

A BIOLOGICAL TREATMENT OF INDUSTRIAL WASTEWATERS: CONTOIS KINETICS

RUBAYYI T. ALQAHTANI^{✉1}, MARK I. NELSON² and ANNETTE L. WORTHY²

(Received 21 October, 2014; revised 22 January, 2015; first published online 30 April 2015)

Abstract

This paper analyses the steady-state operation of a generalized bioreactor model that encompasses a continuous-flow bioreactor and an idealized continuous-flow membrane bioreactor as limiting cases. A biodegradation of organic materials is modelled using Contois growth kinetics. The bioreactor performance is analysed by finding the steady-state solutions of the model and determining their stability as a function of the dimensionless residence time. We show that an effective recycle parameter improves the performance of the bioreactor at moderate values of the dimensionless residence time. However, at sufficiently large values of the dimensionless residence time, the performance of the bioreactor is independent of the recycle ratio.

2010 *Mathematics subject classification*: primary 65P40; secondary 92B05.

Keywords and phrases: bioreactor, chemostat, Contois growth kinetics, stirred tank, water treatment.

1. Introduction

A byproduct of many industrial processes is wastewater that is heavily contaminated by biodegradable organic matter whose concentration must be greatly reduced prior to its discharge into the water supply. A common method of achieving this is to pass the wastewater through a bioreactor containing micro-organisms (biomass) that use the biodegradable organic matter as a food (substrate) source. This results in additional micro-organisms and a variety of products, which may include biological compounds, carbon dioxide, methane and water. The presence of these products is unimportant for the purposes of the present study and, therefore, they are ignored.

After passing through a bioreactor, the effluent stream may enter a settling unit. Some of the micro-organisms in it settle to the bottom of this unit from which they are recycled back into the bioreactor. The settling unit increases the concentration of the

¹Department of Mathematics, Faculty of Science, Al-Imam Muhammad Ibn Saud Islamic University, Riyadh, Kingdom of Saudi Arabia; e-mail: rtaa648@uowmail.edu.au, rtaqahtani@imamu.edu.sa.

²School of Mathematics and Applied Statistics, University of Wollongong, NSW 2522, Australia; e-mail: mnelson@uow.edu.au, annette.worthy@uow.edu.au.

© Australian Mathematical Society 2015, Serial-fee code 1446-1811/2015 \$16.00

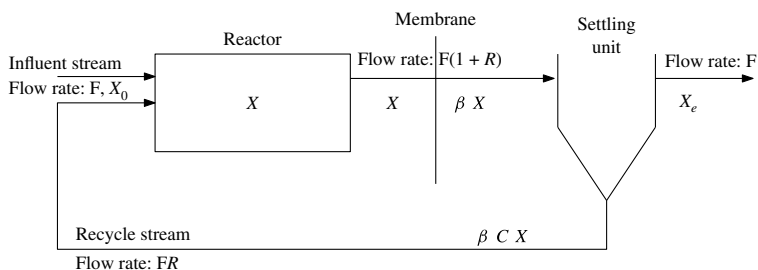


FIGURE 1. Schematic diagram for a bioreactor with recycle.

micro-organisms inside the bioreactor, thereby increasing the efficiency of the process. This reactor configuration is illustrated schematically in Figure 1. An alternative to the settling unit is a permeable membrane, such as a micro-filtration membrane which physically retains micro-organisms inside the bioreactor. In this article, a membrane is thought of as a *filter* through which the effluent stream must pass.

In our model, the bioreactor configuration employed is determined by the value assigned to the reactor parameter β with $0 \leq \beta \leq 1$, which appears in equation (2.2). The extremity, $\beta = 0$, corresponds to an idealized membrane bioreactor, where all the micro-organisms in the fluid stream are retained in the bioreactor. The extremity, $\beta = 1$, represents a continuously stirred bioreactor, where no micro-organism in the fluid stream is retained in the bioreactor. A variety of additional bioreactor configurations are modelled by allowing the reactor parameter to vary between these values [15]. Intermediate values of the parameter β can be viewed as a fraction of the micro-organisms in the fluid stream leaving the bioreactor that are retained in the reactor.

A specific growth rate of the micro-organisms is modelled using Contois kinetics [4]. As outlined in Section 1.1, this gives a better fit to data for some wastewater than alternative expressions. The biological treatment of wastewater using Contois kinetics was investigated previously by Nelson et al. [16]. The difference between their model and ours is in the placement of the membrane. We assume that the membrane is located *after* the bioreactor but before the settling unit, whereas in their study [16] the membrane is placed *after* the settling unit, which is a much less common configuration. For the extreme cases, $\beta = 0$ or $\beta = 1$, the models are identical. However, they differ in the intermediate values.

The objective of this paper is to investigate the performance of the generalized reactor configuration shown in Figure 1 for all possible values of the reactor configuration parameter β . In doing so, we establish some new results for the limiting cases $\beta = 0$ and $\beta = 1$.

1.1. Contois growth kinetics The Contois growth rate expression given by equation (2.3) has been shown to be applicable to the degradation of a range of industrial wastewaters. Table 1 shows some applications in which the Contois model provides a good fit for the experimental data. The second column lists, where applicable, other specific growth rate expressions that have been examined.

TABLE 1. A summary of experimental work on industrial wastewaters where the specific growth was found to be accurately described by Contois kinetics. CH: Chen and Hashimoto model [1].

Substrate/Source of wastewater	Other models used	Reference
Agroindustrial residues	19 kinetic models	Mazutti et al. [14]
Caffeic acid	Monod	Pinna et al. [19]
Hydrolysis of particulate kitchen garbage	First order, Monod	Hidaka et al. [10]
Ice-cream	Monod	Hu et al. [11]
Mining water, sulfate	First order	Hemsi et al. [9]
Municipal solid waste		Gawande et al. [7]
Paper sludge	Monod	Zhang et al. [23]
Palm oil mill	Monod, CH	Abdurahman et al. [1]
Palm oil mill	Monod, CH	Abdurahman et al. [2]
Palm oil mill	CH	Poh and Chong [20]
<i>Penicillium brevicompactum</i>	Verhulst, Exponential	Ardestani [3]
Pharmaceutical	Monod, Tessier	Sun et al. [22]
Synthesized dairy	Monod, Moser, CH	Emerald et al. [6]
Synthetic domestic wastewater		Guerrero et al. [8]
Textile	Monod	Isik and Sponza [12]
Waste-activated sludge	First order, Monod, Hill	Ramirez et al. [21]

2. Model equations and assumptions

2.1. Model assumptions In the process model, we make the standard assumptions that the substrate is not concentrated in the settling unit, and the substrate utilization occurs neither in the settling tank nor in the return line but only in the bioreactor.

2.2. The dimensional model The model equations are

$$V \frac{dS}{dt} = F(S_0 - S) - VX \frac{\mu(S, X)}{\alpha}, \quad (2.1)$$

$$V \frac{dX}{dt} = F(X_0 - \beta X) + RF\beta(C - 1)X + VX\mu(S, X) - K_d VX. \quad (2.2)$$

The parameters in the model are: C , the recycle concentration factor (–); F , the flow rate through the bioreactor (1 day^{-1}); K_d , the death coefficient (day^{-1}); K_x , the saturation constant ($|X||S|^{-1}$); R , the recycle ratio based on volumetric flow rates (–); S , the substrate concentration within the reactor ($|S|$); S_0 , the concentration of substrate in the feed ($|S|$); V , the bioreactor volume (l); X , the concentration of micro-organisms within the bioreactor ($|X|$); X_0 , the concentration of micro-organisms in the feed ($|X|$); t , time (day); α , the yield factor ($|X||S|^{-1}$); β , the reactor parameter ($0 \leq \beta \leq 1$, –); $\mu(S, X)$, the specific growth rate (day^{-1}); μ_m , the maximum specific growth rate (day^{-1}) and τ , the residence time (day).

The first term on the right-hand side of equation (2.1) represents the change in the substrate concentration due to the wastewater flowing through the reactor, whereas the second term models the decrease in the substrate concentration due to consumption of the substrate by micro-organisms.

The first term on the right-hand side of equation (2.2) represents the change in the micro-organism concentration due to the flow of wastewater through the reactor. As explained in Section 1, the value of the parameter β indicates the particular reactor configuration used. The second term models the use of a settling unit. A settling unit is characterized by a concentration factor C and a recycle ratio R . The third term models the increase in the micro-organism concentration due to consumption of the substrate. The final term represents removal of the micro-organisms due to a combination of first-order processes that include endogenous respiration, predation, cell death and cell breakdown [18].

The specific growth rate given by Contois kinetics is

$$\mu(S, X) = \mu_m \left(\frac{S}{K_x X + S} \right), \quad (2.3)$$

and the residence time is defined by $\tau = V/F$. In the following, the quantities $|S|$ and $|X|$ denote concentrations of the substrate S and micro-organisms X , respectively.

For a specific wastewater, a given biological community and a particular set of environmental conditions, the parameters K_x , K_d , α and μ_m are fixed. The parameters that can be varied are C , R , S_0 , X_0 and τ . The parameters C and R are associated with the operation of the settling unit, the parameters S_0 and X_0 characterize the feed and the parameter τ characterizes the operation of the bioreactor.

For our numerical simulations, we use parameter values for the anaerobic digestion of ice-cream wastewater [11]. These are: $\alpha = 0.2116$ (g VSS)(g COD)⁻¹, $\mu_m = 0.9297$ (day⁻¹), $K_d = 0.0131$ (day⁻¹) and $K_s = 0.4818$ (g COD)(g VSS)⁻¹.

2.3. Settling unit model The settling unit is modelled by the values of the concentration factor C and the recycle ratio R . The concentration factor is defined as the ratio of the concentration of micro-organisms leaving the settling unit to the concentration of micro-organisms entering it. As shown in Figure 1, there is a flow rate F associated with the influent stream. There is a corresponding flow rate F that is discharged *downstream* of the activated sludge process. As also shown in Figure 1, there is a flow rate associated with the operation of the settling unit, which is denoted by F_R . By convention, this flow rate is written in the form

$$F_R = RF,$$

where the recycle ratio R is defined by $R = F_R/F$.

The middle term on the right-hand side of equation (2.2) indicates how the rate of change of the micro-organism concentration inside the bioreactor depends on the operation of the settling unit.

The value of C depends on the design and operation of the settling unit and sludge properties such as settling, thickening and compressibility behaviour. The

concentration of micro-organisms recycled from the settling unit back into the reactor is given by the term CX in equation (2.2).

By taking a mass balance over the settling unit, it can be shown that the maximum value of the *concentrating factor* is

$$C_{\max} = 1 + \frac{1}{R}. \quad (2.4)$$

Note that the settling unit does not concentrate the (soluble) substrate. Thus, the value of the concentrating factor for the substrate is 1. Consequently, equation (2.1) is independent of the operation of the settling unit.

2.4. The dimensionless model Equations (2.1) and (2.2) are written in dimensionless form by introducing dimensionless variables for the substrate concentration $S^* = S/S_0$, the micro-organism concentration $X^* = K_X X/S_0$ and the time $t^* = \mu_m t$. The dimensionless equations are

$$\frac{dS^*}{dt^*} = \frac{1}{\tau^*}(1 - S^*) - \frac{S^* X^*}{\alpha^*(S^* + X^*)}, \quad (2.5)$$

$$\frac{dX^*}{dt^*} = \frac{X_0^*}{\tau^*} + \frac{S^* X^*}{(S^* + X^*)} + \frac{\beta(R^* - 1)}{\tau^*} X^* - K_d^* X^*. \quad (2.6)$$

In these equations, the effective recycle parameter $R^* = (C - 1)R$, the dimensionless death rate $K_d^* = K_d/\mu_m$, the dimensionless micro-organism concentration in the feed $X_0^* = X_0/(\alpha^* K_S)$, the dimensionless yield coefficient $\alpha^* = K_S \alpha$ and the dimensionless residence time $\tau^* = V\mu_m/F$.

The effective recycle parameter R^* indicates the *efficiency* of the settling unit at retaining micro-organisms within the bioreactor. When $R^* = 0$, none of the micro-organisms in the feed stream leaving the bioreactor are returned to the reactor. It follows from equation (2.4) that the maximum value of the effective recycle parameter is given by $R_{\max}^* = 1$. When $R^* = 1$, all of the micro-organisms in the feed stream leaving the bioreactor are returned to it. From equation (2.6), it follows that a flow reactor with idealized recycle ($R^* = \beta = 1$) is identical to an idealized membrane reactor ($\beta = 0$). (In both cases, the effluent stream contains no micro-organisms.)

Using the parameter values given in Section 2.2, we have $\alpha^* = 0.1019$ and $K_d^* = 0.0141$. Henceforth, we use a standard assumption that the concentration of micro-organisms flowing into the reactor is zero (that is, $X_0 = X_0^* = 0$). All other parameters in the model are strictly positive.

Since all the terms in equations (2.5) and (2.6) are dimensionless, we typically refer from now on, for example, to the residence time rather than the dimensionless residence time.

In Section 3, we need the Jacobian matrix

$$J(S^*, X^*) = \begin{pmatrix} -\frac{1}{\tau^*} - \frac{X^{*2}}{\alpha^*(X^* + S^*)^2} & -\frac{S^{*2}}{\alpha^*(X^* + S^*)^2} \\ \frac{X^{*2}}{(X^* + S^*)^2} & \frac{-(1 - R^*)\beta - K_d^* \tau^*}{\tau^*} + \frac{S^{*2}}{(X^* + S^*)^2} \end{pmatrix} \quad (2.7)$$

of systems (2.5) and (2.6).

3. Results

In Section 3.1, we establish some global properties of the systems (2.5) and (2.6). In particular, we show that if $K_d^* \geq 1$, then $\lim_{t^* \rightarrow \infty} X^* = 0$. Physically, this means that no micro-organism is present in the reactor and process failure has occurred. Hence, subsequent to this section, we assume that $0 < K_d^* < 1$.

In Section 3.2, we show that there are two steady-state solution branches corresponding to a washout branch and a no-washout branch. Along the former the steady-state micro-organism concentration is zero, and along the latter the steady-state micro-organism concentration is nonzero, except at one point. The point at which these two branches intersect and exchange stability is the *washout point*. We further state the conditions for the latter branch to be physically meaningful. The local stability of the steady-state solutions is determined in Section 3.3. The results obtained in Section 3.1 imply that when a steady-state solution is locally stable, it is, in fact, globally stable.

In Section 3.4, asymptotic solutions are presented for residence times a little higher than the washout point (that is, $\tau^* - \tau_{cr}^* \ll 1$) and for large residence times ($\tau^* \gg 1$). In Section 3.5, we find the value of the residence time at which the biomass concentration is maximized. In Section 3.6, we draw upon the findings of the earlier sections to discuss steady-state diagrams for the effluent and micro-organism concentrations.

3.1. Global behaviour In this section, we establish some global results regarding the systems (2.5) and (2.6), which are new for the limiting cases $\beta = 0$ and $\beta = 1$.

In Appendix A, the region \mathcal{R} defined by

$$\begin{aligned} \frac{\alpha^*}{\alpha^* + \tau^*} &\leq S^* \leq 1, \\ 0 &\leq X^* \leq \frac{\alpha^*}{\mathcal{M}} - \alpha^* S^*, \\ \mathcal{M} &= \min[1, \beta(1 - R^*) + K_d^* \tau^*] \end{aligned}$$

is shown to be positively invariant. This means that if an initial condition is either inside or on the boundary of the region \mathcal{R} , then the corresponding solution of the system cannot leave this region for all values of time with $t^* \geq 0$. Furthermore, we show that the invariant region is exponentially attracting for physically meaningful solutions starting outside the invariant region. Thus, from now on we are free to consider only initial conditions within the invariant region. Note that the invariant region \mathcal{R} is the phase plane of the two concentrations S and X .

In Appendix B, we show that the systems (2.5) and (2.6) cannot have limit cycle solutions. In Appendix C, we establish conditions that ensure that process failure occurs, that is, the biomass dies out or, more formally, $\lim_{t^* \rightarrow \infty} X^*(t^*) = 0$. These conditions are as follows.

- (1) If $K_d^* \geq 1$, then process failure occurs for all values of the residence time (τ^*).
- (2) If $K_d^* < 1$, then process failure occurs when

$$\tau^* \leq \tau_{cr}^* = \frac{1 - R^*}{1 - K_d^*} \beta. \quad (3.1)$$

Later, we show that the critical value of the residence time τ_{cr}^* corresponds to a transcritical bifurcation. Equation (3.1) shows that process failure cannot occur if there is perfect recycle, that is, $R^* = 1$.

3.2. Steady state solution branches In this section, we find the steady-state solutions of the systems (2.5) and (2.6) and characterize when they are physically meaningful. The steady-state solutions are given by:

- (1) washout branch, $(S^*, X^*) = (1, 0)$;
- (2) no-washout branch,

$$(S^*, X^*) = \frac{\alpha^*}{a} \left(1, \frac{(1 - K_d^*)\tau^* - (1 - R^*)\beta}{(1 - R^*)\beta + K_d^*\tau^*} \right), \quad (3.2)$$

where $a = (1 - K_d^*)\tau^* - (1 - R^*)\beta + \alpha^*$.

The no-washout branch (3.2) is physically meaningful only when the substrate and micro-organism concentrations are positive, that is, when $S^* > 0$ and $X^* > 0$. Upon analysing both components of (3.2), we find that this happens when

$$\tau^* > \tau_{cr}^* = \frac{1 - R^*}{1 - K_d^*}\beta. \quad (3.3)$$

Differentiating equation (3.2) with respect to R^* ,

$$\frac{dS^*}{dR^*} = -\frac{\alpha^*\beta}{[-\alpha^* + (1 - R^*)\beta - (1 - K_d^*)\tau^*]^2} < 0. \quad (3.4)$$

The denominator in equation (3.4) is zero when

$$\tau^* = \frac{1 - R^*}{1 - K_d^*}\beta - \frac{\alpha^*}{1 - K_d^*} < \frac{1 - R^*}{(1 - K_d^*)}\beta = \tau_{cr}^*.$$

From inequality (3.3), we deduce that the no-washout solution is not physically meaningful when the denominator is equal to zero. Hence, for physically meaningful solutions the substrate concentration is a decreasing function of the effective recycle parameter R^* . Consequently, at a fixed residence time, the lowest effluent concentration is achieved when the effective recycle parameter takes its maximum value, that is, $R^* = 1$.

Differentiating equation (3.2) with respect to τ^* ,

$$\frac{dS^*}{d\tau^*} = -\frac{(1 - K_d^*)\alpha^*}{[-\alpha^* + (1 - R^*)\beta - (1 - K_d^*)\tau^*]^2} < 0 \quad \text{for } 0 < K_d^* < 1.$$

Hence, the substrate concentration is a decreasing function of the residence time along the no-washout branch.

At the washout point, $\tau^* = \tau_{cr}^*$, given by equation (3.3), the washout and no-washout solution branches intersect at a transcritical bifurcation. The washout value, $\tau^* = \tau_{cr}^*$, represents the maximum residence time at which the treatment process fails. At lower

residence times micro-organisms are removed from the reactor at a rate greater than their maximum growth rate, resulting in process failure. In Section 3.3, we show that at residence times lower (respectively, higher) than the critical value that the washout (respectively, no-washout) solution is the only stable steady-state solution.

The critical value of the residence time is zero when either $R^* = 1$ or $\beta = 0$. Increasing the effective recycle parameter R^* or decreasing the reactor parameter β allows the reactor to operate at lower residence times.

3.3. Stability of the steady-state solutions In Section 3.3.1, the local stability of the washout solution branch is determined. In Section 3.3.2, the no-washout solution is shown to be locally stable whenever it is physically meaningful. The results of Section 3.1 establish that when either steady-state solution is locally stable, it is, in fact, globally stable.

3.3.1. Stability of the washout solution. The Jacobian matrix (2.7) evaluated at the washout steady-state solution is given by

$$J(1, 0) = \begin{pmatrix} -\frac{1}{\tau^*} & -\frac{1}{\alpha^*} \\ 0 & \frac{-(1 - R^*)\beta - K_d^* \tau^*}{\tau^*} + 1 \end{pmatrix},$$

which has the eigenvalues

$$\lambda_1 = \frac{1}{\tau^*} < 0 \quad \text{and} \\ \lambda_2 = \frac{-(1 - R^*)\beta - K_d^*}{\tau^*} \tau^* + 1.$$

Hence, the washout branch is stable when $\lambda_2 < 0$, which occurs when

$$(1 - K_d^*)\tau^* < (1 - R^*)\beta.$$

Note that if:

- $K_d^* > 1$, then $\lambda_2 < 0$ for all τ^* ;
- $K_d^* = 1$, then $\lambda_2 < 0$ provided that neither $R^* = 1$ nor $\beta = 0$;
- $0 < K_d^* < 1$, then $\lambda_2 < 0$ for $\tau^* < \tau_{cr}^* = \beta(1 - R^*)/(1 - K_d^*)$;
- $K_d^* = 1$ and either $R^* = 1$ or $\beta = 0$, then $\lambda_2 = 0$;
- $0 < K_d^* < 1$ and $\tau^* = \tau_{cr}^* = \beta(1 - R^*)/(1 - K_d^*)$, then $\lambda_2 = 0$.

It follows from the results stated in Section 3.1 that in *all five* of these cases the washout solution is globally stable.

3.3.2. Stability of the no-washout solution. The Jacobian matrix (2.7) along the no-washout branch can be written as

$$J(S^*, X^*) = \begin{pmatrix} -\frac{1}{\tau^*} - \frac{X^{*2}}{\alpha^*(X^* + S^*)^2} & \frac{-S^{*2}}{\alpha^*(X^* + S^*)^2} \\ \frac{X^{*2}}{(X^* + S^*)^2} & \frac{-X^*S^*}{(X^* + S^*)^2} \end{pmatrix}.$$

This solution branch is stable if $\det(J) > 0$ and $\text{trace}(J) < 0$. Since

$$\det(J) = \frac{X^*S^*}{(X^* + S^*)^2} \times \left[\frac{1}{\tau^*} + \frac{X^{*2}}{\alpha^*(X^* + S^*)^2} \right] + \frac{X^{*2}}{(X^* + S^*)^2} \times \frac{S_2^{*2}}{\alpha^*(X_2^* + S_2^*)^2},$$

$$\text{trace}(J) = - \left[\frac{X^*S^*}{(X^* + S^*)^2} + \frac{1}{\tau^*} + \frac{X^{*2}}{\alpha^*(X^* + S^*)^2} \right],$$

it follows that $\det(J) > 0$ and $\text{trace}(J) < 0$ whenever $S^* > 0$ and $X^* > 0$. Thus, the no-washout branch is stable whenever it is physically meaningful.

From Section 3.1, we know that all solutions with physically meaningful initial conditions are attracted into a closed and bounded (positively) invariant set. Furthermore, there are no periodic solutions within this set. From Sections 3.2 and 3.3, for any value of the residence time there is only one stable steady-state solution. It follows from the Poincaré–Bendixon theorem [13, page 294] that this steady-state solution must be globally asymptotically stable. This observation is new for the limiting cases $\beta = 0$ and $\beta = 1$.

Note that when the washout solution is stable, the no-washout solution is not located within the invariant region, since it is not physically meaningful. When the no-washout solution is stable, the unstable washout solution has a one-dimensional stable manifold. This manifold is the line $X^* = 0$. Any initial condition not on this manifold is attracted to the no-washout steady-state solution.

3.4. Asymptotic solutions In Section 3.4.1, asymptotic solutions are presented for residence times just higher than the washout point ($\tau^* - \tau_{cr}^* \ll 1$), whilst in Section 3.4.2 they are presented for large residence times ($\tau^* \gg 1$).

3.4.1. Residence time approximations near the washout point ($\tau^ - \tau_{cr}^* \ll 1$).* When the residence time is slightly higher than the critical value, and provided that $\beta \neq 0$, we have the following approximations to the stable steady-state solution $\beta \neq 0$:

$$S^* = 1 - \frac{(1 - K_d^*)}{\alpha^*} \epsilon + O(\epsilon^2), \quad 0 < K_d^* < 1,$$

$$X^* = \frac{(1 - K_d^*)^2}{(1 - R^*)\beta} \epsilon + O(\epsilon^2), \quad 0 < K_d^* < 1,$$

where

$$\epsilon = \tau^* - \frac{1 - R^*}{1 - K_d^*} \beta \ll 1.$$

When $\beta = 0$, corresponding to $\tau_{cr}^* = 0$, the expression for the substrate concentration remains the same, but the expression for the micro-organism concentration becomes

$$X^* \approx \frac{1 - K_d^*}{K_d^*} - \frac{(1 - K_d^*)^2}{\alpha^* K_d^*} \epsilon + O(\epsilon^2).$$

3.4.2. *Large residence times* ($\tau^* \gg 1$). At large residence times, we have the following approximations to the stable steady-state solution:

$$S^* \approx \frac{\alpha^*}{1 - K_d^*} \cdot \frac{1}{\tau^*} + O\left(\frac{1}{\tau^{*2}}\right), \quad 0 < K_d^* < 1, \quad (3.5)$$

$$X^* \approx \frac{\alpha^*}{K_d^*} \cdot \frac{1}{\tau^*} + O\left(\frac{1}{\tau^{*2}}\right), \quad 0 < K_d^* < 1. \quad (3.6)$$

Equation (3.5) shows that the substrate concentration decreases to zero in the limit of infinite residence time. Thus, the effluent concentration can be decreased to any desired level by operating the reactor at a sufficiently large residence time. This is not the case for processes controlled by Monod kinetics, where the substrate concentration has a limiting value $K_d^*/(1 + K_d^*)$ [17], or Tessier kinetics, where the limiting value is $\ln [1/(1 - K_d^*)]$ [15]. Equation (3.6) shows that large values of biomass concentration decrease to zero in the limit of infinite residence time.

These equations show that both the substrate concentration S^* and the biomass concentration are to leading order independent of both the effective recycle parameter R^* and the reactor parameter β .

3.5. Maximizing the micro-organism concentration The emphasis of this paper is on the biological treatment of wastewaters. Consequently, our primary focus is on minimizing the value of the substrate concentration leaving the reactor. In some bioreactor processes it is important to maximize the micro-organism concentration, for instance when the bioreactor is being used to grow the micro-organism. The micro-organism concentration is zero, that is, $X^* = 0$, along the washout solution and in the limit when the residence time increases to infinity. Thus, when the residence time is greater than zero, there is a maximum value for the micro-organism concentration.

Differentiating the steady-state expression for the micro-organism concentration from equation (3.2) with respect to the residence time, we find that the maximum value occurs when

$$\tau^* = \tau_{\max}^* = \frac{(1 - R^*)}{1 - K_d^*} \beta + \frac{\sqrt{K_d^* \alpha^* \beta (1 - R^*)}}{K_d^* (1 - K_d^*)}.$$

3.6. Steady-state diagrams The physically meaningful solutions for the variation of the substrate concentration S^* and the micro-organism concentration X^* as a function of the residence time τ^* are shown in Figures 2–4. The steady-state solutions are only physically meaningful for $0 < S^* < 1$ and $X^* > 0$; as in Section 3.2, this requires that $\tau^* > \tau_{\text{cr}}^*$.

Figure 2 shows the steady-state diagrams for the case of a flow reactor ($\beta = 1$) without a settling unit ($R^* = 0$). Observe that when the residence time is lower than the critical value ($\tau^* < \tau_{\text{cr}}^*$), the stable solution is the washout solution (given by the solid lines $S^* = 1$ and $X^* = 0$); the no-washout solution is not physically meaningful for these values of the residence time and is, therefore, not shown. When the residence time is larger than the critical value ($\tau^* > \tau_{\text{cr}}^*$), the no-washout solution is stable

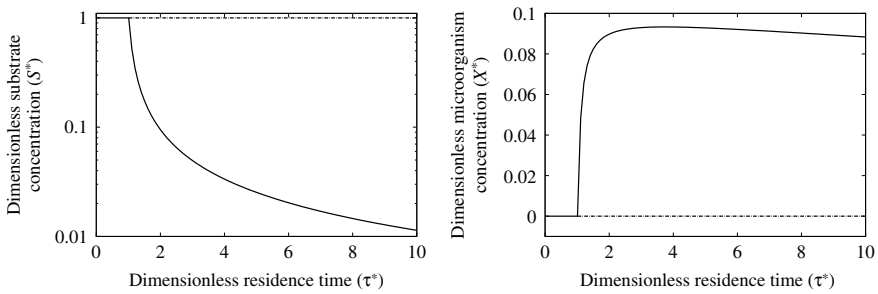


FIGURE 2. Steady-state diagrams showing the variation of the dimensionless substrate and microorganism concentrations with dimensionless residence time. Parameter values: dimensionless decay rate $K_d^* = 0.014091$, dimensionless yield coefficient $\alpha^* = 0.10194$ and $(1 - R^*)\beta = 1$.

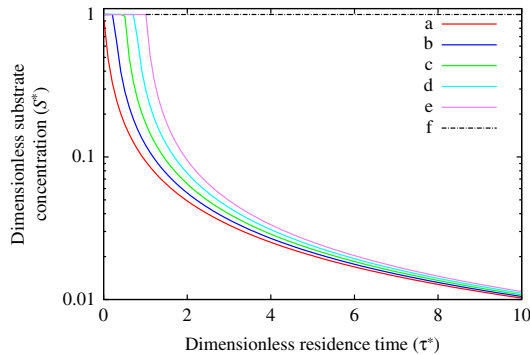


FIGURE 3. Steady-state diagram showing the variation of the dimensionless substrate concentration with dimensionless residence time. Parameter values: $(1 - R^*)\beta = 0$ (a), 0.25 (b), 0.5 (c), 0.75 (d), 1 (e). Other parameter values as in Figure 2. Line (f) shows the washout solution. (Colour available online.)

(as indicated by a solid curve) whilst the washout solution is unstable (indicated by a dotted line). As noted in Section 3.5, there is a value of the residence time at which the biomass concentration is maximized.

Figures 3 and 4 show how the steady-state diagrams for the substrate and microorganism concentrations change as the reactor configuration is changed through reduction of the value of the parameter group $(1 - R^*)\beta$. In these figures, observe that as the value of this parameter decreases, the critical value of the residence time τ_{cr}^* also decreases.

In the following section, we assume that the residence time is sufficiently high (that is, $\tau^* \gg \tau_{cr}^*$) so that the no-washout solution branch is a stable solution.

Figure 3 shows that for a fixed residence time τ^* , the effluent concentration decreases as the value of the reactor parameter $(1 - R^*)\beta$ decreases (from curves (a)–(e)). It also shows that if the value of this group is fixed, then the effluent concentration decreases as the residence time increases. Figure 4 shows that for a

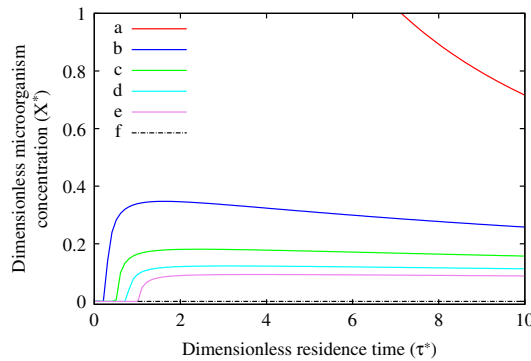


FIGURE 4. Steady-state diagram showing the variation of the dimensionless micro-organism concentration with dimensionless residence time. Parameter values: $(1 - R^*)\beta^* = 0$ (a), 0.25 (b), 0.5 (c), 0.75 (d), 1 (e). Other parameter values as in Figure 2. Line (f) shows the washout solution. (Colour available online.)

fixed residence time the micro-organism concentration X^* decreases as the value of the group $(1 - R^*)\beta$ increases (as illustrated in curves (a)–(e)).

4. Discussion

The steady-state performance of a bioreactor processing industrial wastewaters may be characterized by its treatment efficiency along the no-washout branch, that is, when $\tau^* > \tau_{cr}^*$. The *treatment efficiency*

$$\begin{aligned}
 E &= 100 \left(\frac{S_0 - S}{S_0} \right) \\
 &= 100(1 - S^*)
 \end{aligned}
 \tag{4.1}$$

is the percentage of substrate that has been removed by the reactor. From equation (4.1), it is clear that along the no-washout branch where $0 < S^* < 1$, the efficiency is positive ($E > 0$). Substituting for the substrate concentration from equation (3.2), we obtain the efficiency along the no-washout branch as

$$\begin{aligned}
 E &= 100 \left(1 - \frac{\alpha^*}{\beta(R^* - 1) + \tau^*(1 - K_d^*) + \alpha^*} \right) \\
 &= 100 \left(1 - \frac{\alpha_0^*}{\alpha_0^* + (\tau^* - \tau_{cr}^*)} \right),
 \end{aligned}
 \tag{4.2}$$

where $\alpha_0^* = \alpha^*/(1 - K_d^*)$. The efficiency increases when either the residence time becomes large ($\tau^* \gg 1$) or the critical value of the residence time τ_{cr}^* becomes small. The latter is when the group $(1 - R^*)\beta$ is small.

The efficiency equation (4.2) is shown as a function of the residence time τ^* in Figure 5. This figure shows that at fixed values for the residence time, the efficiency of the reactor increases as the value of the parameter group $(1 - R^*)\beta$ decreases. It also

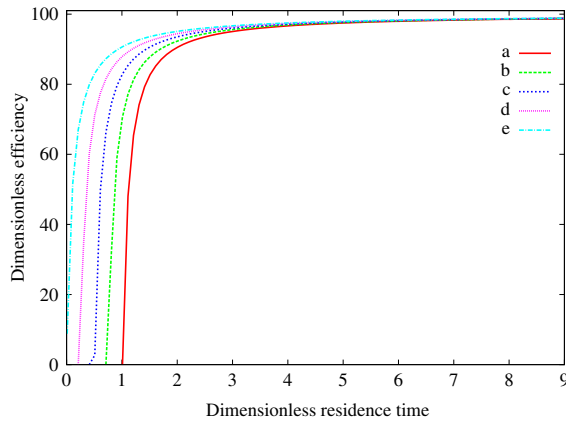


FIGURE 5. The efficiency (E) as a function of the dimensionless residence time. Parameter values: $(1 - R^*)\beta = 0$ (e), 0.25 (d), 0.5 (c), 0.75 (b), 1 (a). Other parameter values as in Figure 2. (Colour available online.)

demonstrates that for a fixed value of the parameter group $(1 - R^*)\beta$, the efficiency increases as the residence time increases.

For values of the residence time slightly larger than the critical value ($\tau^* - \tau_{cr}^* \ll 1$), the efficiency becomes

$$E = 100 \frac{1 - K_d^*}{\alpha} (\tau^* - \tau_{cr}^*) + O(\tau^* - \tau_{cr}^*)^2.$$

At large residence times, the efficiency is

$$E \approx 100 \left(1 - \frac{\alpha^*}{1 - K_d^*} \frac{1}{\tau^*} \right) + O\left(\frac{1}{\tau^{*2}}\right).$$

As the residence time approaches infinity, the efficiency of the process approaches 100% and is independent of the influent pollutant concentration. In contrast with processes controlled by Monod or Tessier kinetics, the maximum efficiency is bounded below 100% and depends upon the influent pollutant concentration S_0 [15, 17]. Finally, at high values of the residence time the process efficiency is independent of both the reactor parameter β and the effective recycle parameter R^* .

Table 2 shows the residence time required to achieve efficiencies of 99%, 99.9% and 99.99% as a function of the parameter group $(1 - R^*)\beta$. The residence time required to achieve a given efficiency increases as the value of this group increases. However, the percentage increase in going from the minimum value 0 to the maximum value 1 is very weak. Furthermore, as the efficiency increases the percentage increase decreases.

5. Conclusion

We have investigated a bioreactor model for the interaction between a micro-organism and a rate-controlling substrate in which the specific growth rate is modelled

TABLE 2. The dimensionless residence time required to achieve an efficiency of 99%, 99.9% and 99.99% as a function of the parameter group $(1 - R^*)\beta$.

Efficiency E^*	$(1 - R^*)\beta$					Percentage increase
	0	0.25	0.5	0.75	1	
99%	11.01	11.28	11.55	11.82	12.10	9.90%
99.9%	111.104	111.37	111.64	111.92	112.19	0.977%
99.99%	1112.04	1112.31	1112.58	1112.86	1113.13	0.098%

using Contois kinetics. We have considered a generalized reactor model in which the idealized membrane reactor and well-stirred flow reactor with or without recycle are limiting cases. These limiting cases were considered in an earlier paper [16]. We have established a number of new results for these limiting cases, in addition to considering the full range of reactor configurations among them.

The steady-state solutions and the stability were found as a function of the residence time. A transcritical bifurcation between the washout and no-washout solutions occurs at the critical residence time τ_{cr}^* given by equation (3.1), when these two solutions intersect and exchange stability. The washout solution is the only stable solution when the residence time is lower than the transcritical value and the no-washout solution is the only stable solution when the residence time is higher than the transcritical value. From our global analysis, it follows that a locally stable steady-state solution is in fact globally asymptotically stable. Furthermore, the washout solution is globally asymptotically stable when the residence time is equal to its critical value (that is, $\tau = \tau_{cr}^*$).

We have shown that the substrate concentration decreases when the parameter group $(1 - R^*)\beta$ decreases. At some large values for the residence time, the substrate concentration is independent of both the reactor parameter β and the effective recycle parameter R^* .

One way to characterize the performance of a bioreactor is the treatment efficiency, which increases by the increase in residence time. Significantly, for processes governed by Contois kinetics, the limiting value of the efficiency as the residence time approaches infinity is independent of the influent concentration.

Appendix A. Invariant region

We show that the region \mathcal{R} is both positively invariant and attracting, that is, a solution starting at any physically meaningful initial condition outside the invariant region eventually enters the invariant region.

Appendix A.1. Solution components may not become negative The systems (2.5) and (2.6) are undefined at the origin. We show that if the initial condition is not defined at the origin, then the solution of the system does not enter this point. Suppose that the

system exists near this point, but with nonzero substrate concentration. Then

$$\begin{aligned}\frac{dS^*}{dt^*} &= \frac{1}{\tau^*}(1 - S^*) - \frac{S^*X^*}{\alpha^*(S^* + X^*)} \\ &\geq \frac{1}{\tau^*}(1 - S^*) - \frac{S^*}{\alpha^*} \\ &> 0\end{aligned}$$

for sufficiently small S^* . Thus, the substrate concentration increases away from zero, making it strictly nonnegative.

Using the classical scalar comparison theorem for ordinary differential equations, the above inequality shows that the region $S^* \geq \alpha^*/(\alpha^* + \tau^*)$ is both positive invariant and attracting. Since

$$\left. \frac{dX^*}{dt^*} \right|_{X^*=0} = 0,$$

the plane $X^* = 0$ is invariant.

Appendix A.2. The substrate component is bounded We show that the region $0 \leq S^* \leq 1$ is both positively invariant and exponentially attracting. Since $X^* \geq 0$ and $S^* > 0$,

$$\begin{aligned}\frac{dS^*}{dt^*} &= \frac{1}{\tau^*}(1 - S^*) - \frac{S^*X^*}{\alpha^*(S^* + X^*)} \\ &\leq \frac{1}{\tau^*}(1 - S^*).\end{aligned}$$

Let Z_1 be the solution of the differential equation

$$\frac{dZ_1}{dt^*} = \frac{1}{\tau^*}(1 - Z_1)$$

with initial condition $Z_1(0) = S^*(0)$. It follows from the classical scalar comparison theorem for ordinary differential equations that $S^* \leq Z_1(t^*)$. Hence,

$$S^*(t^*) \leq 1 - [1 - S^*(0)] \exp\left[-\frac{t^*}{\tau^*}\right].$$

Thus, the region $0 \leq S^* \leq 1$ is invariant, because if the initial condition is within the invariant region, that is, $S^*(0) \leq 1$, then the solution remains within the invariant region, that is, $S^* \leq 1$. Furthermore, if the initial condition is outside the invariant region, $S^*(0) > 1$, then the solution must eventually enter the invariant region in the limit $t^* \rightarrow \infty$, that is, $S^*(t^*) \leq 1$.

Appendix A.3. The biomass component is bounded Let $Z_2 = \alpha^*S^* + X^*$ with initial condition $Z_2 = \alpha^*S^*(0) + X^*(0)$. Then, adding equations (2.5) and (2.6),

$$\begin{aligned}\frac{dZ_2}{dt^*} &= \frac{\alpha^*}{\tau^*} - \frac{\alpha^*S^*}{\tau^*} - \frac{[\beta(1 - R^*) + K_d^*\tau^*]X^*}{\tau^*} \\ &\leq \frac{\alpha^*}{\tau^*} - \frac{M(\alpha^*S^* + X^*)}{\tau^*} \\ &= \frac{\alpha^* - MZ^*}{\tau^*},\end{aligned}$$

where $\mathcal{M} = \min[1, \beta(1 - R^*) + K_d^* \tau^*]$. Hence,

$$Z_2(t^*) = \alpha^* S^*(t^*) + X^*(t^*) \leq \frac{\alpha^*}{\mathcal{M}} - \left[\frac{\alpha^*}{\mathcal{M}} - \alpha^* S^*(0) - X^*(0) \right] \exp\left[-\frac{\mathcal{M}t^*}{\tau^*}\right].$$

Combining this result with our earlier bound on the scaled substrate concentration in [Appendix A.2](#), it follows that the region \mathcal{R}^* defined by $0 \leq S^* \leq 1$ and $0 \leq X^* \leq (\alpha^*/\mathcal{M}) - \alpha^* S^*$ is positively invariant and exponentially attracting.

Appendix B. Periodicity

In this section, we establish the nonexistence of limit cycles. To show the nonexistence of a periodic solution, we use Dulac's criteria.

THEOREM B.1 (Dulac's test [5, 13]). *Consider the system*

$$\frac{dx}{dt} = f(x, y), \quad \frac{dy}{dt} = g(x, y).$$

Let \mathcal{D} be a simply connected region in \mathbb{R}^2 and $\{f(x, y), g(x, y)\} \in C^1(\mathcal{D})$. If there exists a function $\rho \in C^1(\mathcal{D})$ such that

$$\frac{\partial(\rho f)}{\partial x} + \frac{\partial(\rho g)}{\partial y}$$

is not identically zero, and does not change sign in \mathcal{D} , then this system does not have any closed paths lying entirely in \mathcal{D} .

We use the test function $\rho = 1/X^*$, which is acceptable. To see this, note that if a periodic solution exists, it cannot include any part of the line $X^* = 0$, because this line is invariant (see [Appendix A.1](#)).

Applying Dulac's test to the systems (2.5) and (2.6) with the specified choice for ρ ,

$$\frac{\partial(\rho f)}{\partial S^*} + \frac{\partial(\rho g)}{\partial X^*} = - \left[\frac{\alpha^*(X^* + S^*)^2 + X^* \tau^* (\alpha^* S^* + X^*)}{X^* \tau^* \alpha^* (X^* + S^*)^2} \right] < 0.$$

This function is strictly negative inside the positive quadrant. Thus, no periodic solution exists which is entirely contained within the positive quadrant. Since the positive quadrant is positively invariant, there is no periodic solution only partly contained within it.

Appendix C. Global stability of the washout solution

Here we establish conditions that ensure process failure, that is, when the biomass dies out. From equation (2.6),

$$\begin{aligned} \frac{dX^*}{dt^*} &= \frac{S^* X^*}{(S^* + X^*)} + \frac{\beta(R^* - 1)}{\tau^*} X^* - K_d^* X^* \\ &\leq \left[1 - \frac{\beta(1 - R^*)}{\tau^*} - K_d^* \right] X^*, \end{aligned}$$

since $S^*/(S^* + X^*) \leq 1$. (The possibility that $S^*(t^*) + X^*(0) = 0$ is eliminated by the observation that at sufficiently large values of time, $S^*(t^*) \geq \alpha^*/(\alpha^* + \tau^*)$; see [Appendix A.1](#).) Let

$$\frac{\beta(1 - R^*)}{\tau^*} + K_d^* = 1 + \epsilon, \quad \text{where } \epsilon > 0.$$

Then $dX^*/dt^* \leq -\epsilon X^*$, which shows that $\lim_{t^* \rightarrow \infty} X^*(t^*) = 0$. The condition

$$\frac{\beta(1 - R^*)}{\tau^*} + K_d^* = 1 + \epsilon > 1$$

yields the following three cases.

- (1) If either $\beta = 0$, corresponding to an idealized membrane bioreactor, or $R^* = 1$, corresponding to idealized recycle, then the washout solution is globally stable when $K_d^* > 1$.
- (2) If neither $\beta = 0$ nor $R^* = 1$, then the washout solution is globally stable when $K_d^* \geq 1$.
- (3) If $K_d^* < 1$, then the washout solution is globally stable when $\tau^* < \tau_{cr}^* = (1 - R^*)/(1 - K_d^*)\beta$.

In cases 1 and 3, the inequality can be reduced to an equality by observing that on the line $S^* = 1$,

$$\begin{aligned} \frac{dS^*}{dt^*} &= \frac{1 - S^*}{\tau^*} - \frac{1}{\alpha^*} \frac{S^* X^*}{(S^* + X^*)} \\ &= -\frac{1}{\alpha^*} \frac{X^*}{(1 + X^*)} \\ &< 0 \end{aligned}$$

except when $X^* = 0$. Since the point $(S^*, X^*) = (1, 0)$ is a steady-state solution, we deduce that a solution curve that touches the line $S^* = 1$ cannot return to it except at the steady-state solution.

Acknowledgements

We thank the referees for their detailed and constructive comments on our original submission.

References

- [1] N. H. Abdurahman, Y. M. Rosli and N. H. Azhari, "Development of a membrane anaerobic system (MAS) for palm oil mill effluent (POME) treatment", *Desalination* **266** (2011) 208–212; doi:10.1016/j.desal.2010.08.028.
- [2] N. H. Abdurahman, Y. M. Rosli, N. H. Azhari and S. F. Tam, "Biomethanation of palm oil mill effluent (POME) by membrane anaerobic system (MAS) using POME as a substrate", *World Acad. Sci. Eng. Technol.* **5** (2011) 276–281; <http://waset.org/publications/2297/biomethanation-of-palm-oil-mill-effluent-pome-by-membrane-anaerobic-system-mas-using-pome-as-a-substrate>.

- [3] F. Ardestani, "Survey of the nutrient utilization and cell growth kinetic with Verhulst, Contois and exponential models for *Penicillium brevicompactum* ATCC 16024 in batch bioreactor", *World Appl. Sci. J.* **16** (2012) 135–140; <http://citeseerx.ist.psu.edu/viewdoc/download?doi=10.1.1.390.1023&rep=rep1&type=pdf>.
- [4] D. E. Contois, "Kinetics of bacterial growth: relationship between population density and specific growth rate of continuous cultures", *J. Gen. Microbiol.* **21** (1959) 40–50; doi:10.1099/00221287-21-1-40.
- [5] H. Dulac, *Points singulieres des equations differentielles*, Fascicule 61 of *Mém. Sci. Math.* (Gauthier-Villars, Paris, 1934).
- [6] F. M. E. Emerald, D. S. A. Prasad, M. R. Ravindra and H. A. Pushpadass, "Performance and biomass kinetics of activated sludge system treating dairy wastewater", *Int. J. Dairy Technol.* **24** (2012) 609–615; doi:10.1111/j.1471-0307.2012.00850.x.
- [7] N. A. Gawande, D. R. Reinhart and G.-T. Yeh, "Modeling microbiological and chemical processes in municipal solid waste bioreactor, Part I: Development of a three-phase numerical model BLOKEMOD-3P", *Waste Manag.* **30** (2010) 202–210; doi:10.1016/j.wasman.2009.09.009.
- [8] L. Guerrero, S. Montalvo, E. Coronado, R. Chamy, P. Poirrier, D. Crutchik, E. Snchez, M. A. De La Rubia and R. Borja, "Performance evaluation of a two-phase anaerobic digestion process of synthetic domestic wastewater at ambient temperature", *J. Environ. Sci. Health A* **44** (2009) 673–681; doi:10.1080/10934520902847794.
- [9] P. Hemi, C. Shackelford and L. Figueroa, "Calibration of reactive transport models for remediation of mine drainage in solid-substrate biocolumns", *J. Environ. Eng.* **136** (2010) 914–925; doi:10.1061/(asce)ee.1943-7870.0000234.
- [10] T. Hidaka, T. Horie, S. Akao and H. Tsuno, "Kinetic model of thermophilic l-lactate fermentation by *Bacillus coagulans* combined with real-time PCR quantification", *Water Res.* **44** (2010) 2554–2562; doi:10.1016/j.watres.2010.01.007.
- [11] W. C. Hu, K. Thayanythy and C. F. Forster, "A kinetic study of the anaerobic digestion of ice-cream wastewater", *Process Biochem.* **37** (2002) 965–971; doi:10.1016/S0032-9592(01)00310-7.
- [12] M. Isik and D. T. Sponza, "Substrate removal kinetics in an upflow anaerobic sludge blanket reactor decolorising simulated textile wastewater", *Process Biochem.* **40** (2005) 1189–1198; doi:10.1016/j.procbio.2004.04.014.
- [13] D. W. Jordan and P. Smith, *Nonlinear ordinary differential equations*, 2nd edn. *Oxford Applied Mathematics and Computing Series* (Clarendon Press, New York, USA, 1989).
- [14] M. A. Mazutti, M. L. Corazza, F. M. Filho, M. I. Rodrigues, F. C. Corazza and H. Treichel, "Inulinase production in a batch bioreactor using agroindustrial residues as the substrate: experimental data and modeling", *Bioprocess Biosyst. Eng.* **32** (2009) 85–95; doi:10.1007/s00449-008-0225-5.
- [15] M. I. Nelson, E. Balakrishnan and H. S. Sidhu, "A fundamental analysis of continuous flow bioreactor and membrane reactor models with Tessier kinetics", *Chem. Eng. Commun.* **199** (2012) 417–433; doi:10.1080/00986445.2010.525155.
- [16] M. I. Nelson, E. Balakrishnan, H. S. Sidhu and X. D. Chen, "A fundamental analysis of continuous flow bioreactor models and membrane reactor models to process industrial wastewaters", *Chem. Eng. J.* **140** (2008) 521–528; doi:10.1016/j.cej.2007.11.035.
- [17] M. I. Nelson, T. Kerr and X. D. Chen, "A fundamental analysis of continuous flow bioreactor and membrane reactor models with death and maintenance included", *Asia Pac. J. Chem. Eng.* **3** (2008) 70–80; doi:10.1002/apj.106.
- [18] S. G. Pavlostathis and E. Giraldo-Gomez, "Kinetics of anaerobic treatment", *Water Sci. Technol.* **24** (1991) 35–59; <http://www.iwaponline.com/wst/02408/wst024080035.htm>.
- [19] A. Pinna, A. Lallai, G. Mura and M. Grosso, "Comparison across different models for the description of batch biodegradation processes", *Chem. Eng. Trans.* **149** (2009) 1227–1232; doi:10.3303/CET0917205.
- [20] P. E. Poh and M. F. Chong, "Biomethanation of palm oil mill effluent (POME) with a thermophilic mixed culture cultivated using POME as a substrate", *Chem. Eng. J.* **164** (2010) 146–154; doi:10.1016/j.cej.2010.08.044.

- [21] I. Ramirez, A. Mottet, H. Carrère, S. Dèlèris, F. Vedrenne and J. Steyer, “Modified ADM1 disintegration/hydrolysis structures for modeling batch thermophilic anaerobic digestion of thermally pretreated waste activated sludge”, *Water Res.* **43** (2009) 3479–3492; doi:10.1016/j.watres.2009.05.023.
- [22] S. L. Sun, B. Wu, D. Y. Zhao, X. X. Zhang, Y. Zhang, W. X. Li and S. P. Cheng, “Optimization of Xhhh strain biodegradation with metal ions for pharmaceutical wastewater treatment”, *J. Environ. Biol.* **30** (2009) 877–882; http://www.jeb.co.in/journal_issues/200909_sep09_supp/paper_18.pdf.
- [23] J. Zhang, X. Shao, O. V. Townsend and L. R. Lynd, “Simultaneous saccharification and co-fermentation of paper sludge to ethanol by *Saccharomyces cerevisiae* RWB222 Part I: Kinetic modeling and parameters”, *Biotechnol. Bioeng.* **104** (2009) 920–931; doi:10.1002/bit.22464.