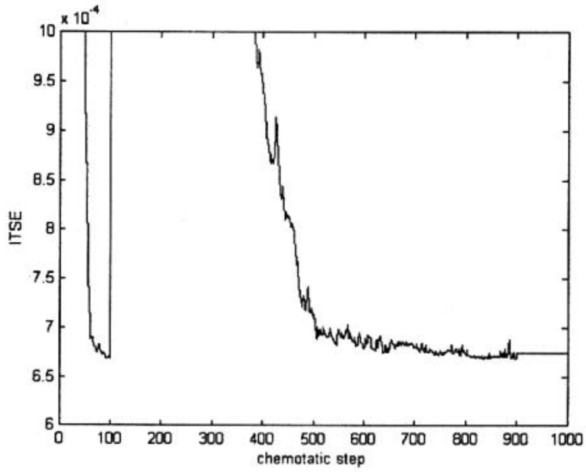

Fig. 7. Search for performance index (ITSE) by bacteria foraging.

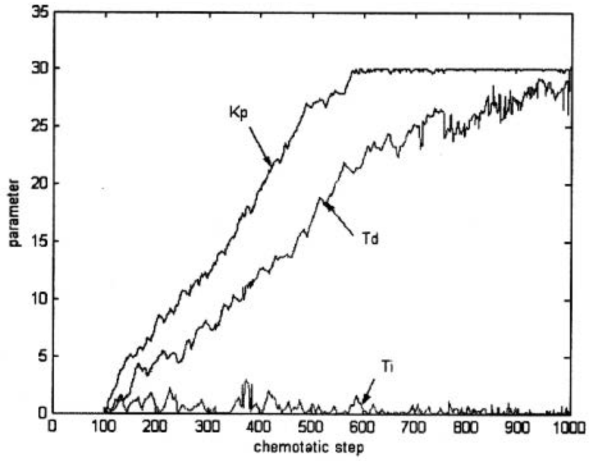

Fig. 8. Search process of optimal PID parameters by bacteria foraging.

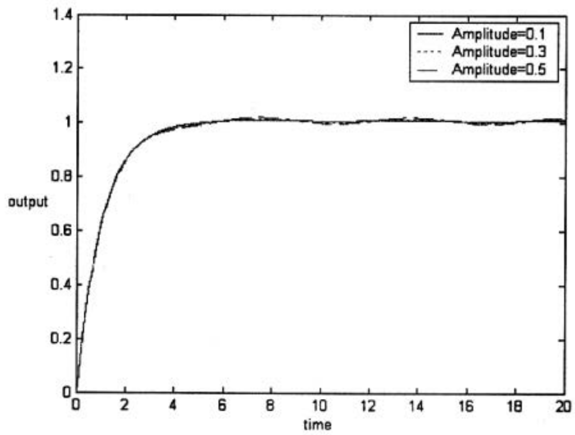

Fig. 9. Step response to a type of sine wave disturbance.

Table 2. PID parameter value and ITSE fersus variation in chemotactic step size.

Chemotactic step size	ITSE	Kp	Ti	Td
Che_size=0.01	0.094163	3.0605	0.076235	1.1411
Che_size=0.05	0.003656	13.704	0.2733	8.773
Che_size=0.15	0.000678	30	0.23208	25.844
Che_size=0.2	0.000668	29.901	0.25813	30

Table 3. Comparison of PID parameter and ITSE of each optimal algorithm.

	Bacteria Foraging	GA[1]	Immune Algorithm
Kp	29.901	29.992	29.739
Ti	0.25813	0.0001	0.39477
Td	30	28.3819	27.277
ITSE	0.000668	0.000668	0.0006352

as large dead time, inverse response, and a highly nonlinear characteristic without any control experience.

Since natural selection of entity tends to eliminate entities with poor foraging strategies for locating, capturing, and ingesting food, they obtain enough food to enable them to reproduce after many generations, poor foraging strategies are either eliminated or shaped into good ones. Optimization is provided for social foraging where groups of parameters communicate to cooperatively forage in engineering.

We propose intelligent tuning of PID controllers by a bacterial foraging-based optimal algorithm for robust control with disturbance resistance in control of motor control loops. Simulation results show satisfactory response. The object function in minimized by gain selection for control, and the variety gain is obtained as shown in **Tables 2** and **3**. The proposed controller is also used effectively in control (**Figs.5–9**).

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