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Genetic Algorithms for Optimal Control of Beer Fermentation

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Abstract-- **This paper uses genetic algorithms to optimise the mathematical model of a beer fermentation process that operates in batch mode. The optimisation is based in adjusting the temperature profile of the mixture during a fixed period of time in order to reach the required ethanol levels but considering certain operational and quality restrictions.**

Index Terms-- **batch fermentation, beer fermentation modelling, genetic algorithms, optimal control**

I. Introduction

The modelling of fermentation processes is a basic part of any research in fermentation process control. Since all the optimisation work to be done is based on the reliability of the model equations, they are important for the right design. These equations are generally non-linear.

In batch or fed batch fermentation processes, there is no steady state. The control of a fermentation process is based on the measurement of physical, chemical or biochemical properties of the fermentation broth and the manipulation of physical and chemical environmental parameters [8], [11].

The heuristic method of trial and error, which is used to find an optimal or pseudo-optimal operating regime by manipulating the process technological parameters, is one of the oldest optimisation methods. Genetic Algorithms are random search methods based on the mechanics of natural selection and natural genetics. In order to use Genetic Algorithms, a solution to the problem as a genome (or chromosome) must be represented. The genetic algorithm then creates a population of solutions and applies genetic operators such as mutation and crossover to evolve the solutions in order to find the best one(s).

Appropriate implementation of Genetic Algorithms includes the following three aspects: definition of the objective function, definition and implementation of the genetic representation, and definition and implementation of the genetic operators. The simulation of the selected model has been accomplished with the help of SIMULINK (Version 2.2) under MATLAB (version 5.2) environment as a modern and improved way for process simulation and possible control. The optimisation of the process have been accomplished with the SHEFFIELD MATLAB GENETIC ALGORITHM TOOLBOX Version 1.2 which is a novel instrument for implementing genetic algorithm methods as script files that can be changed according to the problem requirements [3]. A refining procedure for smoothing the temperature profile obtained with the Genetic Algorithm optimisation has also been included to achieve implementable results.

II. Description of the Process

Fermentation has come to have different meanings to biochemists and to industrial microbiologists. Its biochemical meaning relates to the generation of energy by the catabolism of organic compounds, whereas its meaning in industrial microbiology tends to be much broader.

Batch fermentation refers to a partially closed system in which most of the materials required are loaded on to the fermentor, decontaminated before the process starts and then removed at the end. Conditions are continuously changing with time, and the fermentor is an unsteady-state system, although in a well-mixed reactor, conditions are supposed to be uniform throughout the reactor at any instant of time [5].

Alcoholic brewery fermentation is the main objective of this work. Brewing and the production of organic solvents may be described as fermentation in both senses of the word but the description of an aerobic process as fermentation is obviously using the term in the microbiological context. The microorganisms or biomass concentrations are the central feature of fermentation affecting the rates of growth, substrate consumption and product formation. Growth and product formation rates vary with time due to a dependence on the present state of the batch; characterised by biomass, substrate and product concentrations, dissolved oxygen tension, nutrient feed rates and also on the condition of the culture [7], [10].

III. Mathematical Model

In fermentation, an accurate mathematical model is indispensable for the control, optimisation and the simulation of a process. Models used for on-line control and those used for simulation will not generally be the same (even if they pertain to the same process) because they are used for different purposes; *no model* can be said to be the best. The model is not expected to be a reconstruction of the process, rather it is intended to serve as a set of operators on the identified set of inputs, producing similar output as expected from the process.

The problem is that in real life the process output is usually contaminated with noise and other disturbances, whereas ideally the model should follow the true output of the underlying representative process, which is unknown. Estimation algorithms, if properly chosen, yield the parameter

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values after processing of data coming from measurements on the system.

For the purpose of this work, a kinetic model has been chosen to be part of the simulation and optimisation. This model was developed and published in [2]. The model was obtained from many experimental studies at laboratory scale with the necessary equipment as can be seen in Figure 1. The model has shown good results, and it should be noted that it takes into account realistic aspects of the process, such as the characteristics of wort and yeast.

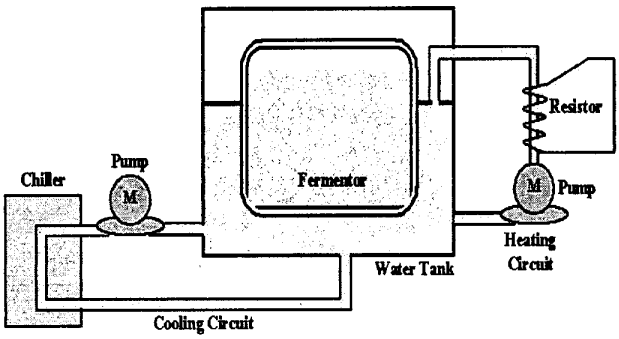

Fig. 1 Experimental Set-up [2]

This model takes into account three components of the biomass: lag, active and dead cells and considers the active cells as the only fermentation agent. It also includes sugar and ethanol concentrations and two important by-products of the fermentation: ethyl acetate and diacetyl, both of them factors that degrade beer quality. A scheme of the process with its main variables is presented in Figure 2.

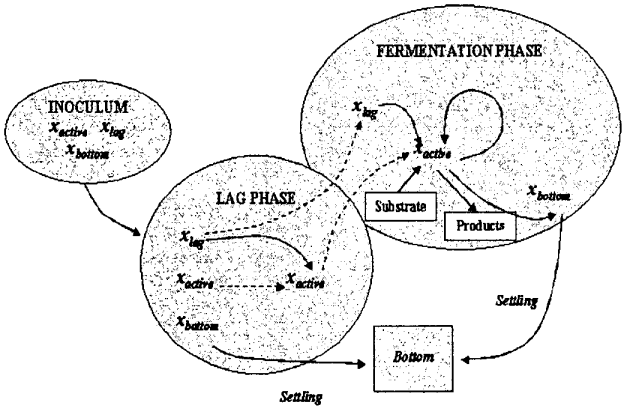

Fig. 2 Process scheme for the kinetic model [2]

Model equations and parameters were adjusted with experimental data values by non-linear regression; with these, good accuracy in the prediction and fitness of the model was achieved. The model is described by the following equations:

$$\mu_x = \frac{\mu_{x0} s}{0.5 s_i + e} \tag{1}$$

$$\mu_D = \frac{0.5 s_i \mu_{D0}}{0.5 s_i + e} \tag{2}$$

$$\mu_s = \frac{\mu_{s0} s}{k_s + s} \tag{3}$$

$$\mu_a = \frac{\mu_{a0} s}{k_s + s} \tag{4}$$

$$f = 1 - \frac{e}{0.5 s_i} \tag{5}$$

$$\frac{dx_{lag}}{dt} = -\mu_{lag} x_{lag} \tag{6}$$

$$\frac{dx_{active}}{dt} = \mu_x x_{active} - k_m x_{active} + \mu_{lag} x_{lag} \tag{7}$$

$$\frac{dx_{bottom}}{dt} = k_m x_{active} - \mu_D x_{bottom} \tag{8}$$

$$\frac{ds}{dt} = -\mu_s x_{active} \tag{9}$$

$$\frac{de}{dt} = \mu_a f x_{active} \tag{10}$$

$$\frac{d(acet)}{dt} = \mu_{eas} \frac{ds}{dt} = \mu_{eas} \mu_s x_{active} \tag{11}$$

$$\frac{d(diac)}{dt} = k_{dc} s x_{active} - k_{dm} (diac) e \tag{12}$$

Most of the parameters of the model have been calculated as Arrhenius functions of temperature (assuming to be affected by the temperature and represented as exponential equations). The constant values of k_{dc} and k_{dm} were calculated with the experimental data for the diacetyl concentration's behaviour:

$$\mu_{x0} = e^{108.31 - \frac{31934.09}{T+273.15}} \qquad k_m = e^{130.16 - \frac{38313}{T+273.15}}$$

$$\mu_{eas} = e^{89.92 - \frac{26589}{T+273.15}} \qquad \mu_{D0} = e^{33.82 - \frac{10033.28}{T+273.15}}$$

$$\mu_{s0} = e^{-41.92 + \frac{11654.64}{T+273.15}} \qquad \mu_{a0} = e^{3.27 - \frac{1267.24}{T+273.15}}$$

$$\mu_{lag} = e^{30.72 - \frac{9501.54}{T+273.15}} \qquad k_s = e^{-119.63 + \frac{34203.95}{T+273.15}}$$

$$k_{dc} = 0.000127672 \qquad k_{dm} = 0.00113864$$

Table 1 describes the nomenclature used:

TABLE 1
NOMENCLATURE USED

Parameter	Description	Unit
μ_a	Ethanol production rate	h^{-1}
μ_D	Specific yeast settling down rate	g/l
μ_{eas}	Ethyl acetate coefficient rate	g/l
μ_{lag}	Specific rate of latent formation	h^{-1}
μ_s	Substrate consumption rate	h^{-1}
μ_x	Specific yeast growth rate	h^{-1}
acet	Ethyl acetate concentration	ppm
diac	Diacetyl concentration	ppm
e	Ethanol concentration	g/l
f	Fermentation inhibitor factor	g/l
k_{dc}	Diacetyl appearance rate	
k_{dm}	Diacetyl reduction rate	
k_m	Yeast growth inhibition parameter	g/l
k_s	Sugar inhibition parameter	g/l
s	Concentration of sugar	g/l
s_i	Initial concentration of sugar	g/l
t	Time	h
T	Temperature	°C
x_{active}	Suspended active biomass	g/l
x_{bottom}	Suspended dead biomass	g/l
x_{lag}	Suspended latent biomass	g/l

IV. DESCRIPTION OF THE OPTIMISATION PROBLEM

Fermentation can be accelerated with an increase of temperature but some contamination risks and undesirable by-products yields (diacetyl, ethyl acetate, etc.) could appear. The objective function was originally defined in order to accelerate the industrial fermentation reaching the required ethanol level in less time, without quality loss or contamination risks [1]. Some modifications to the original sub-objective parameters have been performed in order to achieve equivalent weight values in the cost function. The following terms have been defined:

$$J_1 = 10 \cdot e_{end} \tag{13}$$

$$J_2 = -1.16 \cdot e^{(48 \cdot acet - 66.77)} \tag{14}$$

$$J_3 = -5.73 \cdot e^{(11 \cdot diac - 11.51)} \tag{15}$$

$$J_4 = -\int_0^t 9.91^{-17} e^{(2.31T)} dt \tag{16}$$

$$J_5 = -\sum_{i=1}^{160} \frac{|T_{i+1} - T_i|}{\Delta t} \tag{17}$$

The goal of each sub-objective in the objective function is as follows: J_1 measures the final ethanol production, J_2 limits level of ethyl acetate at the end, J_3 limits diacetyl concentration at the end, J_4 temperature limit along the process, and J_5 penalises brisk changes in temperature.

These terms have been joined to obtain an overall cost function of the process:

$$J = J_1 + J_2 + J_3 + J_4 + J_5 \tag{18}$$

V. USE OF GENETIC ALGORITHMS FOR OPTIMISATION

Genetic Algorithms are search algorithms based on the mechanics of natural selection and natural genetics [6]. They efficiently exploit historical information to speculate on new search points with expected improved performance. GAs have been used in a variety of optimisation tasks, including numerical optimisation and combinatorial optimisation problems as circuit layout and job-shop scheduling [9].

Conventional search techniques are often incapable of optimising non-linear multi-modal functions. In such cases, a random search method might be required. GAs do not use much knowledge about the problem to be optimised and do not deal directly with the parameters of the problem. They work with codes, which represent parameters. The parameters to be optimised are usually represented in a string form since genetic operators are suitable for this type of representation (binary or integer representation method).

VI. IMPLEMENTATION

A SIMULINK model of the Industry Beer Process has been created. The model includes the differential equations, parameters and initial values in an S-Function, together with the necessary terms of the objective function. Figure 3 shows this model under the MATLAB environment.

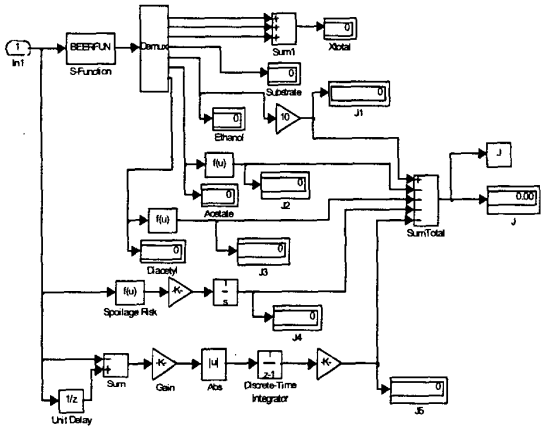

Fig. 3 SIMULINK Model of the Beer Process

In order to optimise the SIMULINK beer fermentation process modelled, a MATLAB script containing the necessary instructions for the genetic algorithm toolbox has been created. In this script some initial parameters needed in the GAs toolbox have been defined, e.g.: number of individuals per subpopulation, maximal number of generations, bounds on decision variables, crossover and mutation rate, etc. Some specific routines can also be chosen and/or changed here, such as: selection, recombination and mutation function for individuals [4].

In order to implement the Genetic Algorithm, the input temperature profile has to be parameterised in terms of chromosomes. Integer numbers for the temperature values (in degrees Celsius) have been used to represent this principle instead of a binary profile. The input profile has been distributed every one hour along the entire process. Consequently, every chromosome or input temperature profile consists of 160 digits (decision variables) that correspond to one different objective function value each. This is the J value to be maximised with the algorithm in order to measure the fitness of each chromosome.

Initial tests were done with a low number of individuals and generations, 100 individuals and 100 generations, generation gap of 50% (how many new individuals are created in every generation), crossover rate of 80% (recombination) and mutation rate set at 1/160 (depending on the number of decision variables). After different runs, the parameters and functions have been set to the following values: number of individuals=1500; maximum number of generations=250; generation gap=80%; crossover rate=80%; mutation rate=1/160; selection function=Roulette Wheel; and recombination function=Double point crossover.

The temperature range for the decision variables have been set from 8 to 16 degrees centigrade taking into account equipment requirements and previous profiles used in the beer fermentation industry (also restricting the algorithm to obtain faster results). With these parameters, a promising temperature profile has been achieved.

VII. Results

First tests had been done with a low number of individuals and generations; generation gap, mutation and crossover rates have also been modified. Different selection and recombination functions for the genetic algorithm have been applied. This has been done in order to achieve a good value of the objective function and a smooth temperature profile. Figure 4 shows how the objective value is maximised with every generation.

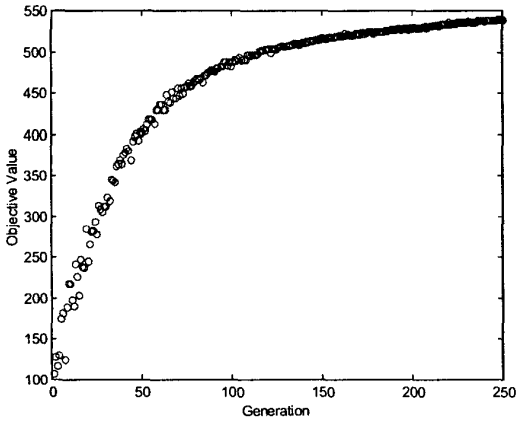

Fig. 4 Objective Value vs. Generation Number

It is clear that with more individuals for the optimisation, smoother results can be obtained; thus, more time will be required by the algorithm in order to obtain an implementable temperature profile. The temperature profile obtained with the GA Toolbox for the selected parameters in this paper is shown in Figure 5.

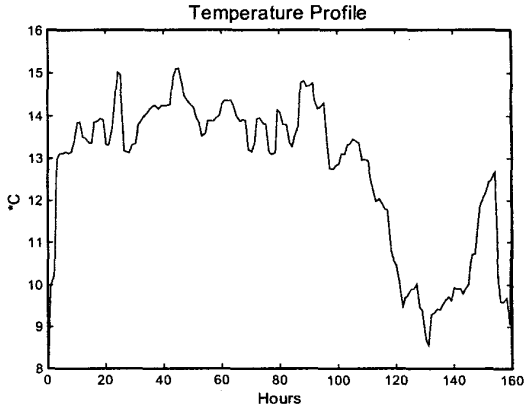

Fig. 5 Non-Smoothed Temperature vs. Time

Given these results, a different smoothing process should be used to improve and make them suitable for implementation. This has been done by means of average calculations for every 40 hours of the initial temperature profile obtained (four in total).

This has been done by means of average calculations for every 40 hours of the initial temperature profile obtained (four in total). With these results, four new temperature values are obtained and placed in the centre point of every average range. Horizontal lines from the previous point and straight lines to the next one have been linked to obtain a piece-wise linearisation. Another MATLAB script has been developed to achieve this purpose. Figure 6 shows the final temperature profile obtained after smoothing the original from the optimisation process.

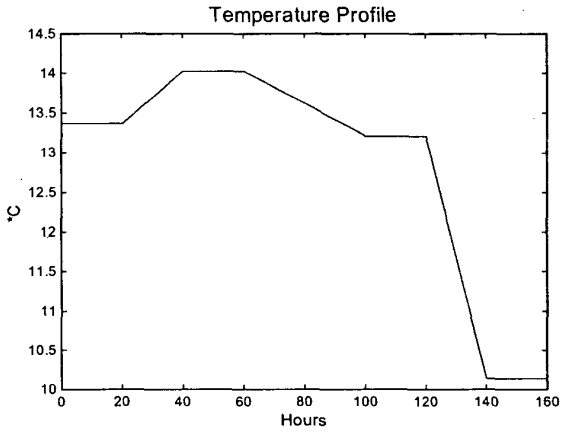

Fig. 6 Smoothed Temperature (°C) vs. Time (Hours)

This improved profile can now be implemented for industrial application. The behaviour of the kinetic variables of the model can be shown in Figures 7, 8 and 9; these were obtained using the smoothed temperature profile applied to the simulated model of the process. Figure 7 illustrates the total suspended biomass and its components: active, latent and dead. Figure 8 encloses the sugar and ethanol concentration curves. Figure 9 includes the by-products concentration.

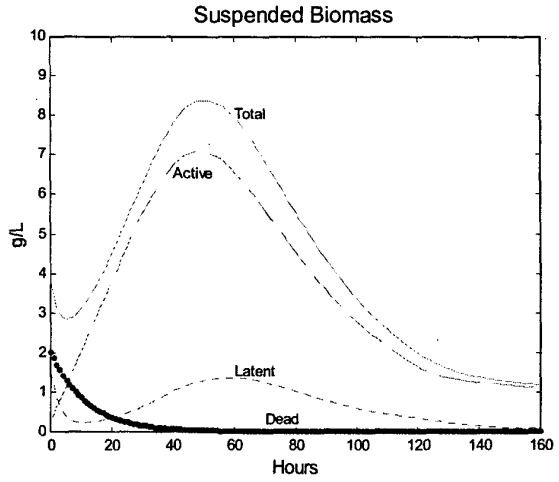

Fig. 7 Suspended biomass behaviour

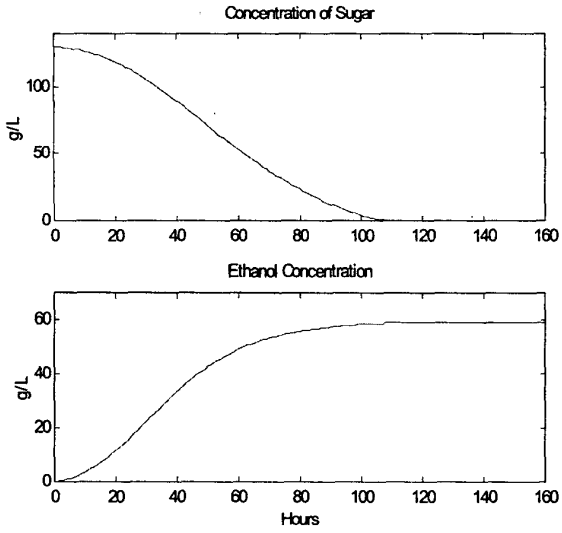

Fig. 8 Sugar and ethanol concentration

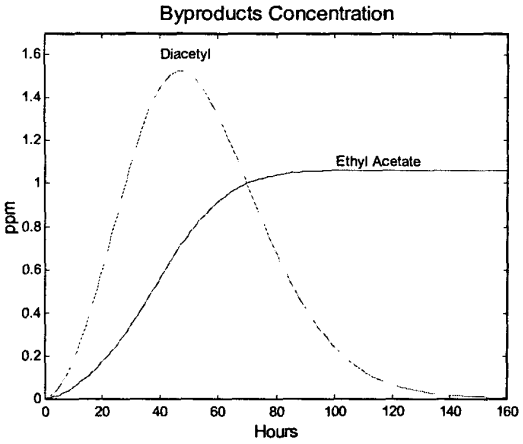

Fig. 9 Byproducts behaviour

VIII. Analysis of Results

Several runs have been made changing the initial parameters related to the genetic algorithm. For instance: number of individuals (starting with 100 up to 1500), number of generations (from 100 to 350), generation gap (0.5 to 0.8), etc. After reviewing these results the best temperature profile with maximum objective value (and with convenient optimisation time) has been selected and smoothed for feasible implementation by means of an average linear approximation.

With this new temperature profile the final objective function value reaches 585.5214, which compared with the original value of 541.5504, that can be obtained using the temperature profile mentioned by [2] for industry application; gives a considerable improvement in the value of the cost function. This value has been obtained not just by maximising the final ethanol production but also minimising the by-products concentration at the end of the fermentation process (Diacetyl and Ethyl Acetate) making sure that no unwanted features are going to be present in the beer.

IX. Conclusions and Further Work

Genetic Algorithms have proved to be suitable in the optimisation of fermentation processes and no previous knowledge, such an initial temperature profile, has been necessary to obtain a satisfactory result.

Previous work done in order to achieve a better profile for implementation have been acceptable and encouraging [1]. The SIMULINK implementation described here appears to be a flexible representation of the model that was easy to interface with the Genetic Algorithm toolbox. In addition, a superior cost-value function has been obtained by means of the Genetic Algorithm Toolbox for the optimisation of the beer process. Also a softer profile by parameterising and calculating average temperatures made results suitable for implementation.

Further work could be done to investigate the benefits of parameterising the temperature profile using a few linear segments. In this way, a smooth profile can be obtained directly and there is no need for an additional smoothing step.

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