Midterm review II

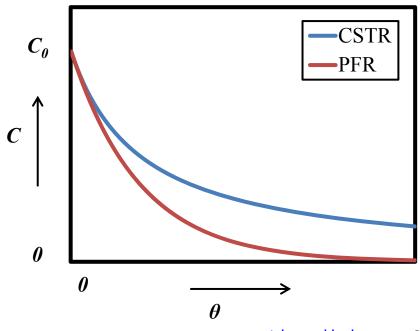
Reactor analysis

• 1st order reaction $\left. \frac{dC}{dt} \right|_{reaction} = -kC$

- Batch reactor:
$$C = C_0 e^{-kt}$$

- PFR:
$$C = C_0 e^{-k\theta}$$

- CSTR:
$$C = C_0/(1 + k\theta)$$



Reactor analysis

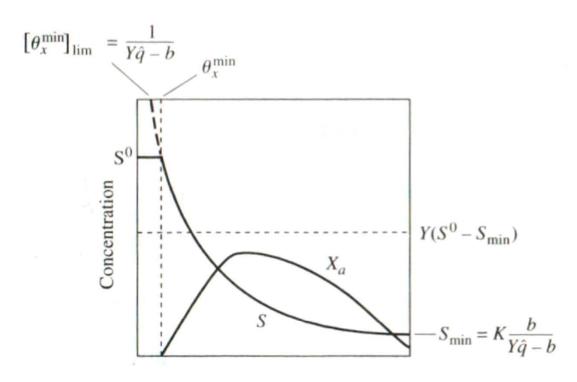
Monod kinetics

$$\frac{dS}{dt}\Big|_{reaction} = r_{ut} = \frac{\hat{q}S}{K+S}X_a$$

$$\frac{dX_a}{dt}\Big|_{reaction} = r_{net} = Y\frac{\hat{q}S}{K+S}X_a - bX_a$$

- Batch reactor: a complicated eq. [5.11] applicable only when decay is negligible
- PFR: a complicated eq. [5.26] applicable only when decay is negligible

- CSTR:
$$S = K \frac{1 + b\theta}{Y\hat{q}\theta - (1 + b\theta)} \qquad X_a = Y \frac{S^0 - S}{1 + b\theta}$$



- 1) $\theta_x \le \theta_{min}$: washout
- 2) $\Theta_x \rightarrow \infty$: $S = S_{min}$
- 3) For $\Theta_{min} < \Theta_x$, S decreases with increase in Θ_x , but X_a peaks at some point

Microbial kinetics in reactors

Q: Calculate the effluent substrate and active biomass concentration of a bioreactor operated as a CSTR when the influent substrate concentration is 100, 1000, and 10000 mg BOD_L/L. The reactor volume is 1000 m³ and the flow rate is 250 m³/hr. Use typical values of Y=0.42 g VSS/g BOD_L , \hat{q} =20 g BOD_L /g VSS-d, K=100 mg BOD_L /L and b=0.15 d⁻¹ for aerobic degradation of typical organic matter.

- Soluble microbial products
 - Production:

$$r_{UAP} = -k_1 r_{ut} \qquad r_{BAP} = k_w X_a$$

– Degradation:

$$r_{deg-UAP} = \frac{-\hat{q}_{UAP}UAP}{K_{UAP} + UAP}$$

$$r_{deg-BAP} = \frac{-\hat{q}_{BAP}BAP}{K_{BAP} + BAP}$$

- Recall a complicated analytical solution in Eqs. [3.38] & [3.39]

Nutrient consumption

$$r_n = \gamma_n Y r_{ut} \frac{1 + (1 - f_d)b\theta_x}{1 + b\theta_x}$$

$$C_n = C_n^0 + r_n \theta$$

• e⁻ acceptor consumption

$$\frac{\Delta S_a}{\Delta t} = \gamma_a Q [S^0 - S - SMP + 1.42(X_v^0 - X_v)]$$
$$= Q [S_a^0 - S_a] + R_a$$

Hydrolysis

- can be reasonably assumed as a 1st-order reaction
- Then, the result is the increase in "effective" influent substrate concentration

$$r_{hyd} = -k_{hyd}S_p$$

$$S_p = \frac{S_p^0}{1 + k_{hvd}\theta}$$

$$S^{0}_{eff} = S^{0} + k_{hyd}S_{p}\theta$$

Q: Compute the effluent COD, BOD_L , and NH_4^+ -N concentration, and the requirement for O_2 supply for a chemostat having

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V = 2500 \, m^3 f_d = 0.8

Q = 10^4 \, m^3/d X_i^0 = X_{in}^0 = 50 \, mg \, VSS/L

Y = 0.5 \, g \, VSS/g S^0 = 400 \, mg \, COD/L

K = 20 \, mg \, COD/L C_N^0 = 50 \, mg \, NH_4^+ - N/L

b = 0.15/d DO^0 = 8 \, mg/L

q = 30 \, mg \, COD/mg \, VSS DO = 3 \, mg/L
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• X_{in} = inorganic VSS

Neglect the production of SMP.

- Our "idealized" biofilm model:
 - Constant X_f and L_f for the entire biofilm
 - External mass transport described by film theory (Fick's 1st law of diffusion with an "effective diffusion layer")
 - Internal mass transport described by Fick's 2nd law of diffusion
 - Deep vs. shallow biofilm

Processes of concern

- External substrate mass transfer: $J = \frac{D}{L}(S S_s)$
- Substrate utilization within biofilm: $r_{ut} = -\frac{\hat{q}X_fS_f}{K + S_f}$
- Internal substrate mass transfer: $r_{diff} = D_f \frac{d^2 S_f}{dz^2}$
- Bacterial growth: $\frac{dX_f}{dt} = Y \frac{\hat{q}S_f}{K + S_f} X_f b'X_f$

 Governing equations & boundary conditions for substrate mass balance

$$0 = D_f \frac{d^2 S_f}{dz^2} - \frac{\hat{q} X_f S_f}{K + S_f}$$
$$0 = \frac{dS_f}{dz} \Big|_{z=L_f} \frac{D}{L} (S - S_s) = D_f \frac{dS_f}{dz} \Big|_{z=0}$$

• Deep biofilm solution: $J_{deep} = \left[2\hat{q} X_f D_f \left(S_s + K \ln \left(\frac{K}{K + S_s} \right) \right) \right]^{1/2}$

• Pseudo-steady state assumption: constant X_f and L_f with time

The assumption gives $0 = YJ - b'X_fL_f$

$$0 = YJ - b'X_fL_f$$

In addition to

$$0 = D_f \frac{d^2 S_f}{dz^2} - \frac{\hat{q} X_f S_f}{K + S_f}$$

$$0 = \frac{dS_f}{dz} \bigg|_{z=L_f} \quad \frac{D}{L} (S - S_S) = D_f \frac{dS_f}{dz} \bigg|_{z=0}$$

- Pseudo-steady state analytical solution: use nondimensionalized variables!
- 1. Compute the non-dimensional parameters

$$S_{min}^* = \frac{b'}{Y\hat{q} - b'} \qquad K^* = \frac{D}{L} \left[\frac{K}{\hat{q} X_f D_f} \right]^{1/2} \qquad S^* = \frac{S}{K}$$

2. Compute α and β

$$\alpha = 1.5557 - 0.4117 \ tanh[log_{10}S_{min}^*]$$

$$\beta = 0.5035 - 0.0257 tanh[log_{10}S_{min}^*]$$

3. Compute S_S^* (recall our first Excel spreadsheet!)

$$S_S^* = S^* - J_{deep}^* \cdot f / K^*$$
 where $f = tanh \left[\alpha \left(\frac{S_S^*}{S_{min}^*} - 1 \right)^{\beta} \right]$ and $J_{deep}^* = (2[S_S^* - ln(1 + S_S^*)])^{1/2}$

- 4. Compute J^* $J^* = K^*(S^* S_S^*)$
- 5. Convert J^* to J $J = J^* (K \hat{q} X_f D_f)^{1/2}$
- 6. Compute $X_f L_f$

$$X_f L_f = YJ/b'$$

- Parameter values
 - $-\hat{q}$, K, Y, and b: obtained from batch experiments
 - D depends on size of a molecule
 - $-D_f$ depends on D but is smaller
 - L depends on D and u
 - b' depends on the tangential shear stress

- Analyzing a completely mixed biofilm reactor
 - Steady state mass balance:

$$0 = QS^0 - QS - J \cdot aV$$
 (substrate)
$$0 = YJ \cdot aV - b'X_fL_f \cdot aV$$
 (active biofilm biomass)
$$0 = -X_aQ + b_{det}X_fL_f \cdot aV$$
 (active suspended biomass)

- Now S as an unknown variable:
 - Iterative approach for *S*: guess *S*, then go through steps 1-6 to get calculated *S*, then guess new *S*, steps 1-6, then until guessed *S* = calculated *S*
 - We did this by our second spreadsheet