RomR model

In this simple model for the RomR concentration in Myxo we are considering the following partial differential equations

$$\frac{\partial u}{\partial t}=\frac{\partial}{\partial x}\left(D\frac{\partial u}{\partial x}\right)+\frac{\left(-u\,At-D\frac{\partial u}{\partial x}Ax\right)}{A}-s1\,u+s2\,v+p1$$

$$\frac{\partial v}{\partial t}=d\,\frac{\partial^2 v}{\partial x^2}+\frac{\left(-v\,At-d\frac{\partial v}{\partial x}Ax\right)}{A}+s1\,u-s2\,v+p2$$

in the previous equations the second terms on the right are due to an area constrain effect and they are turned on only during cell division, otherwise At and Ax are equal to zero.
The term D represent diffusion for the free species and may also be decreased in time during cell division in a more or less big area around the center of the cell. At the moment during cell division we are using only the area constrain effect and not the limiting of diffusion. The

The variable p1 and p2 represent production of the free species u and bounded species v, these rates are proportional to the concentration of the species through a fixed constant p0. At the moment we are considering possible production only close to the poles (in the simulations that we are doing recently production is turned off).

Finally s2 is a fixed dissociation rate for the bounded species on the membrane. Instead the association rate s1 depends on the number of receptors that we are considering along the cell s1=sigma1*n, with n number of receptors per micrometer. At the moment we are considering a continuous piecewise function for n. In these function n=1100 in a narrow zone close to the left pole then drops linearly to 1 and increase again linearly close to the right pole to 600. During cell division we also have an increase in time for n at the center (connecting to a established distance on left and right of center to n=1) up to n=400 the speed of this growth is controlled by a parameter alpha (here our hypothesis is that during division new receptors are produced in the middle of the cells where the new poles are forming).

Also we realized that we needed to establish a carrying capacity for the number of molecules that could bind to the receptors. For the moment we are using a function obtained from some simulation when the production was turned off. The carrying capacity multiplies s1 by the following factor

$$(1-v/fm)^{(1/beta)}$$

where fm is the value for the carrying capacity at that point. We can see that when v is smaller than fm but gets closer this factor is positive but close to zero, meaning that less and less particles may bound to the membrane, and if v is bigger than fm this makes s1 negative inducing more dissociation from the membrane.
This carrying capacity together with the number of receptors n we believe is also important for the reversal mechanism. This is induced in our model reverting both n and the carrying capacity symmetrically respect to the center at the established time of reversal (either fixed time or taken from gamma distribution obtained experimentally).
At the moment this change is done instantaneously, but we want to include the possibility of doing it more gradually.

Future work

In the near future I want to change the way we including the carrying capacity, and make it instead a function of the number of receptors. Moreover, the literature seams to imply that RomR is connected with an other protein FrsZ, maybe through activation and deactivation of receptors. I want first to include different ways of switching more gradually after reversal time and eventually make the reversal time and activation/deactivation of receptors due to the concentration of a second protein (needing therefore a new pde to describe this protein). To do this would be nice to be able to visualize this other protein in experiments both alone and together with RomR (I already mentioned this to Cameron, he said that is possible, but will probably take some time to realize it).
I also want to change a bit the profile for the number of receptor we are using including during division an area that is increasing in time but constant around a small zone centered in the middle (instead of a maximum point like now) I believe this may be more biologically true and may provide with more asymmetry at the center as seen in the experiments.
At the moment experimentally we also have movies with hyper-reversing bacteria where new concentrations for RomR are found and I am waiting to see new data from those to get other ideas. Also I wanted to ask Cameron if is possible to get movies from non reversing and/or hypo- reversing ones, I think that would be really helpful.

Both Cameron, Shant and the Undergrad working on imaging have the last matlab code done before I came back to Italy and I will send them the changes I am doing. Along with any possible relevant simulation I will do, and I think they will keep me posted as well regarding any possible new data from experiments.

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