

Modelling a spatially heterogeneous biofilm and the bulk fluid: selected results from Benchmark Problem 2 (BM2)

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Abstract The numerical simulation of mass transfer and conversion in spatially heterogeneous biofilms on the meso-scale requires an accurate description of the hydrodynamics in the biofilm systems and of spatial effects. This leads to systems of three-dimensional nonlinear partial differential equations that are numerically very expensive to solve and to data requirements that are not easy to meet. In this paper several modeling approaches to reduce the physical complexity and, hence, accelerate the computation are compared. They range from a mere reduction of dimensionality by lumping the problem along a secondary flow direction to global mass balances or empirical correlations, at the core of which a one-dimensional boundary value problem must be solved. It is found that even strongly simplified models can describe the qualitative behaviour of the model with regard to variations in the geometrical and hydrodynamic model parameters quite well. In order to obtain also quantitatively reliable results the hydrodynamics must be considered in an appropriate manner.

Keywords Benchmark problem; biofilm architecture; biofilm model; hydrodynamics; mass transfer; physical complexity

Introduction

The second in a series of three benchmark problems formulated by IWA's Task Group on Biofilm Modeling (Noguera and Morgenroth, 2004; Morgenroth *et al.*, 2004; Rittmann *et al.*, 2004) introduces additional physical complexity into the problem description. It addresses the observation that biofilms in reality form in spatially heterogeneous architectures, which can induce sometimes highly complex flow patterns affecting mass conversion in the system (Picioreanu *et al.*, 2000; Eberl *et al.*, 2000). This effect, however, cannot be taken into account in classical one-dimensional biofilm models in a straightforward manner.

Instead of the assumption of a completely mixed bulk fluid, mass transport by diffusion and advection in the fluid region are considered here. Due to the sometimes complicated geometry of biofilm architectures, the latter requires inclusion of the full hydrodynamics in the flow field explicitly in the simulations. This leads to a system of several nonlinear

three-dimensional partial differential equations, which is numerically expensive to solve. Furthermore, the data requirements for this modelling approach are tremendous. Therefore, engineers are striving for reliable model simplifications that require less information and lead to an accelerated computation.

In a concerted modelling and simulation effort, we investigated whether a detailed description of local physical and geometrical effects on the meso-scale is necessary in reactor (macro-) scale applications, where the purpose of the modelling is often only to calculate the total mass fluxes into the biofilm, i.e., the global mass conversion rates. The goal of this study is to compare global results (i.e., lumped results for the reactor segment) that are obtained by different approaches to tackle the physical complexity. The parameters to be compared are the production rate of biomass in the considered reactor segment, as well as the (average) concentration of the dissolved substrate at the interface between the biofilm and the surrounding water.

System description and governing model

The biofilm system under consideration is a mono-species biofilm with one limiting dissolved substrate in a small rectangular domain, as sketched in Figure 1. It can be represented by liquid and biofilm phases, which are separated by a sharp interface. The liquid phase is defined by the absence of biomass. That is, the actual biofilm is formed by the accumulation of biomaterial. It is assumed to be rigid. The biomass density is assumed to be constant throughout the biofilm. In the liquid region, the dissolved substrate is transported by advection and diffusion. In the biofilm, only diffusive transport is taken into account. In addition, substrate is depleted there by the microorganisms, i.e., by the biomass. This substrate uptake is modelled by standard Monod kinetics as described in Wanner and Morgenroth (2004). At the biofilm/liquid interface, it is postulated that the substrate concentration is the same on both sides and that the diffusive flux across the interface satisfies a simple balance; that is, the diffusive flux out of the liquid region fully enters the biofilm (in other words: no losses due to interface reactions occur; see Eberl *et al.*, 2000). In order to allow for the consideration of advective transport in the liquid phase, the flow field must be taken into account as well. The governing model is given by the incompressible Navier-Stokes equations. As in Morgenroth *et al.* (2004), Rittmann *et al.* (2004), and many previous biofilm modelling studies, the system is considered in a quasi-steady state, based on the usual time-scale arguments. The model description is completed by a set of boundary conditions connecting the biofilm segment under consideration with the exterior world. For the hydrodynamics the following specifications are made: periodic in primary flow directions, symmetric in secondary flow directions parallel to the primary flow; no-slip conditions at the biofilm/liquid interface. At the top boundary, a flow velocity parallel to the substratum is prescribed. Thus, the flow is driven by a Couette flow-like mechanism. This is described and discussed in more detail in Picioreanu *et al.* (2000) and in Eberl *et al.* (2000), where the governing transport equations can also be found. For the dissolved substrates, homogeneous Neumann boundary conditions (i.e., no Fickian flux across the boundaries of the domain) are specified, with the exception of the inflow boundary, where Robin conditions are given such that everywhere the sum of advective and diffusive fluxes into the segment equals an assumed purely advective flux determined by the actual flow field and the bulk concentration of the substrate; this was chosen in order to avoid unwanted inflow effects observed with other boundary conditions applied in earlier studies (Picioreanu *et al.*, 2000; Eberl *et al.*, 2000).

In total, BM2 consisted of 15 experiments, although this first survey only reports on seven. The remaining ones will be reported in a forthcoming publication. In all cases, the same smooth and wavy surface biofilm layer is used but the thickness of the base film varies (see Figure 1). The surface layer was taken from Eberl *et al.* (2000), where a more detailed

description can be found. Physical and biochemical parameters are summarised in Tables 1 and 2. The latter includes some lumped geometric parameters quantifying some aspects of the biofilm structure.

Model simplifications in this study

The numerical simulation of the full three-dimensional model requires the solution of the Navier-Stokes equations in a complicated domain and, therefore, is computationally very expensive. Hence, the description of the physical complexity of the system, expressed in geometrical and hydrodynamic complexity, was simplified in various ways and to varying degrees to obtain faster methods. The modelling approaches taken into account in this study are:

- (M1) A fully three-dimensional numerical simulation of hydrodynamics and mass transfer in the specified biofilm architectures (the original problem; serves as reference data for comparison).
- (M2) A reduction of the three-dimensional biofilm system to a two-dimensional one with comparable characteristic geometrical property; full two-dimensional hydrodynamics and mass transfer.

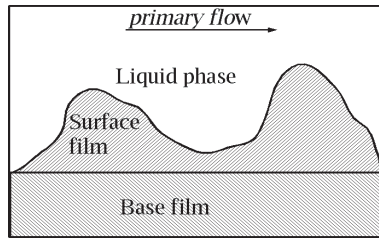


Figure 1 Schematic description of the biofilm system under consideration. The computational domain is divided into a liquid phase (no biomass, white) and the actual biofilm (biomass, grey), separated by an interface. Channels belong to the liquid phase, while clusters belong to the biofilm phase

Table 1 List of parameters that remain unchanged for all numerical experiments

Length of system	1.6 mm
Width of system	94.12 μm
Area enlargement	1.649
Kinematic viscosity	0.00864 m^2/d
Fluid density	1 g/d
Biomass density	10,000 g/m^3
Diffusion coefficient	10^{-4} m^2/d
Monod constant	4 g/m^3
Maximum specific growth rate	5.88 1/d
Yield coefficient	0.63

Table 2 List of changing parameters; the first five columns represent some characteristics of the biofilm structures, while the last two columns describe environmental conditions

	Height of system [mm]	Base film thickness [mm]	Avg. biofilm height [mm]	Max biofilm height [mm]	Volume of biofilm [10^{-12}m^3]	Bulk concentration [g/m^3]	Max. Flow velocity [m/s]
Case 1	0.3953	0.1067	0.1358	0.1694	20.5	5.0	139.97
Case 2	0.3953	0.1067	0.1358	0.1694	20.5	5.0	13.997
Case 3	0.5835	0.2949	0.3241	0.3576	48.8	5.0	139.97
Case 4	0.5835	0.2949	0.3241	0.3576	48.8	5.0	13.997
Case 5	0.3012	0.01255	0.0417	0.07529	6.29	5.0	139.97
Case 6	0.3012	0.01255	0.0417	0.07529	6.29	5.0	13.997
Case 7	0.3953	0.1067	0.1358	0.1694	20.5	0.5	139.97

- (M3) As in M2, but further simplifying the hydrodynamic description by not taking the irregularity of the structure into account for flow field calculations; two different two-dimensional reductions of the biofilm geometry are used (M3a,b).
- (M4) Reduction to a lumped one-dimensional system with completely mixed bulk and concentration boundary layer; variation in the hydrodynamics expressed in terms of a new model parameter (concentration boundary layer thickness) that is determined by model fitting; full numerical simulation of mass transfer by minimising the total deviation between model and reference data. Comparison criterion is the sum of errors in the total flux of substrate across the biofilm surface, J , the average concentration of the substrate at the biofilm surface, S_{surf} as well as the average substrate concentration at the substratum, $S_{substratum}$, and the biomass production rate.
- (M5) As in M4; using (M5a) J , (M5b) S_{surf} and (M5c) $S_{substratum}$ as sole criterion for adjustment of the concentration boundary layer thickness.
- (M6) As in M4, but with a pseudo-analytical solution of the biofilm model; the new parameter is fitted by minimising the sum of the relative deviations in S_{surf} and J .
- (M7) As in M4 but with a simplified analytical solution of the biofilm model; boundary layer thickness is fitted by minimising the error in J , postulating the relative deviations of S_{surf} and J to be equal and enforcing an *ad hoc* global mass balance on the 1d-reactor under completely mixed conditions as in BM1 (see Morgenroth *et al.*, 2004).
- (M8) A one-dimensional description of the biofilm; hydrodynamics incorporated by a global mass balance for the system (derived from the Gauss' Divergence Theorem; Eberl, *in preparation*).
- (M9) A one-dimensional model, concentration boundary layer thickness replaced by a generalised *a priori* correlation for mass transfer based on Comiti *et al.* (2000).
- (M10) One-dimensional approach, biofilm is divided into 2 characteristic regions according to Morgenroth *et al.* (2000). Instead of explicit hydrodynamics an arbitrarily fixed boundary layer is used; this approach does not provide a well defined average S_{surf} but J .

Note that the approaches relying on fitting a new model parameter to the reference data (M4, M5, M6, M7) do not lead to a closed model and, therefore, cannot be considered a solution to BM2 in the sense of a predictive model as long as there is no *a priori* correlation for this parameter found that could be derived directly from the problem description. In this study, they are included for the purpose of a first investigation of the possibility of describing a physically complex situation by standard one-dimensional biofilm models. In particular, it is of interest whether or not a one-to-one correlation between hydrodynamics and boundary layer thickness can be expected.

Results and discussion

The parameters included in the comparison of the approaches M1 through M10 are the average concentration S_{surf} of the substrate at the biofilm/liquid interface and the total mass flux J from the liquid region into the solid biofilm. Under quasi-steady state conditions, J corresponds to the total production rate of new biomass in the system divided by the yield coefficient. The results are collected in Table 3.

Qualitative system behaviour

The dependency of both measured quantities on the physical variations of the experiment according to the fully three-dimensional model M1 can be summarised as follows. As the base film layer gets thicker, S_{surf} decreases and J increases due to increased microbial activ-

Table 3 Selected results of BM2: Reported are average surface concentration S_{surf} [g/m³] and total mass flux J [10⁻⁷g/d] into the biofilm

Model	Case 1		Case 2		Case 3		Case 4		Case 5		Case 6		Case 7	
	S_{surf}	J	S_{surf}	J	S_{surf}	J	S_{surf}	J	S_{surf}	J	S_{surf}	J	S_{surf}	J
1	2.50	4.59	1.48	2.95	2.41	4.76	1.42	2.99	3.59	2.61	2.54	2.10	0.226	0.502
2	2.35	4.38	1.41	2.81	2.26	4.49	1.36	2.84	3.54	2.65	2.41	2.10	0.21	0.47
3a	3.02	5.21	1.38	2.51	2.89	5.48	1.27	2.61	3.82	2.53	2.34	1.85	0.27	0.610
3b	3.03	5.14	1.36	2.52	2.90	5.44	1.29	2.59	3.88	2.51	2.42	1.81	0.26	0.598
4	2.50	4.60	1.50	2.95	2.43	4.741	1.45	2.98	3.56	2.61	2.47	2.13	0.229	0.502
6	2.51	4.58	1.49	2.92	2.41	4.71	1.42	2.94	3.59	2.67	2.54	2.17	0.23	0.496
7	2.66	4.29	1.69	2.54	2.65	4.29	1.65	2.50	3.45	2.71	2.41	2.21	0.32	0.276
8	2.61	4.72	1.60	3.12	2.52	4.89	1.54	3.17	3.64	2.69	2.60	2.20	0.24	0.518
9	2.71	4.83	1.58	3.07	2.63	4.99	1.54	3.11	3.71	2.71	2.58	2.17	0.24	0.529
10	N/A	3.34	N/A	3.34	N/A	3.41	N/A	3.41	N/A	2.10	N/A	2.10	N/A	0.35

ity in the biofilm. On the other hand, a higher hydrodynamic load induces higher J and S_{surf} due to increased availability of nutrients. If the bulk concentration is reduced, both J and S_{surf} decrease.

This qualitative behaviour is found by all other models in this study with the exception of M10, which by construction does not take the variability of the hydrodynamics into account. Accordingly this model cannot be expected to be sensitive to this parameter, although it agrees qualitatively with the other models regarding variations of the biofilm thickness and the bulk concentration. This model will not be considered further in this report. Moreover, comparing for each model the results obtained for varying biofilm thickness under the same hydrodynamic load (Cases 1, 3, 5 and 2, 4, 6, respectively), as well as for the same biofilm structure but with different flow velocities (Cases 1, 2 as well as 3, 4 and 5, 6) pair-wise, all models show the same trends for S_{surf} and J . In some cases, this match is even quantitatively excellent, e.g. the ratio $S_{surf,Case1}:S_{surf,Case3} = \pm 1.04$ for all models M1 through M9. Thus, we observe that all models show approximately the same qualitative trends and sensitivity to variations in both investigated parameters of physical complexity. A more detailed analysis must be omitted here due to space limitations.

Comparing the values obtained for S_{surf} and J by different models also quantitatively, one must be aware that they are affected by two main factors: (i) the model simplification *per se* and (ii) the numerical methods used for the model solution and for the *a posteriori* calculation of S_{surf} and J from the simulation results (where applicable). Although only (i) should be investigated here, the effects of (ii) sometimes cannot be neglected. The results of Morgenroth *et al.* (2004) might serve as a guide to characterise and judge the numerical uncertainties. In the following discussion, the numerical solutions obtained by the complete three-dimensional model description M1 are used as reference data for the other models.

Quantitative comparison of two-dimensional models

In M2, the three-dimensional biofilm structure is reduced to a two-dimensional one, which is chosen such that some characteristic geometrical parameters are preserved, most notably the area enlargement factor Ae as well as minimum, maximum, and average biofilm height and total biomass (and volume) in the system. In Picioreanu *et al.* (2000) and Eberl *et al.* (2000), it was found that Ae is a good descriptor for the correlation of mass transfer, hydrodynamics and geometrical shape in biofilms for both two- and three-dimensional situations. The transport equations become two-dimensional and, hence, acceleration in computing time can be expected. In M3 a further physical simplification was introduced by not solving the full flow equations in the irregular domain, but by a simple approximation

obtained from the Couette flow problem (i.e., disregarding the flow perturbation induced by surface irregularities of the biofilm). Since the calculation of the flow field is the most computing time-consuming step in the multi-dimensional mass transfer problem, this introduces a further acceleration. In the surface biofilm, the Couette-flow field is taken into account in the computation of the substrate concentration, which leads to an over-estimation of transport terms. Two different sets of geometries were used: a) the same as in M2, and b) a two-dimensional description that is obtained by averaging the biofilm height along the direction parallel to the substratum and perpendicular to the main flow direction. This second description is easier and more straightforward to obtain than the first one; however, neither area enlargement, nor maximum and minimum biofilm height are preserved; total mass and volume of the biofilm and average height are the same as in the original three-dimensional description.

A comparison of the simulation results in Table 3 shows that, in general, a good agreement between M1 and M2 is achieved, albeit the discrepancies between two- and three-dimensional models are not negligible. Comparing the results of M2 with the results of M3a shows that giving up the accurate flow description leads to a further increased deviation with reference to M1. The magnitude of this change is in some cases small (<2%, typically at slow bulk flow) and in other cases considerable (>20%, typically at fast bulk flow). Therefore, an *a priori* assessment of the effect of the simplification of the hydrodynamics in a particular case cannot be given without further analysis of the hydrodynamic conditions. On the other hand, comparing the results of M3a and M3b shows that both approaches to reduce the dimensionality of the problem lead to similar results. This allows the conclusion that from a global (lumped reactor scale), quantitative point of view, the model reduction is much more sensitive to the perturbations in the calculation of the hydrodynamic flow field, than to the perturbation in the geometrical description (under the hypothesis that biomass and volume are maintained).

Quantitative comparison of one-dimensional models

All one-dimensional models in this survey rely on a reduction to a homogeneous slab description of the biofilm. Where they differ is the way in which the hydrodynamics are handled. Only two models (M8 and M9) are closed in the sense that they provide a predictive model solution. The models M4 through M7 try to include the hydrodynamics in the reactor by introducing a concentration boundary layer, which is expected to be the thinner the faster the flow regime is. A closed correlation between the reactor hydrodynamics and the boundary layer thickness is not known yet. The approaches M4 through M7 try to determine it from comparison with three-dimensional reference data obtained by M1. A first test for this concept to be a sensible approach to BM2 is that the boundary layer thickness is well-defined as a function of the hydrodynamics.

Parameter fitting of the concentration boundary layer thickness. The task is to find the value for the concentration boundary layer thickness L such that both comparison parameters, S_{surf} and J , best match the values obtained by fully three-dimensional simulation. Clearly, since two quantities must be optimised simultaneously, this is a multi-criteria optimisation problem. It is well known that for this problem neither a unique optimality concept exists nor a unique solution (e.g., Göpfert and Nehse, 1990). Therefore, the optimum value for the boundary layer thickness depends on the formulation of the parameter fitting problem. If the concept of the concentration boundary layer is well defined for BM2, we would expect that different physically sensible formulations lead to comparable values for the parameter L . This was confirmed by M4, M5, M6, and M7 (see above for their description) and is documented in Table 4. L clearly depends on the hydrodynamics by comparing the

Table 4 Concentration boundary layer thickness [μm] obtained by parameter fitting

Model	Case 1	Case 2	Case 3	Case 4	Case 5	Case 6	Case 7
4	75	94	75	94	75	94	75
5a	73.1	132	72.6	133	81.7	141	N/A
5b	73.7	135	74.0	136	70.8	129	74.9
5c	N/A	124	N/A	125	68.9	125	69.7
6	73	93	74	95	71	83	74
7	73.2	109	73.8	116	77.4	88.6	91.3

results of Cases 1, 3, 5, and 7 (fast flow) with the ones of 2, 4, and 6 (slow flow). Further varying influences, such as the bulk substrate concentration and the biofilm thickness, play no or only minor roles in these experiments. The exception to this conclusion is M7, where the obtained values fluctuate more strongly. In this approach, stronger, additional, physical conditions were imposed on the minimisation problem than in all the other approaches. This, together with the values for S_{surf} and J in Table 3, which agree excellently with the reference data, implies that the influence of the flow field could eventually be described by the introduction of a concentration boundary layer as in Wanner and Morgenroth (2004), even if no explicit correlation between its thickness and the flow velocity is found at this point.

Closed models. Only M8 and M9 lead to a closed one-dimensional description in the sense that S_{surf} and J can be calculated on the basis of the problem description without additional information, such as reference data from three-dimensional simulations. Both approaches take the hydrodynamics into account, but do not explicitly consider information about the geometrical structure of the biofilm architecture other than the average biofilm thickness or amount of biomass. Both approaches differ in that M9 is based on an empirical correlation carried over from fixed-bed reactors, while M8 is based on a global mass balance, a heuristic simplification/averaging argument, and straightforward mathematical manipulation. At the core of these models is a one-dimensional biofilm model that is solved numerically. The results summarised in Table 3 show that these one-dimensional models can give results that are as good as the two-dimensional simulations of M2, sometimes even better. M8 seems to be somewhat better than M9 for a higher flow velocity (Cases 1, 3, 5, 7) and *vice versa* for slower hydrodynamics (Cases 2, 4, 6).

Summary and conclusion

The numerical experiments carried out for this study investigated the question whether a detailed three-dimensional study of local biofilm processes is necessary in order to obtain global lumped results about mass transfer in a biofilm reactor segment. This was addressed by starting with a detailed spatial description of biofilm architecture and mass transfer processes and then reducing computational complexity by a reduction of physical complexity in many different ways. More specifically, this was achieved by reducing the geometrical dimensionality and simplifying the hydrodynamic description. The one-, two-, and three-dimensional models considered in this study showed the same sensitivity towards changes in biofilm thickness and hydrodynamic load and were all able to describe the qualitative system behaviour. For the quantitative description, however, a more differentiated result is obtained. Based on the experiments reported here, it appears that the key to a successful quantitative model reduction is a good description of the hydrodynamic conditions in the segment. In a two-dimensional reduction, this can be accomplished by a two-dimensional version of the governing flow equations. One-dimensional approaches required a global mass balance or an empirical correlation that incorporates the hydrodynamics with passable reliability and accuracy. Which simplified predictive models in this

survey would offer the best effort/accuracy/reliability trade-off depends largely on the hydrodynamic regime. Therefore, an analysis of the flow conditions in the reactor is required first before a simplification should be applied. If one aims at a one-dimensional description, M8 is the preferred method for fast flow regimes, while M9 is the method of choice for slower flow velocities. M2 is a safe choice for two-dimensional descriptions in all flow situations, but M3 offers a less computing expensive alternative under slower bulk flow. If local results are desired, one-dimensional models by construction cannot yield a good description for spatially heterogeneous biofilms, but two-dimensional models must be applied. Note, however, that using two- or three-dimensional model descriptions requires much more detailed data about the geometrical structure of the biofilm, while all one-dimensional models tested here only use information about the average thickness or the total amount of biomass. Hence, the choice of the model is also a trade-off between the desired accuracy and the experimental effort.

References

- Comiti, J., Mauret, E. and Renaud, M. (2000). Mass transfer in fixed beds: proposition of a generalized correlation based on an energetic criterion. *Chem. Eng. Sci.*, **55**, 5545–5554.
- Eberl, H.J. (*in preparation*). Integral formulation of one-dimensional biofilm models and applications to BM1, BM2, and BM3.
- Eberl, H.J., Picioreanu, C., Heijnen, J.J. and van Loosdrecht, M.C.M. (2000). A three-dimensional numerical study on the correlation of spatial structure, hydrodynamic conditions, and mass transfer and conversion in biofilms. *Chem. Eng. Sci.*, **55**, 6209–6222.
- Göpfert, A. and Nehse, R. (1990). *Vektoroptimierung*, BSB Teubner, Leipzig.
- Morgenroth, E., Eberl, H.J. and van Loosdrecht, M.C.M. (2000). Evaluating 1d and 3d mathematical models for mass transport in heterogeneous biofilms. *Wat. Sci. Tech.*, **41**(4/5), 347–356.
- Morgenroth, E., Eberl, H.J., Noguera, D.R., Picioreanu, C., Rittmann, B.E., Schwarz, A.O., van Loosdrecht, M.C.M. and Wanner, O. (2004). Comparing biofilm models for a single species biofilm system. *Wat. Sci. Tech.* **49**(11–12), 145–154 (this issue).
- Noguera, D.R. and Morgenroth, E. (2004). Introduction to the IWA Task Group on Biofilm Modeling. *Wat. Sci. Tech.* **49**(11–12), 131–136 (this issue).
- Picioreanu, C., van Loosdrecht, M.C.M. and Heijnen, J.J. (2000). A theoretical study on the effect of surface roughness on mass transport and transformation in biofilms. *Biotech & Bioeng.*, **68**(4), 355–369.
- Rittmann, B.E., Schwarz, A.O., Eberl, H.J., Morgenroth, E., Perez, J., van Loosdrecht, M.C.M. and Wanner, O. (2004). Results from the Multi-Species Benchmark Problem (BM3) Using One-Dimensional Models. *Wat. Sci. Tech.* **49**(11–12), 163–168 (this issue).
- Wanner, O. and Morgenroth, E. (2004). Biofilm modeling with AQUASIM. *Wat. Sci. Tech.* **49**(11–12), 137–144 (this issue).