ITPO 2019, Problem 4: Colony collapse in a nutshell*

(Dated: March 5, 2019)

PROBLEM STATEMENT

Bacteria, such as E. coli, can collectively look for food via a chemotaxis signaling network. When bacteria eat food, they produce attractant molecules in the environment (a liquid medium). By sensing the gradient of attractant concentration, bacteria (in a run-and-tumble motion) swim as random-walkers with bias.

A system of PDEs – the Keller-Segel equations – is often used to describe bacteria chemotaxis:

$$\partial_t b - D_b \nabla^2 b + \kappa \nabla (b \nabla c) = \alpha b \tag{1}$$

$$\partial_t c - D_c \nabla^2 c = \beta b f \tag{2}$$

$$\partial_t f - D_f \nabla^2 f = -\gamma b \tag{3}$$

Here b stands for the bacterial density, c for the attractant concentration, and f for food concentration. The parameters D_b, D_c and D_f are the diffusivity coefficients of the bacteria, the chemoattractant molecules and the food molecules. The parameter κ is the sensitivity of bacteria to the chemo concentration gradient, α is the bacterial growth rate, β is the chemo production rate, and γ is the food consumption rate.

Consider the dynamics of a bacterial colony in an environment of volume V with a hollow shell in the center (volume $V_s \ll V$). Let the hollow shell have a small hole (opening area A_s) on it to connect the inside and the outside. Assume that in the beginning the food concentration is the same everywhere, and we inoculate some bacteria into the environment. Your preliminary experiments show that the bacterial colony collapses into the hollow shell. Model this behavior theoretically and numerically. You may need to modify the Keller-Segel equations.

SOLUTION

The problem above has been solved in [1]. What follows below only highlights the important aspects of the solution; refer to the paper for details.

Although the non-linear coupled differential equations above are not fully amenable to analytic methods, it is worth considering a solution for a simplified case. Also note that the equations above are supplemented

* Email: info@thworldcup.com

by the appropriate no-flux boundary conditions at the walls. Assuming a constant food concentration, a steady-state solution (all time derivatives set to 0) for the system above is given by a solitary wave $b(x) = b_0 \operatorname{sech}^2(x/l)$, where $l = \sqrt{2D_\mathrm{b}D_\mathrm{c}/\kappa b_0 \beta f}$. Note that the width of the "bacteria concentration wave" is inversely proportional to its amplitude, and that the concentration is higher near $x = 0$ (a wall). These solitary waves move along the walls, and, as the bacteria concentration rises, the bacteria move closer and closer to the wall.

[1] simulate the propagation of bacteria waves numerically according to Keller-Segel equations, and observe the described collapse into hollow shells.

A theoretical explanation of such collapse follows from a stability analysis of bacterial population changes within hollow shells. [1] study the evolution of a small perturbation δb in population density inside a cavity — one that in our system can be caused by the passage of a solitary wave through the volume containing the hollow shell. Ordinarily, diffusion equations are stable to such perturbations: over time, the region with higher concentration diffuses out. However, the non-linear Keller-Segel system is unstable to such perturbations.

Given an uptick in bacteria concentration δb inside the shell, [1] find the fluxes of bacteria J_b and the chemoattractant J_c through A_S to first order in perturbation theory to be

$$V_\mathrm{S}\frac{\partial \delta b}{\partial t} = -D_\mathrm{b}A_\mathrm{S}\frac{\delta b}{l_\mathrm{b}} + \kappa A_\mathrm{S} b_0 \frac{\delta c}{l_\mathrm{c}} \tag{4}$$

$$V_\mathrm{S}\frac{\partial \delta c}{\partial t} = -D_\mathrm{c}A_\mathrm{S}\frac{\delta c}{l_\mathrm{c}} + V_\mathrm{S}\beta f \delta b, \tag{5}$$

where l_b and l_c are characteristic lengths for the decay of bacterial and chemoattractant concentrations outside the opening.

It is evident from the flux equations above that a change in bacteria concentration induces a change in chemoattractant density, which, in turn, induces a chemotactic flux that cancels bacteria diffusion. We can find the critical value of bacterial density b_crit at which the fluxes cancel each other out by setting the left-hand sides of equations 4 and 5 to 0:

$$b_\mathrm{crit} = \frac{D_\mathrm{b}D_\mathrm{c}}{l_\mathrm{b}\beta f \kappa}\frac{A_\mathrm{S}}{V_\mathrm{S}}. \tag{6}$$

Notably, the critical density is lower if the area of the opening A_S is small relative to the volume of the cavity V_S.

Above the critical density b_crit, a perturbation in bacteria concentration will lead to a net flux of bacteria *into* the hollow shell. Assuming that the filling of the cavity happens at a rate higher than bacterial and

chemoattractant diffusion, equations 4 and 5 can be used to find:

$$\frac{\partial^2 b}{\partial t^2} = \frac{\kappa A_{\mathrm{S}} b_{\mathrm{crit}} \beta f}{V_{\mathrm{S}} l_{\mathrm{c}}} \delta b, \tag{7}$$

which has an exponential growth in population $b(t)$ inside the hollow cavity as a solution.

[1] S. Park, P. M. Wolanin, E. A. Yuzbashyan, H. Lin, N. C. Darnton, J. B. Stock, P. Silberzan, and R. Austin, Proceedings of the National Academy of Sciences **100**, 13910 (2003).

[2] S. Park, P. M. Wolanin, E. A. Yuzbashyan, P. Silberzan, J. B. Stock, and R. H. Austin, Science **301**, 188 (2003).

[3] M. P. Brenner, L. S. Levitov, and E. O. Budrene, Biophysical journal **74**, 1677 (1998).