Modeling Physiological Resistance in Bacterial Biofilms

N. G. Cogan*
Ricardo Cortez †
Lisa Fauci‡

*Mathematics Department Tulane University New Orleans, LA. 70118 e-mail: cogan@math.tulane.edu FAX: 504 865 5063

†Mathematics Department Tulane University New Orleans, LA. 70118 e-mail: cortez@math.tulane.edu FAX: 504 865 5063

‡Mathematics Department Tulane University New Orleans, LA. 70118 e-mail: ljf@math.tulane.edu FAX: 504 865 5063

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Corresponding Author: N. G. Cogan
Mathematics Department
Tulane University
New Orleans, LA. 70118
E-mail: cogan@math.tulane.edu
Phone: 504 862 3439
Fax: 504 865 5063

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Abstract

A mathematical model of the action of antimicrobial agents on bacterial biofilms is presented. The model includes the fluid dynamics in and around the biofilm, advective and diffusive transport of two chemical constituents and the mechanism of physiological resistance. Although the mathematical model applies in three-dimensions, we present two-dimensional simulations for arbitrary biofilm domains and various dosing strategies. The model allows the prediction of the spatial evolution of bacterial population and chemical constituents as well as different dosing strategies based on the fluid motion. We find that the interaction between the nutrient and the antimicrobial agent can reproduce survival curves which are comparable to other model predictions as well as experimental results. The model predicts that exposing the biofilm to low concentration doses of antimicrobial agent for longer time is more effective than short time dosing with high antimicrobial agent concentration. The effects of flow reversal and fluid/biofilm roughness are also investigated. We find that reversing the flow increases the effectiveness of dosing. In addition, we show that overall survival decreases with increasing surface roughness.

1 Introduction

Although biofilms are beneficial in some environments such as wastewater management [19], sewage treatment [31] and oilfields [4], much of the focus of research is on deleterious properties of biofilms. In industrial settings these properties include fouling, corrosion and contamination [3]. In medical settings, biofilms are responsible for a wide variety of infections [7]. Recently, it was reported that biofilms may be responsible for up to 65% of all infections [21]. Moreover, bacteria within biofilms are more resistant to antimicrobial agents than are planktonic cells of the same type [2], which poses immediate difficulties in treating biofilm infections.

There are many possible resistance mechanisms that have been introduced in the literature. One mechanism is the inability of the antimicrobial agent to fully penetrate the biofilm region. This is probably not due to reduced diffusion within the biofilm matrix. Rather, it is thought that penetration failure is due to a neutralizing reaction between the antimicrobial agent and some component of the biofilm [8, 9, 27]. Reaction limitation cannot completely explain biofilm resistance, since for antimicrobial agents that are not reactive or for thin biofilms where full penetration can be shown, susceptibility is still reduced substantially [9].

Another possible mechanism is that of physiological resistance. If the bacteria within the biofilm are not respiring, susceptibility to antimicrobial agents is typically decreased [15]. Thus, even if the entire bacterial population is exposed to antimicrobial agent, only the respiring fraction of bacteria are susceptible to killing. This mechanism alone cannot fully explain lowered susceptibility. If the antimicrobial agent can fully penetrate the biofilm and if only the respiring bacteria are susceptible, then as the exposure time is increased, the nutrient would penetrate further into the biofilm region causing bacteria deeper in the biofilm to become susceptible. Hence, exposing the biofilm for longer periods would eventually eradicate the bacteria. This is typically not the case in experimental studies. Instead, biofilms

tend to have a small population of 'persister cells' which are not removed by antimicrobial agent challenge [17], so it is unlikely that physiological resistance operates alone.

It has been proposed [13, 23] that quorum-sensing may be a mechanism by which bacteria can up-regulate resistance mechanisms. It is unclear whether this is done by up-regulation of multi-drug efflux pumps [17] or other mechanism such as expression of a non-growing, peristant phenotype [28]; however, there are indications that interfering with the quorum-sensing communication system may increase bacterial susceptibility [28].

We briefly review two mathematical investigations of resistance mechanisms [24, 25]. In the first of these [25], Sanderson and Stewart investigate the role of dosing protocols for the reactive biocide monochlorimine. The authors assume that there is a fixed amount of material within the biofilm region that neutralizes the biocide. The neutralizing agent is depleted by reaction with the biocide. Mass balance equations are derived for the biocide and the neutralizer. These equations are solved using the numerical simulation package AQUASIM [29] which incorporates bulk flow into and out of a one-dimensional well mixed reactor, transport of dissolved constituents within the biofilm, nutrient consumption, advection of cell mass, cell detachment and bacterial growth. Because the bulk fluid is assumed to be well mixed, the fluid dynamics are not addressed. This model captures gross experimental trends such as rapid disinfection followed by steady regrowth. However, the model predicts that the second dose of monochlorimine is more effective than the initial dose, which is contradicted by experimental data obtained in the same study.

In the second study [24], Roberts and Stewart describe a model of biofilm dynamics used to investigate the role of nutrient limitation on bacterial biofilm susceptibility. The model describes the reaction and diffusion of one limiting substrate and one non-reactive antimicrobial agent within a one-dimensional biofilm. The rate of killing by the agent is assumed to be proportional to the growth rate. Zones of no growth are found within the biofilm due to nutrient uptake and subsequent non-uniform spatial patterns of biofilm microorganism killing. Biofilm susceptibility is shown to depend on the biofilm thickness and on the nutrient source concentration. The model is then extended to include a hypothetical damaged cell state, where cells are nonviable but still consume substrate. This resulted in slowed biofilm killing.

In the current study, resistance mechanisms are investigated by coupling fluid flow with the reaction, diffusion and advection of antimicrobial agent and nutrient in two spatial dimensions. No a priori assumptions are made on the antimicrobial agent penetration depth or the concentrations in the bulk fluid. This framework allows for the investigation of spatial inhomogeneities in the susceptibility of bacteria, as well as comparisons between different dosing protocols. If a reaction between the antimicrobial agent and a neutralizing agent within the biofilm is included and external flow is neglected, we obtain quantitative agreement with experimental data [9]. We also find that physiological resistance is capable of capturing the qualitative shape of survival curves as reported in [24]. By direct comparison, we show that plotting survival curves on the scale determined by the product of antimicrobial agent dose concentration and dose duration is not a consistent way to compare dosing protocols. For example, comparing the survival curve for a dosing strategy that calls for continuous dosing of a antimicrobial agent at 10 mg l^{-1} for two hours to a strategy of dosing with concentration 20 mg l^{-1} for one hour is not equivalent on the mixed time scale mg l^{-1}s. The assumption that these survival curves are equivalent has been questioned in the literature

and contradicted by experimental results [12]. Our results also contradict this assumption. Motivated by the spatial distribution of the susceptible population, we study the effect of reversing the bulk fluid flow during the antimicrobial agent application. We find that reversing the flow increases the effectiveness of the antimicrobial agent. We also investigate the effect of surface roughness on antimicrobial agent efficacy by simulating several biofilms with varying fluid/biofilm interfaces. We find that survival decreases with increasing surface roughness and that the decrease depends on the flow velocity.

In the following sections we describe the mathematical model and the numerical methods used to solve the coupled fluid, biofilm, antimicrobial agent, nutrient system of partial differential equations. We then detail several two-dimensional numerical experiments and results.

2 Model Equations

To describe the governing equations for a two-dimensional biofilm in the presence of a single nutrient, oxygen, and a single antimicrobial agent, we assume that the biofilm is immersed in a fluid that is undergoing steady, creeping flow. The physical domain consists of a channel of width mL and length L. There is a biofilm region attached to one wall described by a fluid/biofilm interface, Γ, that does not change in time. Thus, we are neglecting changes in the biofilm morphology due to growth and detachment as well as flow interactions. In this study, the time scale of disinfection is sufficiently shorter than that of biofilm growth; therefore, neglecting morphological changes due to growth is reasonable. While the processes of detachment and fluid/structure interactions are important and are currently being investigated [14, 20], their mathematical treatment is beyond the scope of this paper.

Because the length scale is small and the fluid velocities are low (see Table II) the Reynolds number is on the order of 10^{-4}. Therefore, we assume that the fluid velocity, $\vec{U}$, is governed by the incompressible Stokes equations

$$\mu \Delta \vec{U} = \nabla p - \vec{F} \tag{1}$$

$$\nabla \cdot \vec{U} = 0, \tag{2}$$

where μ is the fluid viscosity and p is the pressure. Applied forces, $\vec{F}$, are specified to introduce effects of the stationary interface on the flow. Although Equations (1) and (2) are defined in the entire physical domain, we restrict the flow to be zero on Γ and the channel walls. This implies that $\vec{U}$ is negligible within the biofilm region [6].

Since the biofilm region does not change, the fluid flow satisfying appropriate boundary conditions on the fluid/biofilm interface and the channel walls is computed only once and assumed to remain steady for the rest of the simulation. Once the steady-state fluid velocity is calculated, the dynamics of the chemical constituents are calculated. Nutrient, $S(\vec{x}, t)$, and antimicrobial agent, $A(\vec{x}, t)$, are introduced into the system at one end of the domain. Both are advected by the fluid and diffuse within the fluid and the biofilm. The diffusion coefficients of nutrient and antimicrobial agent, $D_s(\vec{x})$ and $D_a(\vec{x})$, are assumed to be reduced in the biofilm region. The reduction factors are denoted r_s and r_a, respectively. The consumption of nutrient by the bacteria is modeled by Monod kinetics, where μ_s, Y_s

and K_s denote the maximum specific growth rate, yield coefficient and Monod coefficient, respectively. These assumptions yield the following equations:

$$\frac{\partial S(\vec{x},t)}{\partial t} + \vec{U}(\vec{x},t)\cdot\nabla S(\vec{x},t) = \nabla\cdot(D_s\nabla S(\vec{x},t)) - \mu_s\frac{S}{K_s+S}B(\vec{x},t) \quad (3)$$

$$\frac{\partial A(\vec{x},t)}{\partial t} + \vec{U}(\vec{x},t)\cdot\nabla A(\vec{x},t) = \nabla\cdot(D_a\nabla A(\vec{x},t)) - H_a(A,N). \quad (4)$$

The population of viable bacteria is denoted $B(\vec{x},t)$. H_a denotes the reaction between the antimicrobial agent and the concentration of neutralizing agent, denoted N, within the biofilm. For the simulations below, H_a is either zero or, if $H_a \neq 0$, we assume that the neutralizing agent is consumed by the reaction at a rate proportional to the product of A and N. The dynamics of the neutralizer are,

$$\frac{\partial N(\vec{x},t)}{\partial t} = -k_r Y_n A N, \quad (5)$$

where Y_n denotes the neutralizer/antimicrobial agent yield coefficient.

Finally, the effect of the antimicrobial agent on the bacteria is included in the following equation for the population of bacteria within the biofilm region,

$$\frac{\partial B}{\partial t} = -p_1(A,S)B, \quad (6)$$

where B is zero in the bulk fluid region and $p_1(A,S)$ denotes the disinfection rate.

The description of the disinfection rate, $p_1(A,S)$, differs for various antimicrobial agents and disinfection models. There are many factors that affect this term, including the nature of persister cells and the process of physiological resistance. We assume that bacteria are susceptible to the agent at a rate proportional to the product of the agent concentration and the bacterial growth rate. Because the growth rate depends on the nutrient concentration, bacteria that are in nutrient-limited zones (i.e. deep within the biofilm) are not susceptible. Tacit in this model is that the maximum specific growth rate is constant. In [28], it is suggested that variations in maximum specific growth rate may also affect the spatial variation of bacterial susceptibility. For the simulations presented below, we set $p_1 = \kappa Y \mu_s A\frac{S}{K_s+S}$, where Y is the yield coefficient and κ is a constant of proportionality.

For computational purposes, the equations are nondimensionalized introducing the dimensionless variables $x^* = \frac{x}{L}$, $t^* = \frac{t}{T}$, $\vec{U}^* = \frac{\vec{U}T}{L}$, $P^* = \frac{P\mu}{T}$, $A^* = \frac{A}{a}$, $S^* = \frac{S}{K_s}$ $N^* = \frac{N}{n}$ and $B^* = \frac{B}{b}$ into the system of Equations (1) - (6). The parameters T, a, n and b are typical time and concentration scales. The nondimensional equations are

$$\Delta\vec{U}^* = \nabla P^* \quad (7)$$

$$\nabla\cdot\vec{U}^* = 0 \quad (8)$$

$$\frac{\partial S^*}{\partial t^*} + \vec{U}^*\cdot\nabla S^* = -\mu_s^*\frac{S^*}{1+S^*}B^* + \nabla\cdot(D_s^*\nabla S^*) \quad (9)$$

$$\frac{\partial A^*}{\partial t^*} + \vec{U}^*\cdot\nabla A^* = \nabla\cdot(D_a^*\nabla A^*) - H_a(aA^*, k_sS^*)N^* \quad (10)$$

$$\frac{\partial N^*}{\partial t} = -k_r^* A^* N^* \quad (11)$$

$$\frac{\partial B^*}{\partial t^*} = -p_1^*(aA^*, k_sS^*)B^*, \quad (12)$$

where $\mu_s^* = \frac{\mu_s T}{K_s} b$, $D_s^* = \frac{TD_s}{L^2}$, $D_a^* = \frac{TD_a}{L^2}$, $k_r^* = ak_r Y_n$ and $p_1^* = Tp_1$. The nondimensional domain is $(0,1) \times (0,m)$. The boundary conditions associated with the nondimensional system above are $\vec{U}^* = 0$ on the fluid/biofilm interface, Γ, and the channel walls, $y = 0$, $y = m$. The chemical constituents satisfy $\frac{\partial A^*}{\partial y} = \frac{\partial S^*}{\partial y} = 0$ at $y = 0, y = m$. For the simulations shown below, the concentration of antimicrobial agent and nutrient are the constants C_a and C_s at the upstream end of the domain.

3 Numerical Methods

The numerical solution of the coupled equations of the fluid/biofilm/chemical system described above presents a number of challenges. Foremost is the irregularity of the interface that separates the fluid region from the biofilm region. The gel-like structure of biofilm indicates that this interface is typically diffuse in biofilm settings [30]. The density of the biofilm changes rapidly and diffusion coefficients of dissolved or suspended constituents within the biofilm depend on the density of the biofilm [26]. Hence, this interface supports a transition region across which the diffusion coefficients of the chemical constituents, while continuous, vary rapidly. The width of this transition region is a physical parameter that is chosen to reflect the structure of the biofilm, rather than a numerical parameter that tends to zero.

We adopt a computational framework that discretizes the rectangular region of the channel using a regular, finite difference grid. The biofilm interface is represented by a discrete collection of points that do not coincide with grid points. This discretized interface is used to assign appropriate values of diffusion coefficients to grid points that fall within the transition region. This will be described below. In addition, these interface points, together with the discrete points along the channel walls are used to compute the steady fluid velocity field using the method of regularized Stokeslets. This grid-free method allows us to compute the fluid velocity at any point in the channel using a superposition of exact solutions of the Stokes equations due to the presence of regularized forces. These regularized forces are chosen to enforce zero velocity at the site of the interface and the channel walls. In particular, we can evaluate the fluid velocity field at lattice points on the finite difference grid. Because both the fluid flow and the geometry of the interface are assumed to be steady, we need to compute this velocity field only once at the beginning of the simulation.

The solution of the fluid equations, and the solution of the evolution equations of chemical transport do not treat the interface as a sharp interface, but allow for a smoothed-out region where fluid forces are applied and where diffusion coefficients smoothly vary. Estimates of the thickness of this 'mushy' zone depend on the age of the biofilm, bacterial growth rates and limiting nutrients [3]; however, measurements of biofilm densities [32, 3] indicate that the density typically increases with the depth within the biofilm. For example, Characklis [3], reports that the density of a 730 μm thick biofilm varies from 37 kg m^{-3} in the top 400 μm to 102 kg m^{-3} in the bottom 130 μm. Zhang and Bishop, [32], report a density of 15 mg cm^{-3} in the surface layers and 105 mg cm^{-3} in the bottom layers. We assume that the transition layer is approximately 200 μm thick for the simulations below.

3.1 Fluid Dynamics

Solving Equations (1) and (2) requires enforcing boundary conditions at the channel walls and the fluid/biofilm interface, which is irregular. The solution is obtained using the method of regularized Stokeslets [5] described in more detail below. We first specify a parabolic background flow, with maximum flow rate $\vec{U}_{max}$, in the absence of the interface points. The basic idea of the method is to apply boundary forces, $\vec{F}$, so that the superposition of the background flow and the flow due to the forces satisfies all the boundary conditions simultaneously.

A fundamental solution of the incompressible Stokes equations is called a Stokeslet, and it represents the velocity due to a concentrated force acting on the fluid at a single point in an infinite domain of fluid [18]. The Stokeslet for a single force applied at the origin in two-dimensions is

$$\vec{U}_s(\vec{x}) \;=\; -\frac{\vec{f}_0}{4\pi\mu}\ln(r) + (\vec{f}_0\cdot\vec{x})\frac{\vec{x}}{4\pi\mu r^2}, \tag{13}$$

where $\vec{f}_0$ is the magnitude of the force and $r = |\vec{x}|$.

Because this expression is singular at the origin, it is difficult to evaluate numerically. In [5], Cortez considers the smoothed case where the concentrated force is applied not at a single point, but over a small ball of radius δ centered at the origin. The distributed force is given by

$$\vec{F}(\vec{x}) \;=\; \vec{f}_0\phi_\delta(\vec{x}), \tag{14}$$

for a given cutoff function ϕ_δ. There are many cutoff functions that can be designed, all of which approximate the Dirac δ-function. Once ϕ_δ is specified, we can solve Equations (1) and (2) analytically.

For example, the cutoff function

$$\phi_\delta(\vec{x}) = \frac{3\delta^3}{2\pi(r+\delta^2)^{5/2}}, \tag{15}$$

yields the exact velocity

$$\begin{aligned}\vec{U}_\delta \;=\; & -\frac{\vec{f}_0}{4\pi\mu}\left(\ln\left(\sqrt{r^2+\delta^2}+\delta\right) - \frac{\delta\left(\sqrt{r^2+\delta^2}+2\delta\right)}{\left(\sqrt{r^2+\delta^2}+\delta\right)\sqrt{r^2+\delta^2}}\right)\\ & +\frac{1}{4\pi\mu}\left(\vec{f}_0\cdot\vec{x}\right)\vec{x}\left(\frac{\sqrt{r^2+\delta^2}+2\delta}{\left(\sqrt{r^2+\delta^2}+\delta\right)^2\sqrt{r^2+\delta^2}}\right).\end{aligned} \tag{16}$$

In the limit $\delta \to 0$ we obtain the classical formulas; however, $\vec{U}_\delta$ is not singular.

Since the equations are linear, one may use direct summation to compute the velocity at all points in the domain due to finitely many discrete forces. The forces we are concerned with are those due to the presence of the stationary interface, Γ, and the channel walls. By discretizing the boundaries, we obtain a finite number of points at which there is an applied force. The same points are used to enforce the no-flow condition. That is, the forces to be

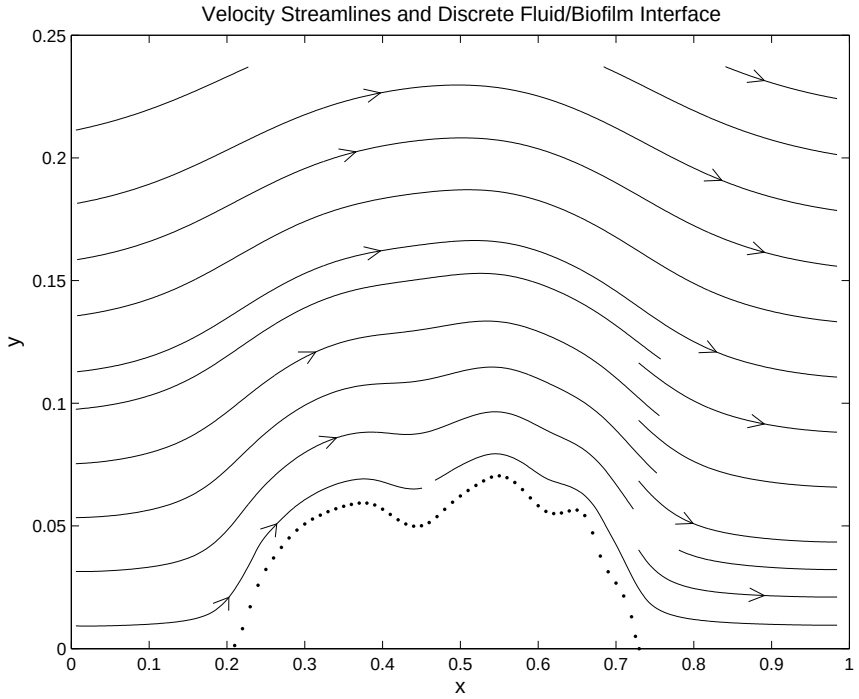

Figure 1: Example of the discretized fluid/biofilm interface with the calculated velocity streamlines. Note that there is no advection within the biofilm region.

computed must cancel the parabolic flow so that after the superposition of the flow due to forces and the parabolic flow, the velocity is zero at the boundary points along the interface and the channel walls. The forces are computed by setting up a linear system based on Equation (13) and inverting the resulting matrix. Streamlines for the velocity around an example region are shown in Figure 1.

The method of regularized Stokeslets is related to boundary integral methods, but has the advantage that forces may be applied at any discrete collection of points. It should be emphasized, that this method is 'grid-free'. That is, $\vec{U}$ is not obtained by solving a discretized problem, but a summation of analytic functions. This summation can then be evaluated on our finite-difference grid.

3.2 Chemical Constituents

Once the steady-state velocity is obtained, Equations (9) - (12) determine the time evolution of the nutrient and biocide concentrations and the bacterial density. The interface between the bulk fluid and the biofilm region is irregular and not aligned with the grid. At the interface, the coefficients experience significant variation.

To incorporate this feature into our model we assume that there is a transition layer of fixed spatial extent where the diffusion coefficients of the constituent particles vary from D_* in the fluid region to r_*D_* in the biofilm. The signed distance from a given point $\vec{x}$ to the interface is $\xi = (\vec{x}^* - \vec{x}) \cdot \vec{\eta}$, where $\vec{x}^*$ is the point on the interface nearest $\vec{x}$ and $\vec{\eta}$ is the outward unit normal at $\vec{x}^*$ (see Figure 2). The diffusion coefficient is given by

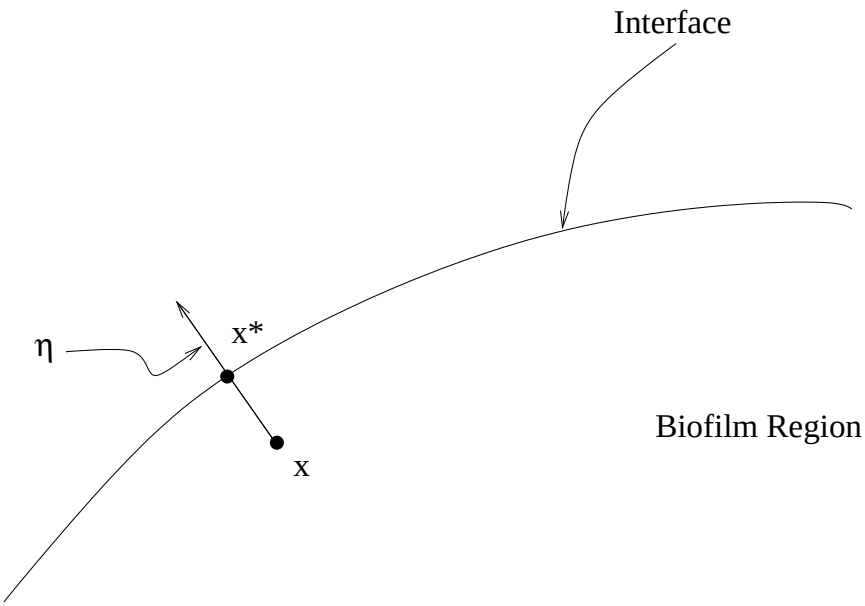

Figure 2: Sketch of the fluid/biofilm interface. The point on the interface nearest to x is x^* and lies in the normal direction.

$$\hat{D}_*(\vec{x}) = \begin{cases} D_*, & \text{for } \xi \le -\delta \\ D_* + (r_* D_* - D_*) H_\delta(\xi), & \text{for } |\xi| \le \delta \\ r_* D_*, & \text{for } \xi \ge \delta. \end{cases}$$

Where the transition function, $H_\delta(\xi)$, is a smooth approximation of a Heaviside function that is one in the biofilm region and zero in the bulk fluid. The width of the transition layer between D_* and $r_* D_*$ is denoted δ and is specified independently of the discretization. Figure 3 shows contours of the smoothed diffusion coefficient for the region shown in Figure 1.

Various transition functions can be designed, two of which are shown in Figure 4, but in our calculations we use the transition function

$$H_\delta(\xi) = \begin{cases} 0, & \text{for } \frac{\xi}{\delta} \le -1 \\ \frac{1}{2}(1 + \frac{\xi}{\delta})^2, & \text{for } -1 \le \frac{\xi}{\delta} \le 0, \\ 1 - \frac{1}{2}(1 - \frac{\xi}{\delta})^2, & \text{for } 0 \le \frac{\xi}{\delta} \le 1 \\ 1 & \text{otherwise.} \end{cases}$$

Once the diffusion coefficients are determined, we use a standard staggered grid approximation of $\nabla \cdot (D(\vec{x}) \nabla c)$ [11]. This, in conjunction with a forward-time-center-space discretization of the parabolic operator $\frac{\partial c}{\partial t} - \nabla \cdot (D(\vec{x}) \nabla c)$ [11] and upwinding for the advective terms, yields an implicit method which is solved using ADI [22]. The method described above has the advantage of specifying the extent of the diffuse interface independent of the grid.

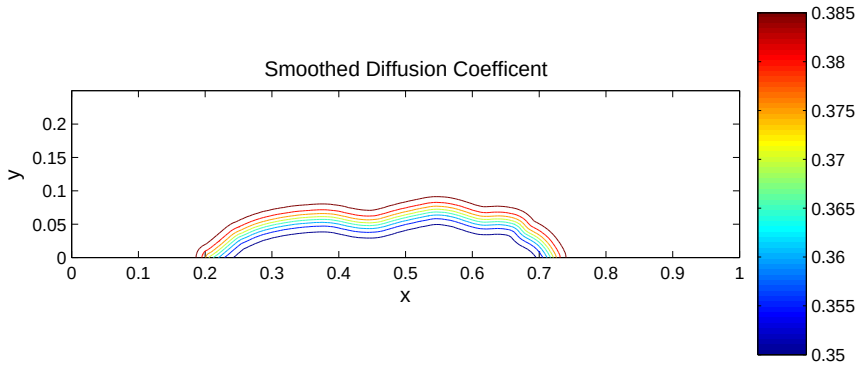

Figure 3: Contours of the diffusion coefficient with diffuse boundary. Notice that the transition region is of uniform width which is independent of the mesh spacing.

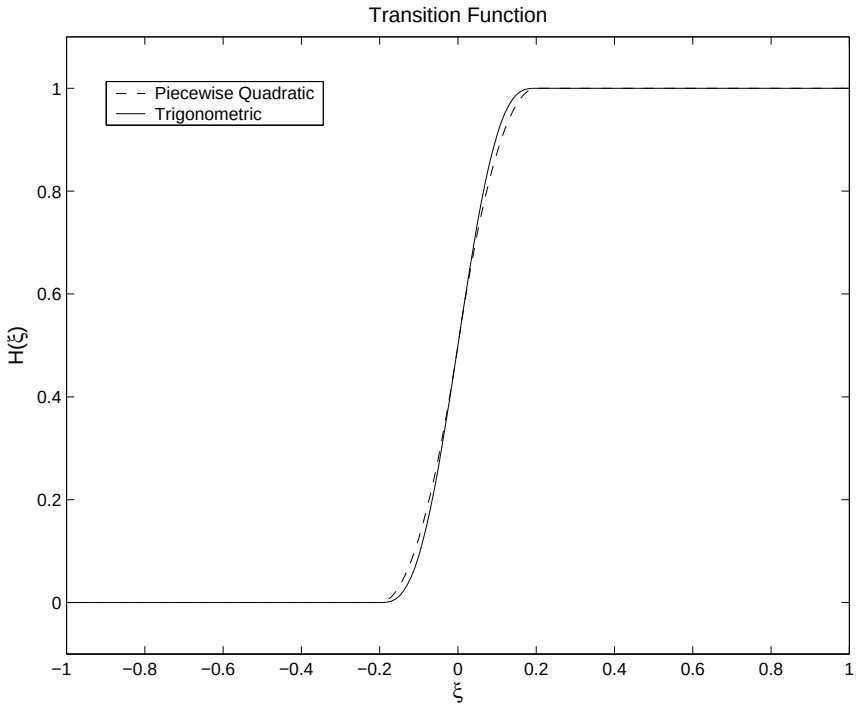

Figure 4: Example of two transition functions, both with transition layer of width 0.2.

3.3 Test problem

To better illustrate the strengths of this method, we consider the steady-state diffusion of a chemical where the diffusion coefficient is spatially dependent. We use the test problem presented in [1]. The computational domain, $(-1,1)\times(-1,1)$, is separated into two regions, one inside the circle of radius 1/2 and the other outside the circle. The diffusion coefficient is specified in each region. Mathematically, we solve the equation

$$\nabla \cdot (\beta_\delta(x,y)\nabla u(x,y)) = f(x,y) \tag{17}$$

where the diffusion coefficient is given by

$$\beta_\delta(x,y) = \begin{cases} b, & \text{outside the circle,} \\ b + (x^2+y^2+1-b)H_\delta(\xi), & \text{in the transition,} \\ x^2+y^2+1, & \text{inside the circle.} \end{cases}$$

The forcing function is $f(x,y) = 8(x^2+y^2)+4$ and b is a constant. The problem is specified by imposing Dirichlet boundary conditions on the computational domain.

For each fixed value of δ, we solve Equation (17) by applying the method described above. If the mesh size used for the finite difference discretization of the derivatives is decreased while keeping δ fixed, we find that the method converges quadratically to the solution of the smoothed problem. In Table I, we compare solutions for $\delta = 0.08$ and decreasing mesh spacing which is chosen small enough to have several mesh points in the transition region.

A weak solution to the problem corresponds to the case of discontinuous coefficient $\beta_0(x,y)$ (or $\delta \to 0$). The solution is:

$$u(x,y) = \begin{cases} x^2+y^2, & \text{for } x^2+y^2 < \frac{1}{4}, \\ (1-\frac{1}{8b}-\frac{1}{b})/4 + (\frac{(x^2+y^2)^2}{2} + x^2 + y^2)/b, & \text{for } x^2+y^2 \geq \frac{1}{4}. \end{cases}$$

The solution is continuous but has a jump in the normal derivative along the circle given by

$$\left[\frac{\partial u}{\partial \eta}\right] = \frac{5}{4b} - 1. \tag{18}$$

Our numerical method approximates this solution. In fact, one can see that for a fixed mesh size, decreasing the value of the smoothing parameter δ results in linear convergence to the weak solution of the problem (Figure 5). By reducing the mesh size and δ simultaneously, our numerical method converges to the solution of the problem with discontinuous coefficients.

h	$\|\|u_h - u_{2h}\|\|_\infty$
0.01	9.307×10^{-4}
0.005	3.065×10^{-4}
0.0025	8.261×10^{-5}

Table I: Comparison between subsequent mesh refinements. The finite difference stencils and numerical convergence are approximately second order. The support of the transition function is $\delta = 0.08$ and $b = 0.5$.

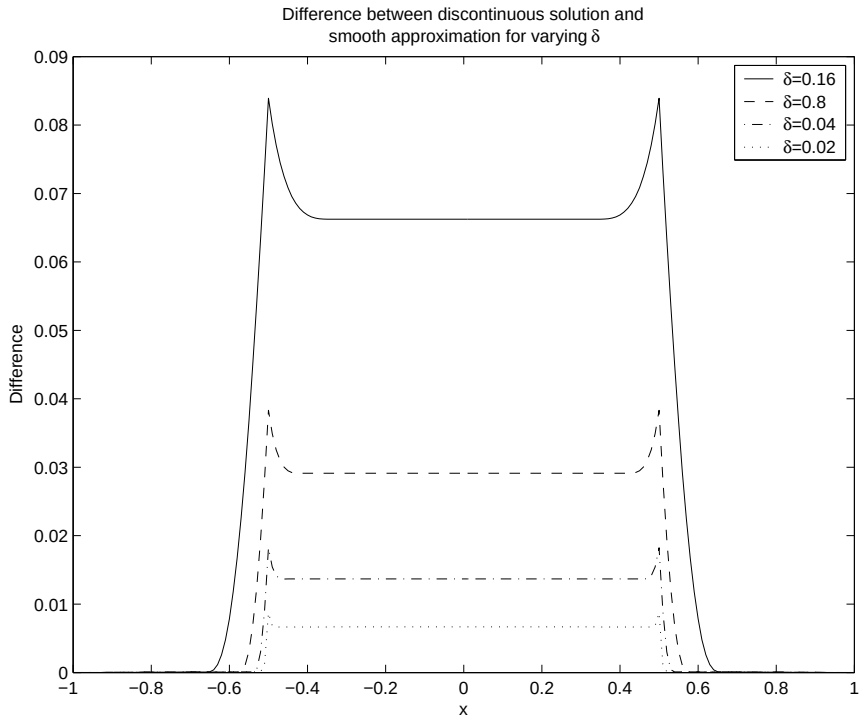

Figure 5: Comparison of errors between the weak solution and the numerical approximation for decreasing δ. The plots show the difference between the true and approximate solution for fixed $y = 0$. The error is localized near the interface $x = \pm\frac{1}{2}$. Here $b = 0.5$ and $h = 0.005$.

Parameter	Symbol	Units	Value	Source
Maximum Specific Growth Rate	μ_s	h^{-1}	0.417	[24]
Yield Coefficient	Y_b		0.8	[24]
Monod Coefficient	K_s	mg l^{-1}	0.1	[24]
Antimicrobial Agent Influent Concentration	C_a	mg l^{-1}	5 - 20	[24]
Nutrient Influent Concentration	C_s	mg l^{-1}	10	[24]
Nutrient Diffusion Coefficient	D_s	m^2h^{-1}	9.67×10^{-6}	[24]
Antimicrobial Agent Diffusion Coefficient	D_s	m^2h^{-1}	1.80×10^{-6}	[24]
Biofilm/Bulk Diffusivity Reduction	r_*		0.9	[25]
Length Scale	L	m	10^{-4}	Assumed
Max. Flow Rate	$\vec{U}_{max}$	m h^{-1}	0-3.4	Assumed
Neutralizer Reaction Rate Coefficient	k_r	m^3 g^{-1} h^{-1}	10	[25]
Neutralizer Reaction Yield Coefficient	Y_n	g g^{-1}	3	[25]
Disinfection Rate Coefficient:	κ			
non-reactive antimicrobial agent			0.044	Assumed
reactive antimicrobial agent			0.4	Assumed

Table II: Parameters used in the simulations

4 Numerical Results

In the following sections we describe results from our simulations. By integrating the bacterial population in space, we can compute the number of surviving bacteria as a function of time (i.e. survival curve). The survival curves are plotted on a logarithmic scale, where the vertical axis is the logarithm of the ratio between the total population of the remaining viable bacteria to the initial population. We assume that oxygen is the limiting substrate. The parameters used in these simulations are given in Table II.

We first demonstrate that, in the absence of flow, but with antimicrobial agent neutralization, we can quantitatively fit experimental data [9]. Then, by incorporating the fluid dynamics into the model, and assuming that the antimicrobial agent is non-reactive, we obtain survival curves that are in qualitative agreement with one-dimensional models [24]. We then show that under the assumptions described above, dosing at low antimicrobial agent concentration for longer durations is more effective than higher dose concentration for shorter periods.

These three simulations are designed to validate the current model; however, one of the strengths of the present study is that it tracks spatial evolution of chemical concentrations and bacterial population. We can use the spatial variability to help determine effectiveness of treatment as well as the distribution of affected cells.

4.1 Simulation 1: No-flow, reactive antimicrobial agent

Although including fluid dynamics is an important part of the current investigation, the model can also be used to simulate no-flow experiments. In [9], Dodds and Stewart incorpo-

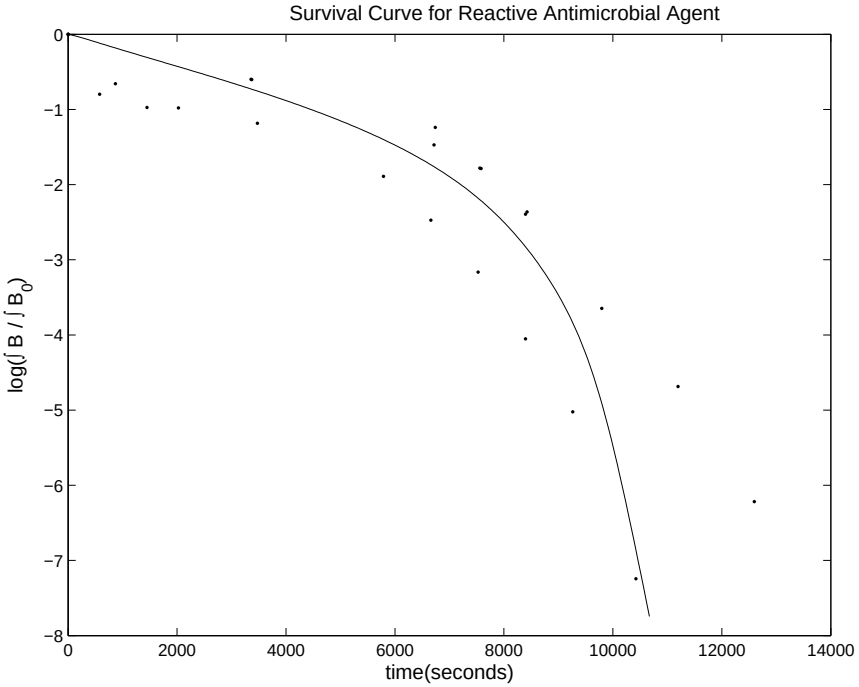

Figure 6: Survival curve for dosing at $C_s = 10\text{mgl}^{-1}$. In this simulation there is no flow and the antimicrobial agent is assumed to react with a neutralizing component of the biofilm. This is consistent with the data collected in [25]. There were multiple samples taken and all the collected data are shown.

rated *Pseudomonas aeruginosa* bacteria into alginate gel beads, forming artificial biofilms. These were incubated in a nutrient broth overnight and then suspended in a hypochlorite solution. Multiple gel beads were removed at regular intervals and dissolved. The surviving bacteria were enumerated from the resulting cell suspensions. Hypochlorite is known to be reactive [25]; therefore, we include reaction with a neutralizing agent within the biofilm. The neutralizing agent is assumed to be uniformly distributed within the biofilm and the initial concentration is set to be 4% of the biomass concentration. The neutralizer reacts with the antimicrobial agent, removing the neutralizer and the antimicrobial agent. Because the antimicrobial agent/neutralizer reaction consumes the neutralizing agent, the antimicrobial agent will eventually fully penetrate the biofilm region. For this simulation we solve Equations (7)- (12) with $\vec{U}$ identically zero. The biofilm domain is the same as in Figure (1). The concentrations of antimicrobial agent and nutrient are fixed at their source values outside the biofilm region. The active bacteria are assumed to be uniformly distributed throughout the biofilm region initially. We then simulate the dynamics for the antimicrobial agent, nutrient, bacteria and neutralizer. Figure 6 shows the survival curve obtained after continuous dosing for 4 hours along with data from [25].

4.2 Simulations 2 and 3: Continuous flow, non-reactive antimicrobial agent

By physiological resistance, we mean that only the bacteria that are respiring are susceptible to antimicrobial agent. It is well known that there are nutrient-depleted zones within the biofilm and that bacteria occupying these zones are typically less susceptible to the antimicrobial agent than actively respiring bacteria [23]. In the following sections we simulate the effect of continuous dosing of a non-reactive antimicrobial agent on a biofilm with a single limiting nutrient.

In this simulation, a background flow from left to right moves in the channel around the biofilm. Initially, the bacteria are uniformly distributed throughout the biofilm region,shown in Figure (1), and the antimicrobial agent and nutrient concentrations are zero within the computational domain, except at the entrance to the channel where they are fixed at their source concentrations. Snapshots of the concentration of antimicrobial agent, nutrient and active bacteria for various times are shown in Figure 7. The nutrient and antimicrobial agent are advected by the fluid outside the biofilm region. Within the biofilm there is negligible flow, so diffusive transport dominates. However, because the bacteria are consuming oxygen, there are zones within the biofilm where the bacteria are in an anaerobic environment. We note that downstream regions of the biofilm have less exposure to nutrient because of consumption by bacteria upstream, so the anaerobic region is located preferentially towards the downstream end of the biofilm. Since the antimicrobial agent is assumed to be non-reactive in this simulation, we fix N to be zero. We see full antimicrobial agent penetration of the biofilm region. Bacteria in regions where there is both nutrient and antimicrobial agent (near the interface) are killed.

The survival curves for several different flow rates are shown in Figure 8. We see that the 'knee' of the curve occurs earlier for the higher flow rate. Moreover, the overall effectiveness of the treatment is improved. These results imply that more bacteria are exposed to the combination of antimicrobial agent and nutrient when the flow is higher. The qualitative survival curves are similar to those found in [24]. Increasing the flow rate has the effect of decreasing the mass transfer boundary layer, which increases the susceptibility. This is also in qualitative agreement with results from [24].

We next consider whether increasing the concentration of antimicrobial agent and decreasing the length of the dosing application yields equivalent survival curves. In particular, we compare three protocols: dose concentrations of 5 mg l^{-1}, 10 mg l^{-1} and 20 mg l^{-1} for duration 5 hours, 2.5 hours and 1.25 hours, respectively. The survival curves are plotted on the scale of mg l^{-1}s (Figure 9). On this mixed time scale, the domains of the survival curves for the three simulations are the same. We find that the final survival fraction for longer exposure is two orders of magnitude less than that of the shortest dose duration, indicating a more effective treatment.

4.3 Simulation 4: Flow reversal, non-reactive antimicrobial agent

Noting that the upstream region of the biofilm has higher nutrient concentration (last row of Figure 7), and is therefore more susceptible to antimicrobial agent, we investigated the survival curve that is obtained when the flow and dose location are reversed during the simu-

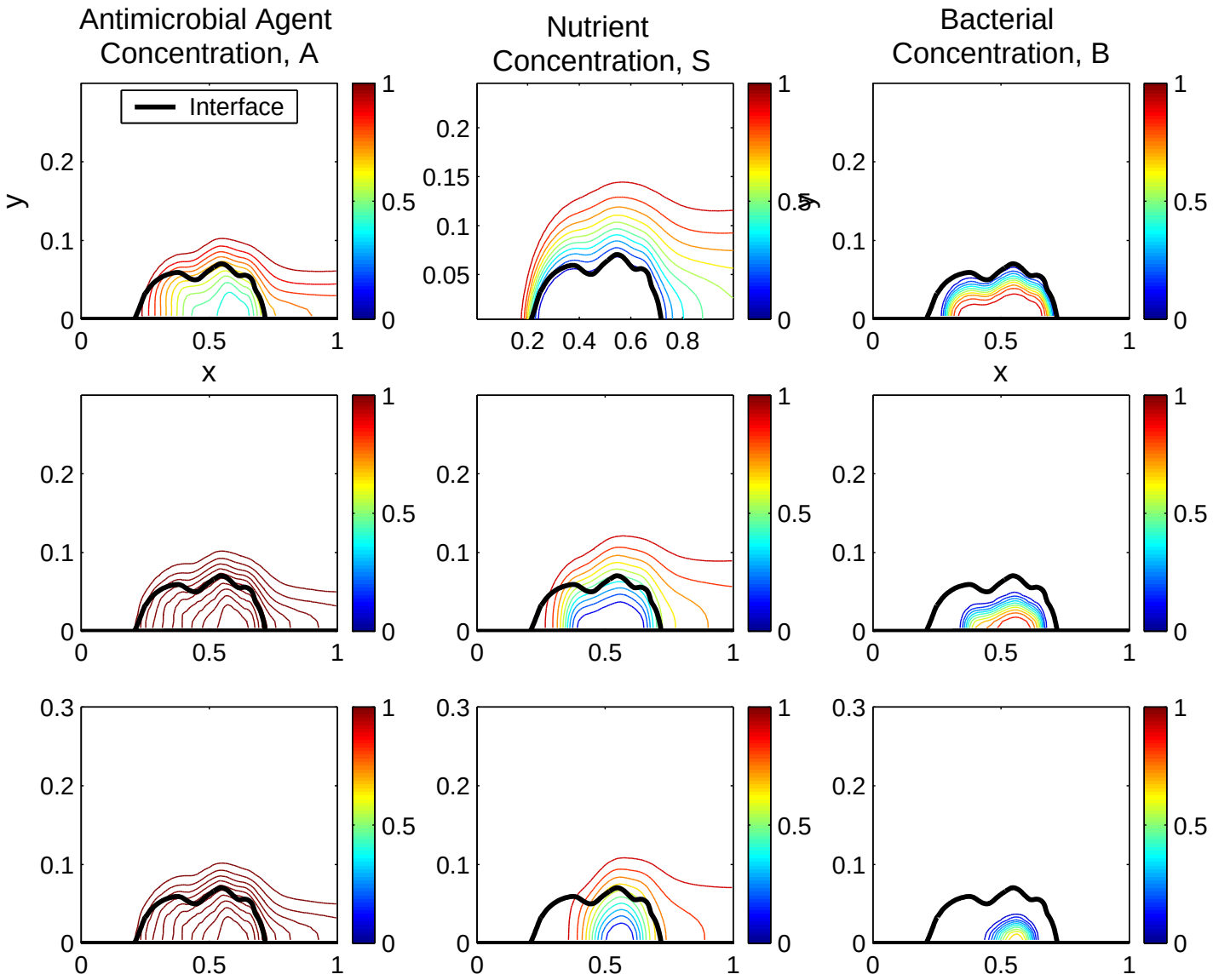

Figure 7: Profiles of antimicrobial agent, nutrient and bacterial concentrations at t=60 minutes (first row), t=120 minutes (second row) and 168 minutes (last row). Note that the antimicrobial agent concentration has equilibrated to the source concentration within two hours (last two rows fo the first column). The maximum flow rate for the parabolic background flow is $U_{max} = 0.0334$ m h^{-1}.

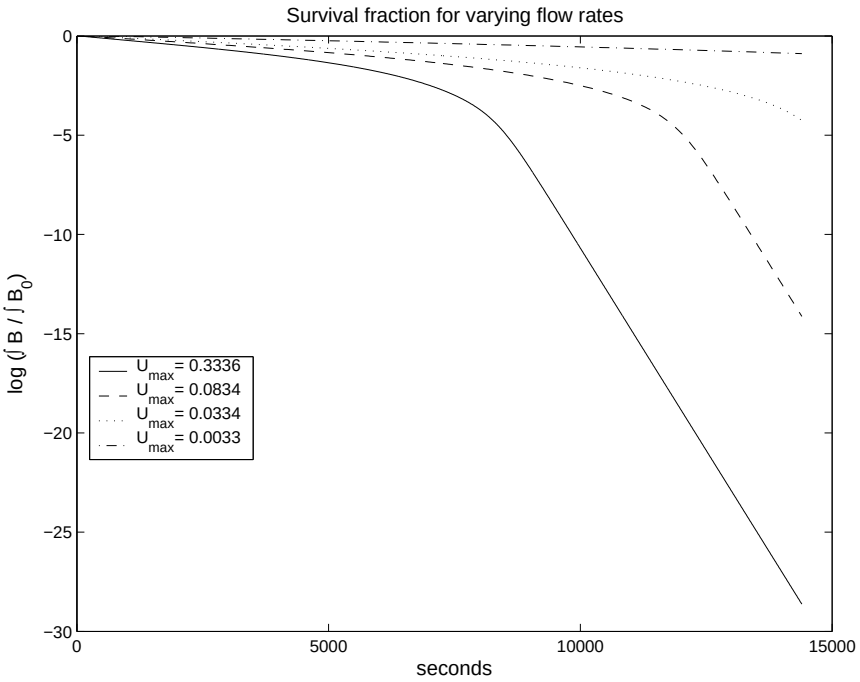

Figure 8: Survival curves for dosing at $C_s = 10\text{mgl}^{-1}$ and four flow rates (0.3336 m h^{-1}, 0.0834 m h^{-1}, 0.0334 m h^{-1} and 0.0033 m h^{-1}). Higher flow increases the susceptibility of the bacterial population resulting in earlier clearing of the bacteria.

lation. Initially, the flow is from left to right. The initial concentrations of the antimicrobial agent and nutrient are zero except at the influent end of the channel. Midway in the simulation, the flow and dose location are reversed. The flow is then continuous from right to left and the concentrations of antimicrobial agent and nutrient are fixed at the right-hand-side of the channel. Although there are many situations where this is not a viable procedure (for example in biofilm infected artificial joints), there are many industrial settings, such as waste water treatment, where flow reversal is feasible. Intuitively, we expect that reversing the flow will increase the susceptibility of the bacteria by providing the downstream biofilm with nutrient during the dose application. We simulate a dosing experiment in which the flow direction and dose location are reversed after 90 minutes. Because bacteria downstream of the source are exposed to less nutrient, they are less susceptible to the antimicrobial agent. When the flow is reversed, these bacteria become more susceptible, increasing the effectiveness of the treatment. Results from this simulation are shown in Figure 10. We see a dramatic decrease in the surviving population compared to the simulation without flow reversal. This indicates that manipulating the flow can increase the effectiveness of treatment.

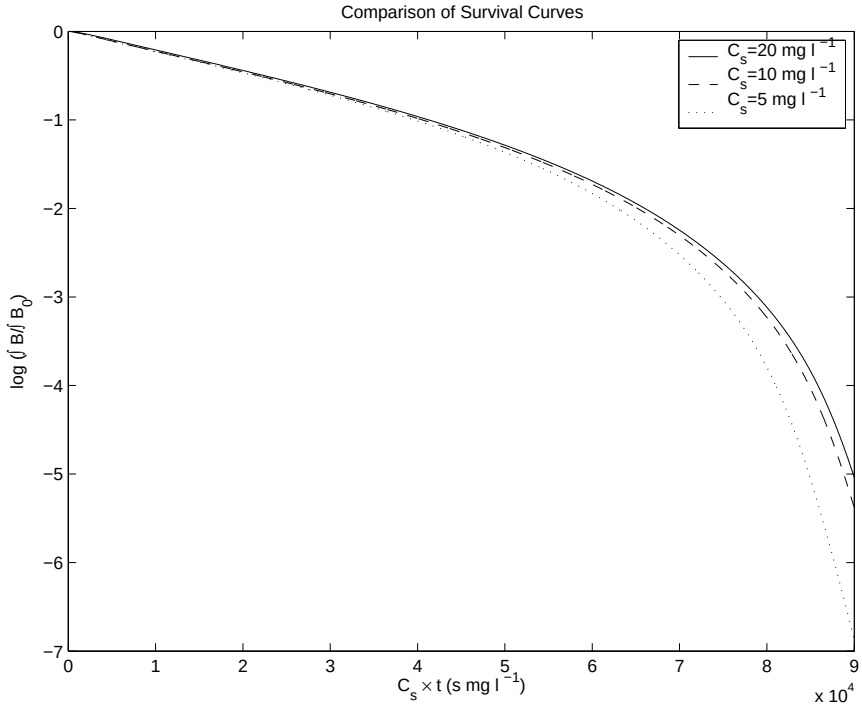

Figure 9: Survival curves for dosing at $C_s = 5\text{mgl}^{-1}$, $C_s = 10\text{mgl}^{-1}$ and $C_s = 20\text{mgl}^{-1}$. The horizontal axis is scaled by the product of the dose concentration and the dose length (chosen so that the product is constant) and the vertical axis is on a logarithmic scale. This comparison clearly illustrates that the dosing protocols do not give the same results. In fact, low concentration dosing for longer time is more effective.

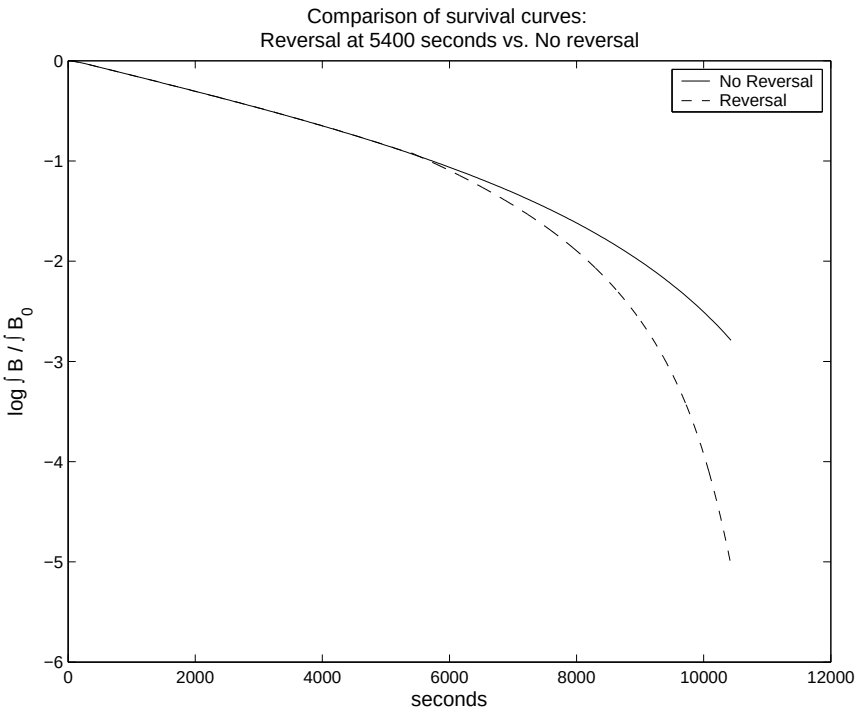

Figure 10: Comparison between two dosing protocols. The solid line shows resulting survival curve for continuous dosing, while the dashed line shows the survival curve when the flow is reversed at 5400 seconds. Because bacteria in regions upstream consume more nutrient, the bacteria in downstream regions are less susceptible to the antimicrobial agent. Reversing the flow exposes different bacteria to antimicrobial agent resulting in a more effective treatment.

4.4 Simulation 5: Continuous flow, non-reactive antimicrobial agent, variable surface roughness

We now examine the effect of surface roughness by comparing the survival curves for regions with three different fluid/biofilm interfaces. The biofilm/fluid interfaces, $\alpha(n)\Gamma(n)$ are given by

$$\Gamma(n) = \begin{cases} 0, & \text{for } x \leq 0.1 \\ (x-.1)(x+14.8) & \text{for } 0.1 < x \leq 0.2 \\ 1.5 + .2\sin\left(\frac{(x-0.2)}{.6} n\pi\right), & \text{for } 0.2 < x \leq 0.8 \\ (x-.9)(x-15.8) & \text{for } 0.8 < x \leq 0.9 \\ 0, & \text{for } 0.9 \leq x, \end{cases} \tag{19}$$

where the scalar parameter $\alpha(n)$ is chosen so that the areas of the biofilm regions are constant. Because the bacteria are uniformly distributed throughout the region, the total population of bacteria is constant for all n. We quantify 'roughness' by n (i.e. roughness increases with n).

The transport of nutrient and antimicrobial agent depends on the steady-state velocity profiles. Therefore the effectiveness of continuous dosing depends on the inflow velocity and the fluid/biofilm interface. To determine the effectiveness of treatment, several numerical simulations were done with varying interfaces and flow velocities. As n increases, we see a decrease in survival. In Figure 11 we show the steady-state flow streamlines, oxygen concentration profiles, interfaces and survival curves for $n = 0, 5$ and 11 for $U_{max} = 0.0334$ m h^{-1} and $U_{max} = 3.336$ m h^{-1}. (Note that the streamlines are the same for each flow rate since the fluid dynamics is governed by the Stokes equations.)

In Figure 12 we show the survival curves with low and high flow rates for the various biofilm regions. We find that for high flow velocities, such as this one, the survival curves are sensitive to the surface roughness. This is not the case for lower flow rates. There is very little difference between survival curves for the same values of n and $U_{max} = 0.0334$ m h^{-1}. Thus the interplay between the roughness and the flow leads to substantially different results.

In Figure 13, the survival curves for low and high flow rates are compared for each of the three regions tested. The general trend of lower survival for higher flow rates is consistent with the simulations in section 4.2.

5 Conclusions

We have presented a model of antimicrobial agent efficacy which couples fluid dynamics with the reaction, diffusion and advection of a single antimicrobial agent and nutrient. We use this model to investigate the mechanism of physiological resistance in two spatial dimensions. Our model reproduces results similar to those in [24], but also predicts spatial evolution of all chemicals and the bacterial population. The model makes no assumption about the mass transfer boundary layer or constituent concentration profiles. Because quantities in the model are spatially dependent, we are able to examine nutrient depleted zones in more detail. This

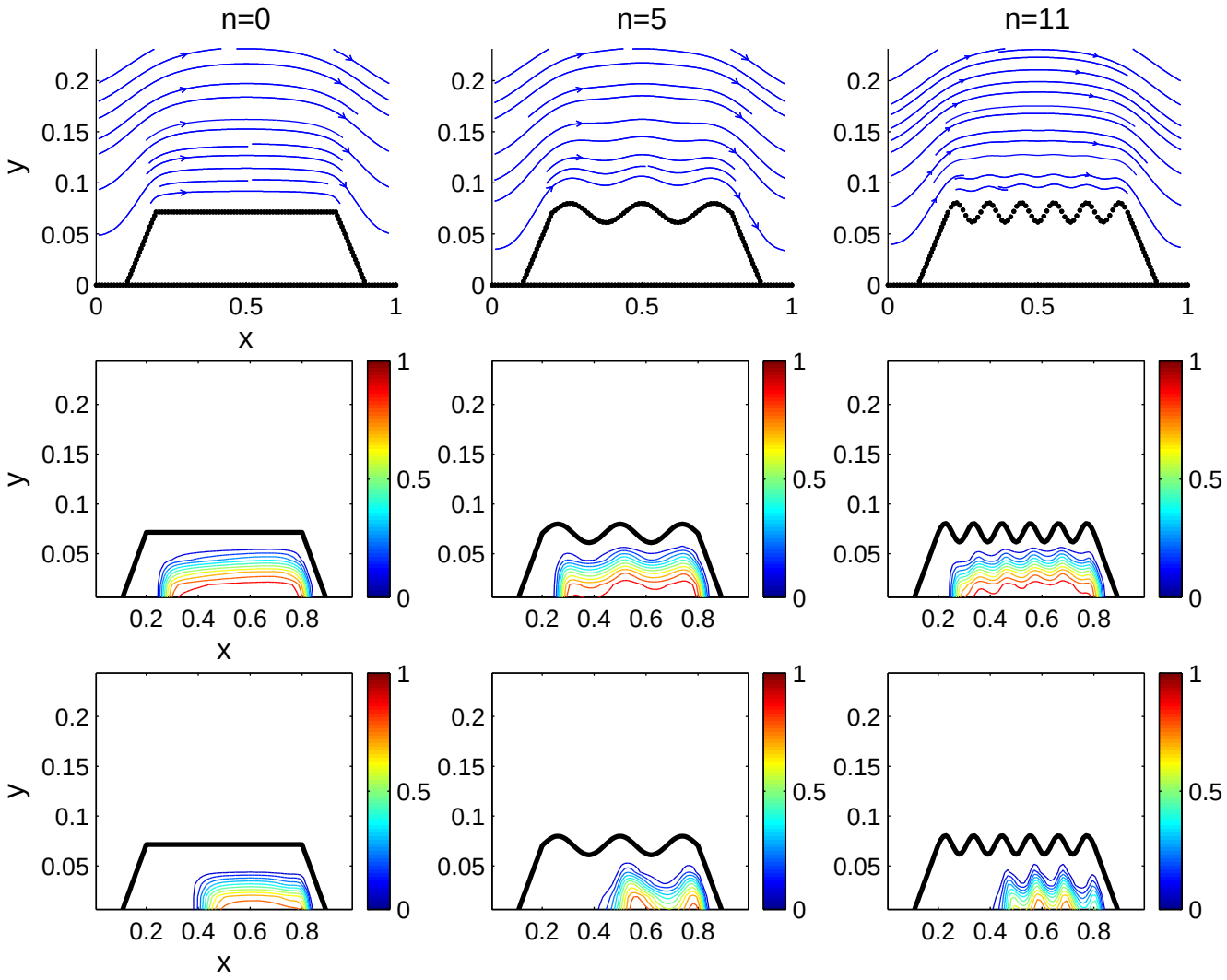

Figure 11: Top row: Streamlines for $n = 0, 5, 11$. Middle Row: Snapshots of the population of viable bacteria with low flow ($U_{max} = 0.0334$ m h^{-1}) at 7200 seconds. Bottom row: Snapshots of the population of viable bacteria with high flow ($U_{max} = 3.336$ m h^{-1}) at 7200 seconds. The roughness is quantified by the mode of the perturbation of the plateau region (see Equation (19)).

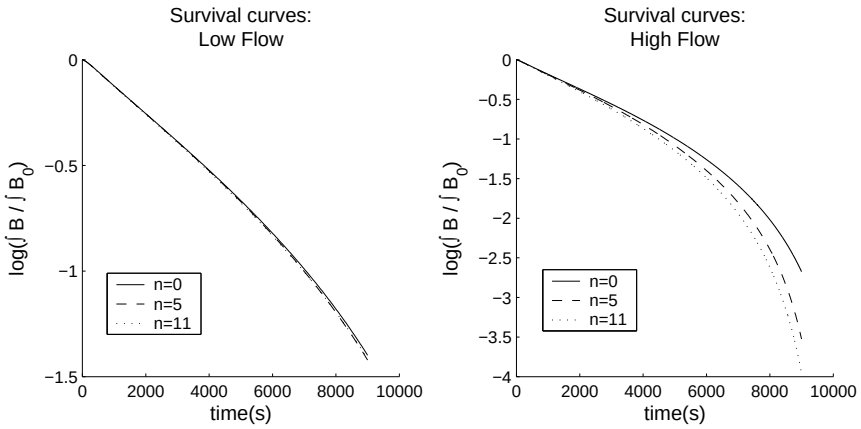

Figure 12: Survival curves for low flow ($U_{max} = .0334$m h^{-1}) and high flow ($U_{max} = 3.336$m h^{-1})showing that the difference in overall survival between the three modes, $n = 0, 5,$ and 11, is more pronounced for higher flow rates.

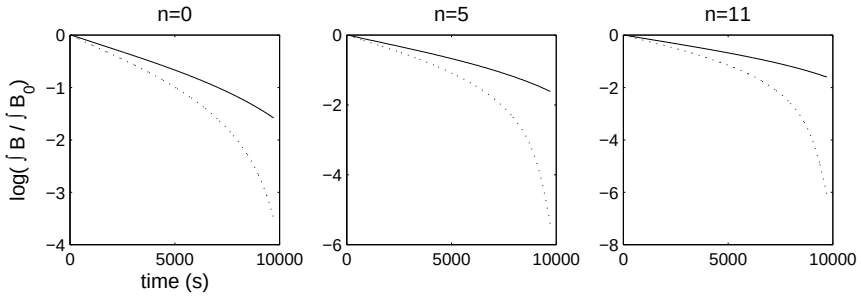

Figure 13: Survival curves for $n = 0, 5$ and 11 for flow rates of $U_{max} = 3.336$m h^{-1} (solid) and $U_{max} = .0334$m h^{-1} (dotted). Again we see that dosing at higher flow rates is more effective than lower flow rates.

motivated a simple dosing protocol which calls for flow reversal. This dosing strategy was shown to increase the effectiveness of dosing substantially. We also showed that long doses with low antimicrobial concentration is more effective in clearing bacteria than short doses of high antimicrobial concentration. Finally, we demonstrate that survival decreases with increasing fluid/biofilm interface roughness. This dependence is more pronounced at higher flow rates.

We believe that the inclusion of comprehensive fluid mechanics, and the tracking of the spatial evolution of chemical constituents and bacterial population presents a robust and versatile method for studying dosing protocols in biofilm treatment. Within the current framework, we plan to model a dynamically evolving biofilm interface that responds both to fluid shear and bacterial growth. In this case, the Stokes equations of fluid dynamics must be solved at each time step due to the unsteady nature of the flow. In addition, this methodology will readily extend to a full three-dimensional implementation. The reaction-diffusion equations will be solved on a regular, finite difference grid. In 3D, the biofilm interface will be represented by discrete lattice points describing a surface, rather than discrete points that represent a one-dimensional curve. The grid-free method of regularized Stokeslets in 3D can easily handle forces distributed along such a surface [6].

A biological issue that has not been addressed in this manuscript is the existence of a small number of persister cells, which are not susceptible to treatment [17]. The nature of these persister cells is an open question. Current hypotheses include variation in multi-drug efflux pumps, maximum growth rates and deactivated programmed cell death (PCD) [17, 28, 13]. Although these hypotheses are not addressed in the current study, the current modeling framework will be used to investigate these theories.

5.1 Acknowledgments

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