

Modeling and Analyzing Hydrodynamic and Physicochemical

Effects in Bacterial Deposition on Surfaces



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Introduction

When bacteria flow through a fluid medium such as water, it tends to accumulate on any available surfaces. In most cases, bacterial deposition on surfaces inflicts damage and causes rapid degradation. This problem is present on ship hulls, measuring instruments, medical devices etc., and is known as biofouling.

Understanding the physical phenomena leading to bacterial deposition is necessary in order to offset biofouling. Current mathematical models describe bacterial deposition inside a parallel-plate flow chamber (PPFC) (Fig. 1), an engineering instrument used for particles and bacteria deposition analysis. However, these models have insufficient accuracy.

The benchmark Smoluchowski-Levich (S-L) approximation shows decreasing flux of bacteria with distance from inlet (Fig. 2a), in total contradiction to the experimental results of Li et al. 2012 (Fig. 2b) [2].

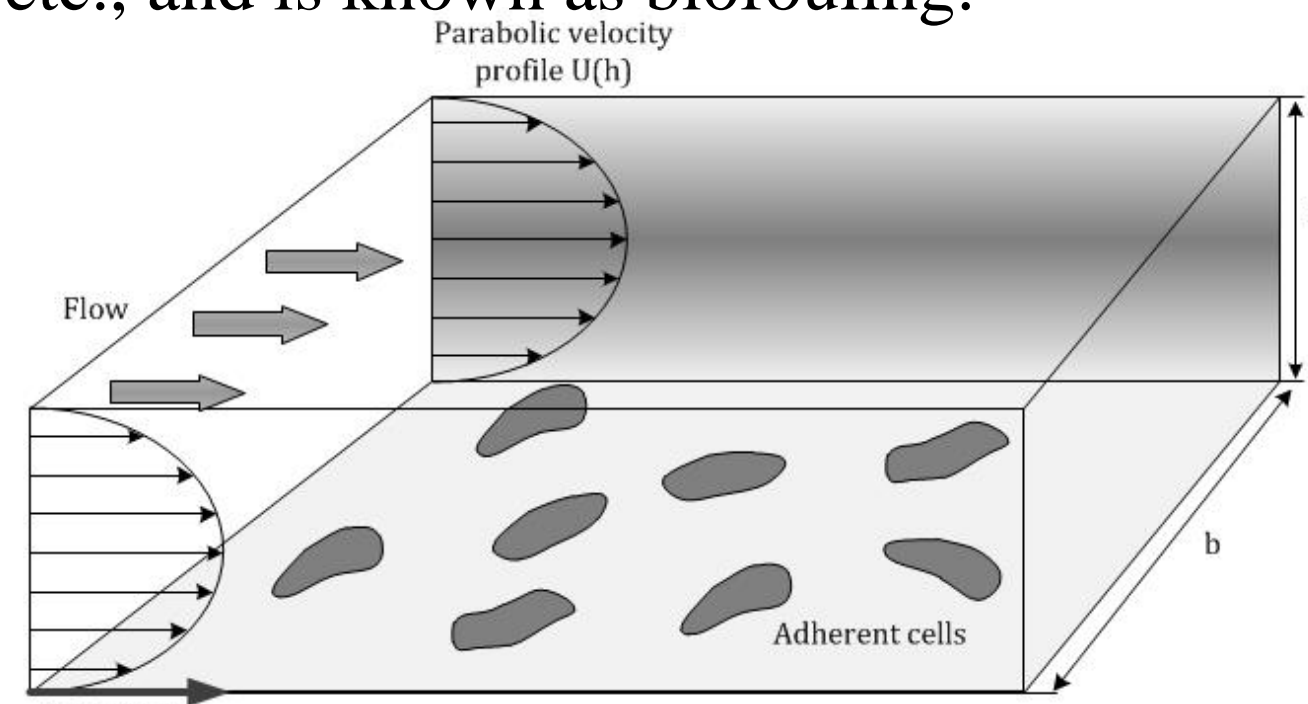


Fig. 1: A parallel-plate flow chamber with a typical parabolic velocity profile [1].

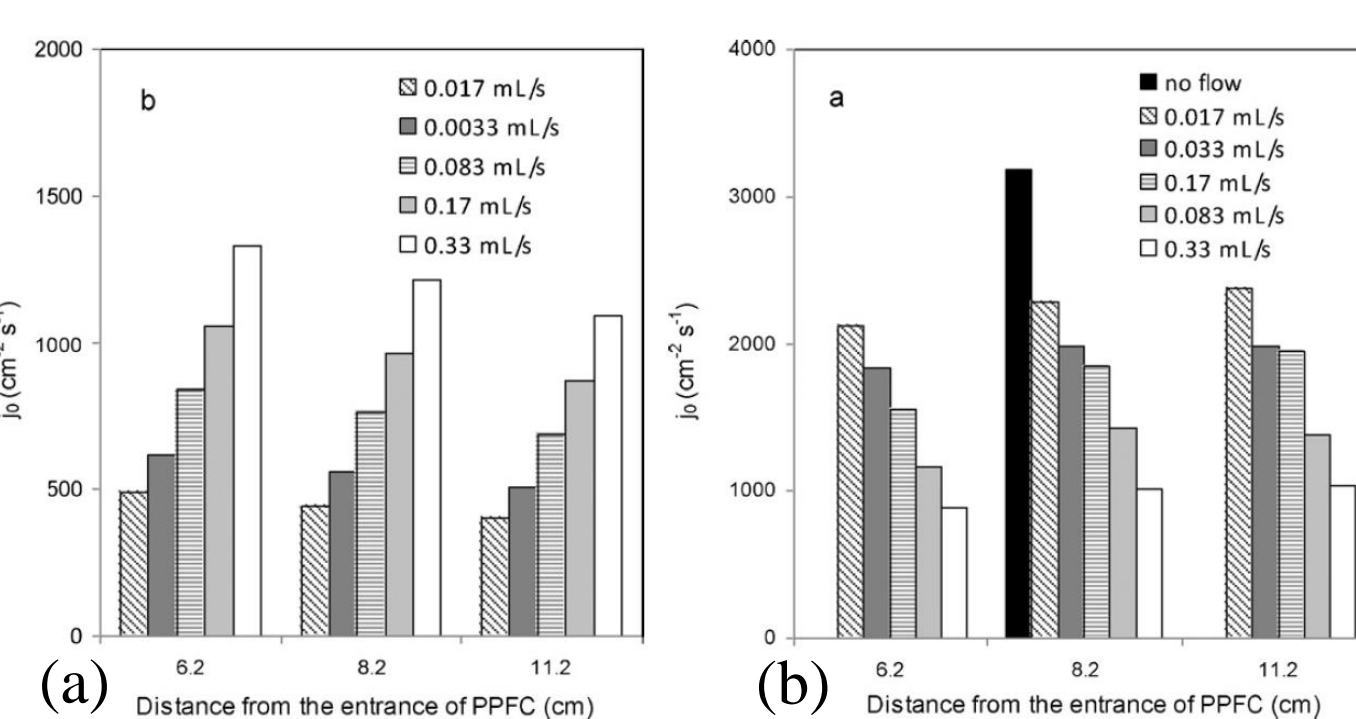


Fig. 2: Bacterial flux vs. distance from channel inlet for different flow rates. (a) Simulation results (S-L approximation). (b) Experimental results [2].

Present Model

We assume a fully developed Poiseuille flow in the channel (Fig. 3).

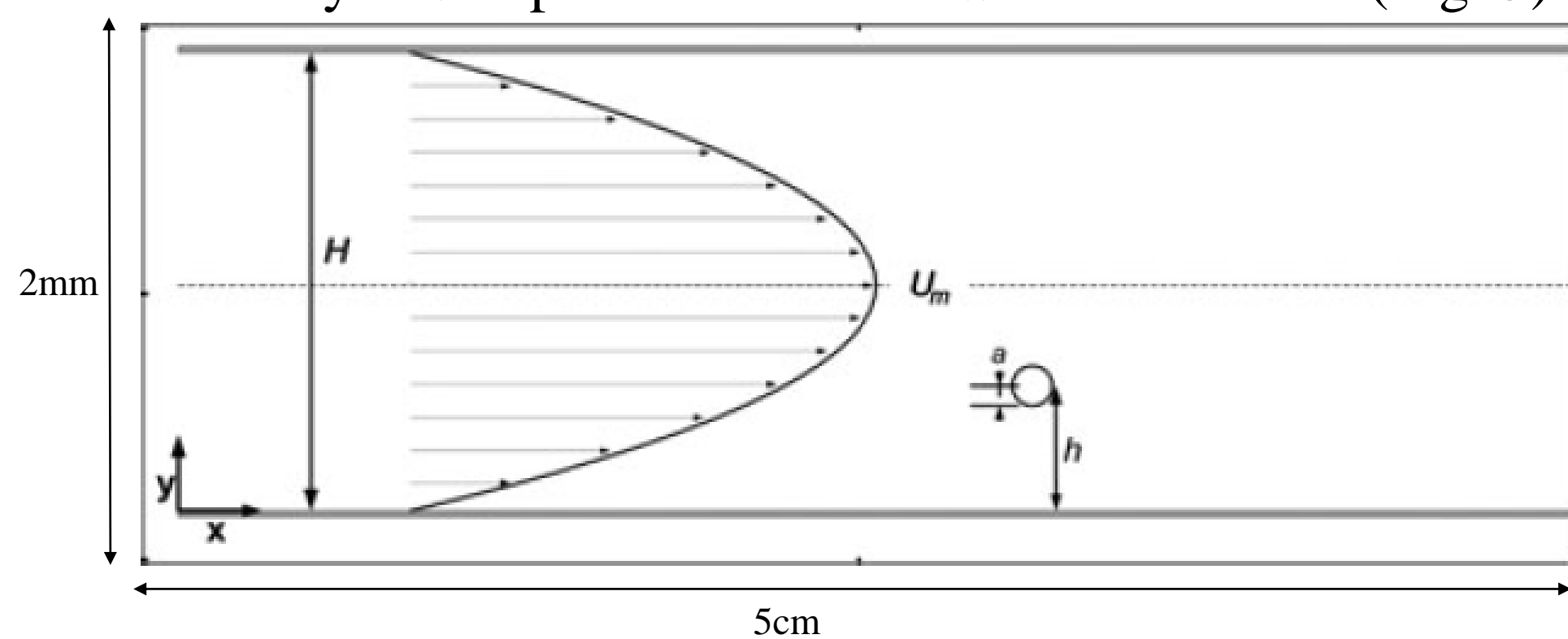


Fig. 3: A 2D cut-plane of the PPFC with a parabolic velocity profile [1].

The general mass-conservation partial differential equation (PDE) solved in the model is:

$$\frac{\partial C}{\partial t} = -\nabla \cdot \mathbf{J} = -\nabla \cdot \left[-D\nabla C + \frac{DC}{k_B T} \mathbf{F} + \mathbf{U}C \right], \quad (1)$$

Accumulation term
Del (partial derivatives)
Flux
Diffusion
Migration (sedimentation+lift)
Convection

Where C is the bacterial concentration, $D \approx 3.49 \cdot 10^{-13} \frac{m^2}{s}$ is the diffusion coefficient, $k_B \approx 1.38 \cdot 10^{-23} \frac{J}{K}$ is Boltzmann's coefficient and $T = 298 K$ is the temperature of the fluid [1].

The sedimentation and lift forces are given by:

$$F_g = -\frac{\pi}{6} a^3 g \Delta \rho, \quad (2)$$

$$F_L = \frac{1}{36} \rho \sigma^2 a^4 G(S), \quad (3)$$

Where $a = 0.7 \mu m$ is the bacterial radius, $\Delta \rho = 100 \frac{kg}{m^3}$ is the difference between the bacterial and fluid density and $\sigma = 600 \frac{1}{s}$ is the shear rate.

In order to solve the PDE, boundary conditions must be set on the channel walls.

Those conditions are given by:

$$J_{y=0,H} = K_{dep} [C_s - C(y=0)] \mathbf{r}, \quad (4)$$

Where \mathbf{r} is the unit vector normal to the wall, C_s is the solution concentration in equilibrium with the surface (taken to be 0), and K_{dep} is the fitting kinetic parameter which describes interactions between the bacteria and the wall [1].

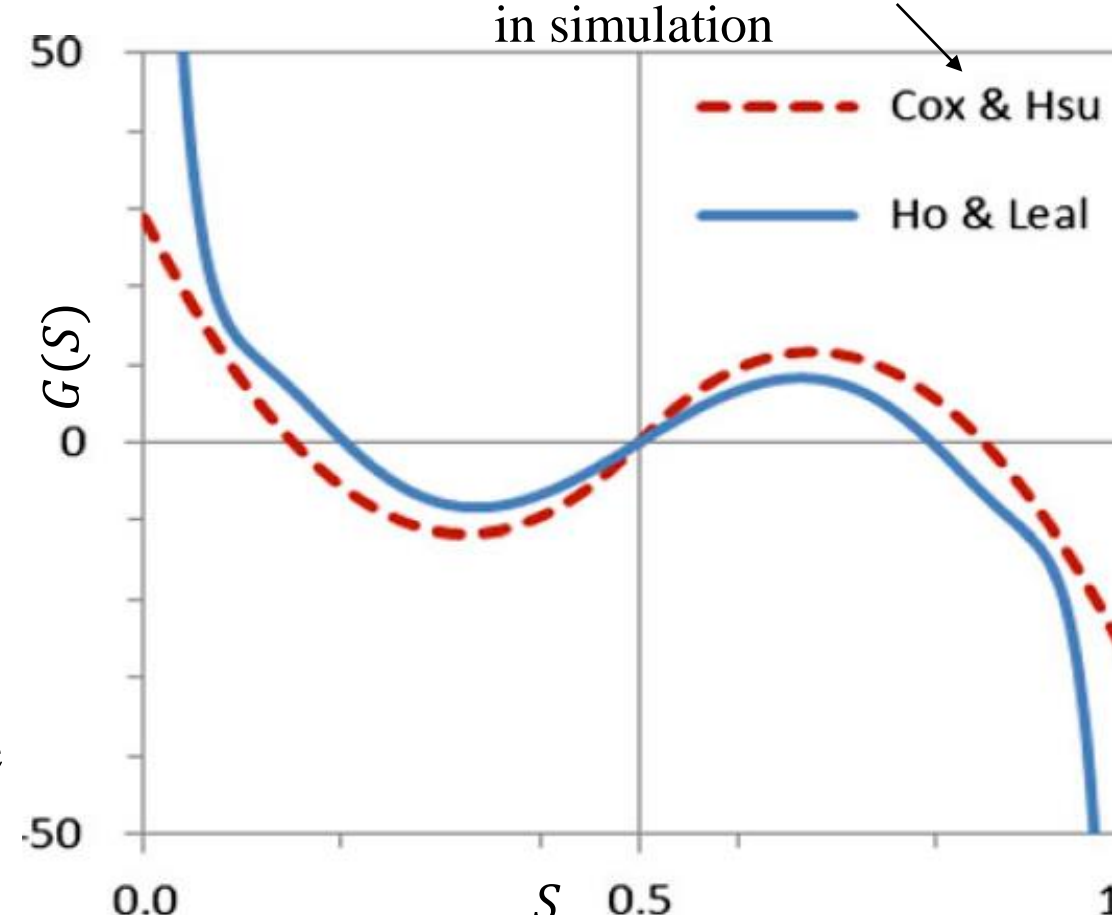


Fig. 4: Variation in lift force as a function of normalized channel height ($S = \frac{x}{H}$) [1].

Sliding Velocity – A Novel Mechanism

- The novelty of this research can be a mechanism called sliding velocity i.e. the drift of bacteria along the channel surface, which we believe is responsible for bacterial increment in flux and density along the channel [3].
- In order to get the bacterial density along the channel's surface, the following continuity equation must be coupled to Eq. (1):

$$\frac{\partial \rho(x,t)}{\partial t} = J(x,t,y=0), \quad (5)$$

- Adding the mean sliding velocity \bar{v}_{slide} to Eq. (5) will result in:

$$\frac{\partial \rho(x,t)}{\partial t} + \bar{v}_{slide} \frac{\partial \rho(x,t)}{\partial x} = J(x,t,y=0), \quad (6)$$

- A typical sliding velocity value of $6.67 \cdot 10^{-8} \frac{m}{s}$ was used in this simulation.

Research Goals

Our goals in this research are to:

1. Refine a mathematical model and obtain reliable simulation results describing the deposition of bacteria on the top and bottom plates of a PPFC by adding the bacterial sliding velocity as a parameter.
2. Solve the model numerically using COMSOL Multiphysics software.
3. Compare our model to present experimental results (Li et al. 2012).

Results and Conclusions

- Solving Eq. (1) numerically for the bottom plate in COMSOL gives the flux as a function of both time and distance from the inlet (Fig. 5). The model was solved for different values of K_{dep} (Fig. 6).
- Incorporating Eq. (6) in the model yields the numerical solution for bacterial density along the channel's bottom plate for different time periods (Fig. 7).

- It can be clearly seen in Figs. 5, 6 and 7 that the bacterial flux and density increase with distance from inlet, time and K_{dep} .

- The resultant trends match those of Li et al. 2012.

- From this simulation we saw that the accumulation term from Eq. (1) contributes the same effect as sliding velocity does in the stationary model.

- Future researches may also consider adhesion forces, non-laminar flow etc.

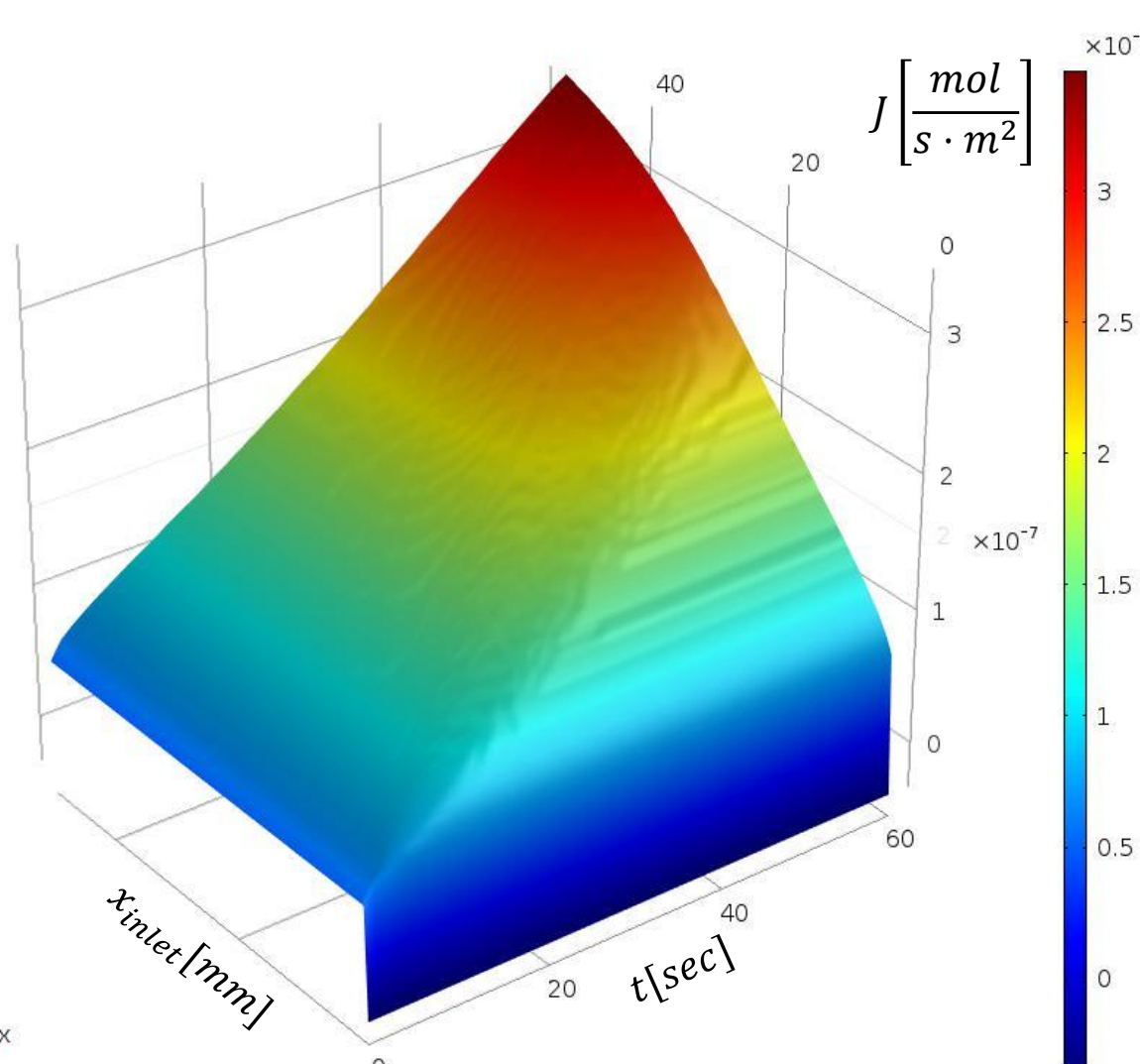


Fig. 5: Bacterial flux on the PPFC's bottom plate as a function of time and distance from inlet.

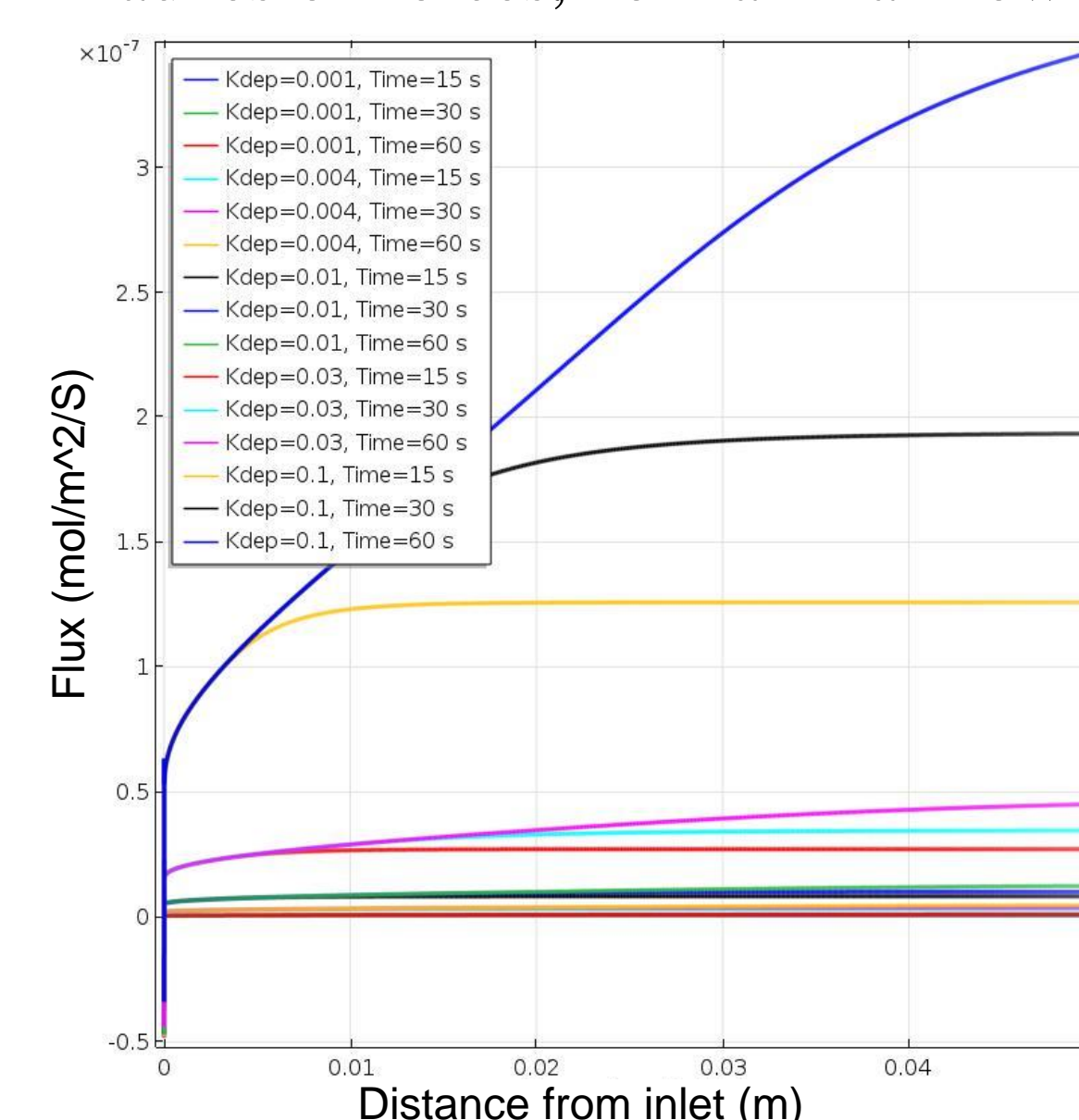


Fig. 6: Bacterial flux on the PPFC's bottom plate vs. distance from inlet for different time and K_{dep} values.

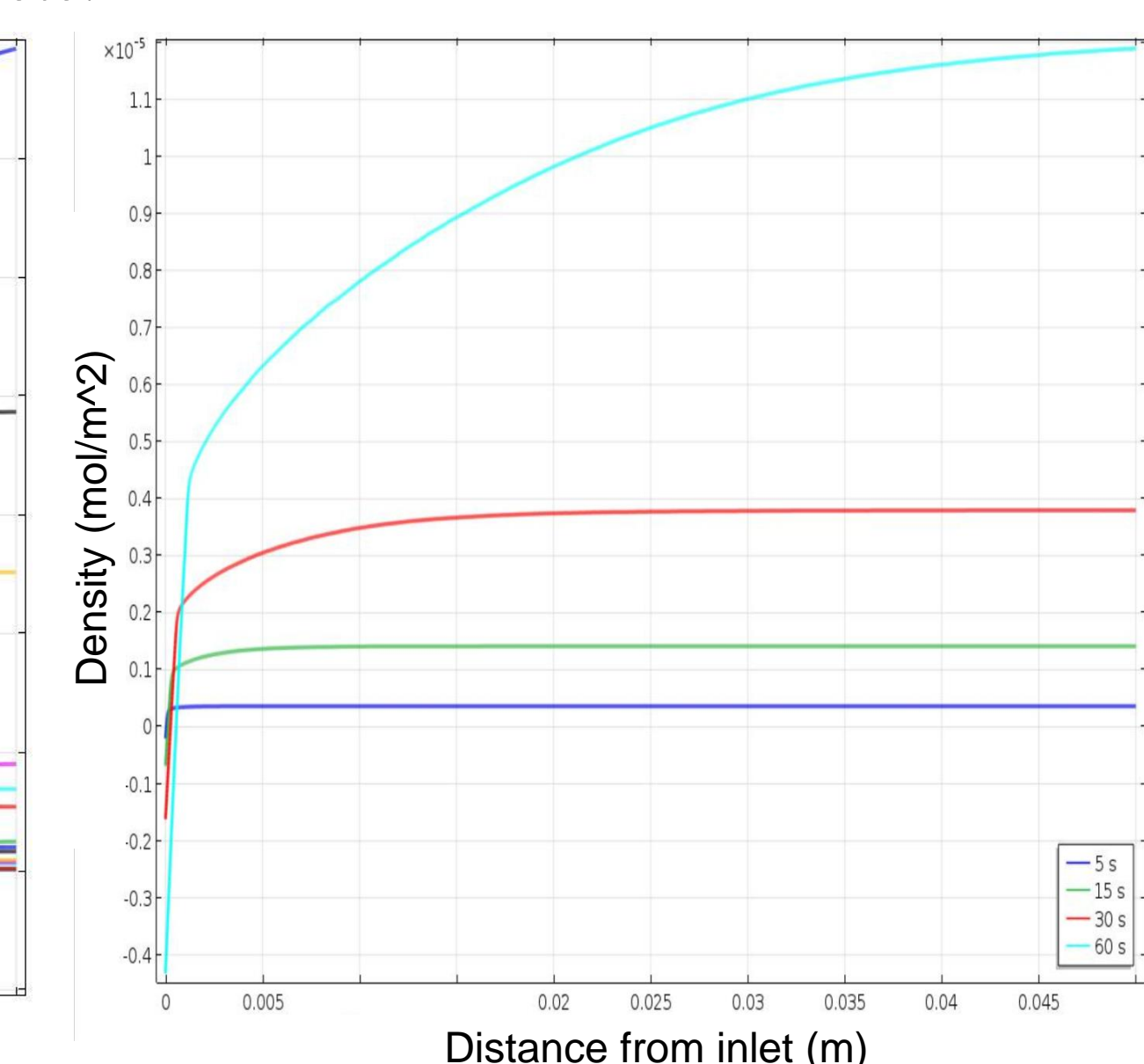


Fig. 7: Bacterial density vs. distance from inlet for different time values.

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