Supplementary Information for

A Traveling-Wave Solution for Bacterial Chemotaxis with Growth

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Supplemental Methods

All of the numerical results shown in the main text were generated using the finite element method (FEM). Numerical simulations of the time evolution of the system of partial differential equations (PDEs) were performed using FEniCS, a computing platform for solving PDEs (1-28). A 1D mesh of resolution 15 μm was used to simulate a moving window of 30 mm (explained below). Finite elements of $P_3A^0$ type were used. The shape function space for $P_3A^0$ consists of all differential 0-forms with polynomial coefficients of degree at most 3, and has dimension 4. The degrees of freedom are given on line segments by moments of the trace weighted by a full polynomial space:

$$u \rightarrow \int_f (\text{tr}_f u) \wedge q, \quad q \in P_2A^1(f).$$

The initial bacterial density was specified with $\rho(x, t) = (\tanh((1 - x^2)) + 1) \times 0.029/2$ in order to initiate a sufficiently localized initial population with a differentiable functional form to avoid singularities. The initial attractant concentration was specified to be constant everywhere (with a value of $a_0$ that was an important model parameter). Neumann boundary conditions of zero flux were specified on both ends of the simulation domain. A difference equation was then solved to approximate the differential equation in time using a small time step (typically between 2 and 25 seconds) The resulting solutions were recorded and used for the subsequent iteration of the difference equation.

As expected, more accurate solutions (with a smaller error in the goal functional) were obtained for higher-resolution simulations, for both spatial and temporal resolution. In particular, lowering the saturation constants for the different reaction and convection terms (i.e., increasing the sensitivity) required substantial increases in the spatial and temporal resolutions. In order to obtain high spatial and temporal resolutions simultaneously, a moving window technique was utilized.

In the moving window technique, only a 30mm window was simulated at a time. When the front of the wave had gone beyond a certain threshold (chosen to be 60-75% of the width of our system) in the simulation domain, the simulation domain for the subsequent iteration was then translated to the right by the distance that the front had moved in the last timestep. The attractant concentrations and bacterial densities were extrapolated for the sections of the new simulation domain for which the values weren’t previously known (which are just the boundary values and are near constant at steady state for our model formulation). This technique holds very well as long as a threshold sufficiently far from the right end of the domain is chosen (this is also desirable to ignore edge effects) such that the linear extrapolation is correct within numerical resolution. Further, this method requires a smaller time interval (especially for fast-expanding solutions) to ensure that the simulation window isn’t translated too much in each timestep.

To analyze the simulations and extract the expansion speeds, the position of the maximum drift velocity was recorded for each timestep. A linear fit over time was then employed for the position to obtain the expansion speed. A sum of least squares fit was used, and only fits with a small enough sum of residuals were used for analysis. The fit was also curated manually to ensure that the expansion speed was calculated using a period of steady and constant expansion speed.

Variation of parameters for Fig. 4B: For Fig. 4B, the value of $a_0$ that maximizes $c$ for different values of $r$, $a_m$, $\rho_c$, and $\mu$ was sought. To do so, the values of $r$, $a_m$, $\rho_c$, and $\mu$ were varied over the ranges given in Table S2 and while the other values were fixed as given in Table S1 (with the exception of $\rho_c$ that was set at 10 OD unless it was being varied). Once all the data was generated, we found the value of $a_0$ between $10^{-3} - 10$ mM that led to the greatest value of $c$ and plotted the corresponding value of $a_0/a_m$ against the corresponding value of $\mu \rho_c/(r a_m)$ while denoting the parameter varied with a marker as specified in the legend of Fig. 4B.

Variation of parameters for Fig. 6B-D: For Figs. 6B-D, all of the data generated for this work was collated and the empirically determined values of $a_{\text{min}}$, $\rho_{\text{min}}$, and $z_m - z_{\text{min}}$ was plotted. This involved over 200 data points in which the following 7 model parameters were varied: $D_1$, $v_0$, $a_m$, $r$, $D_a$, $\mu$, and $a_0$. The ranges of values over which these parameters were varied is given in Table S3. Only results for $\rho_c > 1000$ OD, $\phi > 1$, $a_k = a_m = 1 \muM$, and $D_a > 10 \muM^2/s$ were considered.
Supplemental Figures

**Fig. S1.** The crucial role of growth for traveling-wave solutions. A. Decrease in expansion speed over time upon inclusion of a lower bound in the sensitivity to attractant concentration in the KS model. This is based on the result obtained by Novick-Cohen and Segel (29) for $D_p = 50 \ \mu m^2/\text{s}$ and other parameter values specified in Table S1. B. A schematic of the GE model as introduced by Cremer and Honda et al. (adapted from (30) with permission) The wave front is shown at two different times. First, it is shown at an earlier time in the top half of the panel where the front is propagating to the right with a given expansion speed. The solid green line is a plot of the bacterial density for different distances from the inoculation site. The front of the wave is shaded cyan. Then, the same front is shown with the solid green line after a doubling time in the bottom half of the panel (the earlier front is represented by a dashed green line). A hypothetical wave front that would result with growth and convection but without diffusion is shown in the orange line. Due to diffusion, the increased proportion of bacteria in the front are left behind to give the resulting wave. Thus, diffusion, growth and chemotaxis act together to result in a stable traveling-wave solution in the GE Model. All parameter values are the default values specified in Table S1.
Fig. S2. Comparison of density profiles obtained numerically for the simplified GE model (A) analyzed in this study (using parameters specified in Table S1 for low motility, and $\rho_c = 0.64$) with the general GE model formulated by Cremer and Honda et al. (B) using the experimentally-determined model parameters found in (30). We note that $\rho_c = 0.64$ is the carrying capacity corresponding to the initial nutrient concentration (10 mM) used in (30). Both simulations were performed using the Finite Element Method as detailed in Supplemental Methods. The corresponding expansion speeds are 2.79 mm/h for the version of the GE model analyzed in this study and 3.45 mm/h for the general GE model formulated by Cremer and Honda et al.
Fig. S3. Dependence on the chemotactic sensitivity, $\phi$. Numerical solutions for $D_\rho = 50 \mu m^2/s$ and $D_\rho = 1000 \mu m^2/s$ are shown by red and dark blue circles, respectively. Analytic solution following Eq. 23 are shown by the corresponding solid lines. Parameter values not specified in the legend are provided in Table S1.
Fig. S4. Numerically obtained values of $a_{\text{max}} = a(z_{\text{max}})$, $\rho_{\text{max}} = \rho(z_{\text{max}})$ and $z_{\text{m}} - z_{\text{min}}$ for a broad variation of parameters; seven model parameters in Eqs. 4-5 (other than the carrying capacity, which was $> 1000$ OD for all results here) were varied across many decades (see Supplemental Methods for details of what was done and Supplemental Table S3 for the range of values investigated). Blue lines show $y = x$ to demonstrate agreement with the predicted values of $a_{\text{max}}$, $\rho_{\text{max}}$, and $z_{\text{m}} - z_{\text{min}}$ as derived in Supplementary Note S10. The black line in the plot for $a_{\text{max}}$ shows $y = x/2$, the lower bound derived in Supplementary Note S9.

Supplemental Tables

| Parameter | Description | Value Used for low motility | Value Used for high motility |
|-----------|-------------|-----------------------------|-----------------------------|
| $D_{\rho}$ | Bacterial Motility Parameter | 50 $\mu$m²/s | 1000 $\mu$m²/s |
| $D_a$ | Attractant Molecular Diffusion Coefficient | 800 $\mu$m²/s | 800 $\mu$m²/s |
| $\phi$ | Chemotactic Sensitivity Parameter | 5 | 5 |
| $\chi_0$ | Chemotactic Motility Parameter | 300 $\mu$m²/s | 6000 $\mu$m²/s |
| $a_m$ | Lower Weber Cut-off | $10^{-3}$ mM | $10^{-3}$ mM |
| $a_0$ | Michaelis Constant for Attractant Uptake by Bacteria | $10^{-3}$ mM | $10^{-3}$ mM |
| $\rho_c$ | Background Attractant Concentration | 0.1 mM | 0.1 mM |
| $\mu$ | Rate of Attractant Uptake by Bacteria | 0.77 mM/OD/h | 0.77 mM/OD/h |
| $r$ | Rate of growth of bacteria | 0.69/h | 0.69/h |
| $\rho_c$ | Carrying Capacity | $10^9$ OD | $10^9$ OD |

Table S1. Standard parameters used for numerical simulations. These parameters were always used unless otherwise explicitly specified.

| Parameter varied | Range of Values Used |
|------------------|----------------------|
| $r$              | 0.03-7.7 /h          |
| $a_m$            | $10^{-4} - 3 \times 10^{-2}$ mM |
| $\rho_c$         | 0.9-100 OD           |
| $\mu$            | 0.25-2.3 mM/OD/h     |

Table S2. The range over which individual parameters were varied to determine the optimal value of $a_0$ for each set of parameters for Fig. 4B. Unless varied, the values were the default values given in Table S1 (except for $\rho_c$, for which the default value was 10 OD).

| Parameter varied | Range of Values Used |
|------------------|----------------------|
| $D_{\rho}$       | $10^{-3} - 1000$ $\mu$m²/s |
| $D_a$            | 110 – 800 $\mu$m²/s |
| $\chi_0$         | 100 – 11000 $\mu$m²/s |
| $r$              | 0.44-11.1 /h          |
| $\rho_c$         | 0.9-100 OD           |
| $\mu$            | 0.01 – 1.91 mM/OD/h   |
| $a_0$            | 0.004 – 10 mM         |

Table S3. The range over which individual parameters were varied to determine the numerical values of $a_{\text{min}}$, $\rho_{\text{min}}$, and $z_{\text{m}} - z_{\text{min}}$ for Fig. 6B-D. Unless varied, the values were the default values given in Table S1.

Supporting Information Text
S1. Historical Population Models for Chemotaxis

Chemotaxis, defined as the biased movement of sensitive organisms along gradients of sensible chemicals (known as chemotactants or chemorepellants in the case of movement up the gradient and down the gradient respectively), can be described mathematically by stochastic models for the position and direction-dependent velocity of each individual (31). The mathematical models consider the movement of individuals, independent of each other, that have the following characteristics:

1. The movement of each individual is piece-wise linear (each piece is often called a ‘run’),
2. Each linear ‘run’ stops probabilistically,
3. After stopping, the individual chooses a new direction randomly by a ‘tumble’ process.

This is called the run-and-tumble mechanism of chemotaxis. In the stochastic models, the speed of a linear ‘run’, the probability of stopping, and the probability of a direction being chosen after tumbling can depend on the time, the position, and the direction of the individual (32). These assumptions reflect the observed flagellar motion of many bacteria in liquids and gels (33), but can also be appropriate to describe the movement of other cells migrating on surfaces (32).

The stochastic mathematical models used to describe the motion of individual cells are based on quantitative experimental observations of the statistics for the turning frequency and the turn angle distributions (33). If these distributions are biased in the direction of the chemical gradient, it leads to a biased random walk for each individual. From these stochastic models and reasonable biological assumptions, an effective coarse-grained theory of population-level behavior can be obtained. The ontological components of the population-level theory are the local cell density and the concentration of the relevant chemical species.

A set of deterministic partial differential evolution equations to approximate the density and the mean direction of the population of moving individuals can be obtained rigorously mathematically (32). This was first done by Patlak (34) for a general persistent random walk using Taylor expansions, and then rediscovered by Keller and Segel in the context of chemotaxis through multiple derivations (35, 36). For movements with uniform mean run speed affected by a single attractant, the equation takes the form of a reaction-diffusion equation as follows

\[
\frac{\partial \rho}{\partial t} = \nabla \cdot \left( D_\rho(a) \nabla \rho \right) - \nabla \cdot \left( \rho \bar{v}[a] \right),
\]

where \( \rho \) is the local cell density, \( a \) is the concentration of the attractant, \( D_\rho(a) \) is the effective “diffusion” coefficient of cell motion (also known as the motility coefficient), and \( \bar{v}[a] \) is the drift velocity due to chemotactic cell motion. Further, Keller & Segel were able to show that analogous to Fourier’s law of cooling, the drift velocity must be proportional to the chemical gradient (for sufficiently weak gradients, and ignoring threshold effects) (35). Thus, the drift velocity can be written as

\[
\bar{v}[a] = \chi(a) \cdot \nabla a
\]

where \( \chi(a) \) is known as the chemotactic coefficient function. These phenomenological parameters can be related to microscopic parameters such as the mean run time and the receptor kinetics. It must be reiterated that the above-defined “diffusion” and “convection” processes are not actual molecular diffusion and convection, but rather effective processes resulting from biased random individual movements that are analogous to their molecular counterparts. For a systematic derivation of the above-presented reaction-diffusion equation (along with an extensive review of the assumptions made in the derivation) in an arbitrary number of dimensions, the reader is directed to extensive existing literature reviews (32, 37, 38)).

Eq. S1 can be coupled with reaction-diffusion equations for the attractant, to give rise to several experimentally observed spatial and temporal patterns in the cell density (39). Keller and Segel attempted to employ Eq. S1 to investigate one such pattern: the formation of traveling bands of chemotactic bacteria when placed in a stationary rich medium with a uniform attractant, the first extensive and modern treatment of which was performed by Julius Adler in 1966 (40, 41). This pattern has subsequently been observed in capillary tubes (40, 41), agar plates (42), and microfluidic chambers (43–46). The traveling band observed in these experiments indicates a region of locally maximal bacterial density which appear to be formed by an “accumulation” of fast-moving bacteria. The existence of such a local maximum is in contrast to the resulting fronts from other models of front propagation into unstable states, such as the Fisher-Kolmogorov–Petrovsky–Piskunov Equation (F-KPP Equation), which feature a monotonic front with no local maxima, or periodic front (47).

In their analysis, Keller and Segel assumed that \( D_\rho \) is constant, and that the drift velocity due to chemotactic bacterial motion is determined by logarithmic sensing, i.e., \( \bar{v}[a(z)] = \chi_0 \nabla a(z) \) where \( \chi_0 \) is a phenomenological proportionality constant known as the “chemotactic coefficient” and is a function of the bacterial strain and its internal state, the medium in which the experiment is conducted, and of the attractant being used (48). Such a form for the velocity is inspired by the Weber-Fechner law, which states that the sensitivity to a stimulus is inversely proportional to the background intensity of the stimulus. The Weber–Fechner law was first formulated in 1860 to describe human perception of physical magnitudes in the newly-created field of psychophysics (49, 50), but it has been replicated in hundreds of studies across all sensory modalities and many animal species over the last two centuries (51, 52). In particular, it has been shown that \( E. coli \) cells sense the spatial gradient of the logarithmic ligand concentration for a range of concentrations (53–55).
The dynamics of the attractant field in chemotactic bacteria, are determined by molecular diffusion and uptake and secretion by the bacteria.

\[
\frac{\partial a}{\partial t} = \frac{D_a}{\partial^2 a}{\partial z^2} - \mu(a)\rho + \frac{\delta(a)}{\partial x} \rho.
\]  

In their analysis, Keller and Segel assumed that the molecular diffusion of the attractant is negligible compared to the motility coefficient and the chemotactic coefficient of bacteria, and that the rate of uptake by bacteria is linear in bacterial concentration (which is the case when attractant availability is saturated). Keller and Segel also only considered chemotactic systems in which there is little secretion of the attractant (secretion of attractant can lead to much more complex behaviors (39, 56) and is not considered in this work). Thus, the one-dimensional form of the dynamical system analyzed by Keller and Segel is given by (where \( x \) is the single spatial coordinate):

\[
\frac{\partial \rho}{\partial t} = D \frac{\partial^2 \rho(x)}{\partial z^2} - \frac{\partial}{\partial x} \left( \frac{\chi_0}{a(x)} \frac{\partial a(x)}{\partial x} \right) \tag{S4}
\]

\[
\frac{\partial a}{\partial t} = -\mu\rho \tag{S5}
\]

They also assumed an initially localized population in a uniform attractant background with no finite size boundaries. Keller and Segel were able to solve the system exactly in one dimension and found that Eqs. S4-S5 admit the following travelling wave solutions (where \( z \equiv x - ct \) is the coordinate in the moving frame)

\[
a(z) = a_0 \left[ 1 + \exp\left( -\frac{cz}{D} \right) \right]^{-\frac{D}{\chi_0}} \tag{S6}
\]

\[
\rho(z) = \frac{N_0c}{\chi - Dc} \left[ 1 + \exp\left( -\frac{cz}{D} \right) \right]^{\frac{\chi}{\chi_0}} \exp(-cz/D) \tag{S7}
\]

where \( N_0 \) is the total number of cells in the inoculum. It must be noted that in this case, the total number of cells remains constant, and thus equal to \( N_0 \), as the net growth/death rate is assumed to be 0. The expansion speed (also referred to in literature as the traveling-wave velocity or the linear spreading speed), \( c \), is given by \( \mu N_0/a_0 \equiv c_{KS} \).

The KS model was extremely influential, but its results are highly sensitive to some of the assumptions made, many of which are biologically unrealistic. In particular, Keller and Segel identified that in order to generate traveling-wave solutions under their other assumptions, \( v(a, \nabla a) \) must be singular or constant as \( a \to 0 \) (57). This is unrealistic as cells cannot perform chemotaxis when concentrations fall below detectable values, which are determined by the kinetics of the enzymatic chemical reactions of the attractant. Novick-Cohen and Segel thus later analyzed a model in which \( v \to 0 \) for \( a \to 0 \), by including a lower Weber cutoff in the form of the drift velocity (29):

\[
\bar{v}(a, \nabla a) \equiv \frac{\nabla a}{a + a_m}. \tag{S8}
\]

In line with the original mathematical analysis, unstable wave-like solutions were obtained, with propagation slowing down noticeably during the time scale of the experiment (29) (see Fig. S1) and the front gradually vanishing over time.

Besides being unable to describe the observed stable migration under biological realistic conditions, the KS model also fails to account for a number of important experimental observations such as the independence of the expansion speed on the initial inoculum size (30, 41, 58). Since the original formulation of the KS model, many additional aspects have been considered to explain a stable migrating population (38, 59–61). Soon after the introduction of the KS model, bacterial growth was considered (62–70) to recover the stability of the migrating population. However, the introduced models failed to account for key experimental observations such as the distinct migrating band or the rapid expansion speed (30). A common feature of these models was that they took the attractant to be the same as the substrate for growth. However, by imposing a single substrate which plays both roles, these models unduly constrain the population dynamics and limit the expansion speed as recently pointed out (30). Further, models often preserved the unrealistic form of the drift velocity without a Weber cutoff assumed in the original KS-model (62–65, 69, 71). More recently introduced models consider more complex attractant uptake and excretion dynamics observed for certain environmental conditions (37–39, 72). While these models describe fast and stable expansion, they are not able to describe population migration over several generations since growth is not explicitly included.

**S2. The Crucial Role of Growth**

The logarithmic sensitivity to attractant concentration results in a constant drift velocity even as \( \nabla a(z) \to 0 \) as long as \( a(z) \to 0 \) in the same limit. However, this is unreasonable as in the case of a vanishing attractant, the drift velocity would be expected to also vanish. In their analysis, Keller and Segel demonstrated that for constant per capita uptake of attractant by bacteria, traveling wave solutions to the system of equations require a singularity in the chemotactic coefficient function, \( \chi(a) \) of order one or greater at \( a = 0 \) (73). However, relaxation of the constraint on the uptake by bacteria does not guarantee that the resulting solution would be stable. In fact, without the introduction of any new terms, a vanishing drift velocity would necessarily lead to a “leakage” of cells from the front of the wave. To demonstrate this, we operate in one dimension and
As we require that η → 0 as x → ∞, by performing integration by parts and plugging in Eq. S1, we obtain
\[ \left( c - v(x^*, t) \right) \rho(x^*, t) - D_\rho \left[ a(z) \right] \frac{\partial \rho(x^*, t)}{\partial x} \]
where \( D_\rho \) is the rate of growth of bacteria. By taking a point \( z^* \) sufficiently to the left such that \( v(z^*) < c \),
\[ \frac{dN}{dt} = r N - c \rho(z^*) - D_\rho \frac{\partial \rho(z^*)}{\partial z} \]
As \( z^* \rightarrow -\infty \), we must have that \( \partial_x \rho(z^*) < 0 \) or there exists \( z^* \) such that \( \partial_x \rho(z^*) = 0 \) as \( \partial_x \rho(z^*) > 0 \) just left of the density peak. If we take such a point, we are left with
\[ \frac{dN}{dt} = r N - c \rho(z^*) \]
By mass conservation from the integral form of Eq. S25, we must have that \( c = \mu N / a_0 \).
\[ \implies \frac{dN}{dt} = \left( r - \frac{\mu}{a_0} \rho(z^*) \right) N \]
Further, we may assume (motivated by limiting arguments and scaling relations) that \( \rho(z^*) \) has a positive dependence on \( N \). Thus, there exists a non-trivial \( N = N^* \) for which \( \frac{dN}{dt} = 0 \) and such an \( N \) would be stable as if \( N > N^* \), \( \frac{dN}{dt} < 0 \) and if \( N < N^* \), \( \frac{dN}{dt} > 0 \). Thus, growth leads to a stable fixed point for \( N \) which is the steady state travelling wave solution.

**S3. The Growth-Expansion Model: General Form and Simplification**

Cremer and Honda et al. (30) demonstrated experimentally and numerically that the inclusion of the growth of the bacteria is sufficient to counteract the effect of the leakage due to the lower Weber cutoff and obtain stable migratory bands. They further demonstrated that such an expansion affords a novel physiological benefit to bacteria: guided range expansion which takes place well before the consumption of the nutrient at the inoculation site by the bacteria, and thus allows for rapid colonization. They introduced the generalised Growth Expansion (GE) model given by the following set of equations:

\[ \frac{\partial \rho}{\partial t} = r(n, a) \rho - \nabla (\vec{v} \rho) + D_\rho \Delta \rho, \]
\[ \vec{v} = \chi_0 \nabla \log \left[ \frac{1 + a/a_{\infty}}{1 + a/a_+} \right], \]
\[ \frac{\partial n}{\partial t} = - \frac{\nu(n, a)}{\lambda} \rho + D_n \Delta n, \]
\[ \frac{\partial a}{\partial t} = - \mu(r, a) \rho + D_a \Delta a, \]

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where $\rho$ is the bacterial density, $a$ is the concentration of the attractant, $v$ is the drift velocity of the bacterial population and $n$ is the concentration of the nutrient. All other symbols denote functions and parameters, both environmental and physiological as described below.

1. $r(n, a)$ is the rate of growth of the bacteria. It is assumed to depend on only the local nutrient and attractant concentrations. For bacteria, the Monod equation provides an adequate relation to the nutrient concentrations (74). To simplify the system by eliminating the nutrient, the logistic growth equation may be used to approximate the decrease in growth rate due to the consumption of nutrient (75, 76). A further analysis of the effect of this simplification is explored below. The relation between growth rate and the attractant concentrations depends on the physiological effect of the attractant on the species of bacteria being considered, and the attractant may even hinder growth (39). However, the effect of the attractant on growth is typically much smaller than the other limiting nutrients (30) and may be ignored.

2. $D_n$ is the motility-induced diffusion of the bacteria. Bacteria are too large for Brownian motion to be significant in comparison to their size, however they engage in run-and-tumble motion which leads to a mean run length which is similar to the mean free path of a particle experiencing Brownian motion. Even when chemotaxis is biased in one direction, the movement of the bacteria can be viewed as a diffusion-convection process as described in Section S1. For bacteria such as E. coli in a 0.25% agar gel, it is typically of the order of 50 $\mu$m$^2$/s (30).

3. $a_+$ is the upper Weber cut-off. It has been found empirically that the bacterial sensitivity saturates at high attractant concentration because at high attractant concentrations, the bacteria is chemoreceptor-limited in its ability to sense attractant concentrations. For bacteria such as E. coli and a attractant such as aspartate, it is typically of the order of 30 mM (30).

4. $a_-$ is the lower Weber cut-off. Since the bacteria cannot be infinitely sensitive to attractant concentration, the lower Weber cut-off ensures that at very low attractant concentrations, the chemotaxis induced drift-velocity goes to 0. For bacteria such as E. coli and a attractant such as aspartate, it is typically of the order of 1 mM (30).

It must be noted that an equivalent form for the drift velocity in one dimension is

$$v = \chi \frac{a_+ (a + a_-) \nabla a}{a_- (a + a_+)^2}.$$  

This form, with appropriate substitution of constants, is more commonly found in literature. The case without $a_-$ can be studied by taking $a_- \to 0$, and the case without $a_+$ can be studied by taking $a_+ \to \infty$. In subsequent analysis, for visual clarity, we shall be using the symbol $a_m$ instead of $a_-$ which was used by Cremer and Honda et al. (30).

5. $Y$ is the biomass yield of the nutrient. It reflects a mass conversion factor from the nutrient to the bacterial density. For bacteria such as E. coli and a nutrient such as glucose, it is typically of the order of 0.1 OD/mM (30).

6. $D_a$ is the diffusion constant for the nutrient. For a nutrient such as glucose in a 0.25% agar gel, it is typically of the order of 800 $\mu$m$^2$/s (30).

7. $\mu(n, a)$ is rate of uptake of the attractant by the bacteria per unit bacteria. The nutrient dependence is to allow for a growth-dependent rate of uptake of the attractant. For the case of nutrient saturation, the rate of uptake of the attractant may be taken to be growth-rate independent. The dependence on the attractant is typically of the Michaelis-Menten form:

$$\mu(a(z)) = \mu_0 \frac{a(z)}{a(z) + a_k}.$$  

This is contrasted to the constant form assumed by Keller and Segel, and others. The Michaelis-Menten form is crucial if growth is to be included as for low attractant concentrations the bacterial density may not be small as is the case without growth. Thus, $\mu(a)$ is required to be vanishing for low attractant concentrations and is roughly linear in attractant concentration. For relatively higher attractant concentrations, the constant form of attractant consumption is recovered.

8. $D_a$ is the diffusion constant of the attractant. $D_a$ was typically taken to be negligible in the literature, as it was presumed that it is of a much smaller magnitude than the motility-induced diffusive and chemotactic movements of the bacteria. However, for small molecule attractants such as aspartate, serine and glucose, $D_a$ is typically larger than $D_p$ and $\chi_0$. Moreover, in porous media such as agar, $D_a$ can be significantly larger than $D_p$ (77) as bacteria are not able to complete their full run-and-tumble motions due to collisions with the polymer gel in agar. In their experiments, Cremer et al. found that in agar gels with 0.25% final agar concentration, $D_a$ was 50.2 $\mu$m$^2$/s. In contrast, the diffusivity constant for a typical attractant is around 800 $\mu$m$^2$/s (78).

9. $\chi_0$ is the phenomenological parameter known as the chemotactic sensitivity parameter. It is shown to be strain-dependent and is evolutionary selected by the location of the bacterium relative to other bacteria (79), and for bacteria such as E. coli in a 0.25% agar gel, it is typically of the order of 300 $\mu$m$^2$/s (30).

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While providing excellent numerical agreement to the experimental results, the generalised model of Eqs. S17-S20 is analytically intractable. The system can effectively be understood by making the non-crucial assumptions mentioned above, to recover a system of equations which is much closer to the simplified Keller-Segel equations:

\[
\frac{\partial \rho(z)}{\partial t} = -\nabla (\bar{v} \rho) + D_\rho \Delta \rho(z) + r \rho(z)(1 - \rho(z)/\rho_c),
\]

\[
\bar{v} = \chi_0 \nabla \log[1 + a(z)/a_m],
\]

\[
\frac{\partial a(z)}{\partial t} = -\mu \frac{a(z)}{a(z) + a_k} \rho(z) + D_a \Delta a(z),
\]

where \(\rho_c\) is the carrying capacity of the system. Most notably, we have eliminated the nutrient field since in the GE model the effects of the nutrient and the attractant on the bacterial concentration are decoupled. The effect of limited availability of nutrient can be mimicked by limiting \(\rho_c\). Thus, we reduce the equation to a system of two coupled partial differential equations. The system of equations has a degree of 4 and is accompanied by appropriate initial value and boundary conditions. In our analysis, we specify the initial conditions to be a localized profile of \(\rho(z)\) (any localized profile leads to the same steady state solution; see Fig. S3) and a constant profile of \(a(z)\) at a value of \(a_0\). With some reordering and working in one dimension, we obtain the following equations:

\[
\frac{\partial \rho}{\partial t} = D_\rho \frac{\partial^2 \rho}{\partial x^2} - \chi_0 \frac{\partial}{\partial x} \left( \frac{\rho}{a(z) + a_m} \frac{\partial a}{\partial x} \right) + r \rho(1 - \rho/\rho_c),
\]

\[
\frac{\partial a}{\partial t} = D_a \frac{\partial^2 a}{\partial x^2} - \mu \frac{a(z)}{a(z) + a_k} \rho.
\]

We seek traveling-wave solutions of the forms

\[\rho(x, t) = \rho(z), \ a(x, t) = a(z), \text{ with } z = x - ct\]

where \(c > 0\) is the traveling wave speed (also referred to in previous literature as the expansion speed or the linear spreading speed). This converts the system from a system of partial differential equations to a system of ordinary differential equations as follows:

\[-c \frac{\partial \rho}{\partial z} = D_\rho \frac{\partial^2 \rho}{\partial z^2} + r \rho(1 - \rho) - \chi_0 \frac{\partial}{\partial z} \left( \frac{\rho}{a(z) + a_m} \frac{\partial a}{\partial z} \right),\]

\[-c \frac{\partial a}{\partial z} = D_a \frac{\partial^2 a}{\partial z^2} - \mu \frac{a(z)}{a(z) + a_k} \rho.\]

The boundary conditions of the system are specified such that the concentration of the attractant far to the left of the front is 0, and far to the right of the front is \(a_0\), the initial concentration of the attractant; and the bacteria density is the carrying capacity of the system, \(\rho_c\) far to the left of the front, and 0 far to the right of the front. The boundary conditions can be represented as follows:

\[\rho(\infty) \to 0, \ a(\infty) \to a_0, \ \rho(-\infty) \to \rho_c, \ a(-\infty) \to 0\]

\[\partial_z \rho(\infty) \to 0, \ \partial_z a(\infty) \to 0, \ \partial_z \rho(-\infty) \to 0, \ \partial_z a(-\infty) \to 0.\]

We compared the variation of the expansion speed with \(\chi_0\) for both the full version of the GE model, and our simplified version, and found that the expansion speed remains roughly the same as can be seen in Fig. S2.

S4. The Exponential Ansatz

In the case of no growth and \(a_m, a_k \to 0\) as in the simplified Keller-Segel model (Eqs. S4-S5), away from the right boundary such that \(a_0 \to \infty\), the solution to the system of differential equations is straightforward:

\[a(z) \propto \rho(z) \propto \exp(\lambda_{KS} z) \text{ where } \lambda_{KS} = 0 \text{ or } \lambda_{KS} = \frac{c}{\lambda_0 - D_\rho} \]
We will now show that the error terms that showed up in the calculation for the Diffusion Regime in the main text, such that \( r \ll \lambda c \), can be neglected if \( c \gg a_k \), as shown in the calculation for the Diffusion Regime in the main text, \( \rho(z) \approx \rho_0 \exp(-cz/D_r) \) and \( \rho(z)/a(z)+a_k \approx \frac{C}{a_k} \exp(-cz/D_r) \) where \( \rho_0 \) is the value of \( \rho(z) \) at the interface of the Chemotaxis and Diffusion Regimes. Thus,

\[
\int_{z_t}^{\infty} \frac{\rho(z)}{a(z)+a_k} \, dz = \int_{z_t}^{z_a} \frac{\rho(z)}{a(z)+a_k} \, dz + \int_{z_a}^{\infty} \frac{\rho(z)}{a(z)+a_k} \, dz \approx \beta(z_a-z_t) + \frac{\rho_0 D_r}{a_0 c} \approx \frac{\beta}{\lambda} \ln \left( \frac{a_0}{a(z_t)} \right) + \frac{\beta D_r}{c} \approx O \left( \frac{\beta}{\lambda} \ln \left( \frac{a_0}{a(z_t)} \right) \right)
\]

where the last bound emerges from noting that \( \lambda = c/(\chi_0 - D_r) \) and taking \( \chi_0 > D_r \). We note that since \( \frac{a_0}{a(z_t)} \ll 1 \), the correction term is of a sub-leading order. We will, however, carry it forward to determine the order of the sub-leading term in the final calculation.

\[
\Rightarrow N = c(a_0 - a(z_t)) - D_r a_0 \lambda a(z_t) + O \left( \frac{a_k \beta \log a_0}{a(z_t)} \right)
\]

Now, from the integral of Eq. S24

\[
-c \lambda a_0 = D_r \chi_0 \beta \frac{\partial}{\partial z} \left( \frac{a_0}{a(z)+a_k} \right) + r(a_0 + a_k) + O \left( \frac{a_k \beta \log a_0}{a(z_t)} \right)
\]

We obtain the order of the last term, we note that \( \rho(z) = \beta(a(z)+a_k) \) from \( z_1 \) to a point, \( z_a \) where \( a(z) \sim a_0 \). For \( z > z_a \), as shown in the calculation for the Diffusion Regime in the main text, \( \rho(z) \approx \rho_0 \exp(-cz/D_r) \) and \( \rho(z)/a(z)+a_k \approx \frac{C}{a_k} \exp(-cz/D_r) \) where \( \rho_0 \) is the value of \( \rho(z) \) at the interface of the Chemotaxis and Diffusion Regimes. Thus,

\[
\int_{z_1}^{\infty} \frac{\rho(z)}{a(z)+a_k} \, dz = \int_{z_1}^{z_a} \frac{\rho(z)}{a(z)+a_k} \, dz + \int_{z_a}^{\infty} \frac{\rho(z)}{a(z)+a_k} \, dz \approx \beta(z_a-z_1) + \frac{\rho_0 D_r}{a_0 c} \approx \frac{\beta}{\lambda} \ln \left( \frac{a_0}{a(z_1)} \right) + \frac{\beta D_r}{c} \approx O \left( \frac{\beta}{\lambda} \ln \left( \frac{a_0}{a(z_1)} \right) \right)
\]

Thus, for \( a \ll a_k \), we can solve for \( \lambda \) and we obtain

\[
\lambda = \frac{c}{2(\chi_0 - D_r)} \pm \frac{\sqrt{c^2 + 4\lambda(\chi_0 - D_r)}}{2(\chi_0 - D_r)}
\]

which is the same as the asymptotic form of the solution obtained by Keller and Segel.

**S. Calculation of Expansion Speed with Sub-leading Terms**

We will now show that the error terms that showed up in *Heuristic Derivation of the Expansion Speed* are sub-leading and can be neglected if \( r \ll \lambda c \). To find \( c \), we must use another boundary condition. However, the exponential increase in \( \rho \) does not continue do to the right boundary condition for \( \rho \). Instead, \( \rho \rightarrow 0 \) fast enough for the \( \rho(z) \) to be integrable in the interval \( [z_1, \infty) \) such that \( \rho(z) \ll a(z) \) and \( \partial_r \rho \approx \lambda \rho(z) \). Thus, we integrate Eq. S24 and Eq. S25 and employ suitable approximations:

\[
-\frac{c}{a(z)} = D_r \frac{\partial^2 \rho}{\partial z^2} \bigg|_{z_1}^{\infty} - \mu \int_{z_1}^{\infty} \frac{\rho(z)}{a(z)+a_k} \, dz
\]

\[
\Rightarrow c(a_0 - a(z_1)) = D_r \lambda a(z_1) + \mu \int_{z_1}^{\infty} \rho \, dz - \mu a_k \int_{z_1}^{\infty} \frac{\rho(z)}{a(z)+a_k} \, dz
\]

\[
\approx N \approx O \left( \frac{a_k \beta \log(a_0/a(z_1))}{a(z_t)} \right)
\]

where

\[
\partial_r \rho \approx \lambda \rho(z)
\]

in the asymptotic form of the solution obtained by Keller and Segel.

**S. Calculation of Expansion Speed with Sub-leading Terms**

We will now show that the error terms that showed up in *Heuristic Derivation of the Expansion Speed* are sub-leading and can be neglected if \( r \ll \lambda c \). To find \( c \), we must use another boundary condition. However, the exponential increase in \( \rho \) does not continue to the right boundary condition for \( \rho \). Instead, \( \rho \rightarrow 0 \) fast enough for the \( \rho(z) \) to be integrable in the interval \( [z_1, \infty) \) such that \( \rho(z) \ll a(z) \) and \( \partial_r \rho \approx \lambda \rho(z) \). Thus, we integrate Eq. S24 and Eq. S25 and employ suitable approximations:

\[
-\frac{c}{a(z)} = D_r \frac{\partial^2 \rho}{\partial z^2} \bigg|_{z_1}^{\infty} - \mu \int_{z_1}^{\infty} \frac{\rho(z)}{a(z)+a_k} \, dz
\]

\[
\Rightarrow c(a_0 - a(z_1)) = D_r \lambda a(z_1) + \mu \int_{z_1}^{\infty} \rho \, dz - \mu a_k \int_{z_1}^{\infty} \frac{\rho(z)}{a(z)+a_k} \, dz
\]

\[
\approx N \approx O \left( \frac{a_k \beta \log(a_0/a(z_1))}{a(z_t)} \right)
\]

where

\[
\partial_r \rho \approx \lambda \rho(z)
\]
Collecting the coefficients of $a(z^1)$, we obtain the following two equations:

$$c = (\chi_0 - D_\rho)\lambda - \frac{r(c + D_\rho \lambda)}{\mu \beta} = (\chi_0 - D_\rho)\lambda - \frac{r}{\lambda}$$

(S45)

This is the same relationship between $c$ and $\lambda$ that we had obtained in The Exponential Ansatz by assuming that $\rho(z) = \beta(a(z) + a_m)$. But from comparing the constant terms, we obtain

$$\beta \left(1 + O \left(\frac{a_k}{a_m} \frac{r \log \frac{a_0}{a(z^1)}}{\lambda c} \right) + O \left(\frac{a_k - a_m}{a_m}\right)\right) = \frac{(D_\rho \lambda^2 + c\lambda)}{\mu} \left(1 + O \left(\frac{a_k}{a_m} \frac{r \log \frac{a_0}{a(z^1)}}{\lambda c} \right) + O \left(\frac{a_k - a_m}{a_m}\right)\right) = \frac{ra_0}{\mu a_m}$$

We assume that $r/\lambda c \ll 1$ and the lower order term can be ignored. We also take $a_k - a_m \ll a_m$, but we note that this reveals why we are only getting up to a factor of 2 change even if we relax the assumption that $a_k = a_m$, unless we take $a_k \gg a_m$.

$$\implies \frac{ra_0}{a_m} \approx \lambda^2 (\chi_0 - D_\rho + D_a) - r$$

As $a_m/a_0 \ll 1$, we ignore the second order term on the RHS. Thus, as a final solution, we obtain that:

$$\lambda \approx \sqrt{\frac{r(a_0/a_m)}{\chi_0 - D_\rho + D_a}}$$

$$\implies c \approx (\chi_0 - D_\rho) \sqrt{\frac{r(a_0/a_m)}{\chi_0 - D_\rho + D_a}} - \sqrt{\frac{r(\chi_0 - D_\rho)}{(a_0/a_m)}} \approx (\chi_0 - D_\rho) \sqrt{\frac{r(a_0/a_m)}{\chi_0 - D_\rho + D_a}}$$

For $\chi_0 \gg D_\rho$ and $a_m \ll a_0$, the second term can be ignored. This is self-consistent with the assumption that $r \ll \lambda c$. The error in these calculations is of the order of $a_m/a_0$. Further, this result does not hold for $\chi_0 \sim D_\rho$ (equivalent to the case that $\phi \to 0$ shown in Fig. S4) and in that regime the exponentially increasing profile for $\rho$ disappears and our approximations fail.

S6. Form of Expansion Speed for Finite Carrying Capacity

For $\rho_1 \rightarrow \infty$, we can use the same techniques as earlier, but we have an additional term corresponding to the effect of the carrying capacity. The integral equation now reads:

$$c \rho(z^1) = -D_\rho \frac{\partial \rho}{\partial z}(z^1) + \chi_0 \beta \frac{\partial a}{\partial z}(z^1) + rN - \frac{r}{\rho c} \int_{-\infty}^{\infty} \rho^2(z) dz + O \left(\frac{r(a_0/a_m)}{\chi_0 - D_\rho + D_a} \right)$$

(S46)

, where we have assumed $a_k = a_m$. To progress, we must make some assumptions regarding the form of $\rho^2$ (or equivalently, of $\rho$). Based on the numerical results, we assume a piece-wise exponential form for $\rho$:

$$\rho(z) = \begin{cases} 
\rho_{\text{max}} \exp(\lambda z), & z < 0 \\
\rho_{\text{max}}, & 0 < z < \kappa D_a/c \\
\rho_{\text{max}} \exp(-cz/D_\rho) \exp(\kappa D_a/D_\rho), & z > \kappa D_a/c
\end{cases}$$

(S47)

where $\rho_{\text{max}}$ is the highest value of $\rho(z)$ obtained. The region $0 < z < \kappa D_a/c$ is intended to reflect that there is a transition region between the Chemotaxis Regime and the Diffusion regime where $\rho(z)$ does not behave exponentially is only slowly varying, as observed in numerical simulations. The width of this region has been observed numerically to be set by $D_\rho$ and $c$, with an unknown proportionality constant $\kappa$. As the only relevant variables for $\kappa$ are $D_\rho, D_a, \chi_0$, we hypothesize that it is a function of these variables. This was also motivated by a close inspection of numerical results (Fig. 4). Thus, we find that

$$\int_{-\infty}^{\infty} \rho^2(z) dz = \frac{\rho_{\text{max}}^2(\chi_0/2 + 2D_\kappa)}{2c}$$

(S48)

But we also have that $N = \frac{(\chi_0 + D_\kappa)^{\rho_{\text{max}}}}{c}$. Thus,

$$\int_{-\infty}^{\infty} \rho^2(z) dz = \frac{\chi_0^2 c(\chi_0 + 2D_\kappa)}{2(\chi_0 + D_\kappa)^2}$$

Going back to our previous calculations, we now have that

$$-c \rho \bigg|_{z^1} = D_\rho \frac{\partial \rho}{\partial z}(z^1) \bigg|_{z^1} - \chi_0 \left(\frac{\rho}{a(z) + a_m} \frac{\partial a}{\partial z}\right) \bigg|_{z^1} + rN - \frac{rN^2 c(\chi_0/2 + D_\kappa)}{2 \rho c(\chi_0/2 + D_\kappa)^2}$$

(S49)

$$\implies c \rho(z^1) \approx -D_\rho \frac{\partial \rho}{\partial z}(z^1) + \chi_0 \frac{\partial a}{\partial z}(z^1) + r \frac{(c(a_0 - a(z^1))) - a D_\kappa}{\mu} \approx r \frac{(c(a_0 - a(z^1))) - a D_\kappa}{\mu} \left(\frac{c(a_0 - a(z^1)) - D_\kappa a(z^1)}{\mu}\right)^2$$

(S50)
We ignore terms of \(O(a^2(z^l)/a_0^2)\) as \(a_0 \gg a(z^l)\)

\[
\Rightarrow \ c\beta(a(z^l) + a_m) = -D_\lambda \beta a(z^l) + \chi_0 \beta a(z^l) + \frac{rc(a_0 - a(z^l)) - r D_\lambda a(z^l)}{\mu} - \frac{rc(\chi_0 + 2 D_\lambda \kappa)}{2 \rho_c(\chi_0 + D_\lambda \kappa)^2} \left( \frac{c^2 a_0^2 - 2 c^2 a_0 a(z^l) - 2 c a_0 D_\lambda a(z^l)}{\mu^2} \right) \tag{S51}
\]

Collecting the coefficients of \(a(z^l)\), we obtain the following equation:

\[
c = (\chi_0 - D_\rho) \lambda - \frac{r(c + D_\lambda \rho)}{\mu \beta} + \frac{r(\chi_0 + 2 D_\lambda \kappa)}{\rho_c(\chi_0 + D_\lambda \kappa)^2} \left( \frac{c^2 a_0^2 + c a_0 D_\lambda a}{(D_\lambda \rho^2 + c \lambda) \mu} \right) \tag{S52}
\]

\[
= (\chi_0 - D_\rho) \lambda - \frac{r(\chi_0 + 2 D_\lambda \kappa)}{\rho_c(\chi_0 + D_\lambda \kappa)^2} \left( \frac{c a_0}{\lambda \mu} \right) \tag{S53}
\]

From comparing the constant terms, we obtain

\[
\beta \left( 1 + O \left( \frac{r(\chi_0 - D_\rho) \lambda}{\mu} \right) \right) = \left( D_\lambda \rho^2 + c \lambda \right) \left( 1 + O \left( \frac{r a_m \lambda}{\mu} \right) \right) = \frac{ra_0}{\mu a_m} - \frac{r c^2 a_0^2 (\chi_0 + 2 D_\lambda \kappa)}{2 a_m \mu^2 \rho_c(\chi_0 + D_\lambda \kappa)^2} \tag{S54}
\]

However, for small \(r\) and \(\chi_0 \gg D_\rho\), \(c \approx (\chi_0 - D_\rho) \lambda\) and thus, \(r/\lambda \ll 1\) and the lower order term can be ignored.

\[
\Rightarrow \ \frac{r a_0}{a_m} \approx \lambda^2 (\chi_0 - D_\rho + D_\lambda) - r + \lambda^2 \frac{r(\chi_0 - D_\rho) a_0^2 (\chi_0 + 2 D_\lambda \kappa)}{2 a_m \mu \rho_c(\chi_0 + D_\lambda \kappa)^2} \tag{S55}
\]

where \(\gamma\) is a dimensionless function of \(D_\rho, D_\lambda, \chi_0\) and \(\kappa\). As \(\kappa\) itself is a function of the three variables, \(\gamma\) replaces \(\kappa\) as an equivalent constant. As \(a_m/a_0 \ll 1\), we ignore the term \(O(a_m/a_0)\) on the RHS. Thus, as a final solution, we obtain that:

\[
\lambda \approx \frac{r(\chi_0 - D_\rho) a_0}{\chi_0 - D_\lambda + D_\lambda + \frac{r a_0}{a_m} \gamma} = \frac{\frac{r a_0}{a_m} (\chi_0 - D_\rho + D_\lambda) + \frac{r a_0}{a_m} (\chi_0 - D_\rho) \gamma}{\frac{r a_0}{a_m} (\chi_0 - D_\rho + D_\lambda) + \frac{r a_0}{a_m} (\chi_0 - D_\rho) \gamma} \tag{S56}
\]

\[
\Rightarrow \ c \approx (\chi_0 - D_\rho) \frac{\frac{r a_0}{a_m} (\chi_0 - D_\rho + D_\lambda) + \frac{r a_0}{a_m} (\chi_0 - D_\rho) \gamma}{\frac{r a_0}{a_m} (\chi_0 - D_\rho + D_\lambda) + \frac{r a_0}{a_m} (\chi_0 - D_\rho) \gamma} \tag{S57}
\]

The attractant concentration for the maximum expansion speed found by maximizing \(c_\infty\) with respect to \(a_0\) is given by

\[
\frac{c_\infty^{\text{max}}}{a_m} = \left( \frac{\mu \rho_c}{r a_0 \gamma} \right) \left( 1 + \frac{D_\lambda}{D_\rho} \right) \tag{S58}
\]

The dimensionless function \(\gamma\) is expected to be a non-trivial function of \(\chi_0, D_\lambda\) and \(D_\rho\). It is related to the width of the assumed plateau for the top of the peak, and expected to decrease with higher \(D_\lambda\) as the “smoothening” of the attractant gradient due to \(D_\lambda\) results in a broadening of the density bulge and reduces the effect of the carrying capacity. However, as \(\chi_0, D_\lambda\) and \(D_\rho\) have the same dimensions, \(\gamma\) may be a non-trivial combination of \(\chi_0, D_\lambda\) and \(D_\rho\) which themselves may be raised to powers of combinations of \(\chi_0, D_\lambda\) and \(D_\rho\).

**S7. F-KPP Dynamics in the Growth and Diffusion Regimes**

**A. Diffusion Regime.** To understand the selection of the asymptotic steepness of the front of the wave as \(z \to +\infty\), we operate in the static frame and assume that the initial population is described by a Dirac delta function, i.e., \(\rho(x, 0) = \delta(x)\). Then, the solution to the F-KPP equation is

\[
\frac{\partial \rho(x, t)}{\partial t} = D_\rho \partial_x^2 \rho(x, t) + r \rho(x, t) \tag{S60}
\]

Since it is a second order PDE, we need two boundary/initial conditions, one spatial and one temporal. Our initial condition is given by the Dirac delta function, and we take the boundary condition as a zero population at infinity \((\rho(x \to +, t) = 0)\). The solution is obtained by using the Fourier transform. In our convention, we define the Fourier transform as

\[
\hat{\rho}(k, t) = \int \rho(x, t) \exp(-ix \cdot k) \tag{S61}
\]

and the inverse is

\[
\rho(x, t) = \frac{1}{2\pi} \int dk \hat{\rho}(k, t) \exp(ix \cdot k) \tag{S62}
\]
where \( k \) is the Fourier space dual of the position, and can be understood as a form of spatial frequency.

Going back to our equations, by plugging in the equation for the inverse Fourier transform into the diffusion equation.

\[
\frac{\partial \rho(x, t)}{\partial t} = \frac{1}{2\pi} \frac{\partial}{\partial t} \int dk \hat{\rho}(k, t) \exp(ik \cdot x) = \frac{1}{2\pi} \int dk \frac{\partial \hat{\rho}(k, t)}{\partial t} \exp(ik \cdot x)
\]  \[ \text{[S63]} \]

\[
D_\rho \frac{\partial^2 \rho(x, t)}{\partial x^2} = D_\rho \frac{1}{2\pi} \int dk \hat{\rho}(k, t) \exp(ik \cdot x) = \frac{D_\rho}{2\pi} \int dk \hat{\rho}(k, t) \hat{\rho}(k, t) \exp(ik \cdot x)
\]  \[ \text{[S64]} \]

Thus, plugging everything into the F-KPP equation, we get that

\[
\frac{\partial \hat{\rho}(k, t)}{\partial t} = (-D_\rho k^2 + r) \hat{\rho}(k, t)
\]  \[ \text{[S65]} \]

\[
\Rightarrow \hat{\rho}(k, t) = \hat{\rho}(k, t = 0) \exp(-D_\rho k^2 t + rt)
\]  \[ \text{[S66]} \]

where \( \hat{\rho}(k, t = 0) \equiv \int dk \rho(x, t = 0) \exp(-ik \cdot x) \) \[ \text{[S67]} \]

Consider the initial condition where you start with \( N_0 \) at an infinitesimal volume, which can be taken as a delta function, i.e., \( \rho(x, t = 0) = N_0 \delta(x) \) Then,

\[
\hat{\rho}(k, t = 0) \equiv \int dk N_0 \delta(x) \exp(-ik \cdot x) = N_0
\]  \[ \text{[S68]} \]

Now, we can get the inverse transform:

\[
\rho(x, t) = \frac{1}{2\pi} \int dk \exp(-D_\rho k^2 t + ik \cdot x + rt) = \frac{N_0}{2\sqrt{\pi D_\rho t}} \exp \left( -\frac{x^2}{4D_\rho t} \right) \exp(rt)
\]  \[ \text{[S69]} \]

For the long-term behavior, we take \( x = z + ct \),

\[
\rho(z, t) = \frac{N_0}{2\sqrt{\pi D_\rho t}} \exp \left( -\frac{(z + ct)^2 + 2zt}{4D_\rho t} \right) \exp(rt) = \frac{N_0}{2\sqrt{\pi D_\rho t}} \exp \left( -\frac{z^2}{4D_\rho t} \right) \exp \left( rt - \frac{c^2 t}{4D_\rho} \right) \exp \left( -\frac{-cz}{2D_\rho} \right)
\]  \[ \text{[S70]} \]

The first term signals the transition from \( t = 0 \) to later time, and can be ignored for large \( t \). The second term demonstrates that the speed of the front should be at least \( c_F \equiv 2\sqrt{D_\rho / \tau} \) otherwise the solution doesn’t satisfy the boundary conditions. If the speed were actually lower than \( c_F \), a new front with speed \( c_F \) would emerge and “pull” the front, thus creating a “pulled” wave-front. Any front traveling faster would die over time, unless it is supported by the bulk of the wave. The final term indicates that the steepness of the front must be at least \( c / 2D_\rho \), which would correspond to \( \lambda_F = \sqrt{\tau / D_\rho} \) for the case of pulled waves. However, for speeds propagated by the bulk at speeds faster than \( c_F \), the front is effectively pushed by the bulk. In such a case, the steepness must be at least \( \lambda_F \) as otherwise the asymptotic steepness would be less than the steepness for the Fisher speed, and since a solution with the Fisher speed is always permitted, it would emerge and dominate the front before being overtaken by the bulk. The only stable solution is for the slope to be \( \lambda_F = \frac{c + \sqrt{c^2 - 4D_\rho}}{2D_\rho} \), which is the observed slope. This is the case of a “pushed wave-front” and occurs in the Diffusion Regime of our system.

B. Growth regime. The analysis of the Chemotaxis Regime results in relations for expansion speed as discussed above. To understand the entire traveling wave, we next consider the growth regime, which is defined being left of the density trough and characterized by \( a' \leq a_m \) (Fig. 2). As the drift velocity vanishes with falling attractant concentrations (as \( a' / a_m \rightarrow 0 \) in this regime), convection does not counteract the effects of back-diffusion and cells leave the moving frame. This “leakage” is explored further in Sec. S2 of the Supplemental Text. While the total number of bacteria in the moving front is conserved as growth counteracts this “loss”, cells in the trailing region cannot catch up the fast chemotactic migration and thus “stay behind”. However, cells still grow as long as \( \rho < \rho_c \) and move diffusively. In the growth regime the governing equation for the population is thus given as:

\[
-c \frac{d\rho}{dz} = D_\rho \frac{d^2 \rho}{dz^2} + r \rho (1 - \rho / \rho_c).
\]  \[ \text{[S71]} \]

This is the well-known F-KPP equation. However, in contrast to the standard scenario canonically used to describe range expansion, the right boundary condition is specified by the traveling-wave dynamics of the Chemotaxis Regime. The expansion speed of the population can be obtained in this case by analyzing the “growth front” (the boundary of Growth and Chemotaxis...
Regime in this case), for which \( \rho \ll \rho_c \) and the nonlinear term in Eq. S71 can be neglected. The remaining linear equation yields the solution

\[
\rho \propto \exp(-\lambda_G^2 z), \quad \text{with} \quad \lambda_G^2 = \frac{c \pm \sqrt{c^2 - 4rD_c}}{2D_c},
\]

which relates the expansion speed of the growth front, \( c_G \), in term of the decay parameter \( \lambda_G \) of the density profile. For each value of the allowed expansion speed \( c \geq c_F \equiv 2\sqrt{rD_c} \), the solution is degenerate with two possible values of \( \lambda_G \), except when \( c = c_F \).

A seminal result in the theory of the F-KPP equation is that the marginally stable density profile, with \( \lambda_F = c_F/(2D_c) = \sqrt{r/D_c} \) is selected among all the allowed solutions, for sufficiently compact initial conditions (80, 81). However, as we found for the Chemotaxis Regime the population moves with an expansion speed given by Eq. S45, with \( c > c_F \) as long as \( \phi \) is not too close to 0. Traveling speeds with \( c > c_F \) are permitted as solutions of the F-KPP equation, but they correspond to \( \lambda_F \neq \lambda_F \) and are not marginally stable, thus typically not selected (47). Thus, we may ask, how do the bacteria in this case beat “marginal stability”? Or in other words, how is the propagation speed \( c \) “passed on” from the Chemotaxis Regime to the trailing growth regime which is governed by the F-KPP equation?

This may be understood through another well-known result in the theory of the F-KPP equation that, independent of the precise non-linearities, if the front of the wave is maintained to be shallower than \( \lambda_F \), then the front travels with a speed given by \( c > c_F \) (47). In our case, the shallower slope is \( \lambda_G \approx r/c \). This shallower slope is maintained by the “leakage” of cells from the Chemotaxis Regime into the front of the growth regime which are deposited behind the Chemotaxis Regime along a boundary moving at an expansion speed \( c \). This can be understood through our ansatz \( \rho(z) = \beta(a + a_m) \) as for \( a(z) \to 0 \), \( \rho(z) \to \beta a_m \) and the resulting constant boundary condition for \( \rho(z) \) at the tail of the migrating band. Thus, in this way, the propagation speed \( c \) is “passed on” from the Chemotaxis Regime to the trailing growth regime.

The dynamics of the growth regime reveal how the migrating band may leave behind a small number of “settling” cells, that can then grow exponentially. By continually leaving behind the small number of cells, the back formed by the “settling” cells also keeps up with the migrating band. However, if migrating bands are composed of cells with different motilities starting at the same inoculum spot, fewer cells will be deposited by the faster-moving than by the slower-moving cells. Thus, the slower-moving cells will quickly increase to a higher density and out-compete the cells left behind by the faster-moving band. This leads to the ecological principle that more motile cells have a higher fitness in regions far from the inoculating site, and the less motile cells have a higher fitness in regions close to the inoculating site. This was validated experimentally by Liu et al., who repeatedly selected cells at different distances from the inoculating site, finding that over time the cells close to the starting point formed populations with lower expansion speeds and the cells far from the starting point formed populations with higher expansion speeds (79).

**Growth Regime for \( D_r \to 0 \)**

Beyond the results obtained for the Growth Regime using the modified ansatz, exact mathematical statements can be made regarding the Growth Regime in the case that \( D_r = 0 \). We note that the solutions should not qualitatively change for \( D_r > 0 \) as it can only smoothen the density profile (and subsequently the attractant profile). Numerical simulations performed with \( D_r = 0 \) confirm that all results hold in the limit \( D_r \to 0 \) and all qualitative features are preserved. For simplicity, we will take the limit of large \( \rho_c \) since at the front, \( \rho(z)/\rho_c \to 0 \).

A magnified view of the transition region between the Chemotaxis and Growth Regimes is shown in Fig. 5A, with the location of the density minimum being at \( z_{\text{min}} \). Applying the ansatz to \( z = z_m \) (where ansatz Eq. 7 holds as per the condition Eq. 11, \( a(z) \gg (r/\lambda c)a_m \)), we find the flux of cells due to chemotaxis and diffusion, \( J(z_m) \equiv -v(z)\rho(z) \), to be given by

\[
J(z_m) = -\chi_0 \beta da/dz \bigg|_{z = z_m} = -c\beta a_m,
\]

where we used \( v(z)\rho(z) = \chi_0 \beta da/dz \) based on our ansatz Eq. 7, and \( a(z) \propto \exp(\lambda z) \) with \( \lambda \) given by Eq. 12. Here, a negative value indicates a net flux to the left at \( z_m \), i.e., out of the Chemotaxis Regime. For the wave-front to be at steady state, the loss of cells at \( z_m \) due to chemotaxis and diffusion must be replenished by growth. Recall that in the solution by Novick-Cohen and Segel (29) that also incorporated the lower Weber cut-off but maintained a constant total population size, the population “left behind” the front was the reason that the migrating wave-front slowed down. Incorporating growth, even at very low rates, allows the migrating wave-front to “replenish” itself and maintain stability. This is discussed in more detail in Supplemental Text S2.

Eq. 19 and Eq. S45 also allow us to use Eq. 18 to find \( N(z') \):

\[
N(z') \equiv \int_{z'}^\infty \rho(z)dz \approx N_{\text{band}} \cdot \left( 1 - \frac{\alpha(z')}{\alpha_0} \chi_0 - D_o + \frac{D_a}{\chi_0 - D_o} \right),
\]

with

\[
N_{\text{band}} \approx \alpha_0 / \mu.
\]

Thus, if \( z' \) is sufficiently to the left (such that \( \alpha(z') \ll a_m / (r/\lambda c) \), a regime with a significant overlap with the Chemotaxis Regime), the total population to the right of the position \( z' \) approaches a constant \( N_{\text{band}} \), which is interpreted as the population
size of the migratory band. Thus, from the expression for $\beta$, Eq. 19, and the result Eq. S74 and Eq. S75, we can rewrite Eq. S73 as

$$J(z_m) \approx -rN(z_m), \quad [S76]$$

where $N(z_m)$ is the population size of the wave-front integrated over the range $z_m < z < \infty$. Thus, Eq. S76 explicitly relates the “leakage” of cells out of the front at $z = z_m$ to the growth of cells in the front.

To connect the Growth Regime to the Chemotaxis Regime, we integrate the ODE describing the density $\rho(z)$ in the moving frame, i.e., Eq. S24 (with $\rho_c \to \infty$), from a position $z < z_m$ in the Growth Regime, to the position $z = z_m$ in the Chemotaxis Regime. This results in the exact relation

$$-c \cdot [\rho(z_m) - \rho(z)] = J(z_m) - J(z) + r \int_z^{z_m} \rho(z') dz' \quad [S77]$$

Thus, using Eq. 7,

$$\rho(z) = \beta a_m + \frac{\chi_0}{c} a(z) + a_m \frac{da(z)}{dz} + \frac{r}{c} \int_z^{z_m} \rho(z') dz' \quad [S78]$$

We note that as $a(z) \to 0$, $da(z)/dz \to 0$ as $z \to -\infty$. Now, as $a(+\infty) = a_0 > 0$ and $a(z) \geq 0$, for $a(z) \in C^2$, $da(z)/dz \geq 0$ for at least part of the domain $(-\infty, +\infty)$. Suppose $da(z)/dz \leq 0$ in the domain $(z_p, z_p + \epsilon)$. Then, by continuity as $a(z) \in C^2$

$$\implies \frac{da(z)}{dz} \bigg|_{z_p} = 0, \quad \frac{da(z)}{dz} \bigg|_{z_p - \epsilon} > 0, \quad \frac{da(z)}{dz} \bigg|_{z_p + \epsilon} \leq 0 \quad [S79]$$

$$\implies d^2a(z) \bigg|_{z_p} = 0 < 0. \quad [S80]$$

However, from Eq. S25, $\frac{da(z)}{dz} \bigg|_{z_p} > 0$ as $\mu \frac{a_0}{a(z)+a_m} \rho(z) > 0 \forall z$, which contradicts our supposition. Thus, $da(z)/dz > 0$ in the domain $(-\infty, +\infty)$ and $a(z)$ is always monotonically increasing (even in the Chemotaxis and Diffusion regimes). Since $\frac{da(z)}{dz} > 0$, we have that $\rho(z) > \beta a_m$ from Eq. S78. Further, since $\frac{da(z)}{dz} \big|_{z=z_m} > 0$, we know that $\rho(z_{\text{min}}) < \rho(z_m - \epsilon) < 2\beta a_m$ as $z_{\text{min}} < z_m$. We declare $z^* \in (z_{\text{min}}, z_m)$ such that $\rho(z^*) = 2\beta a_m$ and $\beta a_m < \rho(z) < 2\beta a_m$ for $z \in (z^*, z_m)$.

Now, for $a(z) \gg (r/\lambda)c a_m$, the ansatz holds, and thus Eq. S78 can be written as

$$\rho(z) > \beta a_m + \frac{\chi_0 \lambda}{c} \beta a(z) = \beta(a(z) + a_m) \quad [S81]$$

For $a(z) \ll a_m \implies a(z) \approx \frac{r}{\lambda \lambda_0} a_m$,

$$\frac{r}{c} \int_z^{z_m} \rho(z') dz' > \frac{r}{c} \beta a_m (z_m - z) \quad [S82]$$

As we will show below, $a(z) < a_m \exp(\lambda(z - z_{\text{min}}))$ for $z < z_m$

$$\implies \frac{r}{c} \int_z^{z_m} \rho(z') dz' > \beta \frac{r}{c} a_m \log(a_m/a(z)) > \beta a(z) \quad [S83]$$

And for the chemotactic drift, we have

$$\frac{\chi_0}{c} \frac{\rho(z)}{a(z) + a_m} \frac{da}{dz} > \frac{\chi_0}{c} \frac{\beta a_m}{a(z) + a_m} a(z) \lambda \approx \beta a(z) \quad [S84]$$

Thus, from Eq. S78,

$$\rho(z) > \beta a_m + \beta a(z) = \beta(a(z) + a_m) \quad [S85]$$

Thus, $\rho(z) > \beta(a(z) + a_m)$ for $z < z_m$. From Eq. S25 and this lower bound on $\rho(z)$,

$$\frac{da(z)}{dz} = -\frac{D_s}{c} \frac{d^2a(z)}{dz^2} + \frac{\mu}{c} \frac{\rho(z)}{a(z) + a_m} a(z) \quad [S86]$$

$$> -\frac{D_s}{c} \frac{d^2a(z)}{dz^2} + \frac{\mu \beta}{c} a(z) \quad [S87]$$

$$= -\frac{D_s}{c} \frac{d^2a(z)}{dz^2} + \frac{\chi_0 + D_s}{\chi_0} \lambda a(z) \quad [S88]$$

If $a(z)$ can locally be described as a slowly varying exponential such that $a(z) = \exp(\lambda_0(z))$, then for $(z_m - z_{\text{min}}) \ll 1/(\ln(\lambda_0(z)))$, we may take $a(z) = \exp(\lambda A z)$ where $\lambda_A = \lambda_0(z_{\text{min}})$,

$$\lambda_A a(z) > \lambda a(z) + \frac{D_s}{c} a(z)(\lambda^2 - \lambda_A) \quad [S89]$$

$$\implies \lambda_A - \lambda > \frac{D_s}{c} \frac{(\lambda^2 - \lambda_A)}{a(z)} \quad [S90]$$
This is only possible if $\lambda_A > \lambda$. Thus,
\[
a(z) = a_m \exp(\lambda_A(z - z_m)) < a_m \exp(\lambda(z - z_m)) \quad \text{for } z < z_m. \tag{S91}
\]

Further, for $z^* < z < z_m$, from Eq. S86
\[
\frac{da(z)}{dz} < \frac{\mu c(z_m)}{ca_m} a(z) < \frac{2\beta \mu}{c} a(z) = \frac{2(\chi_0 + D_a)\lambda}{\chi_0} a(z) \tag{S92}
\]
\[
\implies \lambda_A < \frac{2(\chi_0 + D_a)\lambda}{\chi_0} \tag{S93}
\]
This provides bounds on $\frac{da(z)}{dz}$:
\[
\lambda a(z) < \frac{da(z)}{dz} < \frac{2(\chi_0 + D_a)\lambda}{\chi_0} a(z) \tag{S94}
\]
This also gives us bounds on $v(z) = \frac{\chi_0 a(z)}{a(z) + a_m} \frac{da(z)}{dz}$:
\[
\frac{\chi_0 a(z)}{2a_m} < v(z) < \frac{2\chi_0(\chi_0 + D_a)\lambda a(z)}{(\chi_0)} a_m \tag{S95}
\]
\[
\implies v(z) < \frac{2\chi_0(\chi_0 + D_a)\lambda}{\chi_0} \exp(\lambda(z - z_{\text{min}})) \tag{S96}
\]
From Eq. S24, $\frac{da(z)}{dz} = 0$ if
\[
r \rho(z) = \frac{d(v(z)\rho(z))}{dz} = \frac{dv(z)}{dz} \rho(z) \tag{S97}
\]
\[
\implies r = \frac{dv(z)}{dz} = \frac{\chi_0}{a(z) + a_m} \left( \frac{d^2 a(z)}{dz^2} - \frac{(da/dz)^2}{a(z) + a_m} \right) \tag{S98}
\]
\[
= \frac{\chi_0}{a(z) + a_m} \lambda_A^2 \left( a(z) - \frac{a(z)^2}{a(z) + a_m} \right) \tag{S99}
\]
From Eq. 11, we know that for growth to be comparable to the chemotactic drift, $a(z) \ll a_m$, and thus
\[
r \approx \frac{\chi_0}{a_m} \lambda_A a(z_{\text{min}}) \implies a(z_{\text{min}}) \approx \frac{r a_m}{\chi_0 \lambda_A} \tag{S100}
\]
From the bounds on $\lambda_A$ from Eq. S93 and Eq. S91,
\[
\implies \frac{r}{\lambda c} > \frac{a(z_{\text{min}})}{a_m} > \frac{r}{\lambda c} \frac{\lambda_A^2}{4(\chi_0 + D_a)^2} \tag{S101}
\]
Numerically, we find that $a(z_{\text{min}}) \approx r a_m/\lambda c$ (see Fig. 5B), which means that $\lambda_A^2 \approx \lambda c/\chi_0 \approx \lambda^2$ where the final equality holds if $D_f \to 0$. Thus, we find that $\lambda_A \lesssim \lambda = \lambda_a(z_m)$ and $\lambda_a(z_{\text{min}}) \approx \lambda_a(z_m)$, numerically verifying our assumption above that $\lambda_A \approx \lambda_a(z)$ for $z^* < z < z_{\text{min}}$.

Now, at $\hat{z}$ such that $\rho(\hat{z}) = 2\epsilon \beta a_m$, assuming that $\rho(z) \propto \exp(-\lambda_G z)$ for $z^* > z > \hat{z}$:
\[
J(\hat{z}) = -v(\hat{z})\rho(\hat{z}) \tag{S102}
\]
\[
= -\frac{\chi_0}{\lambda_A} \exp\left(-\frac{\lambda_A}{\lambda_G} + \lambda_A(\hat{z} - z_{\text{min}})\right) \rho(\hat{z}) \tag{S103}
\]
\[
< \frac{\chi_0}{\lambda_A} \exp\left(-\frac{\lambda_A}{\lambda_G}\right) 2\epsilon \beta a_m \tag{S104}
\]
As we will show below, $\lambda_A \gg \lambda_G \implies \exp(\lambda_A/\lambda_G) \gg \lambda_A/\lambda_G$, and thus the final term is much smaller than the net growth in time $(z_m - \hat{z})/c$:
\[
- J(\hat{z}) \ll \frac{\chi_0}{\lambda_G} 2(e - 1) \beta a_m < r \int_{\hat{z}}^{z_m} \rho(z')dz' \tag{S105}
\]
Thus, using Eq. S73 and $\rho(z_m) = 2\beta a_m$ (since the ansatz Eq. 7 is valid at $z = z_m$), we can rewrite Eq. S78 for $z < \hat{z}$ as
\[
c \rho(z) \approx c \rho + r \int_{\hat{z}}^{z} \rho(z')dz' \tag{S106}
\]
\[
\rho = \beta a_m + \frac{r}{c} \int_{\hat{z}}^{z_m} \rho(z')dz' \tag{S107}
\]
for \( z \leq \hat{z} \), with the only approximation coming from the condition Eq. S105.

Solving Eq. S106 yields

\[
\rho(z \leq \hat{z}) = \hat{\rho} \exp[\lambda_G (\hat{z} - z)], \tag{S108}
\]

with

\[
\lambda_G = -r / c. \tag{S109}
\]

We note that if \( D_\rho > 0 \), we would have another solution such that \( \lambda_G \approx -c / D_\rho \). However, this solution would be rejected as it corresponds to a solution dominated by diffusion and is an unstable solution at the front of the wave (since growth is greater than or comparable to chemotactic drift, there is no term to balance diffusion in the diffusion-dominated solution and thus lead to the transition to the Chemotaxis regime. Thus, diffusion can only dominate when the right BCs are asymptotic, i.e., \( \rho(z) \to 0 \) as in the Diffusion regime) (47). Thus, as cited earlier, we can see that \( \lambda_A / \lambda_G = \lambda c / r \gg 1 \) in our parameter regime.

To determine the width of the transition zone between the exponentially decreasing and exponentially increasing profiles of \( \rho(z) \) in the Growth and Chemotaxis Regimes respectively, we note that for \( \hat{z} < z < z_m \), \( \beta a_m < \rho(z) < 2e\beta a_m \). Thus, Eq. S107 can be written as

\[
2e\beta a_m = \beta a_m + \frac{r}{c}(z_m - \hat{z})\alpha \beta a_m
\]

where \( 2e > \alpha > 1 \). Thus,

\[
(z_m - \hat{z}) = \frac{c(2e - 1)}{r \alpha} \Rightarrow \frac{(2e - 1)}{2e\lambda_G} < (z_m - \hat{z}) < \frac{(2e - 1)}{\lambda_G}. \tag{S111}
\]

S8. Relation to Chemotactic Pattern Formation and Interfacial Instabilities

Soon after the introduction of the KS model, other models that considered the growth of the bacteria were proposed. Most such models coupled the growth rate and the concentration of the attractant (62–67). Other models require production of attractant by the bacteria. There has been very extensive mathematical literature (38, 72, 82–86) (for a comprehensive review, refer to (87)) focusing on the chemotactic models with attractant production due to crucial experiments that demonstrated that in motile bacterial cells aggregate in response to gradients of attractant which they excrete themselves, and form complex spatial patterns (56). Much work has also been done on traveling-wave solutions and their connection the F-KPP equation (88–92). However, this work has been primarily motivated by the formation of complex patterns, rather than on the relatively simple migratory bands discussed in this paper. Further, the work has been mostly mathematical in nature, focusing on existence and uniqueness proofs, and fail to provide scaling results or concise approximations with phenomenological parameters that can be utilized by experimentalists.

In light of recent experimental evidence for physiological roles of chemotaxis such as range expansion, we hope that tools developed for complex chemotactic pattern formation may be adapted to understanding the relatively simple migratory bands, and build on our simplified model. The minimal nature of our simplified model allows for further analysis upon perturbation of the system to other well-studied systems such as the F-KPP equation, we hope that the understanding of the other systems can be drawn to our system, and that physical, biological and experimental insights related to our system can be utilized for the other systems. We hope that the confluence of the these three systems, which have historically been pursued by different scholastic communities, spur insightful exchange.

Further, we note that because of the similarities between the Diffusion Regime and the pushed wave solutions to the F-KPP equation, fluctuations at the interface of the propagating wave, i.e., the asymptotic limit, will be suppressed (93). This means that the expansion due to chemotaxis will always be highly regular, thus explaining the clean rings observed in experiments (30, 40).

S9. Density Peak

To approximate the maximal bacterial density at the front of the wave, we note that at \( z_{\text{max}} \) (the location of the peak), the integral of Eq. 4 from \( z_{\text{max}} \) to \( \infty \) gives us

\[
\int_{z_{\text{max}}}^{\infty} \rho(z) dz = -D_\rho \frac{d\rho(z)}{dz} \bigg|_{z_{\text{max}}} + v(z_{\text{max}})\rho(z_{\text{max}}) + r \int_{z_{\text{max}}}^{\infty} \rho(z) \frac{a(z)}{a(z) + a_m} dz \tag{S112}
\]

We assume that the total population right of the peak is smaller than the total population between the density dip and the peak

\[
N_1 < \int_{z_{\text{min}}}^{z_{\text{max}}} \rho(z) dz \approx \frac{\rho_{\text{max}}}{\lambda} \ll \frac{c\rho_{\text{max}}}{r}, \tag{S113}
\]

for the parameter regime assumed in this manuscript (i.e., \( \lambda c \gg r \)). Thus, the final term in Eq. S112 can be ignored. Since \( \frac{d\rho}{dz}(z_{\text{max}}) = 0 \), we have that

\[
v(z_{\text{max}}) = c. \tag{S114}
\]
Further, since \( v \equiv \chi_0 \partial_z a(z)/a(z) \), and \( v(z_{\text{max}}) c = (\chi_0 - D_\rho) \lambda \), we have that
\[
\left. \frac{da(z)}{dz} \right|_{z_{\text{max}}} = \frac{c}{\chi_0} a(z_{\text{max}}) \tag{S115}
\]
By integrating Eq. 5 from \( z_{\text{max}} \) to \( \infty \), we have that:
\[
c(a_0 - a(z_{\text{max}})) = \frac{c D_\rho}{\chi_0} a(z_{\text{max}}) + \mu N_1 \tag{S116}
\]
\[
\implies c a_0 = c a(z_{\text{max}}) \left( 1 + \frac{D_\rho}{\chi_0} \right) + \mu N_1 \tag{S117}
\]
We note from Eq. 50 that
\[
a a_0 = \mu N_0 = \mu N_1 + \int_{z_{\text{min}}}^{z_{\text{max}}} \rho(z) dz > 2 \mu N_1, \tag{S118}
\]
where the last inequality comes from our previous assumption that \( N_1 < \int_{z_{\text{min}}}^{z_{\text{max}}} \rho(z) dz \). As a result,
\[
2ca(z_{\text{max}}) \left( 1 + \frac{D_\rho}{\chi_0} \right) = 2ca_0 + 2\mu N_1 = 2ca_0 \tag{S119}
\]
\[
\implies 2ca(z_{\text{max}}) \left( 1 + \frac{D_\rho}{\chi_0} \right) = ca_0 + ca_0 - 2\mu N_1 > ca_0 \tag{S120}
\]
\[
\implies 2ca(z_{\text{max}}) \left( 1 + \frac{D_\rho}{\chi_0} \right) > ca_0 > ca(z_{\text{max}}) \left( 1 + \frac{D_\rho}{\chi_0} \right) \tag{S121}
\]
Alternatively,
\[
a_0 \left( \frac{\chi_0}{\chi_0 + D_\rho} \right) > a(z_{\text{max}}) \geq \frac{a_0}{2} \left( \frac{\chi_0}{\chi_0 + D_\rho} \right) \tag{S122}
\]
This result was numerically verified for a broad range of parameters and is shown in Supplementary Figure S4.

For \( \chi_0 \gg D_\rho \), \( \partial_z \log a(z) \approx \lambda \) for the entire range from \( z_{\text{min}} \) to \( z_{\text{max}} \). Thus
\[
\log a(z_{\text{max}}) - \log a(z_{\text{min}}) \approx \lambda (z_{\text{max}} - z_{\text{m}}). \tag{S123}
\]
This result was also verified numerically and is shown in Supplementary Figure S4.

If our \( \text{ansatz} \), Eq. 7 holds for the density peak (as would be expected by assuming that \( \partial_z \log a(z) \approx \lambda \) for the entire range from \( z_{\text{min}} \) to \( z_{\text{max}} \), we can approximate that
\[
\rho_{\text{max}} \approx \beta (a(z_{\text{max}}) + a_m) \tag{S124}
\]
\[
\implies \frac{\rho_{\text{max}} - \rho_{\text{min}}}{\rho_{\text{min}}} \approx \frac{a(z_{\text{max}})}{a_m} \tag{S125}
\]
\[
\implies \frac{a_0}{a_m} \left( \frac{\chi_0}{\chi_0 + D_\rho} \right) \geq \frac{\rho_{\text{max}} - \rho_{\text{min}}}{\rho_{\text{min}}} \geq \frac{a_0}{2a_m} \left( \frac{\chi_0}{\chi_0 + D_\rho} \right) \tag{S126}
\]
In the regime \( \chi_0 \gg D_\rho \), we can use our main results (Eq. 21 and Eq. 22) to obtain that
\[
\frac{\lambda c}{r} \geq \frac{\rho_{\text{max}} - \rho_{\text{min}}}{\rho_{\text{min}}} \geq \frac{\lambda c}{2r} \tag{S127}
\]
For \( \frac{\lambda c}{r} \gg 1 \),
\[
\frac{\rho_{\text{max}}}{\rho_{\text{min}}} \sim \frac{\lambda c}{r}. \tag{S128}
\]
This scaling relation was also verified numerically and is shown in Supplementary Figure S4.

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