Modeling chemotactic response and contact interactions of amoeboid cells

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Individual cells are connected with the environment, they sense the the exterior with their receptors and process the incoming information. They respond first chemically (polarization) and second mechanically (locomotion) moving toward food, enemy or target direction. It is known that without external signal the cell may randomly swing producing random dynamics, while in other way under a chemical gradient the cell produces a persistent motion in gradient's direction [1, 2, 3].

We apply a phase field for the description of the interior (where the polarization processes takes place) and the exterior of the cells (where the biochemical species diffuse) to model the interaction of both environments at the membrane of the cell. The model we use is described in [2] and has the particularity to include a parameter that tunes the balance between the mechanism of polarity formation and intracellular noise. The model is described as follow

$$\tau\frac{\partial\phi}{\partial t} = \gamma\left(\frac{-G^{'}}{\epsilon^2} + \nabla^2\phi\right) - \beta\left[\left(\int\phi dx - A_0\right) + \alpha c\right] \mid \nabla\phi \mid . \tag{1}$$

In other way, inside the cell there is a reaction-diffusion process governed by a biochemical component c according to

$$\frac{\partial c}{\partial t} = k_\alpha c(1-c)(c-\delta) - \rho c + \frac{1}{\phi}\nabla\cdot(\phi D\nabla c) + \xi(\boldsymbol{x},t)\phi(1-\phi). \tag{2}$$

We tune different parameters of the biochemical reaction rates to compare the resulting dynamics of the computer model of the motion of *Dictyostelium discoideum* in absence and presence of a linear chemical gradients of the chemo-attractant cAMP (cyclic adenosine monophosphate) as shown in Figs. 1 (a) and (b), respectively. One of this parameters is k_α, which is responsible of the transition from slow erratic for small values to fast and persistent motion for large values.

Furthermore, we add to the model the contact interaction among cells under confinement and in absence of chemical gradient where we see that the cells follow circular trajectories as observed in many experiments (see Fig. 2).

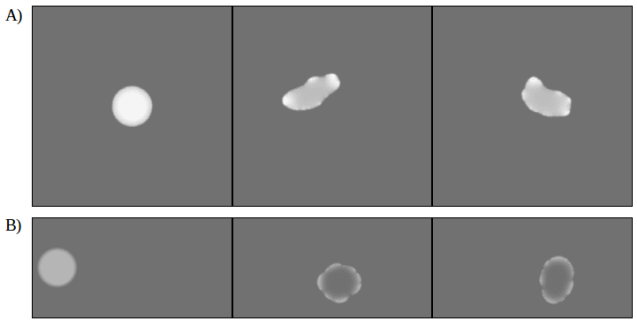

Fig. 1. Screenshots taken every 200 seconds for cell trajectories and parameter $k_\alpha = 2$. (a) Simulation results of a cell in absence of cAMP gradient in a 60×60 μm^2 grid. (b) Simulation results of a cell in presence of cAMP gradient in a 30×60 μm^2 grid.

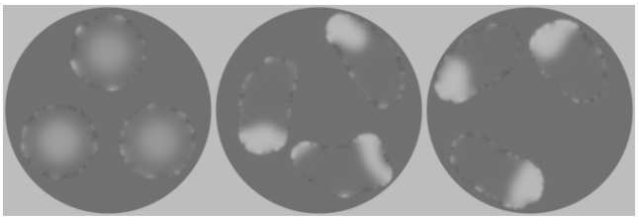

Fig. 2. Simulation Results of three cells under confinement and absence of cAMP in a 33.75×33.75 μm^2 grid. The screenshots were taken every 200 seconds with parameter $k_\alpha = 2$.

[1] L. Song, S. M. Nadkarni, H. U. Bödeker, C. Beta, A. Bae, C. Franck, W.-J. Rappel, W. F. Loomis, and E. Bodenschatz, *Dictyostelium discoideum* chemotaxis: Threshold for directed motion, Eur. J. Cell Biol. **85**, 981-989 (2006).

[2] S. Alonso, M. Strange M, and C. Beta, Modeling random crawling, membrane deformation and intracellular polarity of motile amoeboid motion, (to be published).

[3] G. Amselem, M. Theves, A. Bae, E. Bodenschatz, and C. Beta, A stochastic description of *Dictyostelium* chemotaxis, PLoS ONE **7**, e37213 (2012).