Model

Based on the standard Keller-Segel model, we constructed a kinetic model comprising three key ingredients: cell density (), attractant concentrations (), and oxygen concentrations ():

[1]

[2]

[3]

For each phenotype with a tumble bias , it senses the same external attractant field, following a standard KS chemotactic equation in which the effective diffusion coefficient and chemotactic coefficient are the functions of .

, and

where is the single cell swimming speed. The average speed we measured in semi-2D chamber is around 26 µm/s, corresponding to ~32 µm/s in 3D. is the rate of switching from run state to tumble state for phenotype . is the derivative respect to the internal state which is a function of . is adaptation time scale of the cell, which correlates to tumble bias , . is the receptor gain, . is the rotational diffusion, 0.062 rad/s. is the dimensional rescaling factor, . is the angular correlation factor,

is the perceived signal to cell, , where ,.

The attractant field has two terms, the small molecular diffusion with , and the consumption by the cells. is an oxygen dependent consumption rate, based on the experimental measurement. We choose a hill function form to describe the oxygen dependence:

, where is the consumption rate when oxygen level is saturate, 8.5 µM/min per OD 1 cells. is the external oxygen level, 250 µM. is the threshold, 60 µM. K is basal level, 35%, H is the hill coefficient, 5.

We assume all the phenotypes have the same consumption. The total consumption depends on the total local cell density and the availability of the attractant with a kinetic constant .

The oxygen field also has three key terms, the oxygen diffusion with , the consumption by the cells with a kinetic term per OD 1 cells and , and the supply from the upper surface through PDMS. is the oxygen transfer rate from PDMS to liquid interface .