Development of a simplified model for the fixed biofilm reactor

Sushovan Sarkar and Debabrata Mazumder

ABSTRACT

A simplified fixed biofilm model was developed to formulate the relationship between the substrate concentrations at both the entry and exit, at the biofilm–liquid interface and at the biofilm attached surface along with average substrate flux in the biofilm, substrate flux at the biofilm–liquid interface and effective biofilm thickness. The model considered the substrate mass transport external to the biofilm and into the biofilm as per Fick's law and the steady state substrate as well as biomass balance for attached growth microorganisms. Monod's growth kinetics has been adopted in substrate utilization, incorporating relevant boundary conditions. The numerical solution of model equations was accomplished for calculating average flux and exit substrate concentration and thereafter the Runge–Kutta method was employed for determining effective biofilm thickness. Consequently, two computer programs were developed for the purpose of rapid solution. The model was satisfactorily applied to data available from the literature for checking its accuracy and was validated with the experimental results. The model was found to be an easy, accurate and fast method that can be used for process design of a fixed biofilm reactor.

Key words | experimental validation, fixed biofilm process, mathematical modelling, Runge–Kutta method, simplified solution

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NOTATION

- X_f Attached biomass concentration (mg/cm^3)
- S_0 Substrate concentration of the influent (mg/cm^3)
- S_w Effluent substrate concentration after set batch period (mg/cm^3)
- μ Specific growth rate μmax = maximum specific growth rate (d^{-1})
- θ Hydraulic retention time
- a Specific surface area of supporting media (cm^{-1})
- b_t Total biomass loss rate from biofilm (day^{-1})
- J Flux of rate-limiting substrate into biofilm (mg/(cm^2·day))
- K Half-velocity coefficient (mg/cm^3)
- k Maximum specific rate of substrate use (day^{-1})
- Y Bacteria yield coefficient (mg/mg)
- D Diffusion coefficient in liquid (cm^2/day)
- D_f Diffusion coefficient in biofilm (cm^2/day)
- L Diffusion layer thickness (cm)
- L_f Total biofilm thickness (cm)

INTRODUCTION

Biofilm plays an important role in biological treatment of wastewater as high biomass concentration allows large volumetric loadings and good effluent quality, utilizing low energy consumption, and these can be maintained without the need for sludge separation and sludge recycling (Rittmann 1982). In a fixed biofilm reactor (FBR), the biofilm attached to immobile solid media utilizes substrate as the liquid passes through the reactor in a quasi-plug-flow manner. Besides this, the biofilm process can be easily operated in a continuous flow mode with minimal biomass loss. Biomass is applicable for treating wastewater containing refractory substances and would not introduce any trace of contamination into it. The physical and chemical stability of the biocatalyst can be improved by a biofilm process with low power input (Mudliar *et al.* 2008).

Very limited research works have been performed in the area of steady-state biofilm models with analytical validation for wastewater treatment. All such endeavors also have certain limitations in respect of mode of application. There was

doi: 10.2166/wst.2015.377

no explicit general solution of the second order differential equation of substrate mass balance in the research work by Williamson & McCarty (1976); instead, it was solved for two limiting cases of Monod's equation, i.e. when $S >> K$ and when $S << K$, where S = rate-limiting substrate concentration (mg/l) and K = Monod half-velocity coefficient (mg/cm^3). The Runge–Kutta finite difference technique was applied in an approximate solution of the second order differential equation of mass balance of substrate in the biofilm (Williamson & McCarty 1976). However, the above biofilm model suffered from a drawback that it had not considered such terms as specific surface area, hydraulic retention time etc., which are the crucial parameters in designing an FBR. In the biofilm model by Williamson and McCarty, nomographs were used in the solution of the biofilm model, causing an approximation while deriving the output results. The exit substrate concentration (S_w) could not be determined from these nomographs, while the substrate concentration at the biofilm–liquid interface along with substrate flux and biofilm thickness could be determined by several trial processes.

Later on, thickness of total biofilm in the steady state biofilm model was proposed by Rittmann & McCarty (1980a, b) and by Huang & Jih (1997). However, this model could not determine the effective thickness of biofilm pertinent to a deep biofilm. pseudo-analytical analysis with dimensionless variables was done initially by Rittmann & McCarty (1980a, b) and subsequently by Saez & Rittmann (1991) for solving the steady state biofilm model. However, the said analytical model did not differentiate between a solution for the completely mixed biofilm reactor and one for the FBR. The analytical problems for the FBR were mainly solved by a pseudo-analytical model considering known exit substrate concentration with given kinetic coefficients. The solution process was also found to be approximate, complicated and lengthy. Two levels of iteration are required simultaneously to determine the desired outputs from the steady state biofilm model.

Further, a set of normalized loading curves with dimensionless variables were developed from a pseudo-analytical model (Rittmann & McCarty 1980a, b; Heath *et al.* 1990). This graphical procedure presented an easy but approximate solution in this case. Chances of human error while reading the output results from the normalized loading curves can hardly be avoided in determining an output variable like substrate flux. The main drawback of the normalized loading curve is that it can be used for a given exit substrate concentration (S_w) only and it is unable to determine the effective biofilm thickness (L_e).

A set of nomographs were also developed correlating dimensionless substrate concentration at the biofilm–liquid interface, dimensionless substrate flux, dimensionless biofilm thickness and dimensionless minimum substrate concentration required to sustain the flux (Suidan & Wang 1985). The solution of this model was also an approximate one and only the total biofilm thickness could be determined, as before. In earlier research, AQUASIM programming was used for testing the existing modeling on the biofilm reactor (Wanner & Morgenroth 2004). However, no specific handy flowchart for application of the programming using independent kinetic modeling was created in the research.

To overcome the above drawbacks and limitations, a simplified model solution for the FBR is thus developed with computer programming in FORTRAN. It has been formulated to easily calculate all related output parameters like exit substrate concentration and average substrate flux as well as effective and total biofilm thickness required for the process design of the reactor. The performance of this proposed biofilm model has been examined with a set of representative input variables and standard kinetic data along with the simulated outputs obtained from the literature. The proposed model has also been validated with the experimental results derived from a FBR.

Model description

The conceptual diagram of a typical FBR containing attached-phase biomass is shown in Figure 1.

In the above system, substrate firstly reaches the biofilm media and then flows through the biofilm–liquid interface before penetrating through the biofilm as shown in Figure 2.

From Figure 2, it is evident that the entering substrate concentration S_0 in the bulk liquid becomes the entering substrate concentration S_s and exiting substrate concentration

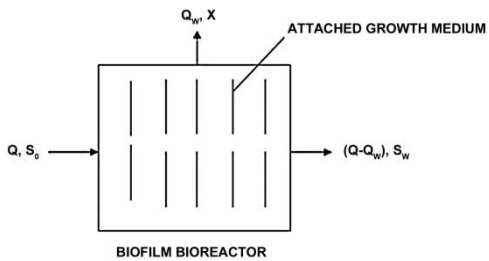

Figure 1 | Schematic diagram of a fixed biofilm reactor.

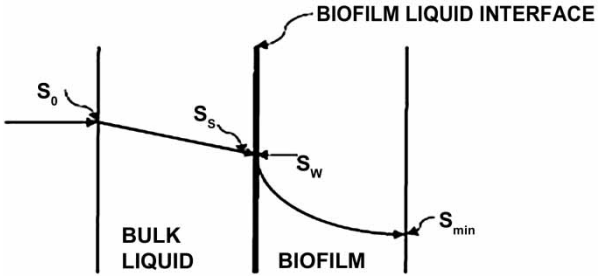

Figure 2 | Profile of substrate concentration in a fixed biofilm reactor.

S_w at the biofilm–liquid interface due to diffusion in the stagnant liquid layer attached to biofilm and it further decreases to S_{min}, i.e. the minimum substrate concentration at the biofilm attachment surface. The substrate flux which is varying over the biofilm thickness can be averaged to account for the substrate mass balance. This average flux must be same as that derived from S_s and S_w in the biofilm–liquid interface.

Now, from the external mass transport according to Fick's fist law

$$J = \frac{D}{L} * (S_0 - S_s) \tag{1}$$

where,

- J substrate flux into the biofilm (mg/(cm^2·day)),
- D molecular diffusion coefficient in liquid (cm^2/day),
- L thickness of effective diffusion layer (cm),
- S_0, S_s entry substrate concentrations in the bulk liquid and at biofilm–liquid interface respectively (mg/cm^3).

The steady state substrate balance for the attached growth is

$$S_s - S_w - a * J_{avg} * \theta = 0 \tag{2}$$

where,

- S_w exiting substrate concentration at biofilm–liquid interface (mg/cm^3)
- a specific surface area of supporting media (cm^{-1}),
- J_{avg} average substrate flux into the biofilm (mg/(cm^2·day)),
- θ empty bed hydraulic retention time (hr).

Again, from the mass balance equation for substrate in the biofilm considering Monod's kinetics,

$$\frac{d^2 S_f}{dz^2} = \frac{k X_f S_f}{D_f (K + S_f)} \tag{3}$$

where,

- S_f substrate concentration at a point in the biofilm (mg/cm^3),
- k maximum specific rate of substrate utilization (per day),
- X_f active biomass density within the biofilm (mg/cm^3),
- D_f molecular diffusion coefficient of the substrate in the biofilm (cm^2/day),
- K half-velocity coefficient (mg/cm^3).

Referring to Figure 2, the boundary conditions for solving the above second order differential equation may be taken as,

(i) at the attachment surface (i.e. at $z = 0$) there will be no flux, i.e. $\frac{dS_{f0}}{dz} = 0$ and effluent substrate concentration is S_{min}

(ii) at the biofilm–liquid interface (i.e. at $z = L_e$) $J = D_f * \frac{dS_f}{dz}$

Methodology of solution

To calculate the average value of 'substrate flux' (J_{avg}) in the biofilm, five divisions in the substrate concentration profile inside the biofilm may be considered as shown in Figure 3.

Equation (2) can be solved to find out 'J' at different points of substrate concentrations as follows:

$$J_1 = \sqrt{2kX_f D_f [(S_1 - S_{min}) + K \ln[(K + S_{min})/(K + S_1)]}} \tag{4}$$

$$J_2 = \sqrt{2kX_f D_f [(S_2 - S_1) + K \ln[(K+S_1)/(K+S_2]] + (J_1/D_f)^2} \tag{5}$$

$$J_3 = \sqrt{2kX_f D_f [(S_3 - S_2) + K \ln[(K+S_2)/(K+S_3)]] + (J_2/D_f)^2} \tag{6}$$

$$J_4 = \sqrt{2kX_f D_f [(S_4 - S_3) + K \ln[(K+S_3)/(K+S_4)]] + (J_3)^2} \tag{7}$$

$$J_5 = \sqrt{2kX_f D_f [(S_w - S_4) + K \ln[(K+S_4/(K+S_w)]] + (J_4)^2} \tag{8}$$

$$S_{min} = K * \frac{b_t}{Y * k - b_t},$$

where b_t = an overall biofilm specific loss rate (day^{-1}), Y = bacteria yield coefficient,

J_1, J_2, J_3 J_4, and J_5 are substrate flux corresponding to substrate concentration S_1, S_2, S_3, S_4 and S_w respectively. It is obvious that the substrate flux (say J_0) corresponding to S_{min} is zero. Therefore, the arithmetic average of J can be calculated as $J_{avg} = (J_0 + J_1 + J_2 + J_3 + J_4 + J_5)/6$.

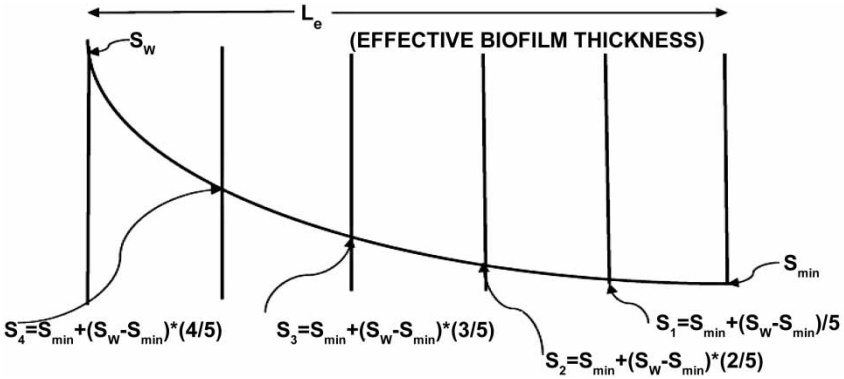

Figure 3 | Divisions in substrate concentration profile within the biofilm.

Again, from Equation (2),

$$S_w = S_s - a*J_{avg}*\theta \tag{9}$$

and from Equation (1),

$$S_s = S_0 - \left(\frac{L}{D}\right)*J_5. \tag{10}$$

Hence, from Equations (8) and (9),

$$S_w = S_0 - \left(\frac{L}{D}\right)*J_5 - a*J_{avg}*\theta. \tag{11}$$

Now, initially a trial value of S_w has been considered somewhat more than the value of S_{min} and the iteration for determining S_w, i.e. exiting substrate concentration, is completed when S_w from Equation (9) exactly matches the assumed trial value.

To calculate the effective biofilm thickness, applying the Runge–Kutta method, the solution of Equation (3) can be obtained as follows:

$$\frac{d^2S_f}{dz^2} = f\left(z, \frac{dS_f}{dz}\right),\ \frac{dS_f}{dz}(z_0) = \frac{dS_{f0}}{dz} = K1 = 0\,[S_{f0} = S_{min} atz = 0]$$

$$L1 = f\left(z_0, \frac{dS_{f0}}{dz}\right) = \frac{d^2S_{f0}}{dz^2} = \frac{kX_fS_{f0}}{D_f(K + S_{f0})}$$

$$\frac{dS_{f1}}{dz} = \frac{dS_{f0}}{dz} + 0.5*L1*h = K2,$$

where h = step = effective biofilm thickness (cm), and is the distance between z = 0 (at the attachment surface) and z = L_e (at the biofilm–water interface)

$$L2 = h*f\left(z_0 + \frac{h}{2}, \frac{dS_{f1}}{dz}\right) = h*\frac{d^2S_{f1}}{dz^2} = \frac{kX_f(S_{f0} + 0.5K1*h)}{D_f(K + S_{f0} + 0.5K1*h)}$$

$$\frac{dS_{f2}}{dz} = \frac{dS_{f0}}{dz} + 0.5*L2*h = K3$$

$$L3 = h*f\left(z_0 + \frac{h}{2}, \frac{dS_{f2}}{dz}\right) = h*\frac{d^2S_{f2}}{dz^2} = \frac{kX_f(S_{f0} + 0.5K2*h)}{D_f(K + S_{f0} + 0.5K2*h)}$$

$$\frac{dS_{f3}}{dz} = \frac{dS_{f0}}{dz} + L3*h = K4$$

$$L4 = h*f\left(z_0 + h, \frac{dS_{f3}}{dz}\right) = h*\frac{d^2S_{f3}}{dz^2} = \frac{kX_f(S_{f0} + K3*h)}{D_f(K + S_{f0} + K3*h)}$$

$$\Delta Y(1) = \frac{h}{6}*(K1 + 2*K2 + 2*K3 + K4) \tag{12}$$

$$\Delta Y(2) = \frac{h}{6}*(L1 + 2*L2 + 2*L3 + L4) \tag{13}$$

where $\Delta Y(1)$ stands for increment of substrate concentration, $\Delta Y(2)$ stands for $\frac{dS_f}{dz}$.

The substrate concentration and the respective flux at the liquid-biofilm interface can be denoted as S_w and J_4 respectively. Therefore,

$$S_w = S_{min} + \Delta Y(1) \tag{14}$$

$$J_5 = D_f*\Delta Y(2) \tag{15}$$

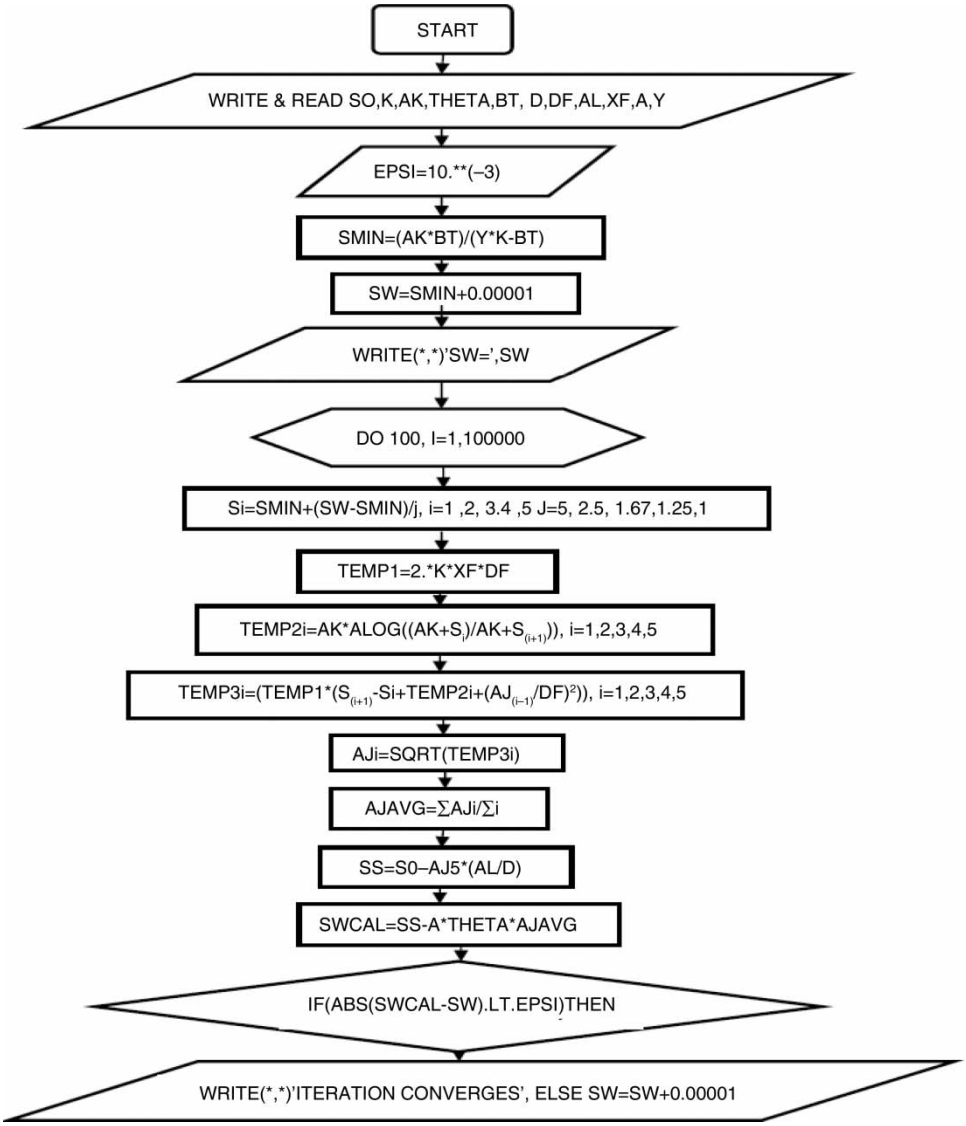

Figure 4 | Flowchart for programming in FORTRAN to calculate unknown exiting substrate concentration S_w and average substrate flux J_{avg}.

Now, from the steady state mass balance of active microorganisms in a biofilm,

$$L_f = \frac{J*Y}{X_f*b_t}, \tag{16}$$

where L_f = total biofilm thickness (cm).

The above model equation is useful to determine the total biofilm thickness in a fixed biofilm reactor system where purely attached growth is considered.

In order to calculate S_w, J and L_e using Equations (4)–(14), i.e. to solve the biofilm model, two flowcharts were constructed as shown in Figures 4 and 5. Consequently, two detailed FORTRAN programs have been developed on the basis of those flowcharts; for the detailed programming please contact the corresponding author.

Essence of flowcharts constructed

Two flowcharts for computer programming in FORTRAN have been prepared approaching the iteration processes, with a view to calculate unknown exiting substrate concentration S_w, substrate flux J (Figure 4) and effective biofilm thickness L_e (Figure 5). In the first flowchart, Equations (4)–(11) are simultaneously iterated to calculate

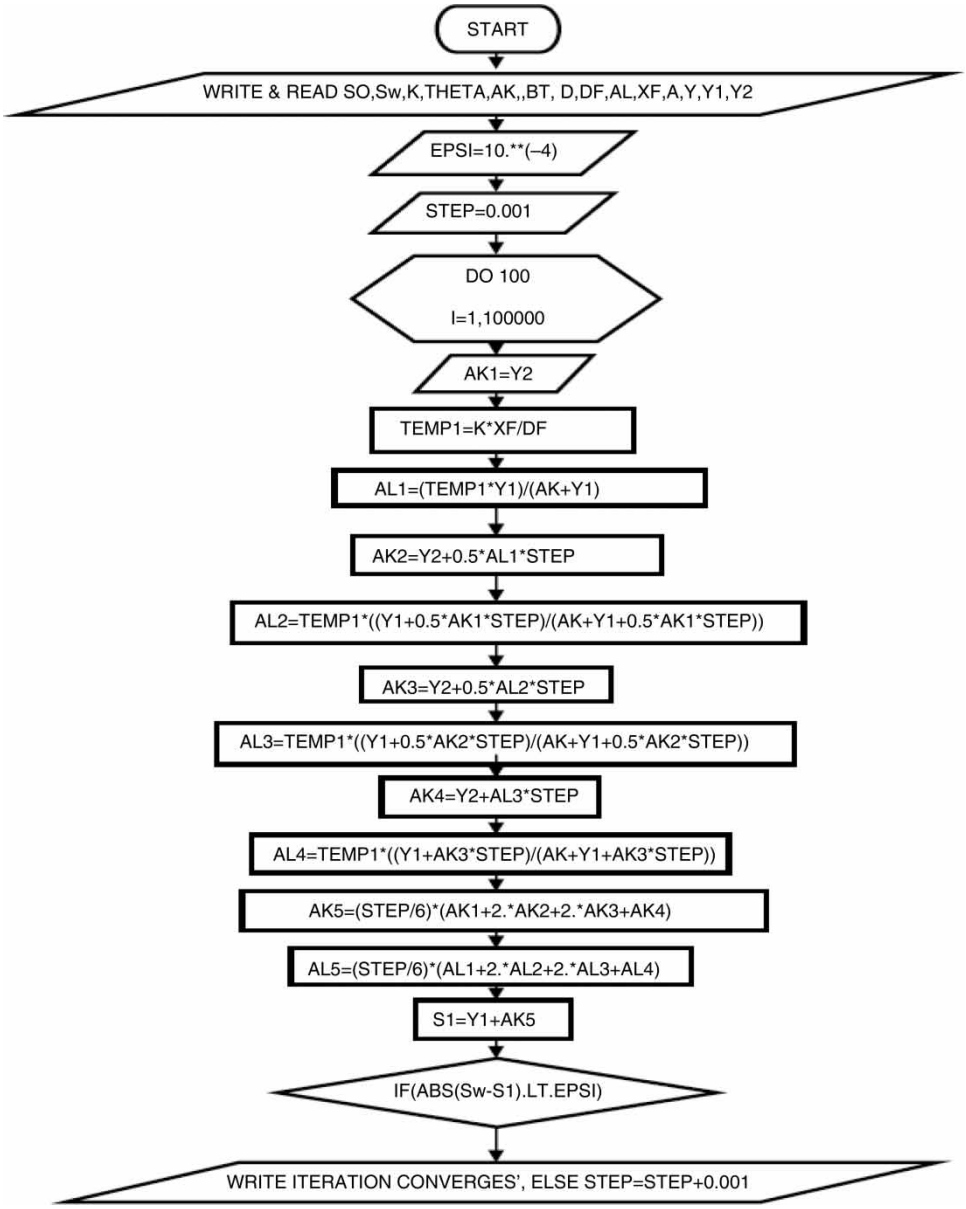

Figure 5 | Flowchart for programming in FORTRAN to calculate effective biofilm thickness (L_e) under a known exiting substrate concentration (S_w).

the unknown exiting substrate concentration S_w at the biofilm–liquid interface and unknown flux J. The initial iteration value S_w was assumed in this flowchart as being a higher value than S_{min} (which is required to sustain a steady biofilm growth). The second flowchart utilized the value of S_w as obtained from the first flowchart to calculate L_e following the concept of the Runge–Kutta method of analysis. The convergence of iteration was attributed at the liquid/biofilm interface when computed substrate concentration (S_w) becomes equal to the assumed one.

Modality of application of the developed model

The developed solution method can be applied to find out the exiting substrate concentration (S_w) at the biofilm–liquid interface and the average substrate flux (J_{avg}) by running the FORTRAN program based on the flowchart as shown in Figure 4. Once the values of S_w and J_{avg} are estimated, the FORTRAN program based on the flowchart as shown in Figure 5 can be run for determining both the total and effective biofilm thickness L_f and L_e.

Table 1 | Comparison of output parameters (S_w, J, L_e and L_f) using various biofilm models

S_o (mg/cm^3)	∂ (hr)	a (cm^{-1})	X_f (mg/cm^3)	S_w (mg/cm^3)			J(mg/(cm^2·day))			L_e(cm)			L_f (cm)		
				Case 1	Case 2	Case 3	Case 1	Case 2	Case 3	Case 1	Case 2	Case 3	Case 1	Case 2	Case 3
0.0025	1.5	1	40	0.0004	0.0005	0.0005	0.024	0.02	0.022	0.0001	***	***	0.003	0.0025	0.00275
0.0035	1.5	1	40	0.0005	0.0006	0.0006	0.0348	0.026	0.029	0.0001	***	***	0.0037	0.0033	0.0036
0.005	1.5	1	40	0.0007	0.0008	0.0008	0.05	0.04	0.05	0.0001	***	***	0.006	0.005	0.006
0.007	1.5	1	40	0.00094	0.001	0.001	0.07	0.052	0.06	0.0001	***	***	0.0087	0.0064	0.0075
0.008	1.5	1	40	0.0011	0.0012	0.0012	0.08	0.063	0.07	0.0001	***	***	0.0100	0.0079	0.0087
0.01	1.5	1	40	0.0014	0.0014	0.0014	0.1	0.076	0.085	0.0047	***	***	0.0125	0.0095	0.01
0.011	1.5	1	40	0.0015	0.0016	0.0016	0.11	0.089	0.1	0.0059	***	***	0.0125	0.0110	0.012
0.012	1.5	1	40	0.0016	0.0018	0.0018	0.12	0.1	0.11	0.0069	***	***	0.0150	0.0130	0.014
0.013	1.5	1	40	0.0018	0.002	0.002	0.13	0.11	0.12	0.0083	***	***	0.0138	0.0140	0.015
0.015	1.5	1	40	0.0021	0.0022	0.0022	0.149	0.13	0.14	0.01	***	***	0.0175	0.0160	0.0175
0.03	1.5	1	40	0.0044	0.0044	0.0044	0.29	0.25	0.27	0.016	***	***	0.0360	0.0320	0.034

***indicates the corresponding values could not be determined by the respective method.

RESULTS OF ANALYSIS

In the present method, the analytical solution has been presented as case 1. At the same time, the pseudo-analytical solution by Rittmann & McCarty (1980a, b) and normalized loading curves by Heath *et al.* (1990) are considered as case 2 and case 3 respectively. The relevant output parameters like S_w, J, L_e and L_f have been computed under 11 distinct input sets in all the three cases, wherever those are suitable for determination. A comparison chart of the output results as stated above with the same kinetic coefficients (as adopted by Rittmann & McCarty (1980a, b)) is shown in Table 1. The kinetic co-efficients and physical data in this regard are as follows: $k = 8\ day^{-1}$, $Y = 0.5$, $K = 0.01\ mg/cm^3$, $b_t = 0.1\ day^{-1}$, $D = 0.8\ cm^2/day$, $D_f = 0.64\ cm^2/day$, $L = 0.01$ cm.

In order to validate the present solution method, the laboratory scale FBR as stated earlier was run under semi-batch mode using municipal wastewater. The results of this study are presented in Table 2.

Case 1 (Proposed fixed biofilm model)

Iteration performed by equating

$$J = (S_0 - S_s)^*(D/L),\ J_{avg} = (S_s - S_w)/(a^*\partial),$$

$$J = \sqrt{2kX_fD_f(S_f - S_w + K\ln(K + S_w/K + S_f))},$$

Runge–Kutta method by solving $\frac{d^2S_f}{dz^2} = \frac{kX_fS_f}{D_f(K+S_f)}$ with iteration of biofilm thickness.

Case 2

As per formula applied in the pseudo-analytical solution as accomplished in Rittmann & McCarty (2001).

Case 3

By using normalized loading curve as per Heath *et al.* (1990).

The kinetic co-efficients and physical data in this regard are as follows: $k = 5\ day^{-1}$, $Y = 0.5$, $K = 0.012\ mg/cm^3$, $b_t = 0.1\ day^{-1}$, $D = 0.8\ cm^2/day$, $D_f = 0.64\ cm^2/day$, $L = 0.01$ cm.

DISCUSSION OF RESULTS

In Table 1, the performance of the present solution method for the FBR has been compared with the well-known

Table 2 | Comparison of output parameters (S_w, J, L_e and L_f) with the experimental data obtained from semi-batch studies

				S_w (mg/cm^3)		J (mg/(cm^2·day))		L_e (cm)		L_f (cm)	
S_0 (mg/cm^3)	∂ (hr)	a (cm^{-1})	X_f (mg/cm^3)	As per proposed model	As per laboratory study	As per proposed model	As per laboratory study	As per proposed model	As per laboratory study	As per proposed model	As per laboratory study
0.1	3	0.402	10	0.0455	0.04	0.739	0.76	0.0883	**	0.369	0.38
0.1	6	0.402	10	0.03	0.027	0.55	0.6	0.0763	**	0.275	0.3
0.1	9	0.402	10	0.0227	0.02	0.439	0.44	0.0692	**	0.22	0.22
0.12	3	0.402	10	0.0567	0.05	0.86	0.88	0.0953	**	0.43	0.44
0.12	6	0.402	10	0.037	0.035	0.67	0.69	0.0821	**	0.34	0.345
0.12	9	0.402	10	0.0284	0.025	0.523	0.55	0.0749	**	0.26	0.275
0.13	3	0.402	10	0.0625	0.055	0.92	0.96	0.0986	**	0.46	0.48
0.13	6	0.402	10	0.0426	0.038	0.704	0.76	0.0863	**	0.352	0.38
0.13	9	0.402	10	0.0314	0.028	0.563	0.593	0.0776	**	0.28	0.296

pseudo-analytical solution by Rittmann & McCarty (1980a, b) and normalized loading curves by Heath *et al.* (1990). In Table 1, the exiting substrate concentration, i.e. S_w at biofilm–liquid interface, was assumed both in case 2 and case 3 as per the simulated results presented in Rittmann & McCarty (1980a, b) for determining the substrate flux. Thus a suitable value of both initial substrate concentration (S_0) and hydraulic retention time (θ) was selected in the simulation study as shown in the comparison table to match with the output results as given in Rittmann & McCarty (1980a, b). The calculated values of S_w as per the present method mostly tallies with the assumed values considered in case 2, i.e. in the pseudo-analytical solution by Rittman and McCarty and in case 3, i.e. in normalized loading curves by Heath *et al.* (1990). Similarly, the average substrate flux (J_{avg}) obtained in case 1 (i.e. in the present method) is in good agreement with that in the pseudo-analytical solution by Rittmann & McCarty (2001) and in the normalized loading curves by Heath *et al.* (1990). The slight deviation of the results from the present solution method may be attributed to the approximation in trial and error analysis in the pseudo-analytical Solution and approximation in studying the values by interpolation from the normalized loading curves, which caused observation error.

The analytical solution process by case 2 was found cumbersome involving a series of tedious calculations. It establishes the simplicity of the proposed biofilm model for determining S_w, the crucial parameter to calculate the substrate flux (J).

It is interesting to note that no existing method (like case 2 or case 3) could determine the L_e (effective biofilm thickness) value. It has been possible to evaluate this by the present simplified method (case 1) only. Therefore, it would be useful to get an idea about the nature of the biofilm (i.e. shallow or deep), provided the total biofilm thickness is already calculated.

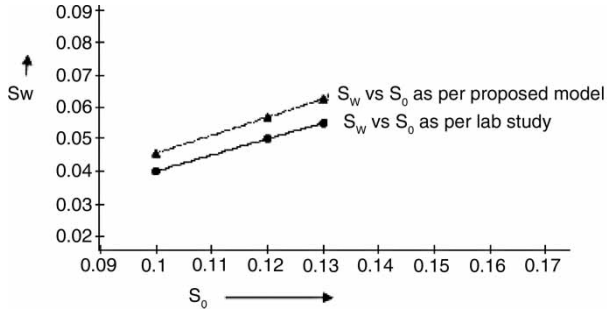

Figure 6 | Comparison of plot S_w vs S_0 between proposed model and laboratory study at $\partial = 3$ hr, a = 0.402 cm^{-1} and $X_f = 10$ mg/cm^3.

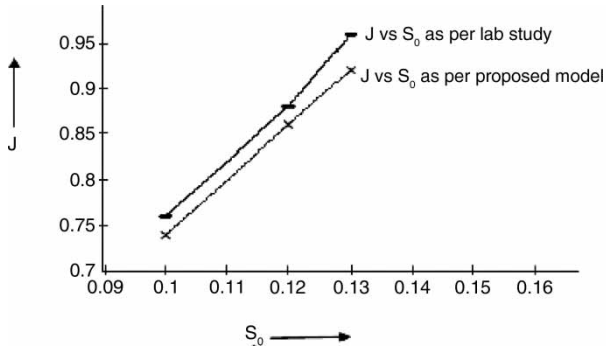

Figure 7 | Comparison of plot J vs S_0 between proposed model and laboratory study at $\partial = 3$ hr, a = 0.402 cm^{-1} and $X_f = 10$ mg/cm^3.

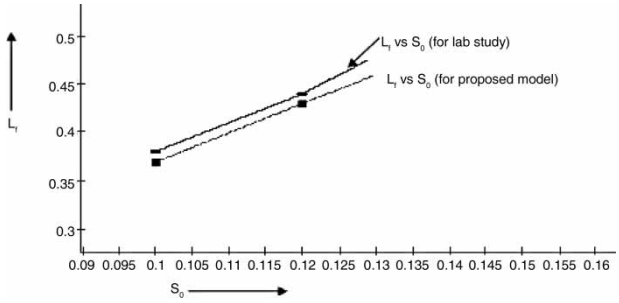

Figure 8 | Comparison of plot L_e vs S_0 between proposed model and laboratory study at $\partial = 3$ hr, $a = 0.402$ cm^{-1} and $X_f = 10$ mg/cm^3.

The value of L_f, i.e. total biofilm thickness in case 2, i.e. in the pseudo-analytical solution by Rittmann & McCarty (1980a, b), is almost equal to that with the proposed biofilm model. However, there is a slight deviation in the value of L_f obtained from the proposed model with respect to case 3, i.e. in normalized loading curves by Heath *et al.* (1990). This deviation is reasonably attributed to the nominal difference in J values under those two respective cases. The experimental outputs as shown in Table 2 are also in a good agreement with those calculated using the present method. The results of the proposed model and laboratory studies have been plotted in Figures 6–8, which also show a similarity between the two. Thus the present solution model not only corroborates the existing methods analytically, but also is validated reasonably with the experimental data. Hence, it can be regarded as a simplified tool for the sake of process design of an FBR.

CONCLUSION

The significant outcomes from the present solution method reveal that it can truly differentiate between an FBR and a completely mixed biofilm reactor (Sarkar & Mazumder submitted) which otherwise cannot be differentiated from the existing classical biofilm models like the pseudo-analytical solution and normalized loading curves. Moreover, no analytical examples were shown with any existing steady state biofilm model in earlier research for determining the unknown exiting substrate concentration, although one classical example was shown by Rittmann & McCarty (1980a, b), where the exiting substrate concentration was assumed for determining the substrate flux in a special case. Again, from the nomographs developed by Williamson & McCarty (1976), no exiting substrate concentration (S_w) can be determined, instead the entering substrate concentration (S_s) at the biofilm–liquid interface can be evaluated along with substrate flux (J) after several trials. The comparison of results using various biofilm models reveals that all relevant outputs like S_w, J, L_e and L_f can be determined only in the present solution model. The effective biofilm thickness L_e could not be found out in case 2, i.e. in pseudo-analytical solution by Rittmann & McCarty (1980a, b), or in case 3, i.e. in normalized loading curves by Heath *et al.* (1990). So there is no scope for ascertaining whether the biofilm is deep or shallow in those two existing methods. It can be further concluded that the exiting substrate concentration in the biofilm–liquid interface (S_w) could not be evaluated by means of calculation under the normalized loading curve, resulting in greater chance of error. The main drawback of the existing models is availability of no rational relationship between the substrate flux and the substrate concentration at the biofilm–liquid interface. The existing biofilm model proposed by Rittmann & McCarty (1980a, b) is complicated, cumbersome and time consuming because of two levels of iterations simultaneously involving various dimensionless parameters.

The accuracy of the present solution model lies with the fact that all the output results are mostly matching those obtained from classical models, especially those of Rittmann & McCarty (1980a, b). The present model provides a simple tool to estimate the exiting substrate concentration in the biofilm–liquid interface, the average substrate flux and the effective biofilm thickness. Since it does not consider any nomograph or normalized loading curves etc., there is no chance of any manual error. Considering all the aspects the present solution method can be proposed for rational design of the fixed biofilm process with a good accuracy.

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First received 14 January 2015; accepted in revised form 7 July 2015. Available online 18 July 2015