A novel model for biofilm growth and its resolution by using the hybrid immersed interface-level set method

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What is a biofilm?



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Biofilm formation



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Why to study a biofilm?

- Bioremediation: technologies to assist the remediation of field sites contaminated with fuel hydrocarbons.
- Waste water treatment
- Bioleaching: A method to extract metals (such as copper) from the ore using only natural ingredients which are very easy to find in the environment: water, air and bacteria.

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The model Pressure equations Substrate equations The full biofilm model

Biofilm modeling Generalities

Basic biofilm models are based upon three principles:

- Transport mechanisms (advection, diffusion): for bringing nutrients into the biofilm.
- ② Consumption and growing mechanisms.
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Modeling

Let $\Omega \subset \mathbb{R}^2$ be the rectangle $\Omega = (0, L_X) \times (0, L_Z)$, divided into two subregions: the biofilm compartment z < h(x, t) and the liquid compartment z > h(x, t), with curve interface z = h(x, t) (the interface need not to be expressible as a function of x).

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Hele-Shaw flow model

The biofilm is modeled as a homogeneous viscous fluid, which satisfies Darcy law

 $\mathbf{u} = -\nabla p$

u, *p* velocity and pressure resp. The biofilm may be growing or decaying, so that

 $abla \cdot \mathbf{u} = g$ in $\Omega_2(t)$

for some g prescribed growing function. Note that g depends on the substrate uptake rate U(S), i.e. g = g(U), where S is a single limiting substrate (e.g., oxygen or glucose).

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The Hele-Shaw flow (revisited) Pressure equations

 $-\nabla^2 p = \begin{cases} g(U) & \text{ in the biofilm region,} \\ 0 & \text{ in the liquid region.} \end{cases}$

The transmissions conditions on the interface $\Gamma(t)$ are:

 $\begin{cases} [p] = d_0 \kappa & \text{(Laplace-Young condition)} \\ \\ \left[\frac{\partial p}{\partial n}\right] = 0 & \text{(kinematic condition)} \end{cases}$

 d_0 , κ are the *amalgamated surface tension coefficient* and the *mean curvature* resp.

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Substrate equations

$$S_t + \nabla \cdot (S\mathbf{u}) - \frac{D_S T}{L_Z^2} \nabla^2 S = 0 \text{ in } \Omega_1(t),$$

$$S_t + \nabla \cdot (S\mathbf{u}) - \frac{D_S T}{L_Z^2} \nabla^2 S = -U(S) \text{ in } \Omega_2(t).$$

The transmissions conditions on the interface $\Gamma(t)$ are the "natural conditions":

$$\begin{bmatrix} S \end{bmatrix} = 0$$
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Modeling of the substrate uptake rate function Monod function

A typical choice for U is the *Monod* function

$$U(S) = \underbrace{\left(\frac{TU_m}{S_m}\right)}_{\nu} \delta_U(1+\mu) \frac{S}{S+K}$$

where T, U_m , S_m , μ , K are the time scale of biofilm growth, reaction rate coefficient, maximum substrate concentration, maintenance coefficient and dimensionless half-saturation, resp. This form is also often used for the growing function g:

$$g(U(S)) = \frac{\nu S_m}{U_m} \delta_g \mu_m \left[(1+\mu) \frac{S}{S+K} - \mu \right]$$

Finally, δ_U and δ_g are scaling parameters.

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External boundary conditions

For the pressure:

 $\begin{cases} p|_{z=H} = 0, & \frac{\partial p}{\partial z} \Big|_{z=0} = 0, \\ p \text{ periodic in } x \text{ direction.} \end{cases}$

For the substrate:

 $\begin{cases} S|_{z=H} = 1, & \frac{\partial S}{\partial z} \\ S \text{ periodic in x direction.} \end{cases}$

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The full biofilm model Main difficulties

Key issue

Evolution of the biofilm front is a *unknown* of the model \Rightarrow problem highly *non-linear*. We so deal with a *free boundary value problem*.

Generalized solutions

The presence of the interface implies that the solution is defined in a weak sense (it is discontinuous). Thus, well-posedness for this problem is a non-trivial issue.

Main novelty

Intensive numerical simulations were successfully carried out. This is achieved by coupling the level set method and the immersed interface method

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Interface evolution Pressure equations Algorithm

Numerical method for the interface evolution (1/3)The level set method

Let $\phi(x, z, t)$ be satisfying $\phi(x, z, t) > 0$ for (x, z) in the liquid region and $\phi(x, z, t) < 0$ for (x, z) in the biofilm region. Then, by continuity $\phi(x, z, t)$ satisfies

$(x,z) \in$ Biofilm front $\Leftrightarrow \phi(x,z,t) = 0.$

Thus, the motion of the biofilm front is modeled by the *level set* equation:

 $\begin{cases} \frac{\partial \phi}{\partial t} + \mathbf{u} \cdot \nabla \phi = \mathbf{0}, & \text{for } (x, z) \in \Omega, \ t > \mathbf{0}, \\ \phi(x, z, \mathbf{0}) = \phi_{\mathbf{0}}(x, z), & \text{for } (x, z) \in \Omega, \end{cases}$

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where $\phi_0(x,z)$ implicitly defines the initial biofilm front.

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Numerical method for the interface evolution (2/3)The reinitialization process

In the level set method $\phi(x, z, t)$ corresponds to the signed normal distance from the point (x, z) to the interface $\Gamma(t)$. Although the level set equation transports the interface at the right velocity **u**, it does not preserve ϕ as a distance function. To overcome this difficulty, we have used the reinitialization process:

 $\begin{aligned} \psi_{\tau} + \operatorname{Sg}(\phi)(|\nabla \psi| - 1) &= 0, \\ \psi(x, z, 0) &= \phi(x, z, t), \end{aligned}$

where $\phi(x, z, t)$ corresponds to the level set function at time t_{n+1} , and Sg(ϕ) is the one dimensional sign function composed with ϕ .

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Interface evolution Pressure equations Algorithm

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Numerical method for the interface evolution (3/3)Numerical methods for the level set equations

We apply this process every 15 time iterations, taking care of obtaining a steady state solution in order to numerically obtain that $|\nabla \psi| \approx 1$. The new function ψ has the same level sets as ϕ and is the signed normal distance to the interface.

Both Hamilton-Jacobi equations are solved by coupling a second-order TVD Runge-Kutta method to update ϕ (resp. ψ) from time t_n to t_{n+1} (resp. τ_n to τ_{n+1}), with a second-order ENO approximation to $\nabla \phi$ (resp. $\nabla \psi$). For an overview of the level set method see [Osher and Fedkiw, 2003].

Interface evolution Pressure equations Algorithm

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Numerical method for the pressure equations Immersed Interface Method (IIM)

- The IIM [LeVeque and Li, 1994] deals with general interface conditions. This method is comparable, but more general than the immersed boundary method [Peskin, 1977].
- The discontinuities of the solution and/or coefficients are imposed in the standard method, by modifying it at *irregular* grid points, i.e., at grid points whose standard five-point stencil centered around it, is located in both sides of the interface (see figure in the next slide).
- If coefficients of the equation are continuous (which is our case), the IIM just adds a correction term in the right-hand side of the discretized equation at the irregular grid points.

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Interface evolution Pressure equations Algorithm

Immersed Interface Method

Interface (dashed line), regular grid (points) and irregular grid points (stars)



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Interface evolution Pressure equations Algorithm

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Algorithm

Step 1. $n \leftarrow 0$. Initialize the initial biofilm front, i.e., set $\phi(x, z, t = 0)$. At t = 0 the substrate is at its maximum level and uniformly distributed in the space, i.e. S(x, z, t = 0) = 1.

- Step 2. Solve the pressure equations, and compute $\mathbf{u} = -\nabla p$ based on the IIM at time $t_n = n\Delta t$.
- Step 3. Solve the substrate equations at time t_n .
- Step 4. Update the position of the interface with the velocity field $\mathbf{u} = -\nabla p$, by solving the level-set equation. Reinitialize the level-set function every 15 time steps.
- Step 5. Update $n \leftarrow n + 1$ and repeat Step 2 to Step 5 to let evolve the system.

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Parameters

We have taken the following common parameters in our simulations [Picioreanu et al., 2000]:

Parameter	Symbol	Value	Units
Time scale of biofilm growth	Т	1000	s
Monod half-saturation constant	K _S	$3.5 \cdot 10^{-4}$	kg m ^{−3}
Diffusion coefficient	D_S	$2.3 \cdot 10^{-9}$	$m^2 s^{-1}$
Surface tension coefficient in water	γ	$72.8 \cdot 10^{-3}$	kg s ^{−2}
Maximum specific growth rate	μ_m	$1.5 \cdot 10^{-5}$	s-1

A key parameter is the ratio (maximum biomass growth rate)/(maximum internal transport rate of substrate) [Picioreanu et al., 1998b], which determines the biofilm heterogeneity. The growth ratio, G, is computed as $G = L_Z^2 U_m / (D_S S_m)$. By setting $S_m = 4$ and 100 mg/L, G is taken as 395 and 16. Moreover, U_m and d_0 are computed accordingly to these values.

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Numerical simulation for a transport-limited regime Fingering formation



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Numerical simulation for a transport-limited regime Fingering formation



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Numerical simulation for a growth-limited regime Compact-shaped biofilm



Numerical simulation for a growth-limited regime Compact-shaped biofilm



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Grid refinement analysis For two simulations



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Conclusions

- Development of a new model that predict real biofilm behavior (finger-like, as well as, more compact structures, depending on the environmental conditions).
- Development of sophisticated numerical techniques (the IIM coupled to the level-set method) in order to evaluate the model.
- We could consider the flow field induced by the liquid and not only by the biofilm growth.
- We could consider two or more substrates as well as biofilm systems with multiple species.
- We could consider biofilm detachment, which also determines biofilm structure.

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- In addition, we could consider that the fluid dynamics is governed by e.g. Navier-Stokes equations.
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Some references

- P. Cumsille, J. A. Asenjo, and C. Conca (2014).
 A novel model for biofilm growth and its resolution by using the hybrid immersed interface-level set method.
 Comput. Math. Appl., 67 (2014), pp. 34–51.
- LeVeque, R. J. and Li, Z. L. (1994).

The immersed interface method for elliptic equations with discontinuous coefficients and singular sources. *SIAM J. Numer. Anal.*, 31(4):1019–1044.

 S. Osher, R. Fedkiw (2003) Level set methods and dynamic implicit surfaces
 Vol. 153 of Applied Mathematical Sciences, Springer-Verlag, New York, 2003.



Peskin, C. S. (1977).

Numerical analysis of blood flow in the heart.

J. Computational Phys., 25(3):220-252.

Picioreanu, C., van Loosdrecht, M. C. M., and Heijnen, J. J. (1998a).

Mathematical modeling of biofilm structure with a hybrid differential-discrete cellular automaton approach.

Biotechnol. Bioeng., 58(1):101–116.

Some references

Picioreanu, C., van Loosdrecht, M. C. M., and Heijnen, J. J. (1998b).

A new combined differential-discrete cellular automaton approach for biofilm modeling: Application for growth in gel beads.

Biotechnol. Bioeng., 57(6):718-731.

Picioreanu, C., van Loosdrecht, M. C. M., and Heijnen, J. J. (2000).
 Effect of diffusive and convective substrate transport on biofilm structure formation: a two-dimensional modeling study. *Biotechnol. Bioeng.*, 69(5):504–515.

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Thank you for your attention!!