

A fundamental analysis of continuous flow bioreactor models and membrane reactor models to process industrial wastewaters

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Abstract

We analyse the steady-state treatment of industrial wastewaters in a continuous flow bioreactor and in an idealised continuous flow membrane reactor. The reaction is assumed to be governed by Contois growth kinetics, which is often used to model the growth of biomass in wastewaters containing biodegradable organic materials. We show that a flow reactor with idealised recycle has the same performance as an idealised membrane reactor and that the performance of a non-idealised membrane reactor is identical to an appropriately defined continuous flow bioreactor with non-idealised recycle. The performance of all three reactor types can therefore be obtained by analysing a flow reactor with recycle. The steady-states of the model are found and their stability determined as a function of the residence time. The performance of the reactor at large residence times is obtained. In the limit as the residence time becomes very large, all three reactor configurations have identical performances. Thus the main advantage of using a membrane reactor, or a flow reactor with recycle, for the treatment of industrial wastewaters and slurries is to improve the performance at low residence times.

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1. Introduction

A continuous flow bioreactor is a well-stirred vessel containing microorganisms (X) through which a substrate (S) flows at a continuous rate. The microorganisms grow in the vessel through the consumption of the substrate to produce more microorganisms and products (P). The products will typically contain carbon dioxide, water and other species, including biological compounds, specific to the process under consideration. The nature of these products is unimportant in this study, as they do not affect the results presented here. Unused substrate, microorganisms, and the product flow out of the reactor. In the treatment of industrial wastewaters, a reactor configuration of this description is also known as an ‘aeration only complete mixing activated sludge system’ or a ‘conventional sewage sludge digester’. In a

bioreactor with recycle the effluent emerging from the reactor is fed into a settling unit. Microorganisms settle to the bottom of the tank, from where they are recycled into the reactor vessel. As a consequence of settling the concentration of microorganisms leaving the settling unit in the recycle stream is higher than that entering it from the biological reactor. The settling of the microorganisms greatly reduces their concentration in the effluent leaving the settling unit, producing a cleaner effluent stream. Recycle enables a higher concentration of microorganisms to be maintained in the bioreactor, which allows the reactor to run at much greater flow-rates and increases its efficiency. This process is illustrated in Fig. 1.

In the treatment of industrial wastewaters, recycle is also known as ‘sludge return’ and a continuous flow bioreactor operating with recycle is known as the ‘activated sludge process’. A practical consideration is to reduce both the substrate concentration and the microorganism concentration in the effluent. This is achieved by having a separate wasting of microorganisms after the reaction mixture has passed through the settling

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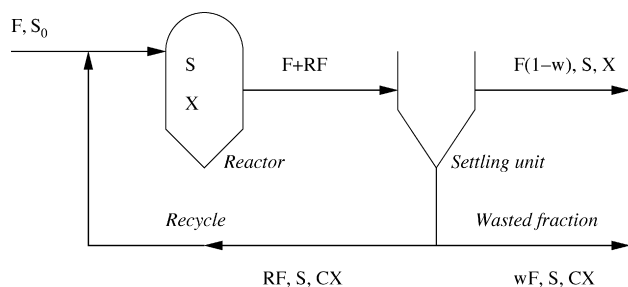


Fig. 1. A bioreactor with recycle and separate wasting of biomass. Nomenclature: C , the recycle concentration factor; F , flowrate through the reactor; R , recycle ratio; S_0 , concentration of substrate in the feed; S , substrate concentration in the reactor; X , cellmass concentration in the reactor; and w fraction of sludge wasted after passing through the settling unit.

unit, $0 < w < 1$ in Fig. 1. This produces an effluent with lower suspended solids.

Flow reactors have long been used in the treatment of industrial wastewaters, where the objective is to reduce the concentration of a soluble organic substrate. One advantage that they offer over other types of reactors is that they produce a greater operational stability in response to toxic or shock loads [1]. This is because mixing dilutes spikes in toxicity levels ('shock loads') across the whole of the reactor volume. A flow-reactor with recycle, augmented by a term representing death of microorganisms, is the simplest model for the biological treatment of industrial wastewaters [2].

Bioreactors sometimes employ a permeable membrane, such as a microfiltration membrane, to physically retain microorganisms inside the reactor. The higher concentrations of microorganisms obtained leads to greater pollutant removal, allowing for a more rapid and efficient process. In ultrafiltration membrane reactors the membrane also retains solids and high-molecular weight compounds that are found in the effluent from a conventional activated sludge reactor. Thus the quality of the water delivered by a membrane reactor can be significantly cleaner than that emerging from conventional reactors. Due to these advantages, membrane reactors have increasingly been used as key elements of advanced wastewater processing schemes. The higher quality water that they can produce and their compactness compared to conventional reactors make membrane reactors particularly suitable for the development of domestic wastewater treatment facilities in urban areas [3]. Although there exists detailed models for wastewater treatment kinetics, such as the IWA ASM model [4], we use a simple two-variable kinetic model in which the degradation of a biodegradable organic material is given by the Contois expression [5]. This choice is motivated by the experimental investigations detailed in Section 1.1 in which this kinetic model was found to accurately describe the processing of certain industrial wastewaters.

The objectives of the current paper are:

- to provide a more detailed investigation of the steady-state behaviour of this process model than previously undertaken;
- to extend the process model to include recycle;

- to consider the restriction of the process to an idealised membrane reactor.

Our analysis will be useful in future experimental studies in which the underlying process kinetics are given by the Contois growth rate expression. It also provides the baseline for investigations into the performance improvement that can be achieved in such systems through the use of reactor cascades.

1.1. Contois growth kinetics

Many industrial processes, particularly in the food industry, produce slurries or wastewaters containing high concentrations of biodegradable organic materials (pollutants). For example, the production of slurries is a feature of large pig and poultry farms and other operations involving animal production. Before the slurry/wastewater can be discharged the pollutant concentration must be reduced. One way to achieve a reduction in the concentration of a biodegradable organic pollutant is to pass the wastewater through a bioreactor containing biomass which grows through consumption of the pollutant.

The Contois growth model, Eq. (3), has been used to model the aerobic degradation of wastewater originating from the industrial treatment of black olives [6], the anaerobic treatment of dairy manure [7,8], the anaerobic digestion of ice-cream wastewater [9], the anaerobic treatment of textile wastewater [10] and the aerobic biodegradation of solid municipal organic waste [11]. Anaerobic conditions are favoured for the processing of waste materials with high levels of biodegradable organic pollutants as these can be removed with low investment and operational costs [12].

The Contois growth expression has been found to model the anaerobic reduction of sulphate by a sulphate-reducing bacteria [13]. This procedure has application in the cleaning of sulphate-containing industrial effluents and in the cleaning of acid mine drainage.

Simulation dynamics based upon Contois kinetics for the hydrolysis kinetics of swine waste, sewage sludge, cattle manure and cellulose have been found to fit experimental data [14]. The Contois growth rate has also been used as a default growth-rate model in simulations of the cleaning of wastewater by microorganisms [15]. Limited theoretical investigation of a continuous flow bioreactor model using Contois kinetics has been carried out by earlier researchers [7–10,13,14]. These investigations were undertaken to aid in the analysis of experimental data and correspond to the choice of parameter values $\beta = 1$, $\gamma = 0$ and $k_d > 0$ in Eqs. (1) and (2). In [7,9,10,14] the maintenance energy was assumed to be zero ($m_s = 0$) whereas in [8,13] the maintenance energy was assumed to be non-zero ($m_s > 0$). The Contois growth model gave predictions that were in excellent agreement with experimental measurements. In some cases the Contois model was shown to give better agreement with data than other growth rate expressions [7,9,10,13]. We extend these earlier theoretical investigations, in particular we consider a flow reactor with recycle and we determine the stability of all solution branches. We note that earlier investigators assumed that the no-washout solution branch is always stable.

2. Model equations and assumptions

2.1. Model assumptions

Wastewater from the food industries contains a complex mixture of biodegradable organic materials, such as fresh and partially decomposed food scraps and crop-residues, that may be in suspension or dissolved. Lumping these into a single substrate species, and the variety of microorganisms existing in the biological reactor into a single microorganism, is a convenient mathematical approximation. Formally, the use of a model containing a single substrate and a single microorganism can be justified if the overall process kinetics are controlled by a process-rate limiting step. The work cited in Section 1.1 suggests that in some cases this provides a reasonable approximation to an undoubtedly more complex process.

It has been suggested that when the Contois growth rate law accurately models experimental data that this indicates that the process is limited by the available surface area, causing mass-transfer limitations. When this interpretation is made, the specific growth rate, Eq. (3), is often written in the equivalent form

$$\mu = \mu_{\max} \left(\frac{S/X}{K_x + S/X} \right).$$

Thus as the population density of biomass increases there is an increasing obstruction to the substrate uptake and growth of any particular microbe. In the limit of large biomass concentration the Contois rate law reduces to

$$r_g = \mu X, \approx \frac{\mu_{\max} S}{K_x},$$

indicating that the limiting factor is the surface area of the particulate substrate. Examples where the Contois model is interpreted as a surface limiting process include [16,17,14].

The equation for the concentration of the substrate, Eq. (1), includes a maintenance energy term $-m_s X$. This recognises that some of the energy that is generated by consumption of the substrate is used for functions other than cell growth, such as maintaining cell integrity and supplying the energy for cellular processes; only the surplus energy is available for growth. The use of maintenance energy in bioreactor models was popularised by Pirt [18], although it had been introduced earlier by Schulze and Lipe [19].

The equation for the concentration of the microorganisms, Eq. (2), includes a term $-k_d X$ which represents a combination of first-order processes. These include endogenous respiration, predation, and cell death and lysis [20].

There are two important assumptions in the process model. These are that the settling unit does not separate the substrate and that utilisation of the substrate only occurs in the reactor, i.e. there is no reaction in either the settling tank or the return line. It follows from these assumptions that, although substrate is recycled, the recycling of substrate does not appear in Eq. (1) [21, p. 248, 493]. It should be further noted that other limiting factors, such as settling problems or membrane fouling, are ignored in the model.

2.2. The dimensional model

The model equations are

$$V \frac{dS}{dt} = F(S_0 - S) - \frac{\mu(S, X)}{\alpha} VX - Vm_s X, \quad (1)$$

$$V \frac{dX}{dt} = \beta F(X_0 - X) + \gamma RF(C - 1)X + VX\mu(S, X) - V k_d X, \quad (2)$$

Specific growth rate

$$\mu(S, X) = \frac{\mu_m S}{K_s X + S}, \quad (3)$$

Residence time

$$\tau = \frac{V}{F}. \quad (4)$$

The units that the concentrations of the substrate species, S , and the microorganisms, X , are measured in are denoted by $|S|$ and $|X|$, respectively. The parameters in the model are: C , the recycle concentration factor (—); F , the flowrate through the reactor vessel ($\text{dm}^3 \text{h}^{-1}$); K_s , the saturation constant ($|S||X|^{-1}$); R , the recycle ratio based on volumetric flow rates (—); S , the substrate concentration within the reactor vessel ($|S|$); S_0 , the concentration of substrate flowing into the reactor vessel ($|S|$); V , the volume of the reactor vessel (dm^3); X , the concentration of cell-mass within the reactor vessel ($|X|$); X_0 , the concentration of cell-mass flowing into the reactor vessel ($|X|$); k_d , the death coefficient (h^{-1}); m_s , the maintenance coefficient ($|S||X|^{-1} \text{h}^{-1}$); t , time (h); α , the yield factor ($|X||S|^{-1}$); μ , the specific growth rate model (h^{-1}); μ_m , the maximum specific growth rate (h^{-1}); and τ , the residence time (h).

For a specific wastewater, a given biological community and a particular set of environmental conditions the parameters K_s , k_d , m_s , α and μ_{\max} are fixed. The parameters that can be varied are S_0 , X_0 and τ .

The parameters β and γ define the reactor model. The choice $\beta = \gamma = 1$ gives a continuous flow reactor. The choice $\beta = \gamma = 0$ gives an idealised membrane reactor, in which all of the microorganisms is constrained to remain in the reactor vessel. Although highly simplified, this approach to modelling a membrane bioreactor was previously used by Yoon et al. [22]. The choice $0 < \beta < 1$ and $\gamma = 0$ gives a non-idealised membrane reactor, in which some of the microorganisms leave the reactor vessel in the effluent stream. For a non-idealised membrane reactor to be operationally effective we require $0 < \beta \ll 1$.

In Eq. (2) the term CX is the biomass concentration in the flow leaving the separating unit. The value of the concentrating factor depends upon the design and operation of the settling unit. It is also highly dependent on sludge properties such as settling, thickening and compressibility behaviour. A mass balance around the settling units shows that the maximum value of the

concentrating factor is given by

$$C_{\max} = 1 + \frac{1}{R}.$$

Thus the maximum value of the product $R(C - 1)$ is

$$[R(C - 1)]_{\max} = 1. \quad (5)$$

This is the simplest possible model for recycle from a settling unit. More detailed models for settling tanks require experimental data to calibrate coefficients. Of the experimental investigations described in Section 1.1 in only one was recycle used [11]. It is not possible to calibrate a more detailed recycle model from the data presented in this paper. The absence of relevant experimental data motivates our analysis of the simplest possible recycle model.

2.2.1. The dimensionless model

By introducing dimensionless variables for the substrate concentration [$S^* = S/S_0$], the cell mass concentration [$X^* = K_s X/S_0$] and time [$t^* = \mu_m t$] the dimensional model, Eqs. (1) and (2), can be written in the dimensionless form

$$\frac{dS^*}{dt^*} = \frac{1}{\tau^*}(1 - S^*) - \frac{1}{\alpha^*} \frac{X^* S^*}{X^* + S^*} - m_s^* X^*, \quad (6)$$

$$\frac{dX^*}{dt^*} = \beta \frac{1}{\tau^*}(X_0^* - X^*) + \gamma \frac{R^*}{\tau^*} X^* + \frac{X^* S^*}{X + S^*} - k_d^* X^*, \quad (7)$$

where the parameter groups are: the effective recycle parameter [$R^* = (C - 1)R$]; the dimensionless biomass concentration in the feed [$X_0^* = X_0 K_s/S_0$]; the dimensionless decay rate [$k_d^* = k_d/\mu_m$], the dimensionless maintenance energy [$m_s^* = m_s/(K_s \mu_m)$], the dimensionless yield coefficient [$\alpha^* = K_s \alpha$] and the dimensionless residence time [$\tau^* = V\mu_m/F$]. All parameters in the model are strictly non-negative.

From now on we assume that the growth medium fed into the bioreactor is sterile, i.e. there are no microorganisms in the influent ($X_0 = X_0^* = 0$), and that $S_0^* > 0$. From Eq. (5) it follows that the maximum value of the effective recycle parameter is $R^* = 1$. The cases $R^* = 1$ and $0 < R^* < 1$ with $\beta = \gamma = 1$ define a flow reactor with idealised and non-idealised recycle, respectively.

With the assumption of sterile feed ($X_0^* = 0$) it follows from Eq. (7) that a flow reactor model with idealised recycle ($\beta = \gamma = R^* = 1$) is identical to the idealised membrane reactor model ($\beta = \gamma = 0$). Furthermore, with the substitution $\beta = 1 - R^*$ the equations for a non-idealised membrane reactor ($0 < \beta < 1, \gamma = 0$) are identical to those of a flow reactor with non-idealised recycle ($\gamma = \beta = 1, R^* > 0$). This is one of the main findings of this research and is independent of the form used for the specific growth rate expression.

3. Results

In this section we analyse the flow-reactor with recycle ($\beta = \gamma = 1, 0 \leq R^* \leq 1$) as we have shown that the results for a membrane reactor ($\beta = \gamma = 0$) immediately follow with

the substitution $R^* = 1 - \beta$. In all our analysis we assume that $k_d^* > 0$.

For what follows it is useful to state the Jacobian matrix for the general form of the model given in Eqs. (6) and (7).

$$J = \begin{pmatrix} -\frac{1}{\tau^*} - \frac{1}{\alpha^*} \frac{X^{*2}}{(X^* + S^*)^2} & -\frac{1}{\alpha^*} \frac{S^{*2}}{(X^* + S^*)^2} - m_s^* \\ \frac{X^{*2}}{(X^* + S^*)^2} & \frac{\gamma R^* - \beta - k_d^* \tau^*}{\tau^*} + \frac{S^{*2}}{(X^* + S^*)^2} \end{pmatrix} \quad (8)$$

In Section 3.1 the steady-state solution branches are given and the condition for the no-washout solution branch to be physically meaningful is identified. In Section 3.2 the stability of the steady-state solutions is determined. In Section 3.3 asymptotic solutions for large residence times are stated.

3.1. Steady-state solution branches

The steady-state solutions of Eqs. (6) and (7) are given by

$$\text{Washout branch } (S^*, X^*) = (1, 0). \quad (9)$$

No-washout branch

$$(S^*, X^*) = \frac{\alpha^*}{A} (1 - R^* + k_d^* \tau^*, R^* - 1 + (1 - k_d^*) \tau^*). \quad (10)$$

$$A = \alpha^* (1 - R^* + k_d^* \tau^*) + [R^* - 1 + (1 - k_d^*) \tau^*] \times [(m_s^* \alpha^* + k_d^*) \tau^* + 1 - R^*], \quad (11)$$

The cases $R^* = 0$, $0 < R^* < 1$, and $R^* = 1$ represent a flow reactor without recycle, a flow reactor with non-idealised recycle, and a flow reactor with idealised recycle respectively. Note that in obtaining the no-washout branch a factor $R^* - 1 + (1 - k_d^*) \tau^*$ is eliminated from the numerator and the denominator of the substrate solution. Thus in what follows we can not have both $R^* = 1$ and $k_d^* = 1$.

The no-washout branch is only physically meaningful when the substrate and cell-mass concentrations are positive ($S^* > 0, X^* > 0$). Recall that the dimensionless yield coefficient is positive ($\alpha^* > 0$). Thus the no-washout branch is physically meaningful when the components of the solution within the parenthesis are positive (negative) provided that the sign of the expression A , Eq. (11), is positive (negative).

The substrate component within the parenthesis of the no-washout branch (10) is positive for any positive residence time, i.e.

$$1 - R^* + k_d^* \tau^* > 0.$$

Thus the case when the components within the parenthesis are negative and the sign of A is negative can immediately be eliminated. The microorganism component within the parenthesis of the no-washout branch (10) is positive when

$$R^* - 1 + (1 - k_d^*) \tau^* > 0. \quad (12)$$

We require that the sign of A be positive. By inspection, the value of A , Eq. (11), is positive, and the no-washout branch

is physically meaningful, whenever inequality (12) holds. The no-washout branch is not physically meaningful when $k_d^* = 1$. When this happens the microorganism component within the parenthesis of the no-washout branch (10) is negative unless $R^* = 1$. Simultaneously, the substrate concentration within the parenthesis is strictly positive. Thus the solution cannot be physically meaningful unless $R^* = 1$. However, as noted following Eq. (11) we can not have $k_d^* = 1$ and $R^* = 1$. Thus in what follows we assume that $0 < k_d^* < 1$.

When $0 \leq R^* \leq 1$ the no-washout branch is physically meaningful when

$$\tau^* > \frac{1 - R^*}{1 - k_d^*}, \quad 0 < k_d^* < 1.$$

For a flow reactor with idealised recycle, or an idealised membrane reactor, ($R^* = 1$), the steady-state solutions on the no-washout branch are given by

$$(S^*, X^*) = \frac{\alpha^*}{\alpha^* k_d^* + (1 - k_d^*)(m_s^* \alpha + k_d^*) \tau^*} (k_d^*, 1 - k_d^*).$$

This expression differs from the equivalent expression for Monod kinetics [23] in the following ways: the expression for the substrate concentration is dependent upon the residence time; the expression for the microorganism concentration is finite in the limit that the residence time approaches zero.

3.2. Stability of solutions

The Jacobian matrix, Eq. (8), evaluated at the washout steady-state solution is

$$J = \begin{pmatrix} -\frac{1}{\tau^*} & -\frac{1}{\alpha^*} - m_s^* \\ 0 & \frac{R^* - 1 - k_d^* \tau^*}{\tau^*} + 1 \end{pmatrix}.$$

The eigenvalues of this matrix are

$$\lambda_1 = -\frac{1}{\tau^*} < 0, \quad \lambda_2 = \frac{R^* - 1 - k_d^* \tau^*}{\tau^*} + 1.$$

It follows that the washout branch is stable when

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

In particular, the washout steady-state is always stable when

$$\begin{aligned} k_d^* &> 1, \\ \Rightarrow \frac{k_d}{\mu_m} &> 1, \\ \Rightarrow k_d &> \mu_m. \end{aligned}$$

This makes physical sense as the above condition implies that the washout steady-state is always stable if the death rate is greater than the maximum growth rate.

When $0 < k_d^* < 1$ the washout steady-state is stable provided

$$\tau^* < \frac{1 - R^*}{1 - k_d^*}.$$

The Jacobian matrix for the no-washout branch is given by

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

Note in obtaining the expression at $J(2, 2)$ we have used the fact that along the no-washout branch

$$\frac{-\beta + \gamma R^* - k_d^* \tau^*}{\tau^*} = -\frac{S^*}{X^* + S^*},$$

which follows from Eq. (7). The no-washout branch is stable when the trace of the Jacobian is negative ($\text{tr} J < 0$) and the determinant of the Jacobian is positive ($\det J > 0$). We have

$$\begin{aligned} \det J &= \frac{X^*}{(X^* + S^*)^2} \left\{ \left[\frac{1}{\tau^*} + \frac{1}{\alpha^*} \frac{X^{*2}}{(X^* + S^*)^2} \right] S^* \right. \\ &\quad \left. + \left[\frac{1}{\alpha^*} \frac{S^{*2}}{(X^* + S^*)^2} + m_s^* \right] X^* \right\}, \\ \text{trace } J &= -\frac{1}{\tau^*} - \frac{1}{\alpha^*} \frac{X^{*2}}{(X^* + S^*)^2} - \frac{S^* X^*}{(X^* + S^*)^2} \end{aligned}$$

Observe that the trace of the Jacobian is negative and that the determinant of the Jacobian is positive for all physically meaningful solutions. Consequently the no-washout solution branch is stable for any physically meaningful solution.

A transcritical bifurcation occurs, as the residence time is varied, when

$$\tau_{\text{tr}}^* = \frac{1 - R^*}{1 - k_d^*}. \quad (13)$$

At this value of the residence time the no-washout solution branch and the washout solution branch intersect at the point

$$(S^*, X^*, \tau^*) = (1, 0, \tau_{\text{tr}}^*).$$

The value of the residence time at the transcritical bifurcation is the highest residence time at which the treatment process fails. At lower residence times microorganisms are removed from the system faster than they can reproduce themselves. This results in process failure, following which the reactor must be reseeded with microorganisms. At residence times lower (higher) than the transcritical value the washout (no-washout) solution is the only stable solution. Eq. (13) shows that the washout condition is a linearly decreasing function of the effective recycle parameter, reaching a zero value when $R^* = 1$, that is for a flow reactor with idealised recycle (or for an idealised membrane reactor). Thus recycle allows the process to operate at lower residence times than would otherwise be the case—allowing a greater throughput of effluent.

Steady-state diagrams showing how the dimensionless substrate concentration (S^*) and the dimensionless microorganism concentration (X^*) change as the dimensionless residence time is varied are shown in Fig. 2. In Section 3.1 we showed that the

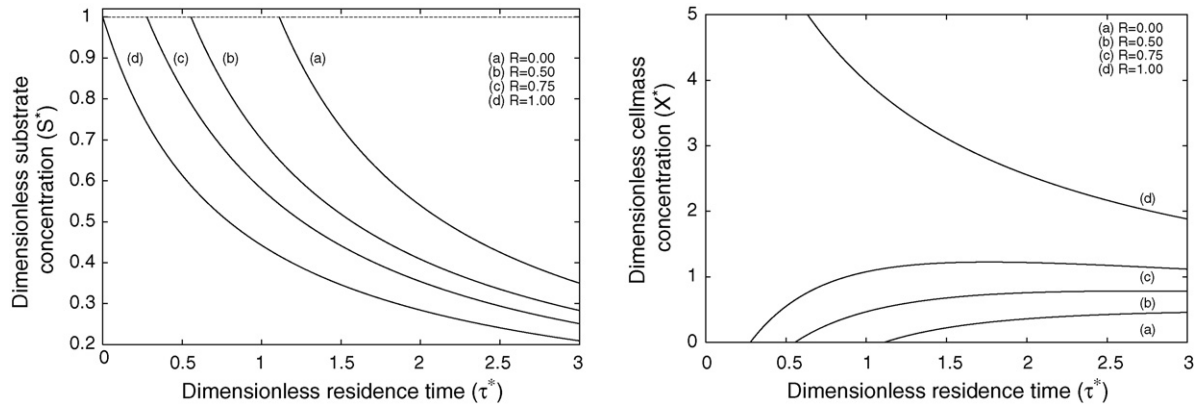


Fig. 2. Steady-state diagrams showing the variation of dimensionless substrate concentration (S^*) and cell mass concentration (X^*) as a function of the dimensionless residence time (τ^*) in a continuous flow bioreactor. Parameter values: dimensionless decay rate, $k_d^* = 0.1$; dimensionless maintenance rate, $m_s^* = 0.04$; dimensionless yield coefficient, $\alpha^* = 1$. The value of the effective recycle parameter is as given.

non-washout branch is only physically meaningful when

$$\tau^* > \frac{1 - R^*}{1 - k_d^*}.$$

When $\tau^* = 1 - R^*/1 - k_d^*$ the solution is given by

$$(S^*, X^*) = (1, 0).$$

In Fig. 2 we do not plot the no-washout solution branch when it is unphysical. This means that in Fig. 2(a) we do not plot solution values which are greater than one ($S^* > 1$) and in Fig. 2(b) we do not plot solution values which are negative ($X^* < 0$). For sufficiently low values of the residence time ($\tau^* < \tau_{tr}^*$) the stable solution is the washout solution, given by the lines $S^* = 1$ and $X^* = 0$ respectively. In the following discussion we assume that the residence time is sufficiently high that the no-washout solution branch is stable.

Fig. 2(a) shows that at fixed residence time the performance of the reactor increases as the effective recycle parameter is increased. For a given value of the effective recycle parameter Fig. 2(a) shows that the performance of the reactor increases as the residence time is increased. In the next section we show that for sufficiently large values of the residence time the performance of the reactor is independent of the value of the recycle parameter.

Fig. 2(b) shows that, provided that the value of the effective recycle parameter is not unity, that the cellmass concentration increases with increasing residence time. In fact this is only true for sufficient small values of the residence time. In the next section we show that at large values of the residence time the cellmass concentration decreases towards zero. Thus the cellmass concentration must increased to a maximum, before decreasing to zero.

3.3. Large residence time approximations

At large residence times we have the approximations

$$S^* \approx \frac{\alpha^* k_d^*}{(m_s^* \alpha + k_d^*)(1 - k_d^*)} \frac{1}{\tau^*} + O\left(\frac{1}{\tau^{*2}}\right) \quad 0 < k_d^* < 1, \quad (14)$$

$$X^* \approx \frac{\alpha^*}{(m_s^* \alpha + k_d^*)} \frac{1}{\tau^*} + O\left(\frac{1}{\tau^{*2}}\right) \quad 0 < k_d^* < 1. \quad (15)$$

At large residence times the steady-state concentrations are, to leading order, independent of the value of the effective recycle factor (R^*), i.e. it is independent of the reactor configuration.

Eq. (14) shows that the effluent concentration can be reduced to any desired level by operating the reactor at a sufficiently large residence time. This is *not* the case when Monod kinetics apply [23]. For Monod kinetics the effluent concentration can not be reduced below the limiting value $k_d^*/1 + k_d^*$. Another difference between biological processes controlled by Monod and Contois kinetics concerns the optimal performance in an idealised membrane reactor ($R^* = 1$). When the process is controlled by Monod kinetics the optimal performance occurs at *any* finite residence time [23], whereas if the process is governed by Contois kinetics then the optimal performance is only reached at an infinite residence time.

4. Discussion

An interesting feature of biological processes that are governed by Contois growth kinetics is that the washout condition, Eq. (13), does not depend upon the influent pollutant concentration (S_0). Consequently, wastewaters containing dilute concentrations of pollutant can be fed through the reactor. In contrast, washout is inevitable for processes controlled by Monod kinetics when the influent substrate concentration is sufficiently low. For systems with Monod kinetics, wastewaters with a low pollutant concentration must be concentrated before they enter the reactor.

There are a number of definitions which are used to characterise the steady-state performance of a continuous flow bioreactor processing industrial wastewaters [24]. The results stated in this section only apply when the no-washout branch is physically meaningful, that is when

$$\tau^* > \tau_{tr}^* = \frac{1 - R^*}{1 - k_d^*} > 0.$$

The specific utilisation (\mathcal{U}), which is also known as the process loading factor, the substrate removal velocity and the food to microorganism ratio, is the rate of substrate utilisation per unit mass of microorganisms and is defined by

$$\mathcal{U} = \frac{S_0 - S}{X} \frac{1}{\tau}.$$

The dimensionless specific utilisation (\mathcal{U}^*) is given by

$$\mathcal{U}^* = \frac{1 - S^*}{X^*} \frac{1}{\tau^*}.$$

Using Eqs. (10) and (11) we obtain

$$\mathcal{U}^* = (k_d^* + m_s^*) + \frac{1 - R^*}{\tau^*}, \quad 0 \leq R^* \leq 1,$$

$$\tau^* > \frac{1 - R^*}{1 - k_d^*}, \quad 0 < k_d^* < 1$$

Hence, for fixed residence time, the dimensionless specific utilisation is a linearly decreasing function of the effective recycle parameter. The dimensionless specific utilisation is a decreasing function of the residence time for reactors with non-idealised recycle and a constant for reactors with idealised recycle ($R^* = 1$). The value for the dimensionless specific utilisation is the same for both Contois and Monod growth rate expressions [23].

From Eqs. (1) and (2) it follows that the specific utilisation is independent of the growth rate law and is given by

$$\mathcal{U} = \left(m_s + \frac{k_d}{\alpha} \right) + \left(\frac{\beta}{\alpha} - \frac{\gamma R(C-1)}{\alpha} \right) \frac{1}{\tau}.$$

The treatment, or process, efficiency (\mathcal{E}) is defined by

$$\mathcal{E} = 100 \frac{S_0 - S}{S_0}.$$

In dimensionless variables this is

$$\mathcal{E}^* = 100(1 - S^*)$$

Note that from this definition it is clear that along the no-washout branch, where $S^* < 1$, the efficiency is positive. Using Eq. (10) we obtain the efficiency as

$$\mathcal{E}^* = 100 \left(\frac{[R^* - 1 + (1 - k_d^*)\tau^*] [(m_s^* \alpha^* + k_d^*)\tau^* + 1 - R^*]}{A} \right),$$

where the expression for the term A is given by Eq. (11). At large residence times, using Eq. (14), this becomes

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

Thus as the residence time approaches infinity the efficiency of the process approaches 100. This is in contrast to the situation in which the process is governed by Monod kinetics, in which the maximum efficiency is bounded below 100 and is given by [23]

$$\mathcal{E}_{\max}^* = 100 \left(\frac{1 - k_d^*}{k_d^*} S_0^* - 1 \right).$$

The rate of waste treatment is defined by

$$\mathcal{W} = \frac{S_0 - S}{\tau}.$$

In dimensionless variables this is

$$\mathcal{W}^* = \frac{1 - S^*}{\tau^*}.$$

From this definition it is clear that along the no-washout branch, where $S^* < 1$, the rate of waste treatment is positive. Using Eq. (10) we obtain the rate of waste treatment as

$$\mathcal{W}^* = \left(\frac{[R^* - 1 + (1 - k_d^*)\tau^*] [(m_s^* \alpha^* + k_d^*)\tau^* + 1 - R^*]}{\alpha^*(1 - R^* + k_d^*\tau^*) + [R^* - 1 + (1 - k_d^*)\tau^*] [(m_s^* \alpha^* + k_d^*)\tau^* + 1 - R^*]} \right) \frac{1}{\tau^*}$$

At large residence times the rate of waste treatment is given by

$$\mathcal{W}^* \approx \frac{1}{\tau^*} + O\left(\frac{1}{\tau^{*2}}\right).$$

5. Conclusion

In this paper we have investigated a bioreactor model for the interaction between a microorganism and a rate-controlling substrate. The specific growth rate used was the Contois expression and the biological model included both a microorganism decay coefficient and a maintenance energy requirement. The reactor model includes both membrane reactors and well-stirred flow reactors with, or without recycle. Our main result is that an idealised membrane reactor is equivalent to a well-stirred flow reactor with idealised recycle, and this is independent of the choice of specific growth rate. The results for a well-stirred flow reactor with non-idealised recycle follow from those of a flow reactor with idealised recycle after a minor re-parameterisation of the model.

Although the Contois expression has a long history, and a number of authors have analysed experimental data using bioreactor models, the performance of a well-stirred bioreactor governed by Contois kinetics and with microorganism death, maintenance energy and recycle has not been reported in the literature. The steady-state solutions of the model were found and their stability determined as a function of the residence time. The residence time at below which process failure occurs (washout) was identified. These results were used to evaluate various performance characterisations of continuous flow bioreactors. It was shown that at large residence times there is very little difference in the performance of the three reactors. The main advantage of using recycle, or a membrane reactor, is therefore to allow operation at lower residence times, thus increasing the throughput of effluent, that can be used in a flow reactor without recycle.

Although there are a number of reports in the literature of waste-waters that can be modelled using Contois kinetics [6–11, 13, 14] we are only aware of one experimental study where recycle was used [11]. Our results in this paper suggest a need

for more experimental investigations using recycle in these type of systems.

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References

- [1] R.E. McKinney, Mathematics of complete-mixing activated sludge, *J. Sanit. Eng. Div. ASCE* 88 (1962) 87–113.
- [2] P.L. McCarty, Kinetics of waste assimilation in anaerobic treatment, in: *Developments in Industrial Microbiology*, vol.7, Society of Industrial Microbiology, 1966, pp. 144–155.
- [3] C. Wisniewski, Membrane bioreactor for water reuse, *Desalination* 203 (2007) 15–19.
- [4] M. Henze, C.P.L. Grady, W. Gujer, G.V.R. Marais, T. Matsuo Jr., A general model for single-sludge wastewater treatment systems, *Water Res.* 21 (1987) 505–515.
- [5] 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.
- [6] J. Beltran-Heredia, J. Torregrosa, J.R. Dominguez, J. Garcia, Ozonation of black-table-olive industrial wastewaters: effect of an aerobic biological pretreatment, *J. Chem. Technol. Biot.* 75 (2000) 561–568.
- [7] S.C. Bhattacharya, P.Q. Khai, Kinetics of anaerobic cowdung digestion, *Energy* 12 (1987) 497–500.
- [8] A.E. Ghaly, S.S. Sadaka, A. Hazza'a, Kinetics of an intermittent-flow, continuous-mix anaerobic reactor, *Energ. Source* 22 (2000) 525–542.
- [9] W.C. Hu, K. Thayanithy, C.F. Forster, A kinetic study of the anaerobic digestion of ice-cream wastewater, *Process. Biochem.* 37 (2002) 965–971.
- [10] M. Işik, D.T. Sponza, Substrate removal kinetics in an upflow anaerobic sludge blanket reactor decolorising simulated textile wastewater, *Process. Biochem.* 40 (2005) 1189–1198.
- [11] L. Krzystek, S. Ledakowicz, H-J. Kahle, K. Kaczorek, Degradation of household biowaste in reactors, *J. Biotechnol.* 92 (2001) 103–112.
- [12] G. Lettinga, Anaerobic-digestion and waste-water treatment systems, *Anton. Leeuw. Int. J. G.* 67 (1995) 3–28.
- [13] S. Moosa, M. Nemati, S.T.L. Harrison, A kinetic study on anaerobic reduction of sulphate, Part I: Effect of sulphate concentration, *Chem. Eng. Sci.* 57 (2002) 2773–2780.
- [14] V.A. Vavilin, S.V. Rytov, L. Ya Lokshina, A description of hydrolysis kinetics in anaerobic degradation of particulate organic matter, *Bioresource Technol.* 56 (1996) 229–237.
- [15] J. Czczot, M. Metzger, J.P. Babary, M. Nihtilä, Filtering in adaptive control of distributed parameter bioreactors in the presence of noisy measurements, *Simulat. Ract. Theory* 8 (2000) 39–56.
- [16] M. Myint, N. Nirmalakhandan, Evaluation of first-order, second-order, and surface-limiting reactions in anaerobic hydrolysis of cattle manure, *Environ. Eng. Sci.* 23 (2006) 970–980.
- [17] S.M. Ruel, Y. Comeau, P. Ginestet, A. Héduit, Modeling acidogenic and sulfate-reducing processes for the determination of fermentable fractions in wastewater, *Biotechnol. Bioeng.* 80 (2002) 525–536.
- [18] S.J. Pirt, The maintenance energy of bacteria in growing cultures, *Proc. R. Soc. Lond. Ser-B* 163 (1965) 224–231.
- [19] K.L. Schulze, R.S. Lipe, Relationship between substrate concentration, growth rate, and respiration rate of *Escherichia coli* in continuous culture, *Arch. Mikrobiol.* 48 (1964) 1–20.
- [20] S.G. Pavlostathis, E. Giraldo-Gomez, Kinetics of anaerobic treatment, *Water Sci. Technol.* 24 (1991) 35–59.
- [21] M.L. Shuler, F. Kargi, *Bioprocess Engineering*, Prentice Hall International Series in the Physical and Chemical Engineering Sciences, second ed., Prentice Hall, New Jersey, USA, 2002.
- [22] S.-H. Yoon, H.-S. Kim, I.-T. Yeom, The optimum operational condition of membrane bioreactor (MBR): cost estimation of aeration and sludge treatment, *Water Res.* 38 (2004) 37–46.
- [23] M.I. Nelson, T. Kerr, X.D. Chen, A fundamental analysis of continuous flow bioreactor and membrane reactor models with death and maintenance included, *Asia Pacific J. Chem. Eng.*, doi:10.1002/apj.106.
- [24] A.W. Lawrence, P.L. McCarty, Unified basis for biological treatment design and operation, *J. Sanit. Eng. Div. ASCE* 96 (1970) 757–778.