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Abstract — Energy consumption in the world is based on two types of sources: fossil fuels and renewable energy. In this case, bioethanol presents itself as an alternative resource to fossil fuels, whose production can occur through specific processes called alcoholic fermentation. In parallel, the growing demand for energy has resulted in the development of even more efficient systems and technologies. In this work, mathematical modeling and simulation was performed to represent the kinetics of alcoholic fermentation in a fed-batch bioreactor. The modeling was developed taking into account the microbial inhibition caused by the presence of excess substrate and product through the Tosetto and Hoppe-Hansford models. In the simulation, Bayesian statistics was used as a tool to estimate the kinetic parameters and the state variables of the bioprocess. The estimates were obtained through the use of a particle filter proposed by Liu and West, with 500 particles and experimental measurements from the literature, whose approach presented 99% accuracy and proved to be effective for describing alcoholic fermentation.

Keywords— *particle filter, bioreactor, kinetic parameters, alcoholic fermentation, mathematical modeling*

I. INTRODUCTION

Bioethanol is a predominant ethanol strand derived from agricultural materials specifically carbohydrates, such as starch (corn grain) and sucrose (sugarcane), and lignocellulosic biomass. Furthermore, the disposal of feedstock in bioprocesses is a characteristic of bioethanol production [1].

By definition, bioprocesses makes the use of microbial, animal and plant cells, and cellular components such as enzymes. Common or innovative products can be originated and harmful waste can be disposed of through by this way. Bioprocessing is an essential part of industries such as food, chemicals, and pharmaceuticals [2].

Bioethanol is produced through a class of bioprocesses called fermentation processes. In turn, a fermentation system

is composed of components such as the living cells of a microorganism (or biomass), the products of metabolism (or metabolites) and nutrients (or substrates) that are arranged in the fermentation medium [3].

These processes differ in the form of operation, such as the mode of substrate addition, product withdrawal, etc. In general, the operation regime of the process is divided into: discontinuous (batch), fed discontinuous (fed-batch) and continuous [4].

In processes involving alcoholic fermentation, fed-batch operation is used in about 75% of Brazilian distilleries, one of the main producing sources in the world, while the remaining 25% operate in continuous mode, using mainly *Saccharomyces cerevisiae* yeast as the ethanol-producing microorganism and agricultural materials as substrate. The operation is conducted at temperatures between 32 and 35 °C. The characteristics of the feed flow, which can last from 4 to 6 hours, are important for the maintenance of the process [5].

The fed-batch alcoholic fermentation consists of an initial stage where the process is discontinuous fed followed by another stage entirely of discontinuous process. The operation regime of the first stage starts with the feeding of a yeast suspension, called inoculum, occupying about 30% of the usable volume of the fermentation vessel, called bioreactor or fermenter. Then, the vessel receives the gradual addition of must, usually a liquid solution consisting of sugarcane juice or molasses diluted with sugarcane juice or water. Afterwards, the process is sequenced in batches until the total consumption of substrate [6].

Studying ways to optimize the fermentation process in order to obtain the maximum yield product is not an easy task. This fact is mainly due to the difficulty in obtaining measurements of the variables that are important in monitoring and controlling the process. To get around these

difficulties, an alternative is to perform indirect measurements through appropriate mathematical models that describe the dynamic behavior of fermentation, including taking into account the action of chemical, physical and biological phenomena [7, 8]. In turn, the kinetics of the fermentative process consists primarily in the analysis of the evolution of the concentration values of one or more components of the system, as a function of fermentation time [3].

In this context, the application of the particle filter technique with the algorithm of Liu and West (2001) will be evaluated to perform the estimates of the state variables (substrate concentration, cell, product and volume) and the parameters of the alcoholic fermentation process, considering the already known mathematical modeling of the process [9].

II. METHODOLOGY

A. Mathematical modeling of alcoholic fermentation

The mathematical modeling considered for this study is phenomenological, unstructured, non-segregated modeling. Phenomenological models consist of a set of mathematical relationships, such as mass balance or conservation equations, among the variables of interest in the system under study. The unstructured aspect is observable when the cellular material is represented by a single variable, usually cell mass, without considering variations of intracellular components. While the non-segregated characteristic concerns the cell population considered homogeneous, that is, all the cells present the same behavior [4].

Due to mass conservation balances, phenomenological mathematical models of fermentative processes can be constituted by Ordinary Differential Equations (ODEs) suitable for representing the dynamic of homogeneous systems [10], as presented in (1–4).

$$\frac{dV}{dt} = F \quad (1)$$

$$\frac{dC_X}{dt} = \left(\mu_X - \frac{F}{V} \right) C_X \quad (2)$$

$$\frac{dC_S}{dt} = \frac{1}{Y_{X/S}} \mu_X C_X + \frac{F}{V} (C_{SF} - C_S) \quad (3)$$

$$\frac{dC_P}{dt} = \frac{Y_{P/S}}{Y_{X/S}} \mu_X C_X - \frac{F}{V} C_P \quad (4)$$

In the ODEs system, V is the volume of medium in the bioreactor in L, C_X is the cell concentration in g.L⁻¹, C_P is the product concentration in g.L⁻¹, C_{SF} is the substrate concentration in g.L⁻¹, C_S is the substrate concentration at feed in g.L⁻¹, F is the substrate flow rate in L.h⁻¹, μ_X is the specific cell growth velocity in h⁻¹, $Y_{P/S}$ is the product yield relative to substrate in g_{CX}.g_{CS}⁻¹ and $Y_{X/S}$ is the cell yield relative to substrate in g_{Cp}.g_{Cs}⁻¹

B. Modeling the specific speed of cell growth

Originally, the modeling of μ_X relies on basic theories of biochemistry. The concept of enzyme kinetics is, by analogy, extended to the microorganism, since it contains a considerable number of enzymes that catalyze the reactions of its metabolism. Thus, it is also assumed that the equations describing the inhibition mechanisms (competitive, noncompetitive, mixed, and acompetitive inhibition) of these agents on a single pure enzyme, are similarly manifested in the microorganism [11]. However, the traditional classification of models for the μ_X parameter is based on the inhibitory agent and can be divided into five groups: those free of inhibition; those that consider inhibition by the substrate, product, or even by the cells themselves; and hybrids that unite the previous inhibition models; as presented in Table I adapted from [1]. The kinetic models for μ_X evaluated in this work are by Tosetto (2002) [12] and Hoppe-Hansford (1982) [13].

Tosetto's model, shown in (15), also propagated as the modified Ghose (1979) model or Andrews/Levenspiel model, is characterized by considering exponential inhibition by substrate and linear inhibition by product [14]. The Hoppe-Hansford model, shown in (12), considers only linear inhibition by the product.

C. Bayesian Statistic

Bayesian statistics is based on Bayes' theorem on three main steps: using accessible knowledge about a given parameter in a model through the a priori probability distribution; assigning the likelihood function using the parameter information available in the observed data; combining both the a priori probability distribution and the likelihood function into the form of the a posteriori probability distribution. The a posteriori probability distribution, as in (19), represents the updated knowledge [15].

$$\pi(P|Y) = \frac{\pi(Y|P)\pi(P)}{\pi(Y)} \quad (19)$$

Equation (19) is in terms of P , which can represent unknown parameters and Y which can denote state variables. The function $\pi(P)$ is the a priori probability density, expressing the information of P prior to the measurement of Y ; $\pi(Y|P)$ is the likelihood function, expressing the observed probability density of Y knowing P ; $\pi(P|Y)$ is the a posteriori probability density function, i.e., the probability density of P given the prior information and the measured value of Y ; $\pi(Y)$ is a normalization constant [16–18].

$$\pi(P|Y) = \alpha \times \pi(Y|P) \times \pi(P) \quad (20)$$

Equation (19) can also be represented by (20), since $\pi(Y)$ represents a normalization constant. Thus, the a posteriori probability density function can be written as being proportional to the product of the likelihood function and the a priori probability density.

TABLE I. KINETIC MODELS FOR SPECIFIC SPEED OF CELL GROWTH

Classification	Author(s)	Model ^a
No Inhibition	Monod (1942)	$\mu_X = \mu_{X,max} \frac{C_S}{K_S + C_S}$ (5)
	Moser (1958)	$\mu_X = \mu_{X,max} \frac{C_S^u}{K_S + C_S}$ (6)
	Contois (1959)	$\mu_X = \mu_{X,max} \frac{C_S}{K_S \times C_X + C_S}$ (7)
Substrate inhibition	Andrews (1968)	$\mu_X = \mu_{X,max} \frac{C_S}{K_S + C_S + \frac{C_S^2}{K_{IS}}}$ (8)
	Wu (1988)	$\mu_X = \mu_{X,max} \frac{C_S}{K_S + C_S + \frac{C_S^v}{K_{IS}}}$ (9)
Product Inhibition	Aiba – Shoda – Nagatani (1968)	$\mu_X = \mu_{X,max} \frac{C_S}{K_S + C_S} e^{(-K_{IP} \times C_P)}$ (10)
	Levenspiel (1980)	$\mu_X = \mu_{X,max} \frac{C_S}{K_S + C_S} \left(I - \frac{C_P}{C_{P,max}} \right)^n$ (11)
	Hoppe – Hansford (1982)	$\mu_X = \mu_{X,max} \frac{C_S}{K_S + C_S} \frac{K_{IP}}{K_{IP} + C_P}$ (12)
Cellular Inhibition	Lee – Pollard – Coulman (1983)	$\mu_X = \mu_{X,max} \frac{C_S}{K_S + C_S} \left(I - \frac{C_X}{C_{X,max}} \right)^m$ (13)
Hybrid Inhibition	Ghose – Thyagi (1979)	$\mu_X = \mu_{X,max} \frac{C_S}{K_S + C_S + \frac{C_S^2}{K_S}} \left(I - \frac{C_P}{C_{P,max}} \right)$ (14)
	Tosetto	$\mu_X = \mu_{X,max} \frac{C_S}{K_S + C_S + \frac{C_S^2}{K_S}} \left(I - \frac{C_P}{C_{P,max}} \right)^n$ (15)
	Levenspiel/Lee – Pollard – Coulman	$\mu_X = \mu_{X,max} \frac{C_S}{K_S + C_S} \left(I - \frac{C_P}{C_{P,max}} \right)^n \left(I - \frac{C_X}{C_{X,max}} \right)^m$ (16)
	Andrews/Lee – Pollard – Coulman	$\mu_X = \mu_{X,max} \frac{C_S}{K_S + C_S + \frac{C_S^2}{K_S}} \left(I - \frac{C_X}{C_{X,max}} \right)^m$ (17)
	Andrews/Lee – Pollard – Coulman/Levenspiel	$\mu_X = \mu_{X,max} \frac{C_S}{K_S + C_S + \frac{C_S^2}{K_S}} \left(I - \frac{C_X}{C_{X,max}} \right)^m \left(I - \frac{C_P}{C_{P,max}} \right)^n$ (18)

^a Kinetic parameters: K_S is the saturation constant, K_{IS} is the substrate inhibition constant, $C_{P,max}$ is the product concentration when cell growth ceases, n is the power of the product inhibition term, u is a dimensionless parameter of the model, v is a dimensionless parameter of the model, K_{IP} is the product inhibition constant and m is a dimensionless parameter of the model.

In possession of this, a specific strategy that makes it possible to obtain inference by simulation is through the use of Sequential Monte Carlo Methods (SMCs), commonly referred to as particle filters. It provides a computational approximation for the a posteriori distribution, which may be in terms of random samples (particles) and associated weights, being able to predict an unknown variable from a data set [19, 20]. From this perspective, Bayesian filters of the particle filter class are probabilistic methods that rely on a recursive algorithm for estimating and updating dynamic

states of a system from models, knowledge bases, and others [21].

Particle filter methods are used in order to produce sequential estimates of the desired dynamic variables. The sequential estimation is done through interleaved prediction and data update steps. This is accomplished in such a way that the error is minimized statistically. Particle filters are traditionally applied with the following algorithms: Sampling Importance Resampling (SIR), Auxiliary Sampling Importance Resampling (ASIR) and Liu and West [20].

In general, simulation methods based on Bayesian sequential analysis of dynamic models initially arise with the proposal to sample the state variables over time using fixed parameters. In such a case, particle "friction" situations are present in resampling-based methods and "weight degeneracy" situations are seen in reweighting-based methods. However, these occurrences are handled by formulating a synthetic method of generating new sample points for parameters by targeting "artificial evolution", in which the non-dependence of parameters with time is still considered [9].

Additionally, the phenomenon of degeneracy occurs because many particles have insignificant weights. More computational effort is required so that particles with small weights can be advanced in time in the same way as large particles. The problem can be minimized by increasing the number of particles, and more efficiently, the resampling technique can be applied in order to select the best particles. The SIR and ASIR algorithms contain resampling steps [9, 20].

Although resampling reduces the effects of degeneracy this can lead to a loss of diversity and the resulting sample may contain a large amount of repeated particles, causing the sample to be impoverished. This is a serious situation in state evolution models with small noises. In this case, the "collapse", or "friction", of all particles into a single particle occurs, especially when there are small time intervals. The ASIR method is qualified to solve this problem [9, 20].

Still, Liu and West present an innovation to use the ASIR algorithm proposing to show how to estimate, besides the state variables, the parameters of the model. Similarly to the state variables, the parameters are updated, or evolved, at each time and this procedure is performed through a combination between the average for all particles and the parameter value for each particle [20].

In the Bayesian view, filter-based sequential simulation using an Auxiliary Particle Filter (APF) that incorporates state variables and parameters has excellent equivalence to Markov chain Monte Carlo (MCMC) analysis. Liu and West demonstrated this by applying and comparing them from a dynamic factor financial model, inherent in the banking industry, to obtain perspectives on a time scale beyond the data set. In this respect, the feasibility of sequential simulation-based filtering induced approximation errors that indicated a tendency to increase over time. In other words, in an analysis it would be convenient to restrict oneself to short time scales because observing a very long horizon increased the possibility of being unrealistic. As a solution, it was proposed to use a longer historical stretch of data and, mainly, it was suggested that methods should always be combined with some form of periodic recalibration based on off-line analysis [9].

D. Simulation of alcoholic fermentation

The analysis of the experimental data aimed to evaluate the kinetic behavior of the state variables and parameters defined in (21–23).

$$X = [C_X, C_S, C_P, V] \quad (21)$$

$$P_{Tosetto} = f(F, \mu_{max}, K_S, K_{IP}, Y_{X/S}, Y_{P/S}) \quad (22)$$

$$P_{Hoppe-Hansford} = f(F, \mu_{max}, K_S, K_{IS}, Y_{X/S}, Y_{P/S}, n, C_{P,max}) \quad (23)$$

The case study estimates of the state variables and parameters were designed using the mathematical modeling of the fermentation simultaneously with the data acquired from the experimental measurements of Borges (2008) [22]. More precisely, they were performed based on the fed-batch fermentation operation in three experimental conditions, named in this paper as FB1, FB2 and FB3. The design parameters and initial conditions are presented in Tables II and III, respectively. Where, t is the fermentation time and t_F is the feeding time, both in hours (h).

The measurements of the state variables are in Table IV–VI, and the already estimated parameter values are shown in Table VII. The values of the experimental measurements, obtained by using a temperature (T) of 32°C, of C_X , C_S , C_P (g.L⁻¹) and V (L) over time (h). In the experimental conditions, C_X is the dry biomass of *Saccharomyces cerevisiae* yeast, C_S is the sucrose concentration, C_P is the ethanol concentration and V is the verified volume in the bioreactor [22].

TABLE II. DESIGN PARAMETER VALUES

Data ^b	C_{SF} (g.L ⁻¹)	t (h)	t_F (h)
FB1	217	8	5.283
FB2	241.4	10	5.217
FB3	285	11	5.2

^b Values obtained from [22].

TABLE III. INITIAL VALUES OF THE STATE VARIABLES USED IN THE ALCOHOLIC FERMENTATION PROCESS

Data ^c	C_X (g.L ⁻¹)	C_S (g.L ⁻¹)	C_P (g.L ⁻¹)	V (L)
FB1	88	0	35.17	1.5
FB2	83	0	36.71	1.5
FB3	83	0	36.78	1.5

^c Values obtained from [22].

TABLE IV. EXPERIMENTAL MEASUREMENTS FOR THE FED-BATCH PROCESS (FB1) WITH $C_{SF} = 217$ G.L⁻¹

t (h) ^d	C_X (g.L ⁻¹) ^d	C_S (g.L ⁻¹) ^d	C_P (g.L ⁻¹) ^d	V (L) ^d
0	88.0	0	35.17	1.500
1	59.0	29.0	42.6	2.116
2	46.6	34.0	47.8	2.820
3	38.2	36.0	52.6	3.479
4	33.1	39.0	55.0	4.139
5.283	27.7	35.8	58.89	4.986
6	28.7	19.85	68.0	4.986
7	29.7	5.2	74.7	4.986
8	29.7	0.894	77.6	4.986

^d Values obtained from [22].

TABLE V. EXPERIMENTAL MEASUREMENTS FOR THE FED-BATCH PROCESS (FB2) WITH $C_{SF} = 241,4 \text{ g.L}^{-1}$.

$t \text{ (h)}^e$	$C_X \text{ (g.L}^{-1})^e$	$C_S \text{ (g.L}^{-1})^e$	$C_P \text{ (g.L}^{-1})^e$	$V \text{ (L)}^e$
0	83.0	0	36.71	1.500
1	56.0	40.0	41.8	2.168
2	44.1	53.0	47.8	2.837
3	36.3	58.11	49.6	3.505
4	31.0	56.0	51.7	4.174
5.217	26.5	64.1	55.3	4.987
6	26.8	40.0	60.4	4.987
7	27.4	21.2	69.94	4.987
8	27.5	8.0	78.2	4.987
9	28.3	2.8	80.4	4.987
10	28.4	0.899	81.2	4.987

^e Values obtained from [22]

TABLE VI. EXPERIMENTAL MEASUREMENTS FOR THE FED-BATCH PROCESS (FB2) WITH $C_{SF} = 285 \text{ g.L}^{-1}$.

$t \text{ (h)}^f$	$C_X \text{ (g.L}^{-1})^f$	$C_S \text{ (g.L}^{-1})^f$	$C_P \text{ (g.L}^{-1})^f$	$V \text{ (L)}^f$
0	83	0	36.78	1.5
1	54	51.8	43.3	2.17
2	44	66.7	47.3	2.84
3	36.6	80	49.3	3.51
4	30.6	82	53.8	4.181
5.2	26.3	88	53.82	4.985
6	26.8	66	65.7	4.985
7	27	44	70.77	4.985
8	27.1	28.3	82.1	4.985
9	27.7	18.4	85.8	4.985
10	27.8	9.8	89.3	4.985
11	28.1	4.57	91.5	4.985

^f Values obtained from [22]

TABLE VII. VALUES OF THE YIELD COEFFICIENTS, GENERAL KINETIC PARAMETERS, AND KINETIC PARAMETERS FOR THE TOSSETTO AND HOPPE-HANSFORD MODELS

Parameters	Values		
Yield coefficients^g	FB1	FB2	FB3
Y_{XS}	0.024	0.021	0.017
Y_{PS}	0.445	0.418	0.413
Flow rate^g	FB1	FB2	FB3
F	0.660	0.668	0.670
General kinetic parameters^g	FB1	FB2	FB3
μ_{max}	0.02686	0.02293	0.02701
K_S	10.40	10.31	32.02
Kinetic parameters for Tossetto model^g	FB1	FB2	FB3
K_{IS}	813.8	693.4	370.0
C_{Pmax}	125.7	129.9	144.1
N	0.1	0.1	0.2861
Kinetic parameters for Hoppe-Hansford model^h	FB1	FB2	FB3
K_{IP}	200	200	200

^g Values obtained from [22].

^h Arbitrarily chosen value.

The deviation used for the experimental measurements was 1% from the maximum concentration value. The estimation results were presented in terms of the 99% confidence interval with 500 particles for Liu and West's algorithm.

E. Statistical analysis

The models were statistically analyzed with the coefficient of determination (R^2), by which the simulation data of the state variables were compared with the experimental data set.

III. RESULTS

A. Estimation of the state variables

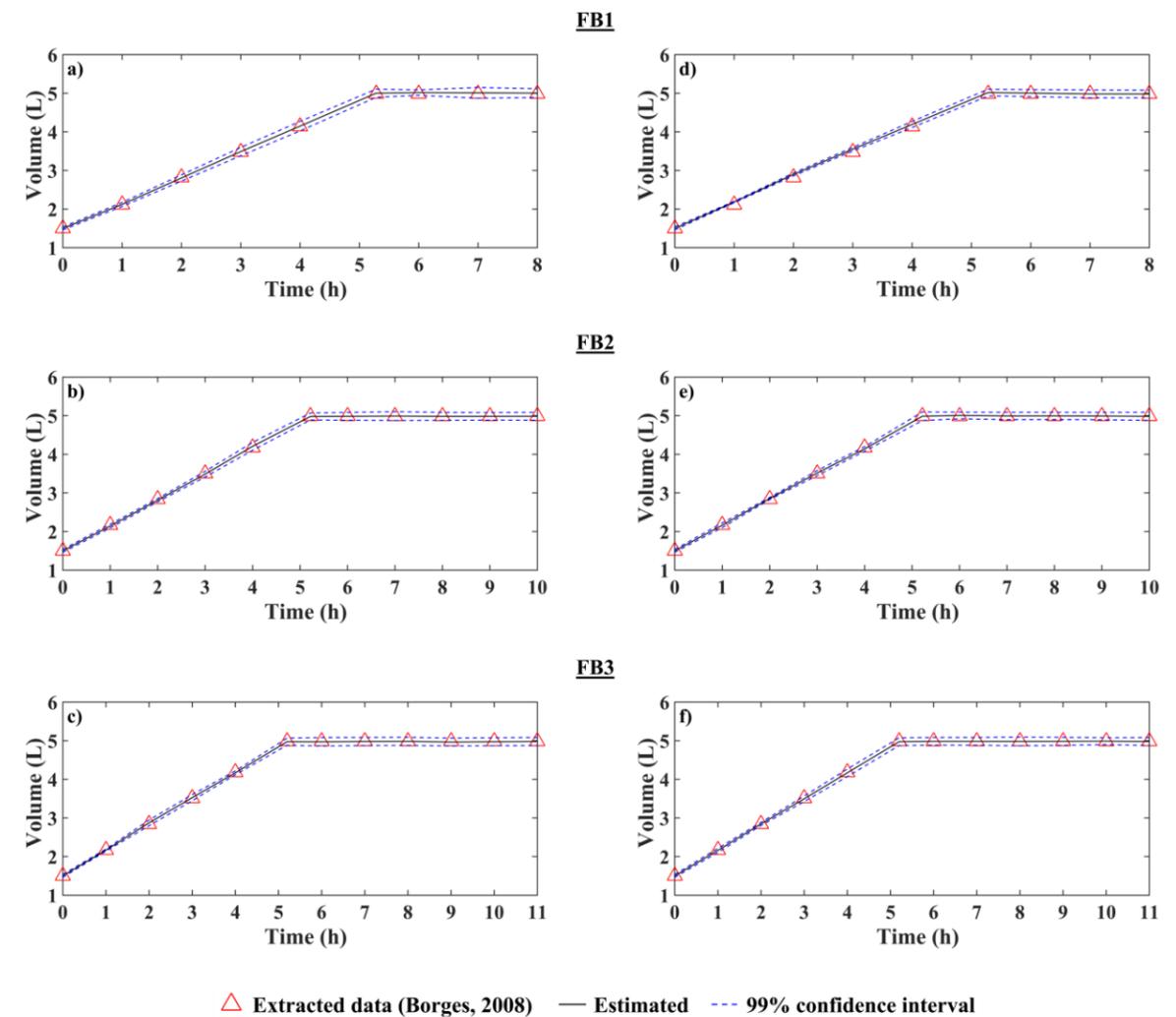


Fig. 1. Obtaining the volume variations (V) by applying the Liu and West filter. (a-c) Tossetto model for μ_X . (d-f) Hoppe-Hansford model for μ_X .

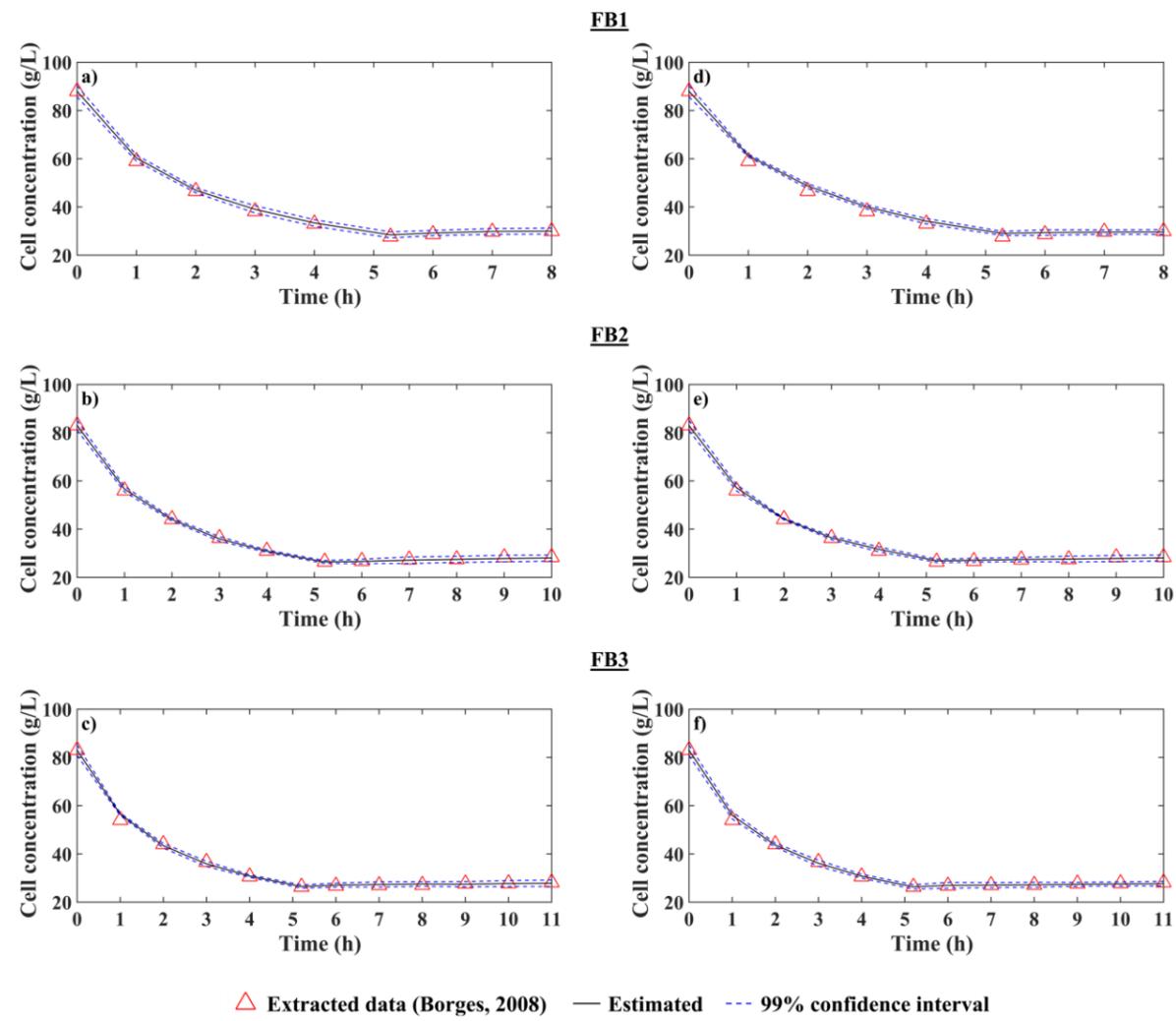


Fig. 2. Obtaining the variations of cell concentrations (C_x) – *Saccharomyces cerevisiae* – by applying the Liu and West filter. (a–c) Tosetto model for μ_x . (d–f) Hoppe–Hansford model for μ_x .

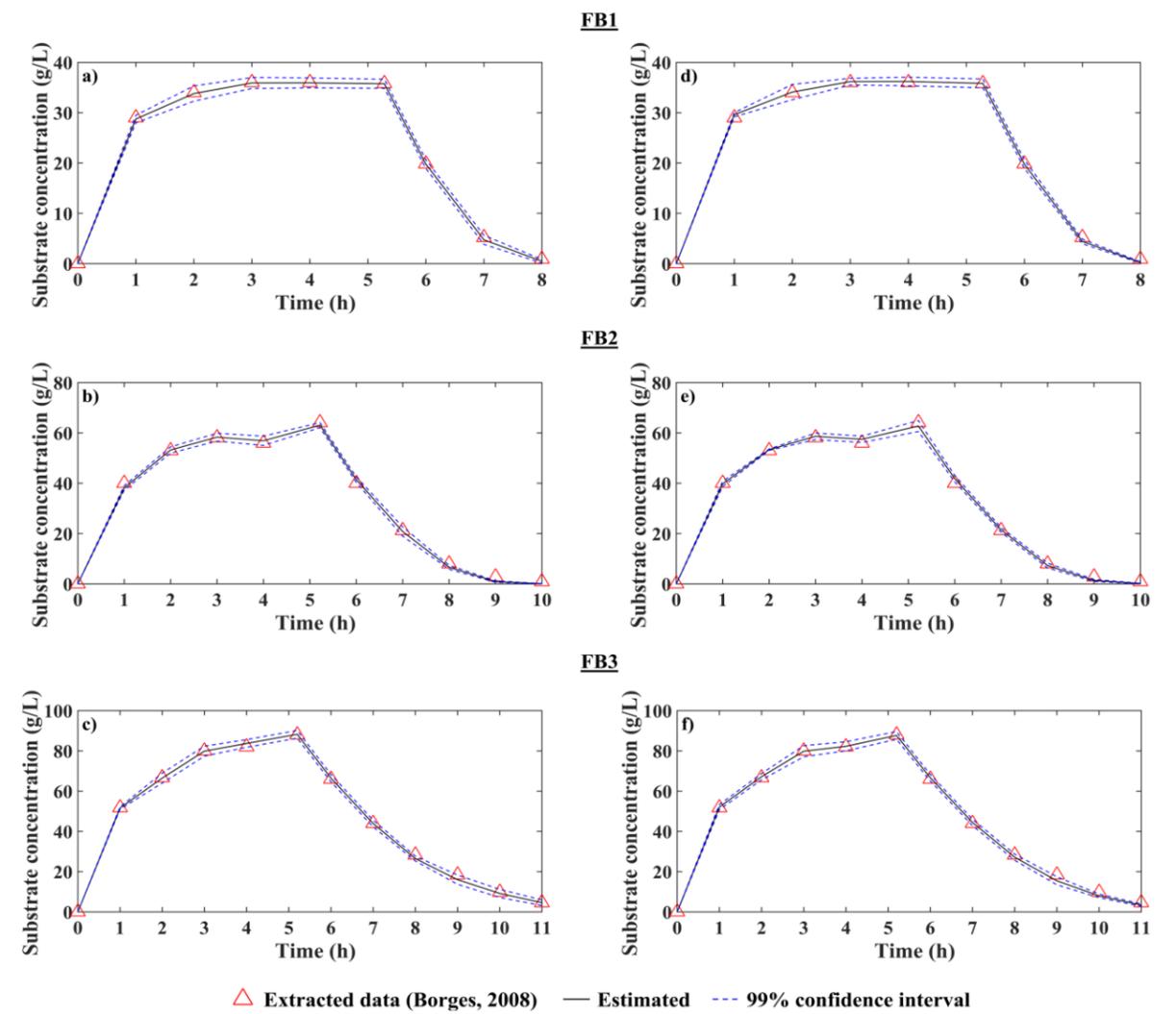


Fig. 3. Obtaining the variations of the concentrations of substrate (C_s) – Sucrose – by applying the Liu and West filter. (a–c) Tosetto model for μ_x . (d–f) Hoppe–Hansford model for μ_x .

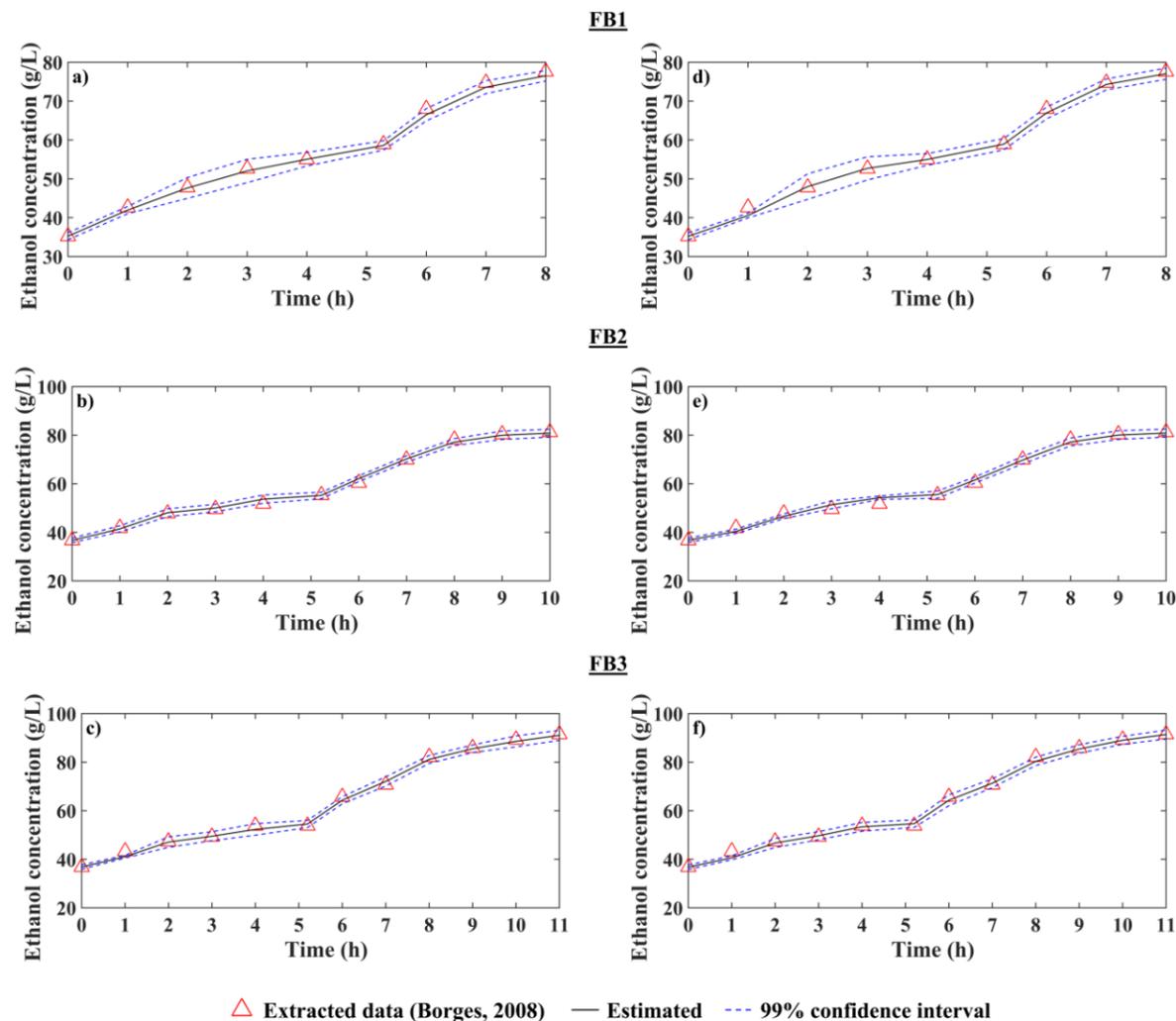
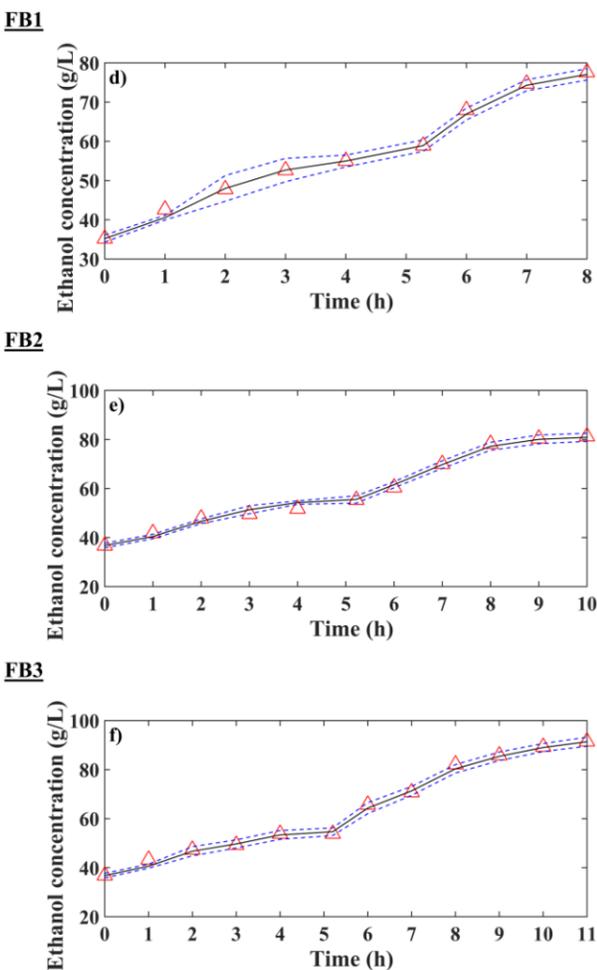


Fig. 4. Obtaining the product concentration variations (C_p) – Bioethanol – by applying the Liu and West filter. (a–c) Tosetto model for μ_X . (d–f) Hoppe–Hansford model for μ_X .

The evolution of the system volume is seen in Fig. 1, where a linear profile is observed during the process of feeding the medium, characteristic of the constant feed flow rate. The total volume becomes constant when the substrate feeding is interrupted.

In Fig. 2, we can see the immediate effects of the substrate-feeding step where initially there is a decrease in cell concentration due to the increase in the volume of the medium and the subsequent stability caused by reaching a constant system volume.

The results for substrate concentration are shown in Fig.3. It is verified that the concentration presents an increase until the time of about 5 hours (end of substrate feeding), followed by a decrease related to its consumption by the yeast cells present in the medium. Consequently, a gradual increase in ethanol production occurs during the fermentation process, as seen in Fig. 4. That is in agreement with what the literature propounds [23], in which ethanol production occurs simultaneously with yeast growth (biomass formation) because it is associated with the energy metabolism of the cell.



B. Kinetic parameters estimation

From the application of the particle filter, new values for the parameters were found for the proposed cases, as presented in Table VIII. Despite the differences in the experimental conditions, mainly referring to the C_{SF} , the yield coefficients and the kinetic parameter μ_{max} showed stable values. While the other parameters values showed a larger difference.

TABLE VIII. UPDATE PARAMETERS VALUES

Parameters	Values					
	Tosetto			Hoppe – Hansford		
Yields coefficients	<i>FB1</i>	<i>FB2</i>	<i>FB3</i>	<i>FB1</i>	<i>FB2</i>	<i>FB3</i>
Y_{XS}	0.0213	0.0184	0.0211	0.0264	0.0230	0.0198
Y_{PS}	0.4155	0.4002	0.4015	0.4402	0.3994	0.3872
Flow rate	<i>FB1</i>	<i>FB2</i>	<i>FB3</i>	<i>FB1</i>	<i>FB2</i>	<i>FB3</i>
F	0.5287	0.7024	0.8052	0.6478	0.5838	0.889
General kinetic parameters	<i>FB1</i>	<i>FB2</i>	<i>FB3</i>	<i>FB1</i>	<i>FB2</i>	<i>FB3</i>
μ_{max}	0.0233	0.0215	0.0303	0.0328	0.0313	0.0285
K_S	12.086	11.528	24.982	7.46111	12.754	24.496
Kinetic parameters for Tosetto model	<i>FB1</i>	<i>FB2</i>	<i>FB3</i>	<i>FB1</i>	<i>FB2</i>	<i>FB3</i>
K_{IS}	794.88	611.09	525.68			
C_{Pmax}	194.29	141.80	92.793			
N	0.0759	0.1061	0.1620			
Kinetic parameters for Hoppe–Hansford model	<i>FB1</i>	<i>FB2</i>	<i>FB3</i>	<i>FB1</i>	<i>FB2</i>	<i>FB3</i>
K_{IP}				207.62	199.89	191.13

C. Statistical Analysis

TABLE IX. CORRELATION COEFFICIENTS (R^2) OF THE SIMULATION THROUGH LIU AND WEST FILTER.

Data	State variable	Kinetics models	
		Tosetto	Hoppe-Hansford
<i>FB1</i>	C_X	0.99902	0.99504
	C_S	0.99974	0.99925
	C_P	0.99665	0.99648
	V	0.99983	0.99868
	Average	0.99881	0.99736
<i>FB2</i>	C_X	0.99967	0.99922
	C_S	0.99788	0.99830
	C_P	0.99664	0.99394
	V	0.99983	0.99988
	Average	0.99851	0.99784
<i>FB3</i>	C_X	0.99766	0.99851
	C_S	0.99888	0.99859
	C_P	0.99682	0.99652
	V	0.99988	0.99997
	Average	0.99831	0.99840

The percent accuracy of the results with μ_X kinetic model by Tosetto was 99.83 – 99.88% and the best accuracy was for condition FB1 (lowest value of C_{SF} and C_P). In the other conditions, the value of the estimated data was decreasing but still with very good accuracy.

For the kinetic model of μ_X by Hoppe–Hansford the range was 99.74 – 99.84%. The best accuracy in this case was for the FB3 data (highest value of C_{SF} e C_P), it was also observed that the accuracy of the simulation was increasing and proportional to the increase in C_P , which confirms the potential of using the model to represent inhibition by the product

IV. CONCLUSION

In this study, mathematical modeling and simulation were performed to represent the alcoholic fermentation kinetics. Using the particle filter method of Liu and West, it was possible to perform the estimates of the state variables and parameters of the alcoholic fermentation process based on three experimental conditions. The applied technique showed good agreement in the estimation of all experimental conditions.

It was possible to verify the inhibition performance by the Tosetto and Hoppe–Hansford specific cell growth rate models. In this respect, the hybrid inhibition by the presence in excess of substrate and product considered by Tosetto fitted the data slightly better, although both models were 99% accurate.

The results obtained made important contributions to research involving fermentation kinetics and computational applications. Since, with the use of the mathematical models combined with the particle filter of Liu and West (2001), one can see the effectiveness of the application of this method and the potential incorporation into methodologies aimed at greater efficiency in bioethanol production, as well as in other fermentative processes.

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