Random Dispersals of Biological Organisms: a theory of non-uniform random dispersal

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ABSTRACT

Diffusion is a PDE model for random movements of Brownian particles and has been used to describe random dispersals in gas, liquid and even in solid. Random dispersals are often non-uniform in heterogeneous environment. Brownian displacement in spatially non-constant temperature is a good example. In many cases biological organisms do not know the correct direction to find a better environment and hence their migration is in a random manner and, hence, diffusion has been used to model such migration phenomena. In particular, biological species usually increase their dispersal rate if the environment becomes hostile and hence they provide excellent examples of non-uniform random dispersals.

The starvation driven diffusion (SDD), recently suggested by the author is designed to understand the effect of motility changes of biological species which increase their migration rate in the event of starvation. The original purpose of this research program was to show that it is not just the size of the dispersal rate, but the motility jumps that makes the key play in the evolutional selection. The current main goal of the project is to explain various biological and physical phenomenon in terms of non-uniform randomness. Chemotaxis without gradient sensing, moving free boundary, evolution of dispersal and thermal diffusion are topics that can be covered by non-uniform randomness.

STARVATION DRIVEN DIFFUSION

The population dynamics of a single species in an heterogeneous environment can be modeled by

$$u_t = \Delta(\gamma u) + u(m - u) = \nabla \cdot ((\gamma + u\gamma_u)\nabla u + u\gamma_m \nabla m) + u(m - u), \qquad (1)$$

where $m(x)$ and $\gamma(u, m)$ are given resource and motility functions, respectively. Unknown solution $u(x, t)$ is the population density of a species. If

$$\gamma_u \geq 0 \quad \text{and} \quad \gamma_m \leq 0,$$

then the above diffusion is called a *starvation driven diffusion* since the motility increases with population and decreases with resource. It is natural to assume that each individual species may not know total resource m and total population u, but they may sense their share of resource m/u. Set

$$s = \frac{u}{m}$$

as a starvation measure under the assumption that $m > 0$. Hence, we assume

$$\gamma = \gamma(s), \quad \gamma'(s) \geq 0.$$

Then the above population model can be written as

$$u_t = \nabla \cdot ((\gamma + s\gamma')\nabla u - s^2\gamma'\nabla m) + u(m - u),$$

which also gives advection term toward the resource. One may consider two competing species, where u and v are the densities. Then, the share of each individuals is $m/(u + v)$. Similarly set

$$s = \frac{u + v}{m}.$$

Then the starvation driven diffusion operator becomes

$$u_t = \Delta(\gamma u) = \nabla \cdot ((\gamma + \frac{u}{m}\gamma')\nabla u + \frac{u}{m}\gamma'\nabla v - \frac{u}{m}s\gamma'\nabla m),$$

which now contains the cross diffusion. This cross diffusion effect produce separation phenomena and pattern formation.

CHEMOTAXIS WITHOUT GRADIENT-SENSING

Models for chemotaxis are based on spatial or temporal gradient-sensing by individual organisms. However, it is puzzling how do microscopic scale bacteria sense the macroscopic scale concentration gradient. The key contribution of Keller and Segel model is showing that erratic movements of individuals may result in an accurate chemotaxis phenomenon as a group. In this program we provide another option to understand chemotactic behavior when individuals do not sense the gradient of chemical concentration by any means. We may show that, if individuals increase their dispersal rate to find food when there is not enough food, an accurate chemotactic behavior may be obtained without gradient-sensing. The resulting equation is written as

$$\begin{cases} u_t = (\gamma\,u)_{xx} = \big((\gamma + \gamma_u u)u_x + \gamma_m u\,m_x\big)_x, & x \in R,\ t > 0, \\ m_t = -k(m)u, \end{cases} \tag{2}$$

This model is surprisingly similar to the original Keller-Segel model. A comprehensive picture of traveling band and front solutions has been provided in [4]. Notice that the above equation is for *Escherichia coli* case. For the *Dictyostelium* case the corresponding equation is

$$\begin{cases} u_t = (\gamma\,u)_{xx} = \big((\gamma + \gamma_u u)u_x + \gamma_m u\,m_x\big)_x, & x \in R,\ t > 0. \\ m_t = dm_{xx} + \alpha u - \beta m, \end{cases}$$

In this case m is not the resource, but the pheromone concentration produced by *Dictyostelium*. Hence, the diffusion is not exactly SDD. However, it is still a non-uniform random dispersal and its traveling wave is being studied. Basically, this project is to develop a chemotaxis theory with non-uniform randomness, but not gradient sensing.