

Observer Design for Saccharomyces Cerevisiae Fermentations

Sánchez López Esperanza Paola*; Sánchez Hernández Bernardo Luis A.*; Marcelino Gutiérrez Villalobos *, J. Luis Zárate Castrejón*, P. Antonio López-Pérez **, Vicente Peña-Caballero*

* Departamento de Ingeniería Agroindustrial, Lic. en Ing. en Biotecnología, Universidad de Guanajuato, Campus Celaya-Salvatierra, División de Ciencias de la Salud e Ingenierías, Mutualismo s/n, Celaya Guanajuato, CP 38060, México USA (e-mail: ep.sanchezlopez@ugto.mx; bla.sanchezhernandez@ugto.mx; jmgutierrez@ugto.mx; jl.zarate@ugto.mx; vicente.caballero@ugto.mx))

**Escuela Superior de Apan, Universidad Autónoma del Estado de Hidalgo, Carretera Apan-Calpulalpan, Km.8., Chimalpa Tlalayote s/n, 43900, Colonia Chimalpa, Apan, Hgo., Mexico (e-mail: <u>pablo_lopez@uaeh.edu.mx</u>)

Abstract: The estimation of the states of a *Saccharomyces cerevisiae* (*S. cerevisiae*) biomass production process using glucose as carbon and energy source in CSTR-type bioreactor cultures was investigated. The biomass estimation was evaluated numerically by implementing the observer in the bioreactor model at a continuous regime. The observer was designed with two terms, one error proportional (Ke) and one sign type (Ksign(e)f(e)). The performance of the proposed observer was compared with the observer published by Bastin and Dochain. For different dilution rates, both observers showed equal performance for the same numerical conditions. Moreover, their response was evaluated for different initial conditions of the model and the estimators with a better performance index of the proposed observer.

Keywords: Software sensors, Observer design, State estimation, Nonlinear systems, batch fermentation

1. INTRODUCTION

The yeast S. cerevisae is a eukaryotic, heterotrophic microorganism belonging to the fungi kingdom (Parapouli et al., 2020), non-pathogenic, and considered to be a generally safe organism (GRAS) (Ostergaard et al., 2000). This yeast has been known for a long time for its use in the fermentation of beverages such as beer, cider, sake, and wine (Jacobus et al., 2021) and even in the production of bread (Lahue et al., 2020) in different processes of the pharmaceutical industry (Ostergaard et al., 2000). This species has been widely studied because it is used as a biological model in basic research and in biotechnological applications such as the production of alcoholic beverages on an industrial scale, the production of biofuels from cellulose sources (Parapouli et al., 2020), and as an input for animal and human food because it contains a high protein content (Parapouli et al., 2020). An advantage of working with this microorganism is its susceptibility to genetic modification by means of recombinant DNA technology or by random mutagenesis or the crossing of two strains (Ostergaard et al., 2000).

Due to the wide knowledge and use of this yeast in the scientific community (academic and industrial), as well as the need to control and optimize these bioprocesses in batch, fed-batch, or continuous bioreactors, the design and implementation of estimators and/or controllers to observe and control the process variables, respectively, continues due to the nonlinear nature of the microorganism and the operating conditions. According to the authors Bastin and Dochain (Chen et al., 1990b, 1990a; Dochain, 2003),

software sensors are programs that apply process models and estimation algorithms to estimate variables and parameters that are not easily measured or that are available. Software sensors use online data to estimate these variables. Different applications of observers in bioprocesses are presented in Table 1 for different modes of bioreactor operation, i.e., batch and fed-batch and continuous. Therefore, in this work a nonlinear observer is designed and numerically implemented to observe the biomass concentration in *S. cerevisiae* cultures in a continuous bioreactor, considering the modeling errors in the proposed observer. The performance of the proposed observer was compared with the observer published by Chen et al. (1990a, 1990b).

Table 1. Biotechnological processes by Saccharomyces cerevisiae are observed and/or regulated through the implementation of

observers and controllers.			
Bioreactor	Methods	Ref.	
type			
Fed-batch	Flow cytometry	(Palomba	
	(FCM)	et al., 2021)	
Fed-batch	Calorimetry-	(Kottelat et	
	based control	al., 2021)	
Batch	UDE-based	(Bangi et	
	hybrid model	al., 2022)	
	approach and		
	the deep hybrid		
	model proposed		
	by Bangi and		
	Knon		

Batch	First-order sliding mode observer, proportional sliding mode observer and high-order	(Alvarado- Santos et al., 2022)
	sliding mode observer	
Fed-batch	Hybrid observer (an asymptotic observer combined with an extended Kalman filtrer applied to high-density cultures of S. cerevisiae)	(Bárzaga- Martell et al., 2021)
Batch	Unsecented Kalman Filter (UKF)	(Yousefi- Darani et al., 2021)
Fed-batch	PID, system identification and parameter optimization.	(Hu et al., 2021; Qin & Zhai, 2024)
Batch	Sliding mode observer	(Spurgeon, 2008)

2. METHODOLOGY

2.1 Basic methodology for writing model equations

Led us write the balances for bioreactor as: Rate accumulation = rate in - rate out (1)

rate in = bulk flow into the volume + generation with thevolume + transfer into the volume across the boundaries other than by bull flow.

 $rate \ out = bulk \ flow \ out \ the \ volume + generation \ with \ the$ volume + transfer out the volume across the boundaries other than by bull flow.

We can now write the balance equations for the quantity.

$$\frac{d[Vy_i]}{dt} = [F_{in}y_{in} + Vr + VN]$$
(2)

Batch fermentation processes $(F_{in}y_{in} - F_{out}y_{out} = 0)$ for Saccharomyces cerevisiae

A general form of these equations is given by:

$$\frac{d[Vx]}{dt} = R_x (3)$$

$$R_x = r_x V (4)$$

$$r_x V = x\mu(x, s, T = Cte., pH = Cte.)V; x(t = 0) = x_0 (5)$$

$$\frac{d[Vs]}{dt} = R_s = -r_s V = -\frac{r_x V}{Y_{xs}} =$$

$$-\frac{x}{Y_{xs}}\mu(x, s, T, pH, ...)V; s(t = 0) = s_0 (6)$$

where x is the biomass concentration (g/L); s represents the substrate concentration (g/L); Y_{xs} represents the yield coefficient of substrate in grams per gram of biomass (g/g); and $\mu(\cdot)$ is the growth rate (or specific growth rate). μ_{max} is the maximum specific growth rate (1/h)

2.2 Observer design (proposed observer)

Yeast cells (S. cerevisiae=X)

$$\frac{d\hat{X}}{dt} = \mu(\hat{X}, \hat{S})\hat{X} + D \cdot [X_{in} - \hat{X}] + k_1 \varepsilon + \zeta_1(\hat{S}, \varepsilon)$$
 (7) Carbon substrate (Glucose=S)

$$\frac{d\hat{S}}{dt} = -Y\mu(\hat{X},\hat{S})\hat{X} + D\cdot[S_{in} - \hat{S}] + k_2\varepsilon + \zeta_2(\hat{S}, \varepsilon)$$
(8)

Initial conditions

 \hat{X}_0 (time zero) = 0.15 g/L

 \hat{S}_0 (time zero) = $10 \ g/L$

In this work, we design of the gains $\zeta_1(\widehat{S}, \varepsilon)$ and $\zeta_2(\widehat{S}, \varepsilon)$ with the following functions:

$$\zeta_{1}(\widehat{S}, \varepsilon) = \gamma_{1} sign(\varepsilon) \left(1 - \left(\frac{\varepsilon}{\beta_{1}}\right)^{2}\right), \zeta_{2}(\widehat{S}, \varepsilon) =
\gamma_{2} sign(\varepsilon) \left(1 - \left(\frac{\varepsilon}{\beta_{2}}\right)^{2}\right) \text{ and with } \varepsilon = S - \widehat{S}. \text{ Also, with }
\zeta_{1}(\widehat{S}, \varepsilon), \zeta_{2}(\widehat{S}, \varepsilon) \in \mathfrak{R}_{\pm}: \{-1, 0, +1\} \text{ and } \gamma_{1}, \gamma_{2}, X_{in}, S_{in}, D, Y, k_{1}, k_{2} \text{ and } \beta \in \mathfrak{R}_{\pm}.$$

Remark 1. Functions $\zeta_i(\widehat{S}, \varepsilon)$ $\{i = 1, 2\}$:

$$\left|\zeta_1(\widehat{S}, \varepsilon)\right| = \left|\gamma_1 sign(\varepsilon)\left(1 - \left(\frac{\varepsilon}{\beta_1}\right)^2\right)\right| \le \gamma_1 \text{ but if } \gamma_1 \le 1,$$

so that, $\zeta_1(\widehat{S}, \varepsilon)$ is bounded, and this assumption, gives opportunity to Assumption 1 (A1)

A1
$$|\zeta_1(\widehat{S}, \varepsilon)| \leq 1$$

Analogously for the function $\zeta_2(\widehat{S}, \varepsilon)$

$$\left|\zeta_2(\widehat{S}, \varepsilon)\right| = \left|\gamma_2 sign(\varepsilon) \left(1 - \left(\frac{\varepsilon}{\beta_2}\right)^2\right)\right| \le \gamma_2 \text{ but if } \gamma_2 \le 1,$$

so that, $\zeta_2(\widehat{S}, \varepsilon)$ is bounded, and this assumption gives opportunity to Assumption 2 (A2).

$$A2 |\zeta_2(\widehat{S}, \varepsilon)| \leq 1$$

Let us derive the general structure of state observers. Consider the following nonlinear system representation for S. cerevisiae fermentations in a bioreactor:

$$\dot{x} = f(x, u) + \Delta \ell; \ y = h(x) = Cx \ (9)$$

With
$$f(\hat{x}, u) = \begin{bmatrix} f_1(X, S) \\ f_2(X, S) \end{bmatrix} = \begin{bmatrix} \mu(X, S)X + D \cdot [X_{in} - X] \\ -Y\mu(X, S)X + D \cdot [S_{in} - S] \end{bmatrix}; y = \begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X \\ S \end{bmatrix}; x = \begin{bmatrix} x_1 \\ x_2 \end{bmatrix} = \begin{bmatrix} X \\ S \end{bmatrix}; C = \begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix}; \text{ and } \dot{x} = \begin{bmatrix} \dot{x}_1 \\ \dot{x}_2 \end{bmatrix} = \begin{bmatrix} \dot{X} \\ \dot{S} \end{bmatrix}$$
where $x \in \Re_+^{1 \times 2}$ is the vector of the state variables; $u \in \Re_+^{1 \times 2}$ is the vector of the state variables.

 $\Re_+^{1\times 2}$ is the control input vector; $f(x,u):\in \Re_+^{1\times 2+1\times 2}\to$ $\Re^{2\times 1}_+$ is a nonlinear smooth vector function and Lipschitz in and uniformly bounded in u; $\Delta \ell$ is the modeling error; and $y \in \Re^{1 \times 2}_{+}$ is the vector of measured states. This proposed (13) presents an estimation technique for systems subject to

modeling errors $\Delta \ell$ (parameter uncertainties), which is a realistic process situation.

Remark 2. The modeling error:

 $|\Delta \ell| \le \alpha$, so that, $\Delta \ell$ is bounded, and this assumption, gives opportunity to Assumption 3 (A3)

A3 $|\Delta \ell| \leq \alpha$

For this purpose, it is proposed the following observer's structure and its corresponding convergence analysis.

The general structure of the state observer for system (9) is:

$$\dot{\hat{x}} = f(\hat{x}, u); \ \hat{y} = h(\hat{x}) = C\hat{x} \ (10)$$

Usually is required, at least that $|\varepsilon| = |x - \hat{x}| = |S - \hat{S}| = 0$, as $t \to \infty$.

Proposition 1. The following dynamic system is an observer for system (9)

$$\dot{\hat{x}} = f(\hat{x}, u) + K\varepsilon + \gamma sign(\varepsilon) \left(1 - \left(\frac{\varepsilon}{\beta} \right)^2 \right); \ \hat{y} = h(\hat{x})$$

$$= C\hat{x} \ (11)$$

Where

$$\varepsilon = x - \hat{x}$$
 (12)

The main advantage of this observer's structure is to couple a class of function bounded to 1, i.e., $sign(\varepsilon)[1 - (\varepsilon/\beta)^2] \le 1$ with a discontinuous sign function in order to provide smoothness to the corresponding output injection; besides, a proportional term $K \cdot \varepsilon$ is considered in order to provide stability to the estimation procedure, which increases the robustness in the states observing.

2.3 Sketch of proof of proposition 1

For the demonstration of proof of convergence of the error to zero, the error dynamics are considered as follows:

$$\dot{\varepsilon} = \dot{x} - \dot{\hat{x}} = f(x, u) - f(\hat{x}, u) + \Delta \ell - K\varepsilon$$
$$- \gamma sign(\varepsilon) \left(1 - \left(\frac{\varepsilon}{\beta} \right)^2 \right)$$
(13)

Taking norm to maximize Eq. (13):

$$\begin{aligned} |\dot{\varepsilon}| &\leq |f(x, u) - f(\hat{x}, u)| + |\Delta \ell| - K|\varepsilon| \\ &- \gamma \left| sign(\varepsilon) \left(1 - \left(\frac{\varepsilon}{\beta} \right)^2 \right) \right| \ (14) \end{aligned}$$

Now, taking into account the following assumption and the corresponding function properties:

Assumption 4 (A4)

$$|f(x,u) - f(\hat{x},u)| \le L|\varepsilon|$$
 (15)

The Lipschitz constant is L > 0

Therefore Eq. (13) considering assumptions A1-A4, can be expressed as:

$$|\dot{\varepsilon}| \le (L - K)|\varepsilon| + (\alpha - \gamma)$$
 (16)

By solving the above differential inequality:

$$|\varepsilon| \le \varepsilon_0 e^{(L-K)t} + \frac{(\alpha - \gamma)}{L} \left[1 - e^{(L-K)t}\right] (17)$$

Considering the matrix (L - K) as a Hurwitz stable matrix. For $t \to \infty$.

Then, eq. 17 yields

$$|\varepsilon| \le \frac{(\alpha - \gamma)}{I}$$
 (18)

Remark 3. Note that the proportional term of the observer structure provide, as usual, stability to the observer, the observer's gain K acts as a convergence rate parameter to lead to the estimation error to the closed-ball with radius proportional to $(\alpha - \gamma)$, moreover the estimation error can be made as small as desired if $\alpha \approx \gamma$, and the property of $e^{(L-K)t}$: if $e^{(L-K)t}$ is nonsingular, $(e^{(L-K)t})^{-1} = e^{-(L-K)t}$.

3. RESULTS AND DISCUSSIONS

3.1 S. cerevisiae batch and continuous mode cultures

Different fermentations (n = 3) were developed in a batch reactor, controlling temperature and pH through the instrumentation systems in the bioreactor. A glucose consumption rate of 0. 60 gS/L was observed during the first 15 hours of the culture. Biomass production was 0.645 gX/Lh with a maximum cell growth rate of 0.4147 1/h. After the estimation process of the kinetic parameters, a value of 0.5080 1/h was obtained for the maximum cell growth rate (Figure 1). For batch cultures, parameter values were obtained by nonlinear regression (data not shown here), giving a fit as shown by the solid line in Fig. 2. With the nominal value of these parameters, the model was extended to continuous operation mode considering the operating parameters D = 0.1, 0.15, and 0.20 1/h with Sin = 5 and 10g/L for different time intervals. The numerical results are shown in Figure 3 for D = 0.10, 0.15, and 0.20 1/h, with Sin = 5 mg/L.

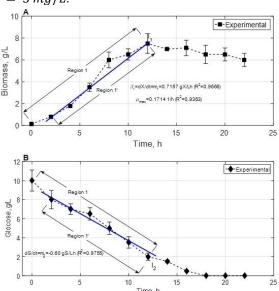


Figure 1. Plot of experimental, data yeast fermentation biomass concentration A and glucose concentration B.

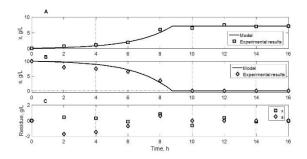


Figure 2. Comparison of model with experimental results: biomass concentration A, substrate concentration B, and residues C.

For D=0.1 h-1 was used to generate the following phase-plane plot for model in (9) under case I conditions (see Figure 4). Notice that all initial conditions converge to equilibrium point $\mathbf{x}=(\bar{X},\bar{S})=(13.2\ 1/h,2.29\ mg/L\ h)$. Thus, $\lambda_1<0$ and $\lambda_2<0$, i.e., $\lambda_1=-\mu(\bar{X},\bar{S})=-0.1$ and $\lambda_2=-Y\dot{\mu}(\bar{X},\bar{S})=-0.3515$

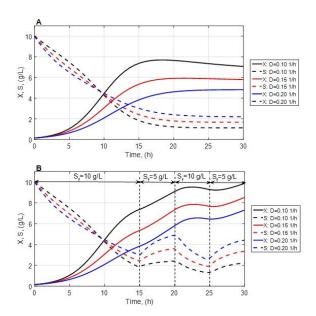


Figure 3. Numerical simulation of the system (23) for different initial conditions.

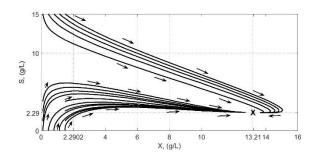


Figure 4. Plot-phase for Contios model, Case I conditions x=stable steady-state

Finally, experimentally for yeast growth in a continuous reactor with a dilution rate of D = 0.2 1/h, the steady state is reached after twenty hours, i.e., after two dilution times (Figure 5). The values of the kinetic parameters of the model in equation (12) obtained by using the *fminsearch* function of MatLab are those reported previously in this section.

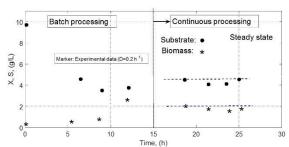


Figure 5. Contonuous processing: Dilution rate D=0.2 h⁻¹ and concentration of feed $S_f = 5g/L$ and V=1 L.

3.2 Proposed observer performance

In this section, the numerical results of the implementation of the observer proposed in (11) to the *S. cerevisiae* biomass production bioprocess (9) are presented and compared with the Bastin and Dochain observer (Chen et al., 1990b) (see appendix) to estimate the biomass concentration by measuring the substrate (glucose) concentration. Specifically, equilibrium state three, i.e., only case 3, is considered.

Figs. 6 and 7 illustrate the performance of both observers and the system in a simulation performed under the following conditions (continuous process): $\mu_{max} = 0.5080 \text{ h}^{-1}$; $K_C = 0.7039$; Y = 0.5838 A square wave influent substrate concentration from 5 to 10 g/L and a constant value for dilution rate (operation parameters). Initial conditions for system (process model Eq. (9)) $X_0 = 0.15 \text{ g/L}$ and $S_0 = 10 \text{ g/L}$ for system Eq. (11) (asymptotic observer) $\hat{X}_0 = 0.15 \text{ g/L}$ and $\hat{S}_0 = 10 \text{ g/L}$ with three sets of eigenvalues λ_1 and $\hat{S}_0 = 10 \text{ g/L}$. The numerical values used in our simulations for the steady-state solution are: Equilibrium point 1 (steady-state solutions): Case 1 Low dilution rate

with D = 0.10 1/h and $S_{in} = 10 g/L$ for nontrivial steady- $\bar{x} = (\bar{X}, \bar{S}) = colum[13.2137 \ g/L \quad 2.2902 \ g/L]$ and the eigenvalues $\lambda_1 = -0.1 \, 1/h$ and $\lambda_2 = -0.3515 \, g/$ Lh with trivial steady-estate $\bar{x} = (\bar{X}, \bar{S}) =$ colum[0 g/L]10 g/L]; Equilibrium point 2 (steady-state solutions): Case 2 Medium dilution rate with D = 0.15 1/h and $S_{in} = 10 \, mg/L$ for nontrivial steady-state $\bar{x} = (\bar{X}, \bar{S}) =$ colum[11.1858 g/L] 3.4719 g/L] and the eigenvalues $\lambda_1 = -0.15 \text{ 1/h}$ and $\lambda_2 = -0.3050 \text{ g/Lh}$; and with trivial steady-estate $\bar{x} = (\bar{X}, \bar{S}) = colum[0 \ g/L \ 10 \ g/L];$ Case 3 Low dilution rate with D = 0.20 1/h and $S_{in} = 10 \text{ mg/L}$ for $\bar{x} = (\bar{X}, \bar{S}) = colum[9.5094 \ g/L]$ 4.4486 g/L] and the eigenvalues $\lambda_1 = -0.20 \text{ 1/h}$ and $\lambda_2 = -0.2711 \text{ g/Lh}$; nontrivial steady-estate $\bar{x} = (\bar{X}, \bar{S}) =$ colum[0 g/L]10 g/L]. For simulation purposes to evaluate the performance of the proposed observer, case 3 was considered.

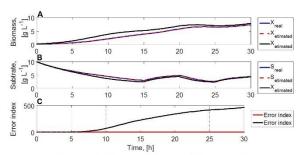


Figure 6. Application of proposed observer with y=S (Eq. (11)) and asymptotic observer (Bastin and Dochain) for Case 3 with low dilution rate D=0.2 h-1 and initial conditions $\hat{X}_0=0.15~g/L$ and $\hat{S}_0=10~g/L$: comparison between systems (x) and (x) and the curve for biomass (A), substrate (B), and error index (C).

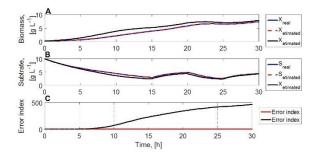


Figure 7. Application of proposed observer with y=X in (11) and asymptotic observer (Bastin and Dochain) for Case 3 with low dilution rate D=0.2 h·¹ and initial conditions $\hat{X}_0=0.135~g/L$ and $\hat{S}_0=10~g/L$: comparison between systems (x) and (x) and the curve for biomass (A), substrate (B), and error index (C).

4. CONCLUSIONS

A conclusion section is not required. Although a conclusion may review the main points of the paper, do not replicate the abstract as the conclusion. A conclusion might elaborate on the importance of the work or suggest applications and extensions.

REFERENCES

- Alvarado-Santos, E., Mata-Machuca, J. L., López-Pérez, P. A., Garrido-Moctezuma, R. A., Pérez-Guevara, F., & Aguilar-López, R. (2022). Comparative Analysis of a Family of Sliding Mode Observers under Real-Time Conditions for the Monitoring in the Bioethanol Production. Fermentation, 8(9), 446. https://doi.org/10.3390/fermentation8090446
- Bangi, M. S. F., Kao, K., & Kwon, J. S.-I. (2022). Physics-informed neural networks for hybrid modeling of labscale batch fermentation for β-carotene production using Saccharomyces cerevisiae. Chemical Engineering Research and Design, 179, 415–423. https://doi.org/10.1016/j.cherd.2022.01.041
- Bárzaga-Martell, L., Duarte-Mermoud, M. A., Ibáñez-Espinel, F., Gamboa-Labbé, B., Saa, P. A., & Pérez-Correa, J. R. (2021). A robust hybrid observer for monitoring high-cell density cultures exhibiting overflow metabolism. Journal of Process Control, 104, 112–125. https://doi.org/10.1016/j.jprocont.2021.06.006
- Chen, L., Bastin, G., & Dochain, D. (1990a). Parameter Identifiability of a Class of Non Linear Compartmental Models for Bioprocesses. IFAC Proceedings Volumes, 23(8), 259–263. https://doi.org/10.1016/S1474-6670(17)51429-9
- Chen, L., Bastin, G., & Dochain, D. (1990b). Structural identifiability of the yield parameters in nonlinear compartmental models for bioprocesses. 29th IEEE Conference on Decision and Control, 1074–1079 vol.2. https://doi.org/10.1109/CDC.1990.203767
- Dochain, D. (2003). State and parameter estimation in chemical and biochemical processes: a tutorial. Journal of Process Control, 13(8), 801–818. https://doi.org/10.1016/S0959-1524(03)00026-X
- Hu, A., Cong, S., Ding, J., Cheng, Y., & Mpofu, E. (2021).
 Differential Evolution Algorithm Based Self-adaptive
 Control Strategy for Fed-batch Cultivation of Yeast.
 Computer Systems Science and Engineering, 38(1),
 65–77. https://doi.org/10.32604/csse.2021.016404

- Jacobus, A. P., Gross, J., Evans, J. H., Ceccato-Antonini, S. R., & Gombert, A. K. (2021). Saccharomyces cerevisiae strains used industrially for bioethanol production. Essays in Biochemistry, 65(2), 147–161. https://doi.org/10.1042/EBC20200160
- Kottelat, J., Freeland, B., & Dabros, M. (2021). Novel Strategy for the Calorimetry-Based Control of Fed-Batch Cultivations of Saccharomyces cerevisiae. Processes, 9(4), 723. https://doi.org/10.3390/pr9040723
- Lahue, C., Madden, A. A., Dunn, R. R., & Smukowski Heil, C. (2020). History and Domestication of Saccharomyces cerevisiae in Bread Baking. Frontiers in Genetics, 11. https://doi.org/10.3389/fgene.2020.584718
- Ostergaard, S., Olsson, L., & Nielsen, J. (2000). Metabolic Engineering of Saccharomyces cerevisiae. Microbiology and Molecular Biology Reviews, 64(1), 34–50. https://doi.org/10.1128/MMBR.64.1.34-50.2000
- Palomba, E., Tirelli, V., de Alteriis, E., Parascandola, P., Landi, C., Mazzoleni, S., & Sanchez, M. (2021). A cytofluorimetric analysis of a Saccharomyces cerevisiae population cultured in a fed-batch bioreactor. PLOS ONE, 16(6), e0248382. https://doi.org/10.1371/journal.pone.0248382
- Parapouli, M., Vasileiadi, A., Afendra, A.-S., & Hatziloukas, E. (2020). Saccharomyces cerevisiae and its industrial applications. AIMS Microbiology, 6(1), 1–32. https://doi.org/10.3934/microbiol.2020001
- Qin, Y., & Zhai, C. (2024). Global Stabilizing Control of a Continuous Ethanol Fermentation Process Starting from Batch Mode Production. Processes, 12(4), 819. https://doi.org/10.3390/pr12040819
- Spurgeon, S. K. (2008). Sliding mode observers: a survey. International Journal of Systems Science, 39(8), 751–764. https://doi.org/10.1080/00207720701847638
- Yousefi-Darani, A., Paquet-Durand, O., Hinrichs, J., & Hitzmann, B. (2021). Parameter and state estimation of backers yeast cultivation with a gas sensor array and unscented Kalman filter. Engineering in Life Sciences, 21(3–4), 170–180. https://doi.org/10.1002/elsc.202000058

Appendix A. (Chen et al., 1990a, 1990b)

Yeast cells

$$\frac{d\hat{X}}{dt} = \mu(\hat{X}, \hat{S})\hat{X} + D \cdot [X_{in} - \hat{X}] + \gamma_1(\hat{X}, \hat{S}) \cdot \varepsilon$$

Carbon substrate

$$\frac{d\hat{S}}{dt} = -Y\mu(\hat{X},\hat{S})\hat{X} + D \cdot [S_{in} - \hat{S}] + \gamma_2(\hat{X},\hat{S}) \cdot \varepsilon$$

Where

$$\varepsilon = x - \hat{x}$$

Initial conditions

 \hat{X}_0 (time zero) = 0.15

$$\hat{S}_0$$
 (time zero) = 10

Remark 1. Measured on-line. Assume the substrate concentration *s* is measured on-line.

Hence, we are in the situation where:

 $\varepsilon = S - \hat{S}$ is the error and γ_1 and γ_2 are the gains.

$$r_X(X,S) = \mu(X,S)X = \frac{\mu_{max}S}{\kappa_c X + S}X$$
 is reaction rate, so that, it governed by the Contois law;

Definition 2. Model of the specific growth rate. Dependence on the substrate concentration s(t) and on the biomass concentration x(t): $\mu(x,s)$.

Contois (1959)

$$\mu(X,S) = \frac{\mu_{max}S}{K_cX + S}$$

With Eq. (1), the experimental data, we assume that the specific growth rate $\mu(x, s)$ obeys the Contoins law. Where μ_{max} and k_s are constant kinetic coefficients.

Definition 1. The gains $\gamma_1(\hat{x}, \hat{s})$ and $\gamma_2(\hat{x}, \hat{s})$

$$\begin{split} \gamma_1(\hat{x}, \hat{s}) &= -\lambda_1 - \lambda_2 - Y(\tilde{r}_x)_s + (\tilde{r}_x)_x - \delta D \\ \gamma_2(\hat{x}, \hat{s}) &= \frac{1}{Y(\tilde{r}_x)_x} \{ -\lambda_1 \lambda_2 - (\lambda_1 + \lambda_2)(D - (\tilde{r}_x)_x)^2 \\ &+ Y(\tilde{r}_x)_x (\tilde{r}_x)_s \} \end{split}$$

Where
$$(\tilde{r}_{\chi})_{S} \triangleq \frac{\partial \tilde{r}_{\chi}}{\partial s}\Big|_{\xi=\hat{\xi}} = \frac{\mu_{max}k_{S}x^{2}}{(k_{S}\hat{x}+\hat{s})^{2}}$$
 and $(\tilde{r}_{\chi})_{\chi} \triangleq \frac{\partial \tilde{r}_{\chi}}{\partial s}\Big|_{\xi=\hat{\xi}} = \frac{\mu_{max}x^{2}}{(k_{S}\hat{x}+\hat{s})^{2}}$

Remark 2. According with the gain $\gamma_2(\hat{x}, \hat{s})$, note that the estimated value \hat{s} must be allowed to be zero in order to avoid division by zero in $\gamma_2(\hat{x}, \hat{s})$.