Abstract. The cell balance equations of Alt are rigorously studied and perturbatively expanded into forms similar to Segel's one-dimensional phenomenological cell balance equations by considering the simplifying case of bacterial density possessing symmetry in the $x$ and $y$ directions responding to an attractant gradient present only in the $z$ direction. We prove that for shallow attractant gradients the lumped integrals involving the tumbling probability frequency distribution and bacterial density distribution in the $\theta$ direction can be explicitly expressed as a product of three quantities: the mean tumbling frequency, the bacterial subpopulation density, and a reversal probability. We also derive expressions for the bacterial net flux in the Fickian form from which two macroscopic transport parameters, the random motility coefficient and the chemotactic velocity, are explicitly related to individual cell properties and chemical gradients.

Key words. chemotaxis, cell balance equations, random motility, chemotactic velocity, perturbation theory

AMS subject classifications. 60G05, 60J60, 92A08

1. Introduction. Studies of bacterial motion and the consequent development of macroscopic transport equations have attracted the interest of researchers in the fields of microbiology and cell physiology for many decades. In recent years, they have also become a focus of interest to researchers in the fields of environmental science, soil hydrology, and chemical engineering. Quantitative characterization of the transport of bacteria has applications to in situ bioremediation, a promising technique for cleaning up environmental contaminants. However, the effectiveness of in situ bioremediation is often limited by the transport of bacteria to the contaminant. Motile bacteria, such as Escherichia coli or Pseudomonas putida, possess the ability to bias their random movements toward a more favorable environment, particularly carbon sources which in bioremediation contexts are often the contaminant itself. This chemical-induced migration of bacterial populations is called chemotaxis and is able to enhance bacterial transport rates. Consequently, the phenomenon of chemotaxis has long been the subject of considerable research.

To investigate and quantify the chemotactic migration of bacterial populations, one approach is to develop mathematical models through which individual bacterial behavior can be incorporated into the macroscopic transport properties. The rigorous three-dimensional cell balance equations derived by Alt [1] have been studied by Ford

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and Cummings [7] to elucidate the relationship between three-dimensional and the one-dimensional cell balance equations and assumptions required to derive one from the other. Due to their generality and rigor, Alt’s equations are the ideal starting point for developing models in which further simplifications are made. The recent paper of Schnitzer [16] further discussed the general theory of random walks in a more extensive fashion, with special applications to the chemotactic bacteria *E. coli*. His mathematical treatments are fairly general so as to make his results quite applicable in many random walks situations. However, in his paper emphasis was directly focused on the higher-dimensional formulation rather than the one-dimensional analogue, though the implicit assumptions and the final conclusions about the Fickian flux expression in his works and ours are both the same. In this paper we study bacterial transport equations and consider the simplifying case of one-dimensional chemical gradients. Using a perturbation analysis, we explicitly show that for this simplifying case the three-dimensional cell balance equation can be reduced to forms similar to Segel’s [17], [18] one-dimensional phenomenological cell balance equations. The relationship between bacterial biological responses and chemical gradients proposed by Berg and Brown [2], [3], who tracked and observed the individual swimming behavior of a chemotactic bacterium *E. coli*, is incorporated. However, our derivation is not limited to this particular empirical relationship. The derivation can be easily extended to other forms of the relationship between bacterial tumbling responses and chemical gradients.

The motivation of this work arises from ongoing confusion between the *intrinsic* and the *apparent* dimension of a system with regard to the expressions for the random motility and chemotactic velocity. The intrinsic dimension here refers to the minimum number of independent spatial coordinates required to describe bacterial motion, and thus cannot be altered. However, one can change the apparent dimension by invoking certain geometric symmetries (e.g., plane, cylindrical, or spherical geometries) from which the number of independent variables of the system degenerates according to the symmetry. Thus the intrinsic dimension for the motile bacteria that are capable of three-dimensional random walks is three, whereas in a one-dimensional model such as Segel’s, which restricts bacterial motion to one dimension, the intrinsic dimension is one. When considering the case in which only a one-dimensional chemical gradient is applied, the apparent dimension for both models is one. Ford and Cummings [7] studied the analogous quantities between the (apparent) one-dimensional cell balance equations which actually result from different intrinsic dimensions (1 and 3) and showed that the equivalent one-dimensional swimming speed in the models of Segel and Rivero et al. [15] should be \( v/2 \), where \( v \) is the three-dimensional speed. This reduced swimming speed \( v/2 \) is based on the linear projection of three-dimensional motion to one single dimension. However, the random motility coefficient derived from Segel’s one-dimensional model with the modified swimming speed does not yield the correct numerical factor that is predicted by three-dimensional analysis. At present there still exists little theoretical investigation regarding the analogous relationship between a three-dimensional model and a one-dimensional model for motile bacterial transport. Thus the way in which the macroscopic transport parameters, such as the random motility coefficient and the chemotactic velocity in a one-dimensional model, are related to their corresponding expressions in a three-dimensional model is still obscure. The goal of this paper is to reconcile the various expressions for such macroscopic transport parameters as the random motility coefficient, which arise from descriptions with different intrinsic dimensions.

The overall structure of this paper can be divided into two parts: in section 2
we reduce Alt’s cell balance equations for the case of one-dimensional chemical gradient into two subpopulation equations and explicitly arrange them in the forms of Segel’s one-dimensional phenomenological equations, and in section 3 we derive a pseudoequilibrium cellular flux from the subpopulation equations. The details are outlined as follows. In the beginning of section 2 we briefly review the three-dimensional Alt equations and the previous works performed by Ford and Cummings [7] in reducing Alt’s three-dimensional equations corresponding to a one-dimensional chemical gradient. In section 2.1 the reduced turning probability density previously defined by Ford and Cummings is analytically derived from the local turning probability density function $W(\alpha)$. The derivation is kept as general as possible in the sense that the explicit form for $W(\alpha)$ is unspecified. In section 2.2 the integral terms accounting for bacterial tumbling and subsequent turning in Alt’s equations are explicitly integrated. In order to explicitly evaluate many $\theta$-integrated quantities, such as the subpopulation densities and cellular flux, the cellular density distribution as a function of the running direction $\theta$ must be known. In section 2.3 the bacterial number density distribution in the $\theta$ direction is sought via perturbation analysis. Using this perturbative solution, Alt’s equations are arranged yielding two one-dimensional subpopulation equations similar to Segel’s in section 2.4. In section 3 we seek the pseudoequilibrium bacterial net flux from which the explicit expressions for the random motility and chemotactic velocity are yielded. The relationship between the flux expressions that are derived from a three-dimensional analysis and from a one-dimensional model with a modified swimming speed projected from three dimensions is also discussed. In section 4 we summarize our analytical results and draw conclusions.

2. Three-dimensional Alt equation. Considering each bacterium as a random walker executing a piecewise linear path, whose speed $v(\vec{r}, t)$ depends on position and time, and by regarding the tumbling and sequential turning to be instantaneous, Alt [1] derived the following differential-integral system describing the bacterial number density $\rho(\vec{r}, s, \tau, t)$ at time $t$ and position $\vec{r}$, with a running direction $\hat{s}$ and run time $\tau$:

$$
(2.1) \quad \frac{\partial \rho(\vec{r}, s, \tau, t)}{\partial t} = -\frac{\partial \rho(\vec{r}, s, \tau, t)}{\partial \tau} - \hat{s} \cdot \nabla_p[v(\vec{r}, t)\rho(\vec{r}, s, \tau, t)] - P_t(\vec{r}, \hat{s}, \tau, t)\rho(\vec{r}, \hat{s}, \tau, t) \quad \text{for } \tau > 0
$$

and

$$
(2.2) \quad \rho(\vec{r}, s, 0, t) = \int_0^\infty \int P_t(\vec{r}, \hat{s}', \tau, t)\rho(\vec{r}, \hat{s}', \tau, t)k(\vec{r}, \hat{s}')\rho(\vec{r}, \hat{s}', \tau, t)d\hat{s}' d\tau
$$

for $\tau = 0$. In (2.1) $P_t(\vec{r}, \hat{s}, \tau, t)$ is the tumbling frequency and $k(\vec{r}, \hat{s}')\rho(\vec{r}, \hat{s}', \tau, t)$ is the turning probability density for a bacterium that was running in the direction $\hat{s}'$ at $\vec{r}$ and time $t$ before tumbling will run in the new direction $\hat{s}$ immediately after the tumbling. Ford and Cummings [7] verified that by invoking the assumption that the probability of tumbling is independent of the run time $\tau$, the Stroock’s equation [20] can be directly

\[\text{perturbation of Alt equations to Segel's 1D equations}\]

\[\text{37}\]
derived from Alt’s equations:

\[
\frac{\partial n(\vec{r}, \hat{s}, t)}{\partial t} = -\hat{s} \cdot \nabla_{\vec{r}} [v(\vec{r}, t)n(\vec{r}, \hat{s}, t)] - P_t(\vec{r}, \hat{s}, t)n(\vec{r}, \hat{s}, t)
\]

\[+ \int P_t(\vec{r}, \hat{s}', t)n(\vec{r}, \hat{s}', t)k(\vec{r}, \hat{s}', \hat{s})d\hat{s}',
\]

(2.3)

where

\[
n(\vec{r}, \hat{s}, t) = \int_0^\infty \rho(\vec{r}, \hat{s}, \tau, t)d\tau.
\]

(2.4)

Ford and Cummings further reduced the three-dimensional cell balance equations of Alt and Stroock to a form similar to the one-dimensional equations of Segel [17], [18] and Rivero et al. [15] by studying the simplifying case of bacterial density possessing symmetry in the \(x\) and \(y\) directions responding to a chemical attractant gradient present only in the \(z\) direction. This means (2.3) can be simplified, after being integrated over the \(x, y,\) and \(\phi\) directions, to become

\[
\frac{\partial n(z, \theta, t)}{\partial t} = -\hat{s}_z \frac{\partial v(z, t)n(z, \theta, t)}{\partial z} - P_t(z, \theta, t)n(z, \theta, t)
\]

\[+ \int_0^\pi P_t(z, \theta', t)n(z, \theta', t)K(\theta'; \theta) \sin \theta' d\theta',
\]

(2.5)

where \(K(\theta'; \theta)\) is defined by Ford and Cummings as a reduced turning probability density

\[
K(\theta'; \theta) = \frac{1}{2\pi} \int_0^{2\pi} \int_0^{2\pi} k(\hat{s}', \hat{s})d\phi'd\phi,
\]

(2.6)

with the further assumption that \(k\) is independent of \(\vec{r}\) and is only a function of the two consecutive running directions characterized by the unit vectors \(\hat{s}'\) and \(\hat{s}\). The unit vectors \(\hat{s}'\) and \(\hat{s}\) can be expressed in spherical coordinates by

\[
\hat{s}' = (\sin \theta' \cos \phi', \sin \theta' \sin \phi', \cos \theta'),
\]

\[
\hat{s} = (\sin \theta \cos \phi, \sin \theta \sin \phi, \cos \theta),
\]

(2.7)

in which \(\theta\) is the polar angle between the running direction and the positive \(z\)-axis and \(\phi\) is the azimuthal angle. \(\hat{s}_z\), the \(z\)-component of \(\hat{s}\), is \(\cos \theta\).

Without knowing the exact form of (2.6), (2.5) can be further simplified by multiplying both sides by \(\sin \theta d\theta\) and integrating over \(\theta\) to yield

\[
\frac{\partial n^+(z, t)}{\partial t} = -\frac{\partial}{\partial z}v(z, t) \int_0^{\pi/2} \sin \theta \cos \theta \cdot n(z, \theta, t)d\theta
\]

\[- \int_0^{\pi/2} P_t(z, \theta, t)n(z, \theta, t) \left[ 1 - \int_0^{\pi/2} K(\theta'; \theta') \sin \theta' d\theta' \right] \sin \theta d\theta
\]

\[+ \int_0^{\pi/2} P_t(z, \theta', t)n(z, \theta', t) \left[ \int_0^{\pi/2} K(\theta'; \theta) \sin \theta d\theta \right] \sin \theta' d\theta',
\]

(2.8)

\[T.T.\]
and
\[
\frac{\partial n^-(z,t)}{\partial t} = -\frac{\partial}{\partial z} v(z,t) \int_{\pi/2}^{\pi} \sin \theta \cos \theta \cdot n(z,\theta,t) d\theta \\
- \int_{\pi/2}^{\pi} P_t(z,\theta,t)n(z,\theta,t) \left[ 1 - \int_{\pi/2}^{\pi} K(\theta;\theta') \sin \theta' d\theta' \right] \sin \theta d\theta \\
+ \int_{0}^{\pi/2} P_t(z,\theta',t)n(z,\theta',t) \left[ \int_{\pi/2}^{\pi} K(\theta';\theta) \sin \theta d\theta \right] \sin \theta' d\theta'.
\]
(2.9)

T.T.\

Here the subpopulation densities \(n^\pm(z,t)\) are defined according to bacterial swimming directions relative to the \(z\)-axis by
\[
(2.10) \quad n^+(z,t) = \int_{0}^{\pi/2} n(z,\theta,t) \sin \theta d\theta,
\]

\[
(2.11) \quad n^-(z,t) = \int_{\pi/2}^{\pi} n(z,\theta,t) \sin \theta d\theta.
\]

We also define the total cell density \(c(z,t)\) as
\[
(2.12) \quad c(z,t) = \int_{0}^{\pi} n(z,\theta,t) \sin \theta d\theta = n^+(z,t) + n^-(z,t).
\]

Equations (2.8) and (2.9) represent the correct forms of the one-dimensional Segel equations by taking into account the spatial effect of bacterial three-dimensional movements on the perceived chemical gradient direction. To proceed further, we need to know the forms of \(K(\theta;\theta')\), \(P_t(z,\theta,t)\), and \(n(z,\theta,t)\) explicitly.

2.1. Reduced turning probability density. Based on the experimental observations of Berg and Brown [2], [3], we assume that when a bacterium chooses the next running direction \(\hat{s}\), the probability in the azimuthal direction \(\phi^*\) measured relative to the previous running direction \(\hat{s}'\) is uniform. However, the turn angle \(\alpha(=\cos^{-1}(\hat{s}' \cdot \hat{s}))\) between two successive running vectors is governed by a probability density function \(W(\alpha)\), for which
\[
(2.13) \quad \int_{0}^{\pi} W(\alpha) \sin \alpha d\alpha = 1.
\]

The coordinate transformation between the global spherical polar coordinates and the local spherical coordinates based on the previous running direction \(\hat{s}'\) is
\[
(2.14) \quad \begin{pmatrix}
\sin \theta \cos \phi \\
\sin \theta \sin \phi \\
\cos \theta
\end{pmatrix} = \begin{pmatrix}
\cos \theta' \cos \phi' & -\sin \phi' & \sin \theta' \cos \phi' \\
\cos \theta' \sin \phi' & \cos \phi' & \sin \theta' \sin \phi' \\
-\sin \theta' & 0 & \cos \theta'
\end{pmatrix} \begin{pmatrix}
\sin \alpha \cos \phi^* \\
\sin \alpha \sin \phi^* \\
\cos \alpha
\end{pmatrix}.
\]

Theoretically, the first step is to transform \(k(\hat{s}';\hat{s})\) into \(k(\theta',\phi';\theta,\phi)\) explicitly and then, according to (2.6), perform the integration over \(\phi'\) and \(\phi\). However, since the symmetry of the turning probability density distribution in \(\phi^*\) in the local coordinates.
vanishes in the global coordinates, the transformation and subsequent integration become very difficult. Rather than perform the transformation and integration of (2.6), a simpler approach is to view \( K(\theta'; \theta) \) as the summation of all such possible events. As depicted in Fig. 2.1, when a bacterium is running in direction \( \hat{s}' \) before a tumble, its possibility of choosing \( \alpha \) and \( \phi^* \) such that \( \alpha \) and \( \phi^* \), respectively, fall between the intervals \( \phi^* \sim \phi^* + d\phi^* \) and \( \alpha \sim \alpha + d\alpha \) is \( W(\alpha) \sin \alpha d\alpha d\phi^*/2\pi \), where \( \alpha \) ranges from zero to \( \pi \) and \( \phi^* \) ranges from \(-\pi\) to \( \pi \). From the coordinate transformation matrix, we have the following relationship:

\[
\cos \theta = -\sin \theta' \sin \alpha \cos \phi^* + \cos \theta' \cos \alpha.
\]

Thus for a specific \( \theta', \phi^* \), and \( \alpha \), there are two specific values of \( \phi^* \)'s that can simultaneously satisfy (2.15), i.e., \( \pm \phi^* \). To make the mapping from \( \phi^* \) to \( \theta \) single valued, we choose the point \( \phi^* = 0 \) on the plane constituted by the z-axis and the vector \( \hat{s}' \) and study only the range where \( 0 \leq \phi^* \leq \pi \). Because \( \cos \phi^* \) is analytic in the range of \( 0 \leq \phi^* \leq \pi \), the probability that a bacterium changes from \( \theta' \) to \( \theta \) for a specific turn angle \( \alpha \) is \( W(\alpha) \sin \alpha d\alpha d\phi^*/\pi \). We should add up all such possible events by allowing the turn angle \( \alpha \) to change freely from zero to \( \pi \). Therefore the sum of all such probabilities is equal to the probability that a bacterium running in \( \theta' \) before a tumble runs into \( \theta \) after its tumble, regardless of the azimuthal \( \phi' \) and \( \phi^* \).

\[
K(\theta'; \theta) \sin \theta d\theta = \int W(\alpha) \sin \alpha \frac{d\phi^*(\alpha, \theta'; \theta)}{\pi} d\alpha.
\]

This gives the reduced turning probability density function

\[
K(\theta'; \theta) = -\frac{\int W(\alpha) \sin \alpha d\phi^*(\alpha, \theta'; \theta)}{\pi \sin \theta d\theta},
\]

where the minus sign is used because \( \partial \phi^*/\partial \theta \), from (2.15), is negative.

Notice that (2.16) is only symbolically correct and the bounds of the integration are left unspecified. The reason is that not every turn angle \( \alpha \) makes a valid contribution to \( K(\theta'; \theta) \) for a specific \( \theta \). This can be understood from Fig. 2.1, in which there exists a valid range for the angle \( \alpha \) to turn from previous direction \( \theta' \) into the desired direction \( \theta \). Similarly, when \( \alpha \) is fixed, the range of valid \( \theta \) is also limited. For a fixed \( \alpha \), the valid range of \( \theta \) can be found from (2.15). For instance, from (2.15) \( \cos \theta \) is linearly proportional to \(- \cos \phi^* \) at constant \( \theta' \) and \( \alpha \). Thus for \( \alpha \) and \( \theta' \) between zero and \( \pi \), \( \cos \theta \) has a valid maximum when \( \cos \phi^* = -1 \) (i.e., \( \phi^* = \pi \)). Likewise, \( \cos \theta \) has a valid minimum when \( \cos \phi^* = 1 \) (i.e., \( \phi^* = 0 \)). Therefore

\[
\cos(\theta' + \alpha) \leq \cos \theta \leq \cos(\theta' - \alpha),
\]

which yields

\[
|\theta' - \alpha| = \theta_1 \leq \theta \leq \theta_2 = \begin{cases} \theta' + \alpha & \text{if } \theta' + \alpha \leq \pi, \\ 2\pi - (\theta' + \alpha) & \text{if } \theta' + \alpha > \pi. \end{cases}
\]

Other valid ranges under various conditions are also shown in Fig. 2.2.

**2.2. Integration of the tumbling terms.** After the reduced turning probability is obtained, we substitute it into (2.8) and (2.9) to calculate the integral terms related to the tumbles. First let us restrict our attention to the case \( 0 \leq \alpha \leq \pi/2 \). Because

\[
\int_0^\pi K(\theta; \theta') \sin \theta' d\theta' = 1,
\]
the bracket in the first tumbling term on the right-hand side of (2.8) becomes

\[ 1 - \int_{0}^{\pi/2} K(\theta; \theta') \sin \theta' d\theta' = \int_{\pi/2}^{\pi} K(\theta; \theta') \sin \theta' d\theta' \]

\[ = \int_{\max(\phi^*, \pi/2)}^{\theta_2'} K(\theta; \theta') \sin \theta' d\theta', \]

where \( \theta_1' \) and \( \theta_2' \), which give the valid integration limits for a fixed \( \alpha \), are defined as

\[ \cos \theta_2' = -\sin \theta \sin \alpha \cos(\phi^* = 0) + \cos \theta \cos \alpha = \cos(\theta + \alpha), \]

\[ \cos \theta_1' = -\sin \theta \sin \alpha \cos(\phi^* = \pi) + \cos \theta \cos \alpha = \cos(\theta - \alpha). \]

Note that in (2.20) an intrinsic restriction is that \( \theta \) be confined between zero and \( \pi/2 \). We also define \( \phi_1^*(\alpha, \theta) \), if it can be found, such that, for fixed \( \alpha \) and \( \theta \),

\[ 0 = -\sin \theta \sin \alpha \cos \phi_1^* + \cos \theta \cos \alpha. \]

Then (2.20) may be written as

\[ \int_{\max(\phi_1^*, \pi/2)}^{\theta_2'} K(\theta; \theta') \sin \theta' d\theta' = -\int_{0}^{\pi} W(\alpha) \sin \alpha \left[ \int_{\phi_1^*(\alpha, \theta)}^{0} \frac{d\phi^*}{\pi} \right] d\alpha \]

\[ = \int_{0}^{\pi} W(\alpha) \sin \alpha \frac{\phi_1^*(\alpha, \theta)}{\pi} d\alpha. \]
Fig. 2.2. Valid ranges for $\theta$ under various conditions.

The angle $\phi^*_1(\alpha, \theta)$ is defined to be the azimuthal integration limit in the local coordinates for the turning direction $\theta'$ after tumbling to cross over the dividing angle $\pi/2$. Thus the first tumbling term (abbreviated as $T.T.^+$) on the right-hand side of (2.8) is

$$T.T.^+ = \frac{1}{\pi} \int_0^\pi W(\alpha) \sin \alpha \left\{ \int_0^{\pi/2} P_l(z, \theta, t)n(z, \theta, t)\phi^*_1(\alpha, \theta) \sin \theta d\theta \right\} d\alpha. \tag{2.23}$$

Similarly, the second tumbling term (abbreviated as $T.T.$) is

$$T.T. = \frac{1}{\pi} \int_0^\pi W(\alpha) \sin \alpha \left\{ \int_0^{\pi/2} P_l(z, \theta', t)n(z, \theta', t)[\pi - \phi^*_1(\alpha, \theta')] \sin \theta' d\theta' \right\} d\alpha. \tag{2.24}$$

To integrate, we need to know $P_l(z, \theta, t)$ and $n(z, \theta, t)$. A particular form for $P_l(z, \theta, t)$ used in the papers of Berg and Brown [2] and Ford and Cummings [7] is adopted here. According to Ford and Cummings, this special form of $P_l$ can be described as

$$P_l(z, \theta, t) = \frac{1}{\tau_0} \exp \left[ -\nu \frac{dN_b}{da} \frac{da}{dt} \right] \exp \left[ -\nu v \frac{dN_b}{dz} \frac{dz}{dt} \cos \theta \right] = P_{l,1}(z, t) \exp[-\xi(z, t) \cos \theta], \tag{2.25}$$
where
\[ \xi(z, t) = \nu v dN_b \frac{\partial a}{\partial z}. \]

Here \( \tau_0 \) is the mean run time in the absence of chemical gradients, \( \nu \) represents a scaling factor relating the material derivative of numbers of bound receptors per bacterium, \( N_b \), and the biological response \( P_t \), and \( a \) is the chemical attractant concentration. When both the temporal and spatial chemical gradients are zero, \( P_t \) reduces to the basal tumbling probability frequency \( P_0 = 1/\tau_0 \). In general, the dynamics of the bound receptors can be described by the law of mass action proposed by Mesibov, Ordal, and Alder [12], \( N_b = \frac{N_t a}{K_d + a} \), where \( K_d \) is the receptor/ligand dissociation constant and \( N_t \) is the total number of cell receptors per cell. Then
\[ \xi = \chi_0 \frac{K_d}{v (K_d + a)^2} \frac{\partial a}{\partial z}, \]

with \( \chi_0 = \nu v^2 N_t \) defined to be the chemotactic sensitivity coefficient which has been measured experimentally. Typical values for \( \chi_0 \) fall in the range of \( 10^{-5} \sim 10^{-4} \) [cm\(^2\)/s] [5], [6], [14]. Thus the parameter \( \xi \) is not a measure of only chemical gradients but a combined parameter that also includes other factors such as chemotactic sensitivity and receptor threshold and saturation. We will show later that \( \xi \) represents the magnitude of deviation of the cell density distribution in velocity space from uniformity (see (2.49)) and thus can also be regarded as a perturbation parameter. In some extreme cases [4], the chemical gradient encountered by bacteria may be considerably large, thus \( \xi \) may exceed unity. However, for many known laboratory experiments and in most environmental applications chemical gradients are usually mild and shallow, which ensures a value of \( \xi \) smaller than one. Consequently, we may expand (2.25) by Taylor series about \( \xi = 0 \):
\[ P_t(z, \theta, t) = P_{t,1}(z, t) \left[ 1 - \xi \cos \theta + \frac{\xi^2}{2} \cos^2 \theta - \cdots \right]. \]

It means that the \( P_t \) with a weak exponential dependence on \( \cos \theta \) can be thought of as a linear combination of various \( P_t \)'s which, respectively, depends on \( \cos \theta \)^0, \( \cos \theta \)^1, \( \cos \theta \)^2, \ldots. The assumption of small chemical gradients within the context of the combined parameter \( \xi \) defined above has been proposed previously in the literature. For example, Lauffenburger and coworkers [14], [15], [19] used linearized (small gradient) expressions for \( \mu \) and \( V_c \) derived in their models to obtain an estimate for \( \chi_0 \) from experimental data available in the literature. They found that, in general, their models agreed reasonably well with experimental data. Lapidus and Schiller [10] employed the same chemotactic velocity expression as derived in this work, (3.26), in their simulations, in comparison with the experiment data performed by Dahlquist, Lovely, and Koshland [4], in which a fixed exponential attractant concentration was established. Their simulations still yielded reasonable agreement at medium and high attractant concentrations. Further discussions regarding the validity of the small gradient assumption can be found in Rivero-Hudec and Lauffenburger [14], Rivero et al. [15], Segel [17], [18], and Staffeld, Quinn, and Lauffenburger [19].

Next we temporarily assume that the multiplication of \( P_t(z, \theta, t) n(z, \theta, t) \) is a polynomial function of \( \cos \theta \), which will be understood and further discussed in section 2.4. That is,
\[ P_t(z, \theta, t) n(z, \theta, t) = \Omega_0(z, t) + \Omega_1(z, t) \cos \theta + \Omega_2(z, t) \cos^2 \theta + \cdots, \]
in which $\Omega_i(z,t)$ are undetermined coefficients. Equation (2.27) allows the study of the influence of the $\theta$-dependence on the cell balance equations. The reason for choosing this particular form is because the number density $n$ will be studied using the perturbation technique later in section 2.3 and expressed as a perturbation expansion function about $\xi \cos \theta$. Thus the multiplication of the perturbed density distribution and the expanded tumbling frequency (2.26) yields a polynomial of $\cos \theta$.

Case 1 ($P_t \cdot n = \Omega_0(z,t)$). For the first case for which $P_t(z,\theta,t)n(z,\theta,t)$ has no dependence on $\theta$, (2.23) becomes

$$T.T. = \frac{\Omega_0(z,t)}{\pi} \int_0^\pi W(\alpha) \sin \alpha \left\{ \int_0^{\pi/2} \phi_1^*(\alpha,\theta) \sin \theta d\theta \right\} d\alpha.$$  

(2.28)

For $0 \leq \alpha \leq \pi/2$, the integral $L$ over $\theta$ in (2.28) is

$$L = \int_{\pi/2-\alpha}^{\pi/2} \phi_1^*(\alpha,\theta) \sin \theta d\theta,$$

(2.29)

where the integration limits $\pi/2 - \alpha$ and $\pi/2$ give the valid integration range such that $\phi_1^*(\alpha,\theta)$ exists. After integrating by parts and noting that $\phi_1^*(\alpha,\pi/2-\alpha) = 0$, this integral yields

$$L = -\phi_1^*(\alpha,\theta) \cos \theta \bigg|_{\pi/2-\alpha}^{\pi/2} + \int_{\sin \alpha}^{\pi/2} \cos \theta \frac{\partial \phi_1^*}{\partial \cos \theta} d\theta,$$

(2.30)

with $w = 1 - \cos^2 \theta$, $\Lambda = \frac{\cos \alpha}{\sin \alpha}$, and (2.21) being employed to calculate $\frac{\partial \phi_1^*}{\partial \cos \theta}$.

Equation (2.30) can be found from standard integration tables to be

$$L = \tan^{-1} \left( \frac{\sqrt{(1+\Lambda^2)w - \Lambda^2}}{\Lambda} \right) \bigg|^{1}_{1-\sin^2 \alpha} = \alpha.$$

(2.31)

Substituting the result back into (2.28) gives

$$T.T. = \frac{\Omega_0(z,t)}{\pi} \int_0^\pi \alpha W(\alpha) \sin \alpha da$$

(2.32)

$$= \Omega_0(z,t) \langle \alpha \rangle \frac{\alpha}{\pi} \text{ for } 0 \leq \alpha \leq \pi/2.$$

Here $\langle \alpha \rangle$ is defined to be the mean average of $\alpha$, or the first moment of $W(\alpha)$, by the expression $\langle \alpha \rangle = \int_0^\pi \alpha W(\alpha) \sin \alpha d\alpha$.

For $\pi/2 \leq \alpha \leq \pi$, the integral $L$ over $\theta$ becomes

$$L = \int_0^{\pi/2} \pi \sin \theta d\theta + \int_{\alpha-\pi/2}^{\pi/2} \phi_1^*(\alpha,\theta) \sin \theta d\theta.$$

(2.33)
Noting that \( \phi^*_\alpha(\alpha - \pi/2) = \pi \), \( L \) can be integrated yielding
\[
L = \pi(-\cos \theta)|^\alpha_{\alpha - \pi/2} + (-\phi^*_\alpha \cos \theta)|^\pi/2_{\alpha - \pi/2} + \int \cos \theta d\phi^*_\alpha \\
= \pi(1 - \sin \alpha) + \pi \sin \alpha + (\alpha - \pi) \\
= \alpha.
\]
(2.34)

Thus we obtain the final conclusion valid for the whole range \( 0 \leq \alpha \leq \pi \)
\[
T.T.^+ = \frac{\Omega_0(z, t)}{\pi} \langle \alpha \rangle.
\]
(2.35)

Likewise, \( T.T.^- \) can be found to be
\[
T.T.^- = \frac{\Omega_0(z, t)}{\pi} \left[ \pi - (\pi - \langle \alpha \rangle) \right] \\
= \frac{\Omega_0(z, t)}{\pi} \langle \alpha \rangle, \quad 0 \leq \alpha \leq \pi.
\]
(2.36)

The results for \( T.T.^+ \) and \( T.T.^- \) for the case of zero \( \theta \)-dependence show that the two opposite tumbling terms can be canceled out by each other in (2.8) and (2.9). That means the tumbling process makes no net contributions to the time-derivatives of \( n^+ \) and \( n^- \), which is not surprising since this case will be shown later to be the unperturbed case in which the tumbling frequency and the bacterial number density are isotropic in all swimming directions. Note that (2.35) and (2.36) are the same results derived by Lovely and Dahlquist [11], who implicitly assumed that the tumbling probability has no \( \theta \)-dependency, i.e., an isotropic case. In this work, we not only consider the isotropic situation, but also study what happens when \( P_t \) and \( n \) are perturbed by anisotropy which arises from the one-dimensional spatial chemical gradient.

**Case 2 (\( P_t \cdot n = \Omega_1(z, t) \cos \theta \)).** If \( P_t(z, \theta, t)n(z, \theta, t) \) linearly depends on \( \cos \theta \), the integral of \( L \) over \( \theta \), following the same procedures as in Case 1, will result in \( \frac{\pi}{4}(1 - \cos \alpha) \) for all values of \( \alpha \). Thus
\[
T.T.^+ = \frac{\Omega_1(z, t)}{2} \int_0^\pi \frac{1 - \cos \alpha}{2} W(\alpha) \sin \alpha d\alpha \\
= \frac{\Omega_1(z, t)}{2} \left( \frac{1 - \langle \cos \alpha \rangle}{2} \right).
\]
(2.37)

and \( T.T.^- \), for which the integral \( L \) gives \( -\frac{\pi}{2} + \frac{\pi}{2}(1 + \cos \alpha) \), is
\[
T.T.^- = \frac{\Omega_1(z, t)}{2} \int_0^\pi \left( -1 + \frac{1 + \cos \alpha}{2} \right) W(\alpha) \sin \alpha d\alpha \\
= -\frac{\Omega_1(z, t)}{2} \left( \frac{1 - \langle \cos \alpha \rangle}{2} \right).
\]
(2.38)

Similarly, \( \langle \cos \alpha \rangle \) is defined to be the mean average of \( \cos \alpha \), or the first cosine moment of \( W(\alpha) \), by \( \langle \cos \alpha \rangle = \int_0^\pi \cos \alpha W(\alpha) \sin \alpha d\alpha \). One can find that \( T.T.^+ \) and \( T.T.^- \) in the anisotropic case have the same magnitude but with opposite signs. In general, \( \Omega_1 \) is negative, as will be shown later in section 2.4, and \( 1 - \langle \cos \alpha \rangle \geq 0 \). Thus \( -T.T.^+ + T.T.^- \) is positive, which will contribute to the increase of the time-derivative of \( n^+ \) and the decrease of the time-derivative of \( n^- \) in (2.8) and (2.9), respectively.
2.3. Distribution of $n(z, \theta, t)$ in $\theta$ direction. Theoretically one can infer little a priori information for $n(z, \theta, t)$. The most common and intuitive guess is that the bacterial density distribution is uniform in all directions, which will be proved in this section to be the correct solution for $n(z, \theta, t)$ in an isotropic environment (i.e., no chemical gradients). When a weak chemical gradient is suddenly imposed, we hypothesize that the uniformly distributed density profile will be perturbed by a small amount. If the spatial variation in the bacterial density is negligible, i.e., $\partial (vn)/\partial z \approx 0$, we can substitute the initial guess for $n(z, \theta, t)$ into

$$n'(z, \theta', t + \Delta t) \approx [1 - \Delta t \cdot P_t(z, \theta', t)]n(z, \theta', t)$$

(2.39)

$$+ \Delta t \int_0^\pi P_t(z, \theta, t) n(z, \theta, t) K(\theta; \theta') \sin \theta d\theta$$

to calculate the new bacterial density distribution at the next time, $t + \Delta t$.

The direct interpretation of (2.39) is that the bacterial density in the $\theta'$ direction after $\Delta t$, $n'(z, \theta', t + \Delta t)$, is composed of those that have already been in $\theta'$ before $\Delta t$ and do not tumble after $\Delta t$ and those that moved in other directions before $\Delta t$ and change into direction $\theta'$ after $\Delta t$. The product of $\Delta t$ and $P_t$ on the right-hand side of (2.39) represents the probability a bacterium tumbles during the interval $\Delta t$. Therefore, a restriction in the use of (2.39) is $\Delta t \leq 1/P_t$.

Equation (2.39) is derived directly from (2.5) by dropping the convective term. This is an acceptable approximation if the magnitude of the dimensionless group $\xi$ is smaller than unity. That is, the smallest distance $\Delta t$ over which there exists an obvious density variation is much larger than bacterial swimming velocity $v$ times the maximum allowable time interval $1/P_t$. Discussion of the validity of (2.39) can also be found in [16].

2.3.1. Isotropic case. For simplicity let us first consider the case without spatial chemical gradients ($\xi = 0$). Consequently, bacteria are in an isotropic environment and the tumbling probability frequency $P_t$ has no $\theta$ dependence ($P_t(z, \theta, t) = P_{t,i}(z, t)$). By assuming that the bacterial density distribution is uniform in $\theta$, we have $n(z, \theta, t) = c(z, t)/2$ such that $\int_0^\pi n(z, \theta, t) \sin \theta d\theta = c(z, t)$.

First, the valid range of $\theta$ for fixed $\theta'$ and $\alpha$ is found from Fig. 2.2 to be

$$|\theta' - \alpha| = \theta_1 \leq \theta \leq \theta_2 = \begin{cases} \theta' + \alpha & \text{if } \theta' + \alpha \leq \pi, \\ 2\pi - (\theta' + \alpha) & \text{if } \theta' + \alpha > \pi. \end{cases}$$

Using (2.16) for the expression of $K(\theta; \theta')$ and (2.15) to calculate $\partial \theta'/\partial \phi^\ast$, the integral $I$ in (2.39) becomes

$$I = \frac{c(z, t)P_{t,i}(z, t)}{2\pi} \int_0^\pi \left[ \frac{W(\alpha) \sin \alpha d\alpha}{-\sin \theta' \frac{d\theta'}{d\alpha}} \sin \theta d\theta \right]$$

(2.40)

$$= \frac{c(z, t)P_{t,i}(z, t)}{2\pi} \int_0^\pi W(\alpha) \left[ \int_{\theta_1}^{\theta_2} \frac{1}{\sin \phi^\ast(\alpha, \theta)} d\theta \right] d\alpha.$$

By (2.15) the integrand in the square brackets can be replaced by

$$\frac{1}{\sin \phi^\ast(\alpha, \theta)} = \frac{\sin \theta \sin \alpha}{\sqrt{\sin^2 \alpha - (\cos \theta - \cos \alpha \cos \theta')^2}}$$

(2.41)
Let \( u_1 = \sin \alpha \sin \theta', \ u_2 = \cos \alpha \cos \theta', \) and define a new variable \( s = \cos \theta - u_2. \) Equation (2.40) is reduced to

\[
I = \frac{c(z, t) P_{t,1}(z, t)}{2\pi} \int_0^\pi W(\alpha) \sin \alpha \left[ \int \frac{-ds}{\sqrt{u_1^2 - s^2}} \right] d\alpha.
\]

The integration in the bracket yields an arc-sine function

\[
\int \frac{-ds}{\sqrt{u_1^2 - s^2}} = -\sin^{-1} \left( \frac{\cos \theta - \cos \alpha \cos \theta'}{\sin \alpha \sin \theta'} \right)_{\theta = \theta' + \alpha}^{\theta = \theta' - \alpha} = \pi,
\]

which gives us the final result

\[
n'(z, \theta', t + \Delta t) = \left[ 1 - \Delta t P_{t,1} \right] \frac{c(z, t)}{2} + \Delta t P_{t,1} \frac{c(z, t)}{2} \int_0^\pi W(\alpha) \sin \alpha \, d\alpha
\]

\[
= \frac{c(z, t)}{2}
\]

that does not depend on \( \theta' \) and is equal to \( n(z, \theta, t). \)

This result verifies the intuitive hypothesis that in an isotropic environment the bacterial density distribution in \( \theta \) is uniform. Due to the random nature of bacterial swimming behavior, this uniformity is not surprising. One thing to notice, however, is that the uniformity is not affected by the turn angle distribution \( W(\alpha). \)

Substituting this result into (2.5), we find that under isotropic conditions (2.5) simplifies to

\[
\frac{\partial c(z, t)}{\partial t} = -\nabla_z \cdot (\vec{v}(z, t) c(z, t)),
\]

which is merely a restatement of mass conservation.

### 2.3.2. Anisotropic case.

Still assuming that the chemical gradient is shallow, i.e., \( \xi \) is a small parameter, we will write \( P_t(z, \theta, t) \) explicitly in terms of \( P_t(z, \theta, t; \xi) \) although \( \xi \) is also a function of \( z \) and \( t. \)

To start with, \( P_t \) is approximated by

\[
P_t(z, \theta, t; \xi) = P_{t,1}(z, t) \left[ 1 - \xi \cos \theta \right] + O(\xi^2 \cos^2 \theta),
\]

and the uniform distribution of \( n(z, \theta, t) = c(z, t)/2 \) is used as the initial condition. Note that the same linear expansion for the anisotropic tumbling frequency was also used in Schintzer’s work [16]. We are curious about the evolution of \( n(z, \theta, t) \) after a chemical gradient is imposed at \( t = t_0. \) The integral \( I \) in (2.39) now becomes

\[
I = \frac{c(z, t_0) P_{t,1}(z, t_0)}{2\pi} \int_0^\pi W(\alpha) \left[ \int_{\theta_1}^{\theta_2} \frac{1 - \xi \cos \theta}{\sin \phi_1(\alpha, \theta)} \, d\theta \right] d\alpha + O(\xi^2 \cos^2 \theta').
\]

Splitting the integral in the bracket into two parts,

\[
\int_{\theta_1}^{\theta_2} \frac{1 - \xi \cos \theta}{\sin \phi_1(\alpha, \theta)} \, d\theta = \int_{\theta_1}^{\theta_2} \frac{1}{\sin \phi_1(\alpha, \theta)} \, d\theta - \xi \int_{\theta_1}^{\theta_2} \frac{\cos \theta}{\sin \phi_1(\alpha, \theta)} \, d\theta.
\]
we note that the first part is the same as the isotropic case. The second part can be found to be $-\pi (\sin \alpha \cos \alpha) \xi \cos \theta'$. This gives the expression for $n'(z, \theta', t_0 + \Delta t; \xi)$ after the first substitution

$$n'(z, \theta', t_0 + \Delta t; \xi) = \left\{ 1 - \Delta t P_{t,1}(1 - \xi \cos \theta') \right\} \frac{c}{2}$$

$$+ \Delta t P_{t,1} \frac{c}{2} \left\{ 1 - \xi (\cos \alpha) \cos \theta' \right\} + O(\xi^2 \cos^2 \theta')$$

(2.48)

$$= \frac{c}{2} \left\{ 1 + \Delta t P_{t,1}(1 - \langle \cos \alpha \rangle) \xi \cos \theta' \right\} + O(\xi^2 \cos^2 \theta').$$

Successively substituting the new expression of $n'(z, \theta', t + \Delta t; \xi)$ into (2.39) is also possible but not necessary. The information conveyed from (2.48) is that we may postulate that $n(z, \theta, t; \xi)$ can be perturbed from the uniform solution $c(z, t)/2$ by the small parameter $\xi \cos \theta$ and thus be represented by the expansion form

$$n(z, \theta, t; \xi) = \frac{c(z, t)}{2} [1 + n_1(z, t) \xi \cos \theta + \cdots].$$

(2.49)

It should be understood that the perturbation in the density distribution does not directly result from the one-dimensional chemical gradient, but deviously from the anisotropic tumbling frequency that results from the spatial gradient. Substituting (2.46) and (2.49) into (2.5) and equating to zero the coefficients of successive powers of $\xi \cos \theta$, we obtain the following sequence of PDEs:

$$\frac{\partial c}{\partial t} = -\nabla_z \cdot (\vec{v}c),$$

(2.50)

$$\frac{\partial (\xi n_1)}{\partial t} = -\nabla_z \cdot (\vec{v}n_1) + \xi P_{t,1}(1 - \langle \cos \alpha \rangle)(1 - n_1).$$

(2.51)

Equation (2.50) is the mass balance of bacterial density. Its solution, although not helpful in analyzing our problem, is $c(z, t) = \text{constant}$ along the Lagrangian path. Equation (2.51) can be further simplified if $\xi$ is a very weak function of $z$ and $t$. That is, if $\xi$ remains constant and thus can be canceled out, (2.51) may be rewritten as

$$\frac{Dn_1}{Dt} = P_{t,1}(1 - \langle \cos \alpha \rangle)(1 - n_1), \quad \text{Initial condition (I.C.) : } n_1(z, t_0) = 0.$$  

(2.52)

The solution is

$$n_1(z, t) = 1 - \exp \left\{ -1(1 - \langle \cos \alpha \rangle) \int_{t_0}^{t} P_{t,1}(z, t') Dt' \right\},$$

(2.53)

where the integral notation $Dt'$ in the exponent of (2.53) is meant to indicate that the integration is carried out along the Lagrangian path. Note that the value of $n_1(z, t)$ can range only from zero to unity.

Now substituting $n_1(z, t)$ back into (2.49) yields

$$n(z, \theta, t; \xi) = \frac{c(z, t)}{2} \left\{ 1 + \left( 1 - e^{-1(1 - \langle \cos \alpha \rangle) \int_{t_0}^{t} P_{t,1}(z, t') Dt'} \right) \xi \cos \theta \right\} + O(\xi^2 \cos^2 \theta).$$

(2.54)

For a very short time, just after $t_0$, $n_1(z, t_0 + \Delta t) \simeq P_{t,1}\Delta t(1 - \langle \cos \alpha \rangle)$ and (2.54) reduces back to (2.48). This agreement confirms that our postulate for the perturbative form of (2.49) is correct.
2.4. Simplification of (2.8) and (2.9). Employing (2.49) as the perturbative expression for \( n(z, \theta, t; \xi) \), we can explicitly find \( n^+(z, t; \xi) \) and \( n^-(z, t; \xi) \) from their definitions as follows:

\[
(2.55) \quad n^+(z, t; \xi) = \frac{c(z, t)}{2} \left[ 1 + \frac{\xi}{2} n_1(z, t) \right] + O(\xi^2)
\]

and

\[
(2.56) \quad n^-(z, t; \xi) = \frac{c(z, t)}{2} \left[ 1 - \frac{\xi}{2} n_1(z, t) \right] + O(\xi^2).
\]

The multiplication of \( P_t(z, \theta, t; \xi) n(z, \theta, t; \xi) \) can also be perturbatively expanded as

\[
(2.57) \quad P_t(z, \theta, t; \xi) n(z, \theta, t; \xi) \sim P_{t,1} [1 - \xi \cos \theta] \frac{c}{2} [1 + n_1 \xi \cos \theta]
\]

\[
\Omega_0(z, t) + \Omega_1(z, t) \cos \theta + O(\xi^2 \cos^2 \theta),
\]

with

\[
\Omega_0(z, t) = \frac{c}{2} P_{t,1} \quad \text{and} \quad \Omega_1(z, t) = -\frac{c}{2} P_{t,1} (1 - n_1) \xi
\]
as defined in (2.27). Here \( \Omega_1 \) is nonpositive since \( n_1 \) ranges between zero and unity. Of course, we also implicitly assume \( \xi \) to be positive, which means that the bacteria perceive spatial gradients of chemoattractants rather than repellents. Therefore, the analytical results for the tumbling terms (\( T.T.^+ \) and \( T.T.^- \)) from the previous section are readily applicable:

\[
(2.58) \quad T.T.^+ = \frac{c}{2} P_{t,1} \left\{ \frac{\langle \alpha \rangle}{\pi} \right\}_\pi - \frac{\xi}{2} (1 - n_1) \left( \frac{1 - \langle \cos \alpha \rangle}{2} \right) + O(\xi^2).
\]

Likewise

\[
(2.59) \quad T.T.^- = \frac{c}{2} P_{t,1} \left\{ \frac{\langle \alpha \rangle}{\pi} \right\}_\pi + \frac{\xi}{2} (1 - n_1) \left( \frac{1 - \langle \cos \alpha \rangle}{2} \right) + O(\xi^2).
\]

The difference between them is given by

\[
(2.60) \quad T.T.^+ - T.T.^- = -\frac{c}{2} P_{t,1} \xi (1 - n_1) \left( \frac{1 - \langle \cos \alpha \rangle}{2} \right) + O(\xi^2),
\]

which is negative for the case of chemoattractant gradients (\( \xi \geq 0 \)) and positive for the case of chemorepellent gradients (\( \xi \leq 0 \)).

If we define the mean tumbling frequencies by

\[
\overline{P_t^+} = P_{t,1} \exp \left[ -\int_0^{\pi/2} (\xi \cos \theta) \sin \theta d\theta \right]
\]

\[
= P_{t,1} \exp \left[ -\frac{\xi}{2} \right]
\]

\[
\simeq P_{t,1} \left[ 1 - \frac{\xi}{2} + \cdots \right]
\]

(2.61)
and
\[
\overline{P_t^+} = P_{t,1} \exp \left[ -\int_{\pi/2}^{\pi} (\xi \cos \theta) \sin \theta d\theta \right] \\
= P_{t,1} \exp \left[ \frac{\xi}{2} \right] \\
\simeq P_{t,1} \left[ 1 + \frac{\xi}{2} + \cdots \right],
\]
(2.62)
we also have
\[
\overline{P_t^+ n^+} - \overline{P_t^- n^-} = \frac{c}{2} P_{t,1} \left[ 1 - \frac{\xi}{2} (1 - n_1) \right] - \frac{c}{2} P_{t,1} \left[ 1 + \frac{\xi}{2} (1 - n_1) \right] + O(\xi^2)
\]
(2.63)
\[
= -\frac{c}{2} P_{t,1} \xi (1 - n_1) + O(\xi^2).
\]
It is interesting to note that the way the mean tumbling frequencies are defined is equivalent to assuming \( v / 2 \) as the one-dimensional swimming speed for the one-dimensional tumbling frequencies in the model of Rivero et al. [15], since the above \( \theta \)-integrations yield the factors of \(+1/2\) and \(-1/2\), respectively, in the positive and negative \( z \) directions.

Comparing (2.63) to (2.60) suggests we define another parameter \( P_r \) by
\[
P_r = \frac{1 - \langle \cos \alpha \rangle}{2}
\]
(2.64)
such that for the leading terms,
\[
T.T.^+ - T.T.^- = (\overline{P_t^+ n^+} - \overline{P_t^- n^-}) P_r.
\]
This parameter \( P_r \) is termed by Rivero et al. [15] as the one-dimensional reversal probability.

The convective terms now can also be evaluated explicitly. Therefore, the apparent one-dimensional convective velocities \( v_{1D}^\pm \) can be defined by equating \( v_{1D}^\pm n^\pm \) to the integrals of the convective terms. That is,
\[
v_{1D}^+ = v \int_0^{\pi/2} v \sin \theta \cos \theta n(z, \theta, t; \xi) d\theta / \int_0^{\pi/2} \sin \theta n(z, \theta, t; \xi) d\theta,
\]
(2.65)
\[
v_{1D}^- = -v \int_{\pi/2}^{\pi} v \sin \theta \cos \theta n(z, \theta, t; \xi) d\theta / \int_{\pi/2}^{\pi} \sin \theta n(z, \theta, t; \xi) d\theta.
\]
(2.66)
Thus one obtains
\[
v_{1D}^+(z, t; \xi) \simeq v \left( \frac{1}{2} + \frac{\xi}{12 n_1} \right) + O(\xi^2)
\]
(2.67)
and
\[
v_{1D}^-(z, t; \xi) \simeq v \left( \frac{1}{2} - \frac{\xi}{12 n_1} \right) + O(\xi^2).
\]
(2.68)
Note that the one-dimensional convective velocities are actually defined as the ensemble averages, a definition which is, however, unsuitable for the one-dimensional mean tumbling frequencies to achieve the leading-term matches.
3. Fickian expression. Segel [17], [18] showed that the bacterial equilibrium flux $J_z$ can be derived from his one-dimensional model with a form similar to the Fickian expression. His result is correct when considering bacterial movements that are confined to one dimension only. However, when interpreting experimental data that are based on a one-dimensional projection of three-dimensional motion, equations derived from the one-dimensional model may not be completely applicable. Consequently, the application of Segel's equations to the various experiments for random motility must be made with consideration for the dimensionality of the actual motion and the dimensionality of the projected motion being analyzed experimentally. In particular, considerable confusion exists in the literature concerning the correct expression for the random motility of a bacterial population. Without recourse to any cell balance equations, Lovely and Dahlquist [11] derived independently the expression (in our notation)

$$\mu_0 = \frac{v^2}{3P_0(1 - \langle \cos \alpha \rangle)},$$

(3.1)

where $\mu_0$ is the random motility coefficient and $P_0$ is the tumbling probability in the absence of chemical gradients. If one projects three-dimensional motion onto a single dimension and measures the diffusion of the projected motion, the same expression for the random motility applies. This is a straightforward consequence of the Einstein relation. Thus (3.1) is the correct expression for the random motility independent of the number of dimensions into which the motion is projected.

Some confusion over this point has arisen in the published literature. Rivero et al. [15] showed that the Segel equations implied

$$\mu_0^{1D} = \frac{s^2}{P_0(1 - \langle \cos \alpha \rangle)},$$

(3.2)

where $s$ is the one-dimensional swimming speed. It should be noted that the term $(1 - \langle \cos \alpha \rangle)$ was introduced rather arbitrarily by Rivero et al., whereas we demonstrate that it comes in quite naturally in the projection from three-dimensional motion to one-dimensional space. Othmer, Dunbar, and Alt [13] suggested that in N-dimensional motion,

$$\mu_0^{N-D} = \frac{(v^{N-D})^2}{NP_0(1 - \langle \cos \alpha \rangle)}.$$

(3.3)

Since $N$ is the system’s intrinsic dimension, the result of Othmer, Dunbar, and Alt is independent of the apparent dimension.

There is a real discrepancy underlying these results. For example, even when one corrects (3.2) by using the correct projected one-dimensional speed, $s = v/2$ (see Ford and Cummings [7]), (3.2) disagrees with (3.1). Equation (3.3) agrees with (3.1) for $N = 3$ but not for $N = 2$ or 1. Hence, one would like to find the source of these discrepancies. In this section, we will show that when correctly projected from three-dimensional to one-dimensional motion, the projected cell subpopulation equations yield (3.1), not (3.2). Equation (3.3) is not incorrect when taken in context: (3.3) refers to motion confined to $N$ dimensions, not motion projected from higher dimensions to $N$ dimensions.

From our previous analysis, we showed that Alt’s equations can be reduced to

$$\frac{\partial n^+}{\partial t} = -\frac{\partial (v_1^+ n^+)}{\partial z} - (P_1^+ n^+ - P_1^- n^-)P_r,$$

(3.4)
When considering only the leading terms up to $O(\xi)$. The net flux in the $z$ direction, from (2.5), should be defined as

$$J_z(z,t;\xi) = v(z,t) \int_0^\pi \sin \theta \cos \theta n(z,\theta,t;\xi) d\theta = v(z,t) \int_0^{\pi/2} \sin \theta \cos \theta n(z,\theta,t;\xi) d\theta + v(z,t) \int_{\pi/2}^\pi \sin \theta \cos \theta n(z,\theta,t;\xi) d\theta$$

Substituting the expressions of $n^\pm$ and $v^\pm$ into (3.6), the flux becomes

$$J_z(z,t;\xi) = c \frac{\xi}{3} n_1 + O(\xi^2).$$

Similarly

$$v^+_1 n^+ + v^-_1 n^- = \frac{c}{2} \left( \frac{1}{2} + \frac{\xi}{3} n_1 \right) + \frac{c}{2} \left( \frac{1}{2} - \frac{\xi}{3} n_1 \right) + O(\xi^2)$$

$$= \frac{c}{2} + O(\xi^2).$$

The addition of (3.4) and (3.5) gives the conservation equation of the total bacterial density,

$$\frac{\partial c}{\partial t} = -\frac{\partial J_z}{\partial z},$$

and the difference of the two equations yields

$$\frac{\partial (n^+ - n^-)}{\partial t} = -\frac{\partial (v^+_1 n^+ + v^-_1 n^-)}{\partial z} - 2(P^+_t n^+ - P^-_t n^-) P_r.$$

Substituting the expressions of $n^+$ and $n^-$ and (3.8) into (3.10), we obtain

$$\frac{\partial (c \xi n_1)}{\partial t} = -\frac{1}{2} \frac{\partial (vc)}{\partial z} - c \left[ \frac{P^+_t - P^-_t}{2} + \xi n_1 (P^+_t + P^-_t) \right] P_r.$$

Comparing (3.11) to (3.7), the argument of the time-differentiated term on the left-hand side of (3.11) is $J_z/(\frac{2}{3} v)$, and the last term on the right-hand side of (3.11) can be matched by

$$\frac{3}{2} J_z(P^+_t + P^-_t) P_r + \frac{vc (P^+_t - P^-_t) P_r}{2} = \frac{vc}{2} n_1 (P^+_t + P^-_t) P_r + \frac{vc (P^+_t - P^-_t) P_r}{2}$$

Thus (3.11) can be rewritten as

$$\frac{\partial J_z/(\frac{2}{3} v)}{\partial t} = -\frac{1}{2} \frac{\partial (vc)}{\partial z} - \frac{3}{2} J_z(P^+_t + P^-_t) P_r + \frac{vc (P^+_t - P^-_t) P_r}{2},$$

$$= \frac{3}{2} J_z(P^+_t + P^-_t) P_r + \frac{vc (P^+_t - P^-_t) P_r}{2},$$

$$= \frac{3}{2} J_z(P^+_t + P^-_t) P_r + \frac{vc (P^+_t - P^-_t) P_r}{2},$$

$$= \frac{3}{2} J_z(P^+_t + P^-_t) P_r + \frac{vc (P^+_t - P^-_t) P_r}{2}.$$
Next we must assume that the three-dimensional swimming speed $v(z, t)$ is constant in order to obtain the flux equation similar to Segel's. Multiplying (3.13) by $2v/3$ yields

$$\frac{\partial J_z}{\partial t} = -\frac{v^2}{3} \frac{\partial c}{\partial z} - J_z (P^{-}_t + P^{+}_t) P_r - v \frac{2}{3} (P^{+}_t - P^{-}_t) P_r \cdot c.$$  \tag{3.14}

Following the same reasoning of Segel in assuming $\partial J_z/\partial t \simeq 0$, we obtain the equilibrium bacterial flux in a Fickian form where

$$J_z = -\frac{1}{3} \frac{v^2}{(P^{-}_t + P^{+}_t) P_r} \frac{\partial c}{\partial z} + \left(\frac{2}{3} v\right) \frac{P^{-}_t - P^{+}_t}{P^{-}_t + P^{+}_t} \cdot c.$$  \tag{3.15}

Comparing (3.15) with Segel's flux expression, one finds that only the numerical coefficients differ. This difference can be understood if one recalls that in Segel’s one-dimensional formulation bacterial flux is defined as $J_z = \frac{v}{2} (n^+ - n^-)$ with a one-dimensional swimming speed $v/2$. However, in the case of three dimensions the ratio of $J_z$ and $n^+ - n^-$ is

$$\frac{J_z}{n^+ - n^-} = \frac{vc\xi/3}{c\xi/2} = \frac{2}{3} v,$$  \tag{3.16}

which still remains valid even in the limit of $\xi \to 0$.

From Segel’s one-dimensional model that assumes bacteria swim one-dimensionally with a constant swimming speed $v/2$, the corresponding cellular flux is

$$J_z^{1D\text{-Segel}} = -\frac{v^2/4}{(P^{-}_t + P^{+}_t) P_r} \frac{\partial c}{\partial z} + \left(\frac{v}{2}\right) \frac{P^{-}_t - P^{+}_t}{P^{-}_t + P^{+}_t} \cdot c,$$  \tag{3.17}

while (3.15) can be rewritten as

$$J_z^{1D\text{-Proj.}} = -\frac{4}{3} \frac{v^2/4}{(P^{-}_t + P^{+}_t) P_r} \frac{\partial c}{\partial z} + \frac{4}{3} \left(\frac{v}{2}\right) \frac{P^{-}_t - P^{+}_t}{P^{-}_t + P^{+}_t} \cdot c.$$  \tag{3.18}

This is equivalent to saying that the cellular flux predicted from the one-dimensional Segel model is underestimated by a factor $4/3$ compared to the rigorous result in (3.18), even when the swimming speed in the Segel model is modified to be $v/2$ as required by projection from three dimensions to one dimension.

The random motility coefficient $\mu$ and chemotactic velocity $V_c$ are thus defined as

$$\mu = \frac{2}{3} \frac{v^2}{(P^{-}_t + P^{+}_t) (1 - \langle \cos \alpha \rangle)}$$  \tag{3.19}

and

$$V_c = v \frac{2}{3} \frac{P^{-}_t - P^{+}_t}{P^{-}_t + P^{+}_t}.$$  \tag{3.20}

If the temporal and spatial chemical gradients are both zero, $P^{-}_t = P^{+}_t = P_0$. The random motility coefficient in the absence of chemical gradients in (3.19) is consistent with (3.1), as obtained by Lovely and Dahlquist [11] using a very different derivation.
Notice that the numerical factor of $2/3$ in (3.19) is independent of the explicit relationship of the tumbling frequency with chemical gradients. In fact, one can easily verify that the expression for the pseudoequilibrium flux remains unchanged as long as the assumption of small $\xi$ is valid and the tumbling frequency $P_t$ is expanded to be a linear form of $\xi \cos \theta$. This is because for the bacterial number density distribution the term including $\cos \theta$ is odd in the range of $\theta$, $[0, \pi]$, and thus does not contribute to the $z$-derivative term in (3.14). In addition, if the density distribution in velocity space deviates from the unperturbed distribution only by a small amount, the random motility coefficient is still dominated by the unperturbed part. In other words, the factor $2/3$ results from the unperturbed bacterial density distribution and dominates the magnitude of $\mu$ at small $\xi$. Therefore the numerical factor in the leading term for $\mu$ is unaffected by the explicit tumbling frequency relationship.

The chemotactic velocity in (3.20) is also found to be in agreement with the result of Lovely and Dahlquist [11]. If we define the corresponding one-dimensional mean run times in the positive and negative $z$ directions as $T^+ = 1/P_t^+$ and $T^- = 1/P_t^-$, (3.20) can be rewritten in terms of the mean run times,

$$
(3.21) \quad V_c = \frac{2}{3} \frac{T^+ - T^-}{T^+ + T^-}.
$$

Lovely and Dahlquist [11] derived the chemotactic velocity $V_c$ at an equilibrium state in the following fashion:

$$
(3.22) \quad V_c = \frac{1}{3} \frac{\int_0^\pi T(z, \theta, t) \cos \theta \sin \theta d\theta}{\int_0^\pi T(z, \theta, t) \sin \theta d\theta},
$$

where $T(z, \theta, t)$ is the mean run time distribution in the $\theta$ direction and is defined to be the inverse of the tumbling frequency

$$
(3.23) \quad T(z, \theta, t) = \frac{1}{P_t} \exp[\xi \cos \theta].
$$

After expanding (3.23) in a series about $\xi \cos \theta$ and defining

$$
(3.24) \quad T^+ = \int_0^{\pi/2} T \sin \theta d\theta \approx \frac{1}{P_t} \int_0^{\pi/2} (1 + \xi \cos \theta + \cdots) \sin \theta d\theta = \frac{1}{P_t} \left[ 1 + \frac{\xi}{2} + \cdots \right],
$$

and

$$
(3.25) \quad T^- = \int_{\pi/2}^\pi T \sin \theta d\theta \approx \frac{1}{P_t} \int_{\pi/2}^\pi (1 + \xi \cos \theta + \cdots) \sin \theta d\theta = \frac{1}{P_t} \left[ 1 - \frac{\xi}{2} + \cdots \right],
$$

it immediately follows that the denominator of (3.22) equals $T^+ + T^-$ and the numerator equals $\frac{2}{3}(T^+ - T^-)$. Hence our expression for $V_c$ agrees with (3.22) defined by Lovely and Dahlquist. It can also be verified by substitution that both definitions yield the same final result

$$
(3.26) \quad V_c = \frac{1}{3} \xi + O(\xi^2)
$$

after linearly expanding the tumbling frequencies (or mean run times) in terms of $\xi$. 
The prediction of (3.26) is in agreement with the well-known experimental finding that under the small gradient condition, the migration speed of a chemotactic population band is approximately proportional to the rate of increases of bound receptors. Note that this proportional relationship with $\xi$ does not yield linearity to the chemical gradients in the sense that $\xi$ also includes such factors as receptor saturation and threshold. We found that (3.26) is the same equation adopted by Lapidus and Schiller [10], who modified the Keller–Segel logarithmic model [8], [9] for $V$, and Rivero et al. [15] except for the numerical factor $1/3$. It is clear that the factor must have been included in the chemotactic sensitivity $\chi_0$ that is determined experimentally. Interestingly, Lapidus and Schiller applied (3.26), which is derived based on the assumption of small gradients, to simulate the sharp-gradient experiment of Dahlquist, Lovely, and Koshland [4] and still found good agreement between their simulations and the experiments of Dahlquist, Lovely, and Koshland [4] and Mesibov, Ordal, and Alder [12]. Hence it seems to us that although (3.19) and (3.20) are derived based on the small gradient assumption, their applications to various experimental conditions appear to be satisfactory over a quite larger range of chemical gradients.

4. Conclusion. Using perturbation theory, Alt’s three-dimensional equations can be approximately simplified into the same forms as Segel’s one-dimensional phenomenological cell balance equations for the case in which an attractant gradient is present in only one dimension:

\[
\frac{\partial n^+}{\partial t} = -\frac{\partial (v^+_1 n^+)}{\partial z} - (P^+_t n^+ - P^-_t n^-) P_r,
\]
\[
\frac{\partial n^-}{\partial t} = \frac{\partial (v^-_1 n^-)}{\partial z} + (P^+_t n^+ - P^-_t n^-) P_r.
\]

The results obtained from perturbation analysis are summarized as follows. For shallow chemical gradients, the following relationships hold:

\[
n(z, \theta, t; \xi) = \frac{c(z, t)}{2} [1 + n_1(z, t) \xi \cos \theta] + O(\xi^2 \cos^2 \theta),
\]
\[
n^+(z, t; \xi) = \frac{c(z, t)}{2} \left[ 1 + \frac{\xi}{2} n_1(z, t) \right] + O(\xi^2),
\]
\[
n^-(z, t; \xi) = \frac{c(z, t)}{2} \left[ 1 - \frac{\xi}{2} n_1(z, t) \right] + O(\xi^2),
\]
\[
P^+_t(z, t; \xi) = P_{t,1}(z, t)e^{-\xi/2},
\]
\[
P^-_t(z, t; \xi) = P_{t,1}(z, t)e^{+\xi/2},
\]
\[
v^+_1(z, t; \xi) = \frac{v(z, t)}{2} \left[ 1 + \frac{\xi}{6} n_1(z, t) \right] + O(\xi^2),
\]
\[
v^-_1(z, t; \xi) = \frac{v(z, t)}{2} \left[ 1 - \frac{\xi}{6} n_1(z, t) \right] + O(\xi^2).
\]

We proved that under an isotropic environment, the bacterial density distribution is uniform in the $\theta$ direction regardless of the turn angle probability distribution $W(\alpha)$. When there exists a small spatial chemical gradient, this uniformity is perturbed as a result of the self-adjustment of the bacterial population in $\theta$ through the direction-dependent tumbling mechanism. The mean average tumbling frequencies
happen to be the same ones used in the one-dimensional model of Rivero et al. [15] by adopting \( v/2 \) as the one-dimensional swimming speed in the exponent. The one-dimensional convective velocities \( v^\pm_1 \) are the results of the perturbed bacterial density in \( \theta \) direction due to the presence of a small spatial chemical gradient. They do not necessarily reflect the bacterial one-dimensional projected swimming speed \( v/2 \), but they reduce back to \( v/2 \) as the spatial chemical gradient \( \xi \to 0 \).

The pseudoequilibrium cellular flux can be expressed in exactly the same form as the Fickian expression: the sum of a diffusion-like term and a convection-like term

\[
J_z(z,t;\xi) = -\frac{1}{3} \frac{v^2}{(P_t^- + P_t^+)P_t} \frac{\partial c}{\partial z} + \left( \frac{2}{3} v \right) \frac{P_t^- - P_t^+}{P_t^- + P_t^+} \cdot c.
\]  

Our analysis shows that the expression of the random motility coefficient based on the consideration of bacterial three-dimensional motion is consistent with the result of Lovely and Dahlquist [11]. Moreover, from our analysis we are also able to obtain the correct expression for the chemotactic velocity. The random motility coefficient and the chemotactic velocity, after substituting in (2.61) and (2.62) for the mean average tumbling frequencies, can be explicitly expressed by

\[
\mu = \frac{v^2}{3P_{t,1}(1 - \langle \cos \alpha \rangle)}
\]

and

\[
V_c = \frac{1}{3} v \xi,
\]

both of which are consistent with Schnitzer’s [16] derivations in three dimensions considering only expanding the anisotropic tumbling frequency to a linear form.

REFERENCES


