THE UNIVERSITY of EDINBURGH
School of Physics and Astronomy

Modelling Bacterial Aggregation

Ross Slater

Supervisors: Prof. R.J.Allen
Dr. G.Melaugh

Introduction

The aggregation of bacteria is important in many fields including medicine, waste water treatment and engineering. We have focused on modelling the aggregation of the bacteria *Pseudomonas aeruginosa*, a very common bacteria known to have high antibiotic tolerance due to its ability to readily form biofilms. We set out to model two experiments carried out by researchers in the Institute for Condensed Matter and Complex Systems; aggregation of growing cultures and the reaggregation of bacteria from aggregates that have been broken down.

Methods

The Smoluchowski coagulation equation[1] was time discretised to give the following equation

$$[N_j](t+\Delta t) = [N_j](t) + \frac{k}{2}\sum_{i<j}[N_i](t)[N_{j-i}](t)\Delta t - k[N_j](t)\sum_{i=1}^{n}[N_i](t)\Delta t$$

A growth contribution to the population change was added and the rate coefficient approximated using the diffusion constant of swimming *E. coli*. This allowed the modelling of bacteria aggregating during growth. Probability distribution functions were produced for experimental and simulated data sets to allow for comparison of aggregate concentration change over time.

Results

The reaggregation of disrupted aggregates in suspension was first modelled and compared to experimental data. The data compared well, with similar trends in the data as seen in Fig. 1 and Fig. 2 . Adapting the model to simulate growth in the bacteria gave less promising results, with a lack of growth in single bacteria. Following this we then investigated varying the growth rate used in the simulation.

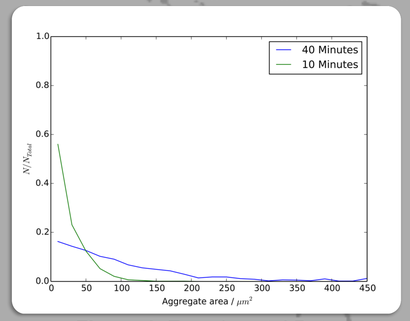

Figure 1: Experimental Data

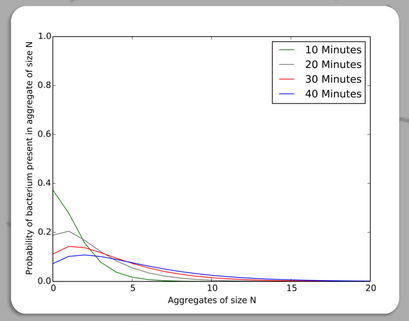

Figure 2: Model

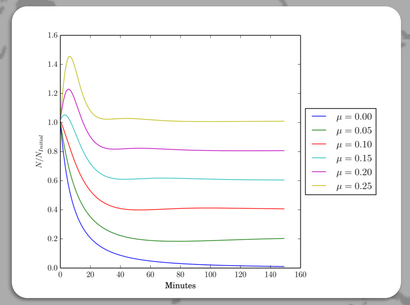

Figure 3: Varying growth rates

Fig. 3 shows the result of varying the growth rate μ between 0 and 0.25 on the concentration of single bacteria in the system. Two regimes were identified, one in which the concentration of monomers decays rapidly before reaching a steady state where the growth and aggregation are roughly balanced. The other regime shows very rapid initial growth followed by the same decay in population to a steady state.

Conclusions

This model captures the behaviour of the reaggregating bacteria well, but underestimates the growth of the bacteria in the system. Determining a new rate constant, or adding a collision efficiency parameter may resolve this, by reducing the rate of aggregation of monomers, giving them more time to grow. Our model calculates the number of bacteria in aggregates of size j, the experimental data conversely measured aggregate area. This lead to difficulty in comparing our simulation to the experiment. Methods such as confocal microscopy may in the future allow us to calculate the volume of aggregates and therefore number density of bacteria in them, allowing for much better comparisons with our model. Although the model does not capture the growth of the bacteria well, it does model the aggregation of *Pseudomonas aeruginosa with some success.*

References

[1] D. F. Evans and H. Wennerstrom. The colloidal domain: where physics, chemistry, biology, and technology meet. Second edition. Wiley-VCH, 1999.

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