BE 159 Spring 2014
Homework #3
Due at the start of lecture, May 20, 2014.

Problem 3.1 (Spontaneous flow of an active viscous fluid (50 pts))**.**
In the Mayer, et al. paper, the authors used the following equation of motion to describe the dynamics of an active viscous fluid.

$$\frac{\partial \zeta \Delta\mu}{\partial x} = -\eta \frac{\partial^2 v}{\partial x^2} + \gamma v, \tag{3.1}$$

where I have used $\zeta\Delta\mu$ for the active stress, as we did in lecture. It is useful to think of $\zeta\Delta\mu$ as a single variable, which happens to be proportional to the change of chemical potential due to ATP hydrolysis, $\Delta\mu$. (This is why it is written this way.)

In the Mayer paper, $\zeta\Delta\mu$ was assumed to be a function of myosin density. It could, of course, be a function of any regulator of active stress, be it myosin, a protein that regulates myosin, actin-binding proteins, etc. Let c be the concentration of an active stress regulator, such that $\zeta\Delta\mu = \zeta\Delta\mu(c)$. For convenience, we will define a dimensionless function f such that

$$\zeta\Delta\mu = (\zeta\Delta\mu)_0 f(c). \tag{3.2}$$

Now, if we have a regulator in the active fluid, it naturally must obey a conservation of mass equation.

$$\frac{\partial c}{\partial t} = D \frac{\partial^2 c}{\partial x^2} - \frac{\partial}{\partial x}(vc). \tag{3.3}$$

This equation gives temporal dependence to the regulator concentration, i.e., $c = c(x,t)$. If we have a uniform concentration of active stress regulator, then $\zeta\Delta\mu$ is constant, and we can have no flow. This prompts the question: if we start with a uniform concentration of active stress regulator, can we get spontaneous active stress-driven flow? We will address this question in this problem.

a) Assume we have 1-D system of length L with periodic boundary conditions, analogously to the treatment of the *C. elegans* cortex in the Goehring, et al. paper. Let the homogeneous steady state be $c = c_0$. How do we know this is the only homogeneous steady state?

b) Let $c_1(x,t)$ be a small perturbation of the steady state such that $c(x,t) = c_0 + c_1(x,t)$. As we did in lecture, we assume a form of c_1 of

$$c_1(x,t) = c_1^0 \mathrm{e}^{st+ikx}. \tag{3.4}$$

Insert this expression for $c(x,t)$ into the equation of motion to solve for the flow velocity as a function of c_1. Keep only terms up to first order in the perturbation. Your expression will also include

$$f_0' \equiv \left.\frac{\mathrm{d}f}{\mathrm{d}c}\right|_{c_0}. \tag{3.5}$$

c) We define the Péclet number, Pe as

$$\mathrm{Pe} = \frac{(\zeta\Delta\mu)_0}{D\gamma}. \tag{3.6}$$

Why is this an appropriate definition of the Péclet number?

d) Insert your expression for v from part (b) into equation (3.3). Perform a stability analysis on this equation to show that the homogeneous steady state is linearly unstable if

$$\frac{\mathrm{Pe}\, c_0 f_0'}{1 + (2\pi\ell/L)^2} > 1, \tag{3.7}$$

where ℓ is the hydrodynamic length scale defined in the Mayer, et al. paper. Comment on the significance of this result.

Problem 3.2 (Flow as a big perturbation (50 pts))**.**
In the paper by Goehring et al., the authors claim that cortical flow provides the large perturbation to bring the distribution of PAR proteins on the membrane away from the stable homogeneous steady state where the anterior-like complex occupies the entire membrane. How strong much the flow be? We will investigate this question with numerical calculations in this problem.

The wild type flow can be approximately described by

$$v(x,t) = ax\, \mathrm{e}^{-x^2/2b^2}\, r(t), \tag{3.8}$$

$$r(t) = \frac{1}{2}\left[\mathrm{erf}\left(\frac{t - t_{\mathrm{on}}}{t_s}\right) - \mathrm{erf}\left(\frac{t - t_{\mathrm{off}}}{t_s}\right)\right], \tag{3.9}$$

where L is the total system length and $x \in [-L/2, L/2)$, with periodic boundary conditions. Here, $r(t)$ serves to turn the flow on and off. Nate Goehring performed curve fits of wild type flow profiles to deduce the parameter values $a = 0.014$ s^{-1}, $b = 14$ µm, $t_{\mathrm{on}} = 150$ seconds, $t_{\mathrm{off}} = 650$ seconds, and $t_s = 50$ seconds. (This flow profile was not used in the paper, but is a good approximation to the actual profile.)

We will leave the parameter b fixed in our analysis, as this sets the shape of the cortical flow velocity profile, but will vary the parameter a, which sets the scale of the flow speed. We will also vary t_{off}. Leave all other parameters fixed to their values reported in Table S1 of the Goehring paper.

a) Numerically solve for the homogeneous steady state (i.e., find the values of A_{ss} and P_{ss}) in which the anterior-like complex is enriched on the membrane.

b) Using the approximate expression for $v(x,t)$, numerically solve the system of PDEs defined by equations (2) and (3) of the Goehring paper. Use the steady state determined in part (a) as your initial condition. Use the parameters listed above.

c) Argue why $U = ab$ is a good choice for the characteristic flow velocity. We will use this with equation S5 from the Goehring paper to define the Péclet number.

d) Vary the Péclet number by varying the parameter a and perform numerical solutions of the dynamical equations. How large must Pe be in order to polarize the cell?

e) Now, keeping $a = 0.014$ s^{-1}, vary t_{off} and perform numerical solutions. How long must the flow be on in order to polarize the cell?

Problem 3.3 (Simulations of Delta-Notch signaling on a hexagonal lattice (extra credit))**.**
I am writing some code that you can use to do simulations of Delta-Notch signaling on a hexagonal

lattice, similar to what is seen in developmental systems, e.g., in *Drosophila* development. If I manage to get it ready and post it, you can play with the simulation to investigate the patterning dynamics resulting from Delta-Notch-based regulation of gene expression.