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Controller Tuning Of A Biological Process Using Optimization Techniques

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Abstract: PID(Proportional-Integral-Derivative) control is one of the earlier control strategies. It has simple control structure which was understood by plant operators and which they found relatively easy to tune. Many techniques have been developed to obtain the optimum PID parameters for a particular system. In this paper Genetic algorithms (GA) are proposed as a method for proportional-integral (PI) parameters optimization for controlling a bioreactor in which cell growth follows substrate inhibition kinetics. The performance of the proposed controller has been compared with the performance of the internal model control (IMC) tuning scheme in terms of time domain specifications, servo and regulatory problems.
Keywords: Bioreactor, GA, IMC,pi tuning.

I. INTRODUCTION

Biochemical reactors are used in a wide variety of processes from waste treatment to fermentation for the production of biochemical. They are inherently nonlinear. The control of nonlinear processes like bioreactors by conventional tuning does not give satisfactory responses. This is due to the change of process gain and time constant with the operating conditions. This stimulates the development of tools that can assist engineers to achieve the best overall PID control for the entire operating range of a given process. Over the past few years many different techniques have been developed for obtaining the optimum proportional, integral control parameters for PI controllers.

This paper describes the application of genetic algorithms to the optimal tuning of the classical PI controllers being used to regulate nonlinear Processes [1]-[3]. The use of genetic algorithms in this field of PI optimization is expected to overcome weaknesses of other conventional approaches in non-linear situations. Genetic algorithms are very effective at finding optimal Solutions to a variety of problems. This innovative technique performs well when solving complex problems
because it does not impose many limitations of traditional techniques.

II. THE DYNAMIC MODEL OF A CONTINUOUS STIRRED TANK REACTOR

In this section we present the dynamic model of a continuous stirred tank bioreactor where a single population of microorganism is cultivated on a single limiting substrate [4]. A typical control and

instrumentation diagram of the bioreactor with biomass concentration as the measured output is shown in Fig 1.

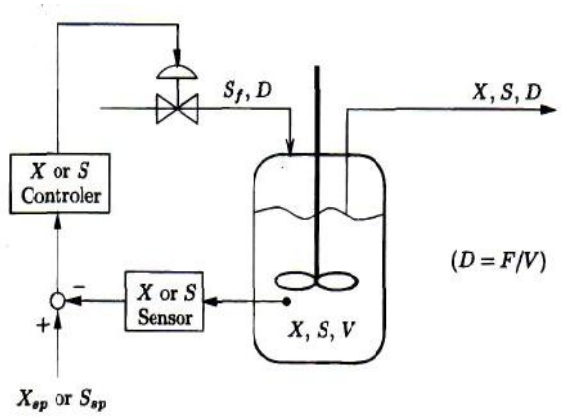

Fig 1 Schematic diagram of a continuous bioreactor

A variety of fermentation processes can be described by the unstructured model [5]

$$\frac{dx}{dt} = (« - D).x. \qquad (1)$$

$$\frac{dS}{dt} = D(S_f - S) - «.x - \frac{1}{Y_{x/s}} \qquad (2)$$

$$\frac{dP}{dt} = «.x.Y_{p/x} - D.P \qquad (3)$$

Where x, S, P and « are the biomass concentration, substrate concentration, product concentration and the specific growth rate respectively.

D = dilution rate = F/v = $\frac{Vol.\ flow\ rate}{reactor\ volume}$

S_f, is the substrate feed concentration, $Y_{x/s}$ is the yield coefficient for cell mass and $Y_{p/x}$ is the yield co-efficient for product

III. SUBSTRATE INHIBITION MODEL:

Many empirical expressions have been proposed for the function μ(s) and we consider the substrate inhibition model [6] which is the most commonly used classical function:

$$\mu = \frac{\mu_{max}.S}{Ks + S + K_i.S^2} \qquad (4)$$

where «max is the maximum growth rate constant and *Ks* is saturation constant and Ki is the saturation constant.

In the present control study the parameters used for the substrate inhibition model are

«max = 0.53 h^{-1}, *Ks* = 0.12 *g/l*, $Y_{x/s}$= 0.4, $Y_{p/x}$ = 0.5, S_f = 4.0 *g/l*, Ki=0.4545,D=0.3h^{-1}

The nonlinear process has the following steady state for a dilution rate of 0.3 h^{-1} at which the production rate xD is maximum,
Biomass concentration *x* =1.5302 g/l
Substrate concentration *s* = 0.1746 g/l
Product concentration *p* = 0.7651 g/l

The process is controlled at this operating point.

The state space formulation [7] is used to linearize the nonlinear equations around the steady state operating point. The transfer function relating the dilution rate to the biomass concentration is,

$$Gp(s) = \frac{-1.53s^2 - 0.9181s - 0.1377}{s^3 + 2.862s^2 + 1.447s + 0.2036}$$

On approximation, the above transfer function is modeled as a first order system and the transfer function is given by,

$$Gp(s) = \frac{-0.6764}{0.4491s + 1}$$

IV. CONTROLLER DESIGN

A. Conventional Design Techniques

The basic PI controller parameters are given as, proportional gain, Kp and integral gain Ki. Over the last fifty years, numerous methods have been developed for setting the parameters of a PID controller. In this paper it is considered to proceed with IMC tuning technique proposed by Skogestad for PI tuning.

B. IMC Tuning Technique

The Internal Model Control technique is one of the recent traditional tuning techniques that yield better values among the techniques available for conventional methods For a First order model of the IMC tuning values basedon Skogestad proposal is given as, $K_p = \frac{1}{K}(\tau/\tau_c + \tau_d)$

where τc =τd as per Skogestad, integral time constant Ti is given as Ti = τ and hence we have Ki = Kp/Ti. Applying the technique we get the IMC tuning parameters as Kp= -0.664, Ki = -1.4784 for the proposed model.

V. GA BASED PI CONTROLLER

A. Genetic Algorithm

GAs is a powerful search algorithm that performs an exploration of the search space that

evolves in analogy to the evolution in nature. The power of GAs consists in only needing objective function evaluations instead of derivatives or other auxiliary knowledge, to carry out their search[8],[9].They use probabilistic transition rules instead of deterministic rules, and handle a population of candidate solutions (called individuals or chromosomes) that evolves iteratively. Each iteration of the algorithm is called generation. The evolution of the species is simulated through a fitness function and some genetic operators such as reproduction, crossover and mutation.

During the **reproduction** phase the fitness value of each chromosome is assessed. This value is used in the selection process to provide bias towards fitter individuals. Just like in natural evolution, a fit chromosome has a higher probability of being selected for reproduction. This continues until the selection criterion has been met. The probability of an individual being selected is thus related to its fitness, ensuring that fitter individuals are more likely to leave offspring. Multiple copies of the same string may be selected for reproduction and the fitter strings should begin to dominate.

Once the selection process is complete, the **crossover** algorithm is initiated. The crossover operations swaps certain parts of the two selected strings in a bid to capture the good parts of old chromosomes and create better new ones. Genetic operators manipulate the characters of a chromosome directly, using the assumption that certain individual's gene codes, on average, produce fitter individuals. The crossover probability indicates how often crossover is performed. A probability of 0% means that the .offspring. will be exact replicas of their .parents. and a probability of 100% means that each generation will be composed of entirely new offspring. Using selection and crossover on their own will generate a large amount of different strings. However there are two main problems with this: 1. Depending on the initial population chosen, there may not be enough diversity in the initial strings to ensure the GA searches the entire problem space. 2. The GA may converge on sub-optimum strings due to a bad choice of initial population. These problems may be overcome by the introduction of a mutation operator into the GA.

Mutation is the occasional random alteration of a value of a string position. It is considered a background operator in the genetic algorithm The probability of mutation is normally low because a high mutation rate would destroy fit strings and degenerate the genetic algorithm into a random search. Mutation probability values of around 0.1% or 0.01% are common, these values represent the probability that a certain string will be selected for mutation for an example for a probability of 0.1%; one string in one thousand will be selected for mutation. Once a string is selected for mutation, a randomly chosen element of the string is changed or .mutated. The fittest individuals will survive generation after generation while also reproducing and generating offspring's that might be stronger and stronger. At the same time, the weakest individuals disappear from each generation. Individuals must be encoded in some alphabet, like binary strings, real numbers, vectors and other. In a practical application of genetic algorithms, a population pool of chromosomes has to be installed and they can be randomly set initially. In each cycle of genetic evolution, a subsequent generation is created from the chromosomes in the current population. The cycle of evolution is repeated until a termination criterion is reached. The number of evolution cycles, or a predefined fitness value can set this criterion. In this paper, the magnitude of the error will be used to assess the fitness of each chromosome.

VI. IMPLEMENTATION OF GA

The optimal values of the conventional PI controller parameters Kp and Ki, is found using GA. All possible sets of controller parameter values are chromosomes whose values are adjusted so as to minimize the objective function, which in this case is the error criterion, which is discussed in detail. For the PI controller design, it is ensured the controller settings estimated results in a stable closed loop system.

A. Initialization of Parameters

To start up with GA, certain parameters need to be defined. It includes the population size, bit length of chromosome, number of iterations, selection, crossover and mutation types etc. Selection of these parameters decides to a great extent the ability of designed controller. The range of the tuning parameters is considered in the range of 0-10. Initializing the values of the parameters for this paper is as follows:

Population size – 100
Bit length of the considered chromosome – 6
Number of Generations – 100
Selection method – 'Maximum Geometric selection'
Crossover type – 'Single point crossover'
Crossover probability – 0.8
Mutation type –'Uniform mutation'
Mutation probability – 0.05

B. Objective Function for the Genetic Algorithm

The objective functions considered are based on the error criterion. A number of such criteria are available and in this paper controller's performance is evaluated in terms of Integral time absolute error (ITAE) error criteria. The error criterion is given as a measure of performance index given by the equation:

$$I_{ITAE} = \int_0^T t|e(t)|dt$$

In this paper we consider the limits for the equation from time, t=0 to t=Ts, where Ts is the settling of the system to reach steady state condition for a unit step input.

C. Termination Criteria

Termination of optimization algorithm can take place either when the maximum number of iterations gets over or with the attainment of satisfactory fitness value. Fitness value, in this case is nothing but reciprocal of the magnitude of the objective function, since we consider for a minimization of objective function. In this paper the termination criteria is considered to be the attainment of satisfactory fitness value which occurs with the maximum number of iterations as 100.For each iteration the best among the 100 particles considered as potential solution are chosen. Therefore the best values for 100 iterations is sketched with respect to iterations, and are as shown in Fig 2 and 3..

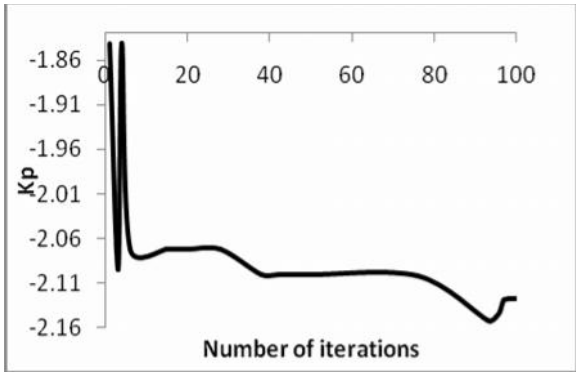

Fig 2. Best solutions of Kp for 100 iterations

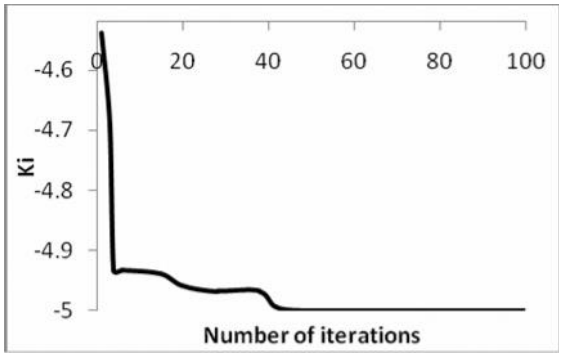

Fig 3. Best solutions of Ki for 100 iterations

The PI controller was formed based upon the respective parameters for 100 iterations, and the global best solution was selected for the set of parameters, which had the minimum error. A sketch of the error based on ITAE criterion for 100 iterations is shown in Fig 4.

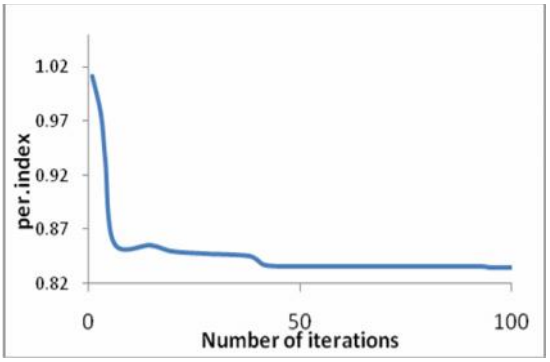

Fig 4. ITAE values for 100 iterations

It was seen that the error value tends to decrease for a larger number of iterations. As such the algorithm was restricted to 100 iterations for beyond which there was only a negligible improvement.

Based on GA for the application of the PI tuning we get the PI tuning parameters for the model as, Kp=-2.1275, Ki = -4.9995

VII. RESULTS AND DISCUSSION

The PI values obtained by the GA are compared with those of the results derived from skogested method in various perspectives, viz. set point changes and regulatory changes.

A tabulation of the time domain specifications comparison and the performance index comparison for the obtained models with the designed controllers is presented. All the simulations were implemented using Matlab.

In this study we present the simulation results of servo and regulatory responses of IMC tuned and GA based controllers for a dilution rate D = 0.3 h^{-1} is presented.

The servo response of the IMC tuned controller and GA based controller of a bioreactor for positive set-point change in cell concentration for 5% from stable steady state (x=1.5302 g/l) are shown in fig 5. For the feed concentration 4 g/l the steady state cell mass concentration X cannot be more than 1.6. since, the steady state cell mass concentration is the product of feed concentration and yield co-efficient.

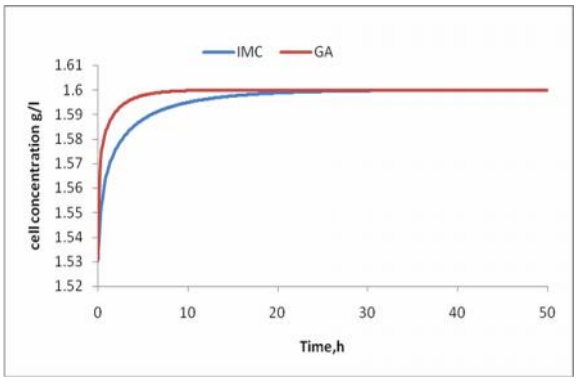

Fig 5.Servo response of the bioreactor for positive setpoint change in cell concentration for 5% from stable steady state (x=1.5302g/l)

The servo response of the IMC tuned controller and GA based controller of a bioreactor for negative set-point change in cell concentration for 5% from stable steady state (x=1.5302 g/l) are shown in fig 6.

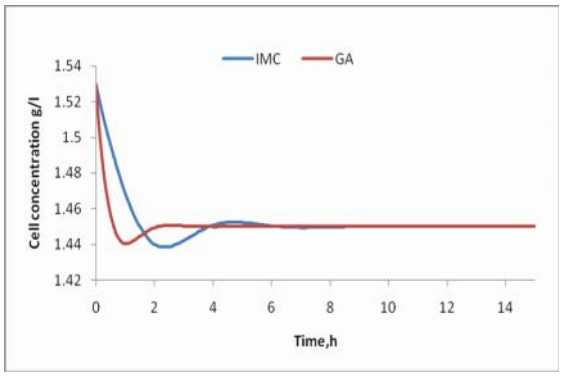

Fig 6.Performance of controllers for negative setpoint change(5%)in cell concentration

The responses of the bioreactor for a step change in both setpoint and the disturbance(substrate concentration from 4.0g/l
to 5.0 g/l) are shown in fig.7

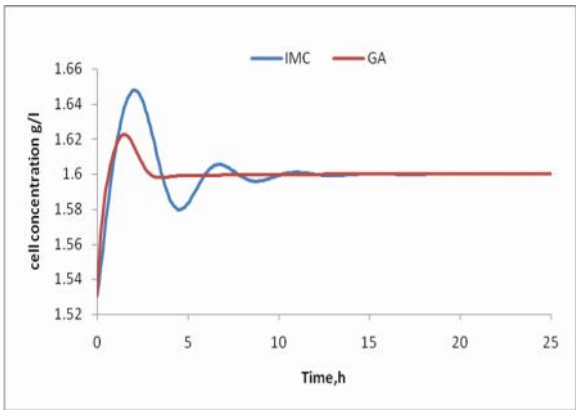

Fig 7 Response to a step change in both setpoint and the feed concentration(SP=1.5302 to1.6,D=0.3,S_f =4.0 to 5.0)

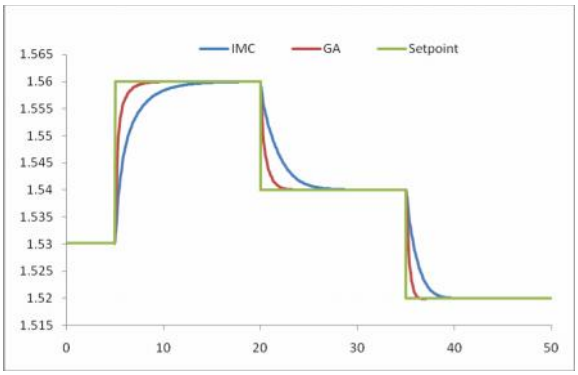

Figure 8 performance of controllers for multiple setpoint changes in cell concentration

The regulatory response of the IMC tuned controller and GA based controller of a bioreactor for a step disturbance in feed concentration (Sf) from 4.0g/l to 5.0g/l is shown in Fig 9.

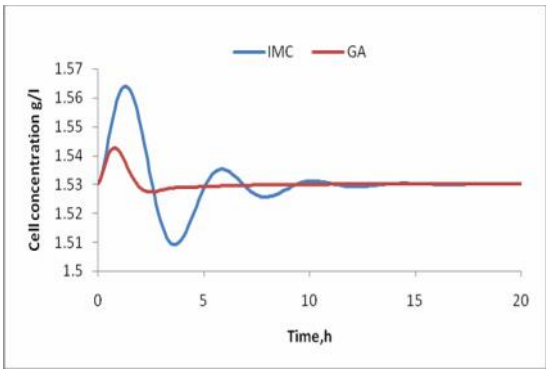

Fig 9. Regulatory responses of the bioreactor for step disturbance in feed concentration ($s_{f)}$ from 4.0 g/l to 5.0 g/l)

TABLE I -COMPARISON OF TIME DOMAIN SPECIFICATIONS

	IMC CONTROLLER	GA CONTROLLER
Settling time (seconds)	25	8

TABLE II -COMPARISON OF PERFORMANCE INDEX OF IMC TUNED AND GA TUNED CONTROLLERS

	IMC CONTROLLER	GA CONTROLLER
ITAE	9.9939	0.2298
IAE	10.5107	2.0941
ISE	5.5174	1.3755
MSE	0.0183	0.0046

VIII. CONCLUSION

In the present work the design and implementation of GA based PI controller and IMC tuned PI controller for biochemical reactors with Substrate inhibition kinetics have been presented. Based on the simulation results it is concluded that for a continuous bioreactor, the performance of the GA controller is much superior compared to the IMC tuned controller.GA controllers allow to have a faster and more precise control of the process, both for setpoint and disturbance step changes. The simulation responses reflect the effectiveness of the GA based controller in terms of time domain specifications. The performance index under the various error criterions of the GA based controller is always less than the IMC tuned controller.

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