

# Summer Project Proposal: Complex Fluid Models and Cellular Motility

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Microorganism motility in a Newtonian fluid is a classical field of study, but the typical Newtonian model for fluid dynamics can be inadequate to describe the environment microorganisms actually move in. Microorganisms typically operate in a complex environment composed of fluid with suspended microstructures such as elastic polymers and filamentous networks. To account for the extra microstructures in the fluid, we can add an additional stress term to the Navier-Stokes equations to model the stretching and bending of the structures in response to fluid flow. The simplest model of this form is the Oldroyd-B model. This model is based on Maxwell elements which consist of a spring and dashpot in series [1]. The constitutive equations become

$$\begin{aligned}\rho \left( \frac{\partial \mathbf{u}}{\partial t} + \mathbf{u} \cdot \nabla \mathbf{u} \right) &= -\nabla p + \mu \Delta \mathbf{u} + \xi \nabla \cdot \boldsymbol{\tau} \\ \nabla \cdot \mathbf{u} &= 0 \\ \overset{\Delta}{\boldsymbol{\tau}} &= \frac{\mu}{\lambda} 2\mathbf{D} - \frac{1}{\lambda} \boldsymbol{\tau}\end{aligned}$$

where  $\overset{\Delta}{\boldsymbol{\tau}}$  is the upper convective derivative and  $\mathbf{D}$  is the rate of strain tensor. Moving from an Oldroyd-B model to more realistic models of complex fluids involves a fairly straightforward adjustment of the constitutive equations as more realistic models have similar structures to the Oldroyd-B model. For example, the Giesekus model adds in a nonlinear term,  $(\boldsymbol{\tau} \cdot \boldsymbol{\tau})$ , to the equation for the extra stress.

We are currently working on a project to numerically solve the above equations and building the solver into IBAMR (Immersed Boundary Adaptive Mesh Refinement). This software package already has a fluid solver implemented. The current project is discretizing the Oldroyd-B model using central differences, and then solving the equations above using the built-in fluid solver and time-stepper from IBAMR.

For the summer under the guidance of Dr. Boyce Griffith, we plan on adopting a finite volume method approach to solving the Oldroyd-B model, leaving the more realistic models to a later date. This approach utilizes the transport phenomena that is inherent in the problem to conservatively update the solution at each time step yielding more accurate and stable solutions [2]. We can try to use rheological data of tracked particles gathered by Dr. Sam Lai's group in the School of Pharmacy and Dr. David Hill in the Physics Department to match our model with experimental data [3]. We can also do a comparison of various constitutive models that have an upper convected Maxwell model such as the Giesekus model.

Once this method has been implemented, we can utilize IBAMR's fluid structure interactions to model locomotion. Previous studies have shown that organisms with a fixed gait can gain a speed boost as they swim through complex fluids when compared to Newtonian fluids [4] [5]. Other studies have shown that viruses can become trapped inside complex fluids when attached with antibodies [6]. A natural extension to this question is how bacteria locomotion is affected by the presence of antibodies when swimming through these complex fluids. We can use experimental data obtained by Dr. Lai's group to set up the numerical simulations.

An additional extension to this project involves cellular locomotion. Experiments have shown that the actin cytoskeleton determines the structure of the cell [7]. The network of actin filaments changes and reacts to external stimuli and is theorized to play a major role in the locomotion of cells [8]. The interior of cells consists of a highly viscous and elastic cytosol and can accurately be modelled with a complex fluid. Using IBAMR, we can couple the motion of the cell's elastic membrane that is largely determined by the traveling waves of actin with the the motion of the cytosol. This will allow us to match experimental data of the cell's ability to move using it's actin cytoskelton. This project is done in conjunction with Dr. Tim Elston in the Pharmacology Department and Dr. Greg Forest in the Mathematics Department.

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