Commun Nonlinear Sci Numer Simulat 15 (2010) 60–70

Contents lists available at ScienceDirect

Commun Nonlinear Sci Numer Simulat

journal homepage: www.elsevier.com/locate/cnsns

A stochastic Keller–Segel model of chemotaxis

Pierre-Henri Chavanis

Laboratoire de Physique Théorique (CNRS UMR 5152), Université Paul Sabatier, 118, route de Narbonne, 31062 Toulouse Cedex 4, France

ARTICLE INFO

Article history:
Received 2 May 2008
Accepted 2 September 2008
Available online 12 September 2008

Keywords:
Chemotaxis
Self-organization
Nonlinear dynamics
Fluctuations
Stochastic processes
Long-range interactions

ABSTRACT

We introduce stochastic models of chemotaxis generalizing the deterministic Keller–Segel model. These models include fluctuations which are important in systems with small particle numbers or close to a critical point. Following Dean's approach, we derive the exact kinetic equation satisfied by the density distribution of cells. In the mean field limit where statistical correlations between cells are neglected, we recover the Keller–Segel model governing the smooth density field. We also consider hydrodynamic and kinetic models of chemotaxis that take into account the inertia of the particles and lead to a delay in the adjustment of the velocity of cells with the chemotactic gradient. We make the connection with the Cattaneo model of chemotaxis and the telegraph equation.

1. Introduction

In biology, many organisms (bacteria, amoebae, cells,...) or social insects (like ants, swarms,...) interact through the process of chemotaxis [1–3]. Chemotaxis is a long-range interaction that accounts for the orientation of individuals along chemical signals that they produce themselves. Famous examples of biological species experiencing chemotaxis are the slime mold amoebae *Dictyostelium discoideum*, the flagellated bacteria *Salmonella typhimurium* and *Escherichia coli*, the human endothelial cells etc. When the interaction is attractive, chemotaxis is responsible for the self-organization of the system into coherent structures such as peaks, clusters, aggregates, fruiting bodies, periodic patterns, spirals, rings, spots, honeycomb patterns, stripes or even filaments. This spontaneous organization has been observed in several experiments [4–16] and numerical simulations [17–33]. Chemotactic attraction is therefore a leading mechanism to account for the morphogenesis and self-organization of biological systems. For example, it has been advocated to explain aggregation patterns in bacteria, tissue organization during embryonic growth, cell guidance, fish skin pigmentation patterning, angiogenesis in tumour progression and wound healing, formation of plaques in Alzheimer's disease, dynamics of blood vessel formation etc [24,34]. It is fascinating to realize that the self-organization of chemotactic species in biology shares some analogies with the self-organization of galaxies in astrophysics and large-scale vortices (like Jupiter's great red spot) in two-dimensional turbulence.[1] A first successful model of chemotactic aggregation is provided by the Keller–Segel (KS) model [41] introduced in 1970. The standard KS model can be written as

E-mail address: chavanis@irsamc.ups-tlse.fr

[1] These analogies are intrinsically due to the long-range attractive nature of the interaction. In particular, self-gravitating systems, 2D vortices and chemotactic species interact through a field produced by the distribution of particles via a Poisson equation (or its generalizations). Furthermore, the process of self-organization is described by relatively similar relaxation equations corresponding to nonlinear mean field Fokker–Planck equations [35]. Therefore, self-gravitating systems, 2D vortices and chemotactic species share many analogies despite their very different physical nature. These striking analogies have been emphasized by the author in several papers [36–40,35].

1007-5704/$ - see front matter © 2008 Elsevier B.V. All rights reserved.
doi:10.1016/j.cnsns.2008.09.002

$$\frac{\partial\rho}{\partial t}=\nabla\cdot(D_*\nabla\rho-\chi\rho\nabla c), \tag{1}$$

$$\frac{\partial c}{\partial t}=D_c\Delta c-kc+h\rho. \tag{2}$$

It consists in two coupled differential equations that govern the evolution of the density of cells (or other biological entities) $\rho(\mathbf{r},t)$ and the evolution of the secreted chemical $c(\mathbf{r},t)$. The first Eq. (1) is a drift-diffusion equation. The cells diffuse with a diffusion coefficient D_* and they also move in a direction of a gradient of the chemical (chemotactic drift). The chemotactic sensitivity χ is a measure of the strength of the influence of the chemical gradient on the flow of cells. The coefficient χ can be positive or negative. In the first case (chemoattraction), the particles climb the chemical gradient and form clusters. In the second case (chemorepulsion), they descend the chemical gradient and repell each other. In that case, the chemical acts like a poison. The second Eq. (2) in the KS model is a reaction-diffusion equation. The chemical is produced by the bacteria with a rate h and is degraded with a rate k. It also diffuses with a diffusion coefficient D_c. When chemotactic attraction prevails over diffusion, the KS model describes a *chemotactic collapse* leading to aggregates or Dirac peaks. There is a vast literature on this subject. We refer to Perthame [42] for numerous references in applied mathematics and to Chavanis [43] for additional references in physics.

The first equation of the KS model can be interpeted as a mean-field Smoluchowski equation describing a system of Brownian particles in interaction. On the other hand, in the limit of large diffusivity of the chemical, we can make a quasi-stationary approximation $\partial c/\partial t\simeq 0$ in the second equation and obtain the screened Poisson equation. We are led therefore to the simplified Keller–Segel model

$$\frac{\partial\rho}{\partial t}=\nabla\cdot(D_*\nabla\rho-\chi\rho\nabla c), \tag{3}$$

$$\Delta c-k_0^2c=-\lambda\rho, \tag{4}$$

where we have set $k_0^2=k/D_c$ and $\lambda=h/D_c$. In the absence of degradation of the chemical ($k_0=0$), the field equation (4) reduces to the Poisson equation $\Delta c=-\lambda\rho$ (see [44] and Appendix C of [32] for a precise justification of these approximations). In that case, the Keller–Segel (KS) model becomes isomorphic to the Smoluchowski–Poisson (SP) system

$$\frac{\partial\rho}{\partial t}=\nabla\cdot\left[\frac{1}{\xi}\left(\frac{k_BT}{m}\nabla\rho+\rho\nabla\Phi\right)\right], \tag{5}$$

$$\Delta\Phi=S_dG\rho, \tag{6}$$

describing a system of overdamped self-gravitating Brownian particles in the mean field approximation [45,25,28,30,46,31,47,43,48,49]. We have the correspondances: $D_*=k_BT/\xi m$, $\chi=1/\xi$, $c=-\Phi$, $\lambda=S_dG$. In particular, the concentration of the secreted chemical $c(\mathbf{r},t)=-\Phi(\mathbf{r},t)$ in biology plays the role of the gravitational potential (with the opposite sign) in astrophysics.[2] More generally, when we consider a system of Brownian particles interacting via an arbitrary binary potential $u(\mathbf{r}-\mathbf{r}')$ and make a mean-field approximation [53–55], we obtain the mean-field Smoluchowski equation

$$\frac{\partial\rho}{\partial t}=\nabla\cdot\left[\frac{1}{\xi}\left(\frac{k_BT}{m}\nabla\rho+\rho\nabla\Phi\right)\right] \tag{7}$$

$$\Phi(\mathbf{r},t)=\int\rho(\mathbf{r}',t)u(\mathbf{r}-\mathbf{r}')\,\mathrm{d}\mathbf{r}'. \tag{8}$$

The main difference between models (1)–(2) and (7)–(8) comes from the equation for the field $c(\mathbf{r},t)$ or $\Phi(\mathbf{r},t)$. Eq. (2) is non-markovian since the concentration of the chemical $c(\mathbf{r},t)$ at time t depends on the concentration of the bacteria and of the chemical at earlier times. By contrast, Eq. (8) is markovian since the potential $\Phi(\mathbf{r},t)$ is assumed to be instantaneously produced by the distribution of particles.

It is important to note that the Keller–Segel model is a *mean field* model which ignores fluctuations. This implicitly assumes that the number of cells $N\to+\infty$ and that we are far from a critical point. Now, in biology, the number of particles in the system can be relatively small. Furthermore, from the statistical physics viewpoint, it is natural to investigate the role of fluctuations during chemotaxis. In order to go beyond the mean field approximation, some authors [17,56,57,32] have proposed to return to a corpuscular description of the dynamics and to describe the motion of the particles (chemotactic species or "active" walkers) by N coupled stochastic Langevin equations of the form

$$\frac{\mathrm{d}\mathbf{r}_i}{\mathrm{d}t}=\chi\nabla c_d(\mathbf{r}_i(t),t)+\sqrt{2D_*}\mathbf{R}_i(t), \tag{9}$$

$$\frac{\partial c_d}{\partial t}=D_c\Delta c_d-kc_d+h\sum_{i=1}^{N}\delta(\mathbf{r}-\mathbf{r}_i(t)), \tag{10}$$

[2] One great achievement of Keller and Segel [41] was to interpret slime mold aggregation as a manifestation of a fundamental instability in a uniform distribution of amoebae and acrasin (chemoattractant). As noticed in [50,51], this instability is closely related to the Jeans gravitational instability in astrophysics [52].