BE 159 Spring 2015
Homework #4
Due at the start of lecture February 26, 2015.

Problem 1 (Flow as a big perturbation)**.**
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.

In the Goehring, et al. paper, the authors employed periodic boundary conditions, doing the calculation around the whole cortex. In our calculation, we will use no-flux boundary conditions going from pole to pole. This essentially means Neumann boundary conditions on the concentrations of the anterior and posterior PAR complexes and enforcing that $v = 0$ at the poles. We define the anterior pole to be at $x = 0$ and the posterior pole to be at $x = L/2$ to stay consistent with Goehring's notation.

The wild type flow can be approximately described by

$$v(x,t) = ax\, \mathrm{e}^{-x^2/2b^2}\, r(t), \tag{1}$$

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

where L is the total system length and $x \in [0, L/2]$. 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.) Note that with these parameters $v(L/2, 0)$ is very close to zero, so we do not need to worry about advective flux through the boundary.

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. *Hint*: You can use numerical root finding packages, such as SciPy's `scipy.optimize.fsolve`.

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?

You can use any of a variety of techniques for solving the PDEs. You might find the tutorial on numerically solving reaction-diffusion equations for Turing patterns available on the handouts page of

the course website useful. When reading that tutorial, note that you should choose `banded=False` for the PAR system. You will also need to do numerical quadrature to compute A_{cyto} and P_{cyto}. You can use standard functions, like `scipy.integrate.trapz`, to do this.