A Multispecies Biofilm Growth Model

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INTRODUCTION

WHAT IS A BIOFILM?
A biofilm is a structured collection of bacteria that adheres to a surface. The development of biofilms is relevant to many fields including wastewater management, industrial processes, natural aquatic ecology, and medicine. In a typical formation of biofilm, bacteria compete in a bulk liquid for nutrients, called substrates. The bacteria reproduce until they attach to a surface where it then forms a protective biofilm. As substrate diffuses into the biofilm, it grows in thickness until it can release bacteria into the bulk liquid to colonize additional surfaces.

WHY IS IT IMPORTANT?
The protective layer allows tolerance to antibiotics and other threats greatly increasing the resilience of the bacteria. Applications of biofilms are widespread, for example, most water treatment plants now use biofilms for secondary filtration.


Figure 1. The Biofilm Life Cycle
From Dirckx, P. A Brief Introduction to Biofilms

PROJECT GOALS:
The Fundamentals of Biofilm Engineering (EBIO 566) course taught by Dr. Phil Stewart in Chemical and Biological Engineering needs a new program to numerically model biofilm growth and dispersion in a continuously stirred tank reactor. The existing software is old, difficult to use, and the source code is no longer available making it impossible to update or modify. The goal of this project is to develop a new program to model biofilm growth in the presence of multiple substrates. Such a model would need to both accurately predict biofilm thickness and be easy to use for those unfamiliar with coding languages. A successful model would need to account for microbial growth, the effects of multiple substrates and biofilms on growth rates, the diffusion of substrates into the biofilm, the dispersion of biomass into the bulk liquid, and concentrations of substrates in the bulk liquid.

METHODS
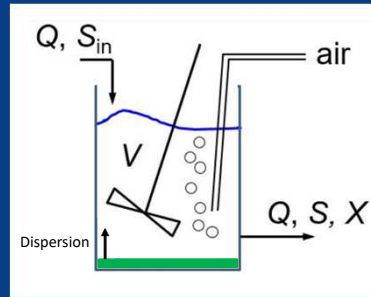
There are four main parameters that are needed to model biofilm thickness.

Substrate Concentration in the Tank:

$$\frac{dS}{dt} = -\frac{\mu(S)x}{Y_{xs}} + \frac{QS_{in}}{V} - \frac{QS}{V} - \frac{AB_{flux}}{V}$$

Tank Species Growth   Inflow   Outflow   Biofilm Species Growth

Substrate Concentration in the Biofilm:

$$\frac{dS_b}{dt} = D_e \frac{d^2 S_b}{dz^2} - \frac{\mu(S_b)X_b}{Y_{xs}}$$

Diffusion   Biomass Consumption/Production

Species Concentration in the Tank:

$$\frac{dx}{dt} = \mu(S)x - \frac{Qx}{V} + \frac{v_{det}AX_b}{V}$$

Tank Biomass Growth   Outflow   Biofilm Dispersion

Species Concentration in the Biofilm:

$$\frac{\partial X_b}{\partial t} = e[\mu(z)\epsilon - \frac{\partial(v\epsilon)}{\partial z}]$$

Growth   Velocity

These parameters are used to update growth rates throughout the model. The volume fractions of each species within the biofilm are then calculated. Using the volume fractions and growth rates, a growth velocity for each species is determined. These are combined resulting in a total growth velocity for the biofilm. This can then be used to find biofilm thickness.

A fourth order Runge Kutta scheme is used to solve the concentrations in the tank. Diffusion of substrate into the biofilm is discretized using the Finite Difference method. Trapezoidal integration is used to calculate the growth velocities.

RESULTS

The model shows good agreement with analytical solutions for a test case in which the biomass consumes one substrate and produces another. Implementations including multiple biomass species have yet to achieve such agreement.
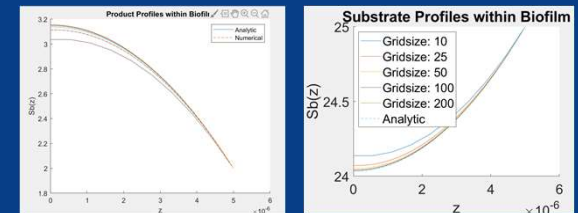
CONCLUSION

The model has been shown to accurately predict biofilm growth in simplified with multiple substrates and a single biofilm species cases where a solution is known. The program developed in this project is easier to use and more versatile than previous tools. It can be used as an agile tool in the research and instructional setting to get preliminary results without the time-consuming process of cultivating biofilm colonies for each initial test.

FUTURE WORK

Next semester, comprehensive testing and verification of the model will be performed. Results will be compared to the existing BAM program. A graphical user interface will be implemented to enable usage without existing MATLAB experience.

ACKNOWLEDGEMENTS AND CITATIONS

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