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Modeling the Dynamic Response of an Activated Sludge Process

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ABSTRACT

Previously collected data describing aerated synthetic waste water, treated in a continuous stirred-tank reactor, are analyzed to understand better the dynamic response to step changes in the dilution rate, D. Comparing a change in D between steady states leads to hysteresis trajectories on both the graph of specific growth rate, μ, vs limiting substrate level (S) and the graph of (S) vs the cell level (X). Qualitative differences between the three different monitored cases will be compared to simulations of simple models at various dilution level changes in order to gain understanding of the dynamics of the process.

Index Entries: Dynamic response; modeling; activated sludge; fermentation; hysteresis.

INTRODUCTION

Laboratory experiments in which a mixed culture of microorganisms continuously degrade synthetic media were analyzed to describe the response in specific growth rate, μ, to a step change in the feed flow rate. The dynamic response covers the transition from the steady-state conditions corresponding to one feed flow (dilution rate) to the new steady-state

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conditions corresponding to a higher feed flow rate. For all three experiments considered, the response trajectory of μ vs the limiting substrate concentration (S) was observed to be a counterclockwise hysteresis curve. Since this is different from the expected Monod-type hyperbolic response, an alternative mathematical model is proposed to account qualitatively for this observed transient trajectory. In inferring the structure of the experimental μ vs (S) response relationship, a sharper model, suitable not only for description, but also prediction, thus may be developed to account for dynamic upsets in waste-treatment operations.

MATERIALS AND METHODS

The data from this study were collected previously (*1*) and are exhibited in Figs. 1 and 2. The experiments are summarized here. Five steady states were obtained at various dilution rates. The measured variables were (X), the cell concentration (determined as mixed-liquor suspended solids [MLSS]) and residual substrate level (determined as glucose). Three experiments were conducted following the dynamics from one steady state to another steady state using a mixed-culture sludge in which step changes in the dilution rate, D (the feed volumetric flow rate divided by the volume of liquid in the aeration tank) were made from: 0.1 → 0.2 h^{-1}, 0.2 → 0.3 h^{-1}, and 0.4 → 0.5 h^{-1}. The composition of the synthetic waste medium was comprised of glucose (1000 mg/L), $(NH_4)_2 SO_4$ (500 mg/L), $MgSO_4 \cdot 7H_2O$ (100 mg/L), $FeCl_3 \cdot 6H_2O$ (0.5 mg/L), $CaCl_2$ (0.5 mg/L), $MnSO_4 \cdot H_2O$ (10 mg/L), KH_2PO_4 (527 mg/L), and K_2HPO_4 (1070 mg/L). Further details of the experiment are given in (*1*).

Modeling

The two generally used dynamic equations for describing microbial growth in a CSTR are:

$$d(X) / dt = -D(X) + \mu(X) \tag{1}$$

and

$$d(S) / dt = D[S_F - (S)] - (\mu / Y)(X) \tag{2}$$

Equation (1) is the microbial cell balance (assumed to be one organism or at least describable by a monoculture), and Eq. (2) is the substrate mass balance. S_F is the substrate feed concentration, and Y, a constant, is the cellular yield relative to the substrate utilized, i.e., for a batch system, $Y = -d(X)/d(S)$. The specific growth rate, μ, for a batch system is often depicted by the Monod equation:

$$\mu = [\mu_{MAX}(S)] / [K_S + (S)] = [1 / (X)] [d(X) / dt] \tag{3}$$

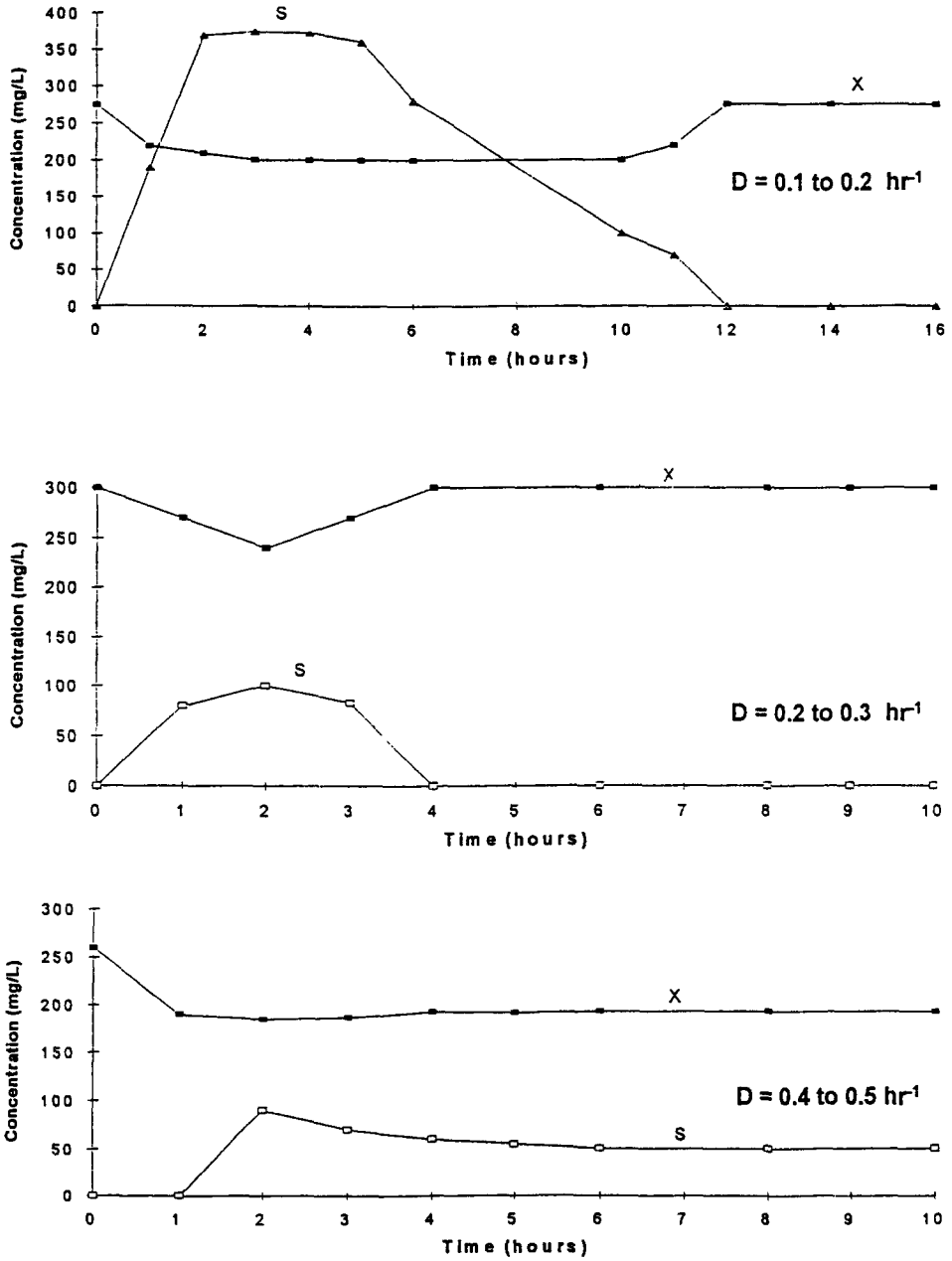

Fig. 1. Change of concentrations of (X), the cell dry weight (MLSS), and (S), the residual substrate (glucose) during unsteady-state operation. (**A**) D: 0.1 → 0.2 h^{-1}, (**B**) D: 0.2 → 0.3 h^{-1}, and (**C**) D: 0.4 → 0.5 h^{-1}.

where μ_{MAX} is the maximum (asymptotic) growth rate and K_s is the saturation constant. We observe from Eq. (1) that at steady-state operation, when $d(X)/dt = 0$:

$$\mu = D = [\mu_{MAX}(S)] / [K_S + (S)] \quad (4)$$

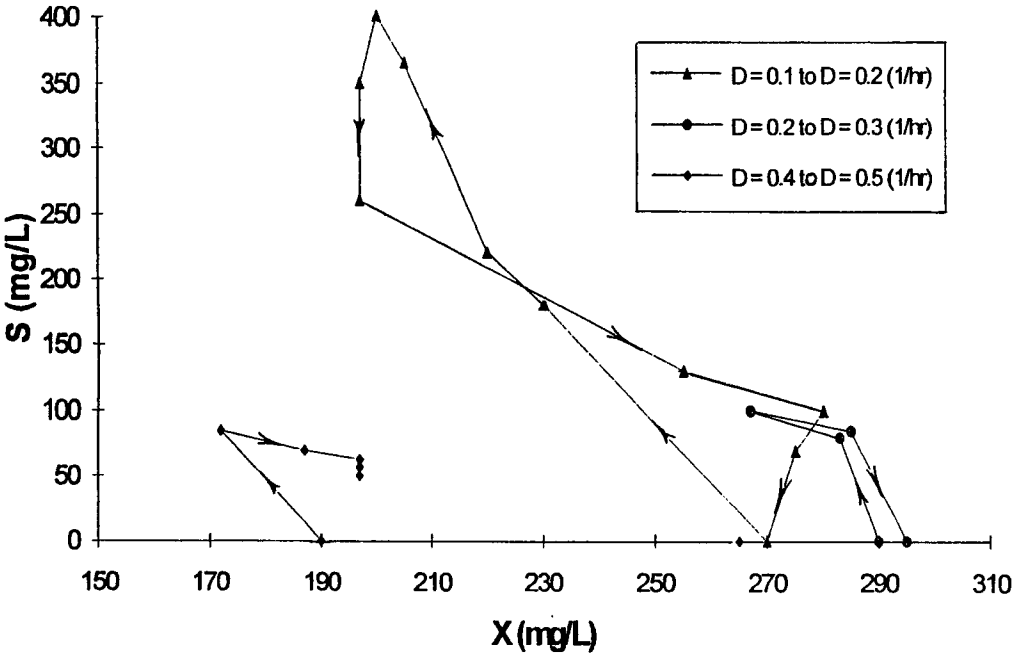

Fig. 2. Phase plane plot of the experimental data: substrate level as a function of cell level during the response to the step change of the dilution rate. (**A**) D: 0.1 → 0.2 h^{-1}, (**B**) D: 0.2 → 0.3 h^{-1}, and (**C**) D: 0.4 → 0.5 h^{-1}.

Therefore, since five of the six reported steady-state values for $(S) = \bar{S}$ are reported as negligible or "zero" values, μ has a very sharp slope,

$$Lim\ (d\mu / d(S) \mid (S) \rightarrow 0 = \mu_{MAX} / K_S \tag{5}$$

or

$$Lim\ \mu / S \rightarrow 0 = [\mu_{MAX} / K_S]\,(S) \tag{6}$$

where K_S is very small. In other words, the $\mu(S)$ hyperbola looks almost like a step function with slope of μ_{MAX}/K_S and a horizontal asymptote μ_{MAX}.

$S = S_F - X/Y$ from the steady-state solution, $d(S)/dt = 0$, to Eq. (2), implying that as S approaches 0, X goes to YS_F. This nearly linear steady-state relationship between (S) and (X) seems to be followed by the data for the D = 0.2–0.3 h^{-1} case in Fig. 2.

μ is calculated from the dynamic data for (S) and (X) presented in Figs. 1 and 2 by differencing Eq. (7), a rearrangement of Eq. (1):

$$\mu = [1 / (X)]\,[d(X) / dt] + D \tag{7}$$

The data for μ as a function of (S) developed from Eq. (7) are plotted in Fig. 3 showing counterclockwise hysteresis trajectories for all three cases. In order to obtain a model that describes non-Monod-type single-valued hyperbolic functions of μ and high late time values of μ, we propose to modify the Monod model as follows: K_s is allowed to be a linear function

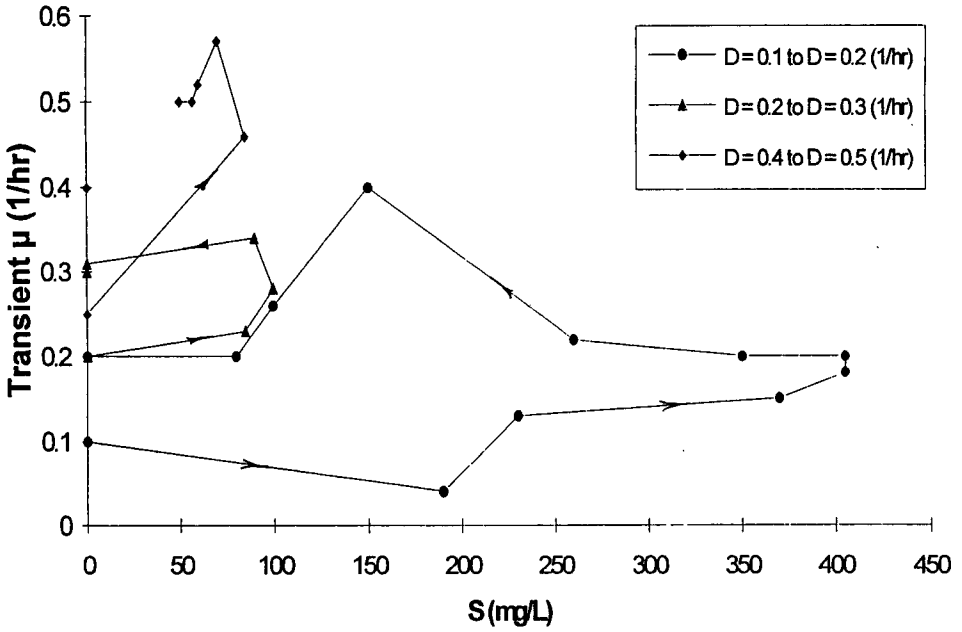

Fig. 3. Hysteresis response of the experimental data: specific growth rate as a function of substrate concentration during the response to the step change of the dilution rate. (**A**) D: 0.1 → 0.2 h^{-1}, (**B**) D: 0.2 → 0.3 h^{-1}, and (**C**) D: 0.4 → 0.5 h^{-1}.

of (*X*), whereas μ_{MAX} is held constant. The simplest case to model seems to be the $D = 0.4$ to $D = 0.5$ h^{-1} response in Fig. 1. There (*X*) decays from an initial value to a new lower steady-state value. (*S*) rises from the initial value to a higher steady-state value. K_S is proposed to be of the form:

$$K_S = A + B\,(X) \tag{8}$$

This enables the model of μ in Eq. (3) to have low values when (*X*) is high (since K_s is relatively large) and higher values when (*X*) is lower (since K_s becomes smaller) for a given (*S*) value. μ then tracks a Monod-type hyperbola for the lower value initially as (*S*) increases and curves upward to a higher μ hyperbola as (*X*) decreases.

The exploration of K_s as a variable to describe dynamic hysteresis responses to step changes in the feed substrate concentration has been previously discussed for pure culture systems (2). In that study, linear relationships between K_s and (*X*) were shown to determine whether the response hysteresis trajectories were clockwise or counterclockwise depending on the sign of B. That study did not lead to clear results for step changes in the feed flow rate, hence, the need for further study described in this article. An additional complication here is that the data describe mixed cultures, not pure cultures. It is assumed here that the pure culture model is a good first approximation for qualitatively describing the mixed-culture data.

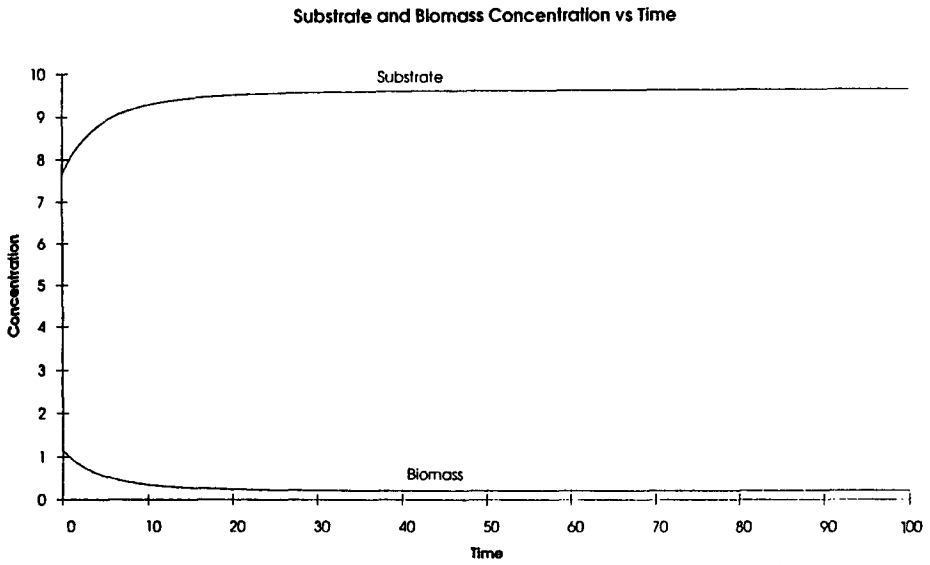

Fig. 4. Simulated concentrations. Change of concentration of cell dry wt and residual substrate during unsteady state.

One possible "derivation" of the $K_s = f(X)$ relationship can be seen in the linear relationship between K_s and K in an earlier paper (*3*), where K is the conversion factor from the genetic machinery variable ("total ribosomes") and cell concentration (*3*). When that conversion factor is a negatively linear function of cell level, then the relationship $K_s = A + B(X)$ can be developed.

RESULTS AND DISCUSSION

Typical simulation results for the proposed modified Monod model are displayed in Figs. 4, 5, and 6 for the following set of parameters:

$\mu_{MAX} = 0.5$;
$Y = 0.5$;
$K_S = 2 + 10(X)$, or A = 2 and B = 10; and
$S_F = 10$

for the case of $D = 0.1$ to $D = 0.3\ h^{-1}$.

The linear rise of the (S) vs (X) simulation shown in Fig 5 is somewhat like the experimental data for the $D = 0.2$ to $D = 0.3\ h^{-1}$ case in Fig. 2. It does differ qualitatively from the "Figure 8" hysteresis for the $D = 0.1$ to $D = 0.2\ h^{-1}$ case and the clockwise hysteresis for the $D = 0.4$ to $D = 0.5\ h^{-1}$ experimental case shown in Fig. 2.

The clockwise response (quarter turn) of the simulated μ vs (S) trajectory in Fig. 6 does indeed correspond to the three experimental cases of μ vs (S) displayed in Fig. 3. Thus, the main objective of this study to mimic

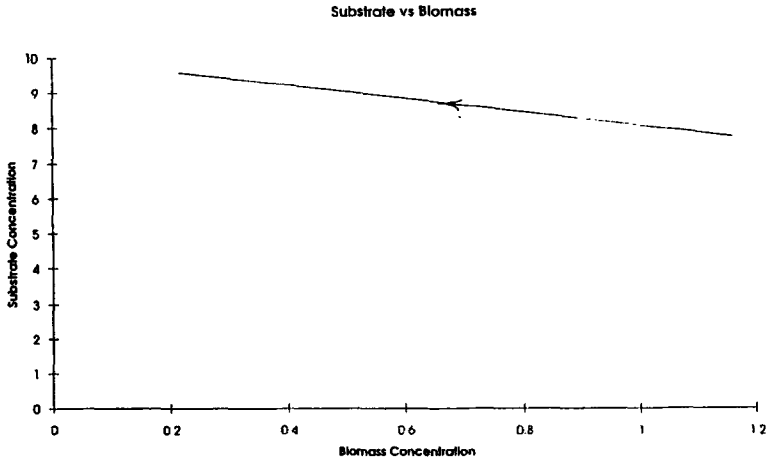

Fig. 5. Simulation of the phase plane response: substrate concentration as a function of the cell concentration following the dilution rate step change.

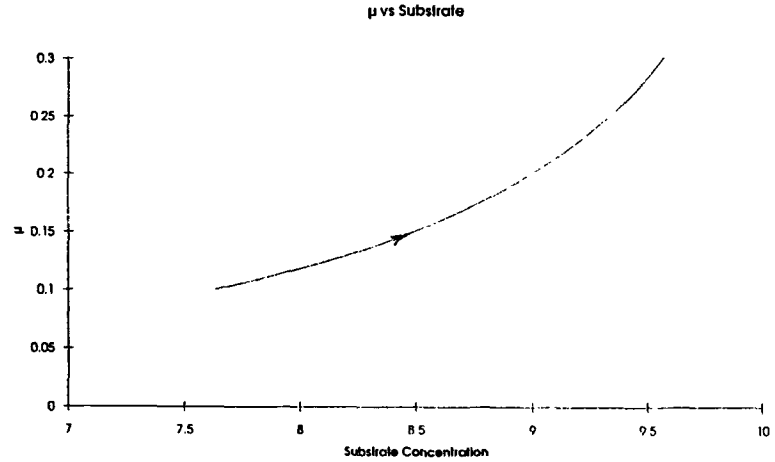

Fig. 6. Simulation of the hysteresis response: specific growth rate as a function of substrate concentration following the dilution rate step change.

the clockwise nature of the μ vs (S) response through the addition of a linear (X) term in K_S in the Monod model was achieved. What still needs to be accomplished by simulation of a more complete model is to develop complete clockwise loops, which in turn require the (S) to have a distinct peak with respect to time.

CONCLUSIONS

A qualitatively more accurate description of the dynamic response to a step function input to a laboratory waste-treatment system has been developed by modifying the K_s term in the Monod equation:

$$\mu = [\mu_{MAX}(S)] / [K_S + (S)] \quad (9)$$

as follows:

$$K_S = A + B(X) \quad (10)$$

In particular, the modification in K_s incorporates into the growth term, μ, the ability to describe the counterclockwise μ vs (S) dynamic responses resulting from an abrupt rise in the feed flow rate.

Three views for the (S) and (X) data give additional perspectives on dynamic model building. In addition to the traditional (S) and (X) vs time plots, the phase plane plot of (S) vs (X) and μ vs (S) provides valuable insight into the development of sharper microbial growth models.

Merely modifying K_s from a constant to a linear function of (X) is only a first step toward building a more descriptive model capable of qualitatively and quantitatively describing upsets in waste-treatment systems. With sharper models, better control strategies can be developed to minimize noncompliant substrate effluents.

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