Traveling pulses in bacterial populations

The journey of *Escherichia coli*

Vincent Calvez
CNRS, ENS Lyon, France

Workshop "Deterministic and stochastic front propagation"

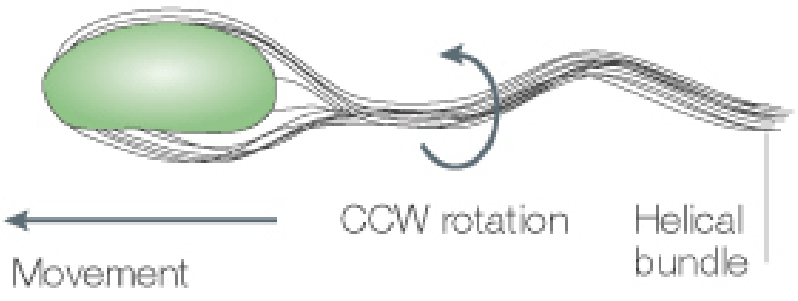
BIRS, March 2010

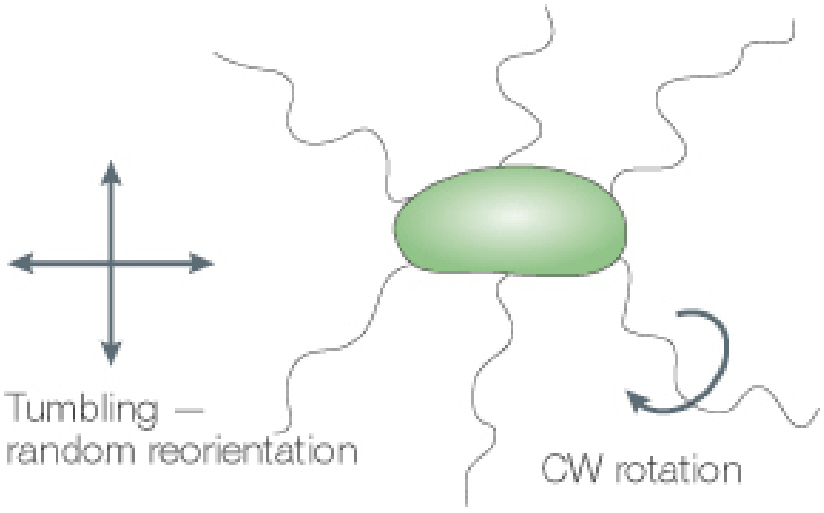
Joint work with **Nikolaos Bournaveas** (*Univ. Edinburgh*), **Benoît Perthame** (*Univ. Paris 6*) and **Axel Buguin**, **Jonathan Saragosti**, **Pascal Silberzan** (*Institut Curie, Paris*).

Contents

Contents

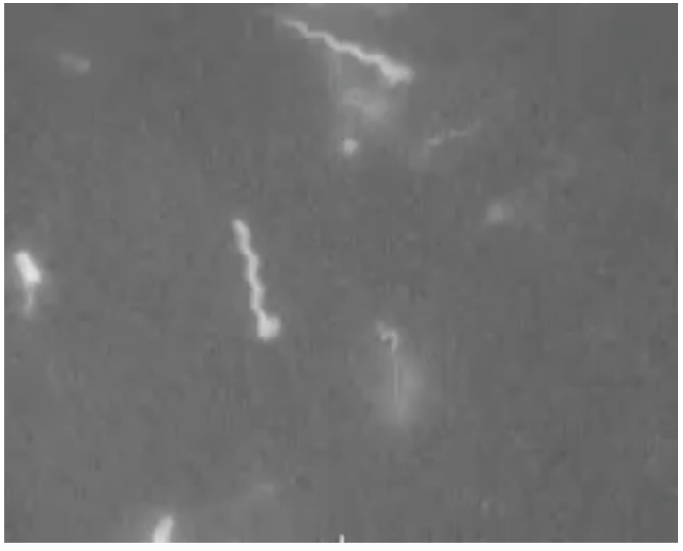
Description of *E. coli* movements





Alternatively:

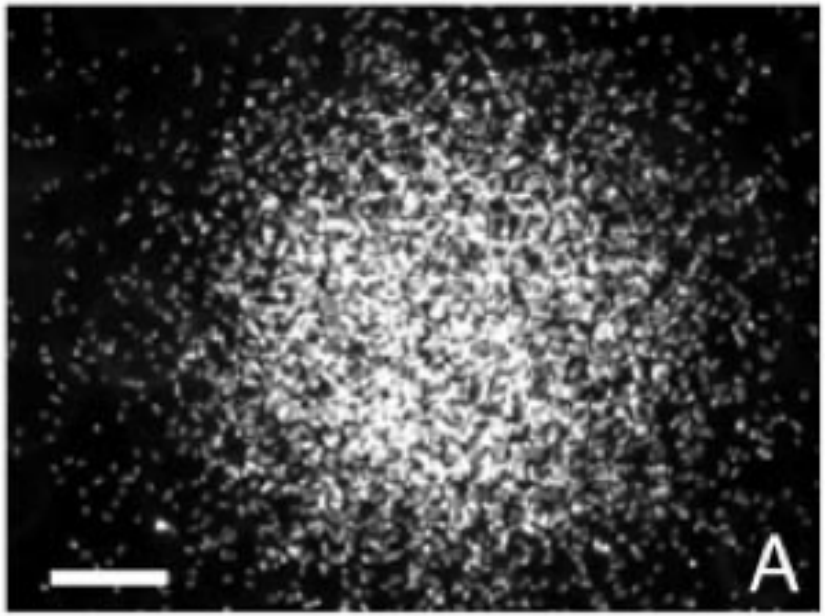
- Straight swimming trajectories ($\sim$ 1sec.): *run*
- Reorientation events ($\sim$ 0.1sec.): *tumble*



Howard Berg's lab

Chemical signaling

- Bacteria can sense multiple chemical substances along their trajectories.
  Chemoattractants: amino-acids (*e.g.* aspartate), glucose...
- Bacteria are able to produce themselves some of these chemicals.
  Positive feedback: accumulation of bacteria in opposition to the natural dispersion.



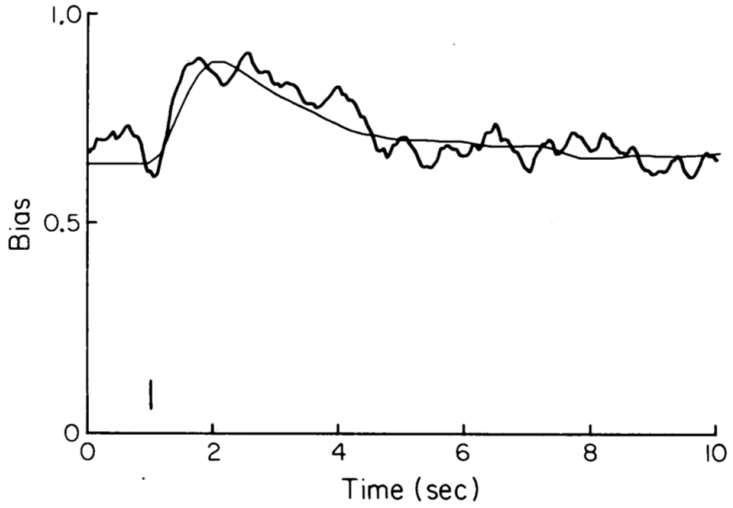
N. Mittal, E.O. Budrene, M.P. Brenner, A. van Oudenaarden, PNAS

Response to the chemical signal

E. coli reacts to the time variations of the signal: tumbling events decrease when the signal concentration increases.

Complex signal integration inside each individual:

- Memory effects
- High sensibility to signal changes (excitation)
- Adaptation



J.E. Segall, S.M. Block, H.C. Berg, PNAS

Contents

Kinetic modeling

- Bacterial density $f(t,x,v)$ is described in the space $(0,T)\times\mathbb{R}^2\times V$ (time×position×velocity).
- Velocity space V is bounded (speed of bacteria is almost constant $\approx 20\mu ms^{-1}$).

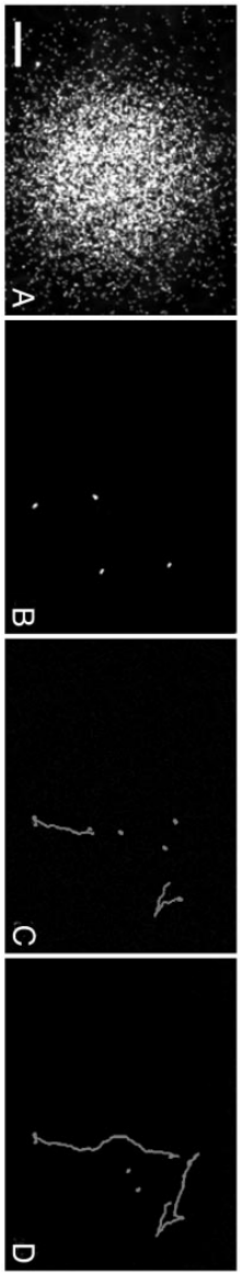
The Othmer-Dunbar-Alt model ('80) :

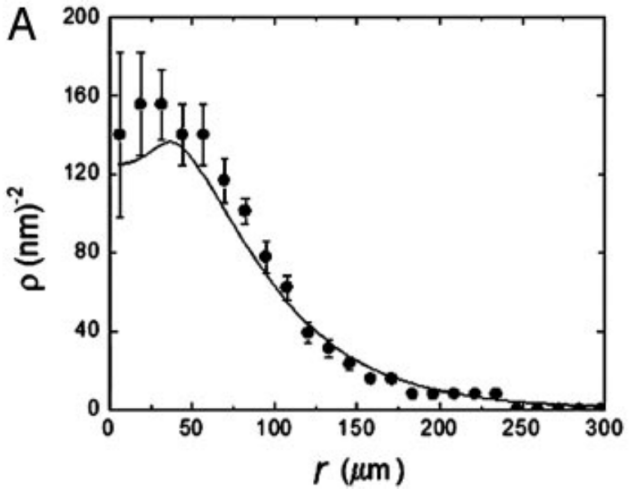
$$\underbrace{\partial_t f + v\cdot\nabla_x f}_{run} = \underbrace{\int_{v'\in V}\mathbf{T}[S]f(t,x,v')\,dv' - \int_{v'\in V}\mathbf{T}^*[S]f(t,x,v)\,dv'}_{tumble}$$

- The tumbling kernel $\mathbf{T}[S](v,v')$ denotes the frequency of reorientation $v'\to v$.
- The chemical signal is secreted by the bacteria, following a reaction-diffusion equation:

$$\partial_t S = D_S\Delta S - \alpha S + \beta\rho\,,\quad \rho(t,x) = \int_{v\in V} f(t,x,v)\,dv$$

What about the tumbling frequency?





- First approach, not including memory effects (Dolak and Schmeiser):

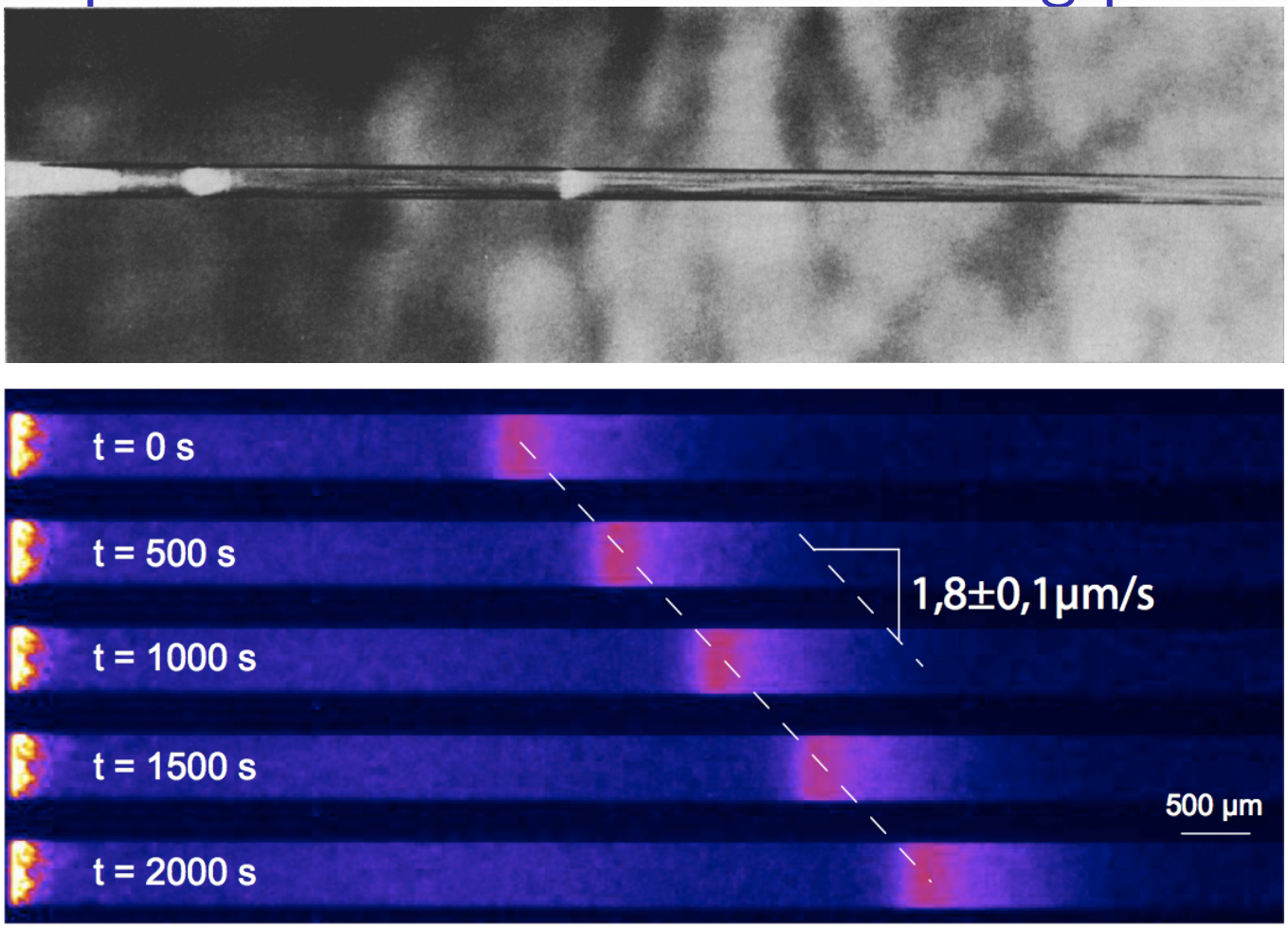
$$\mathbf{T}[S](v, v') = \psi\left(\left.\frac{DS}{Dt}\right|_{v'}\right) = \psi\left(\partial_t S + v' \cdot \nabla_x S\right)$$

- Phenomenological approach by Segall *et al.*: memory effect = time convolution along the past trajectory:

$$\mathbf{T}[S](v, v') = \psi\left(\int_{0\text{sec.}}^{4\text{sec.}} K(s) S(t - s, x - sv')\, ds\right)$$

Contents

Experimental evidence for traveling pulses



- Bacteria initially lie on the left side of a channel,
- They secrete a chemoattractant (presumably glycine),
- A fraction travels to the right with constant speed and constant profile (asymmetric).

One possible scenario

- Bacteria gather due to secretion of a chemottractant (as for cluster formation),
- They consume another chemical (the *nutrient* N). This triggers the motion of a pulse.

Kinetic description:

$$\partial_t f + v \cdot \nabla_x f = \mathbf{Q}[S, N] f$$

And reaction-diffusion equations:

$$\partial_t S = D_S \Delta S - \alpha S + \beta \rho$$
$$\partial_t N = D_N \Delta N - \gamma \rho N \, .$$

Derivation of a simpler model

Analysis of the previous system is not that simple. In adimensional form it writes:

$$\varepsilon \partial_t f + v \cdot \nabla_x f = \frac{1}{\varepsilon} \mathbf{Q}[S, N] f$$

Taking the limit when $\varepsilon \longrightarrow 0$ leads to a parabolic equation for the density $\rho(t, x)$:

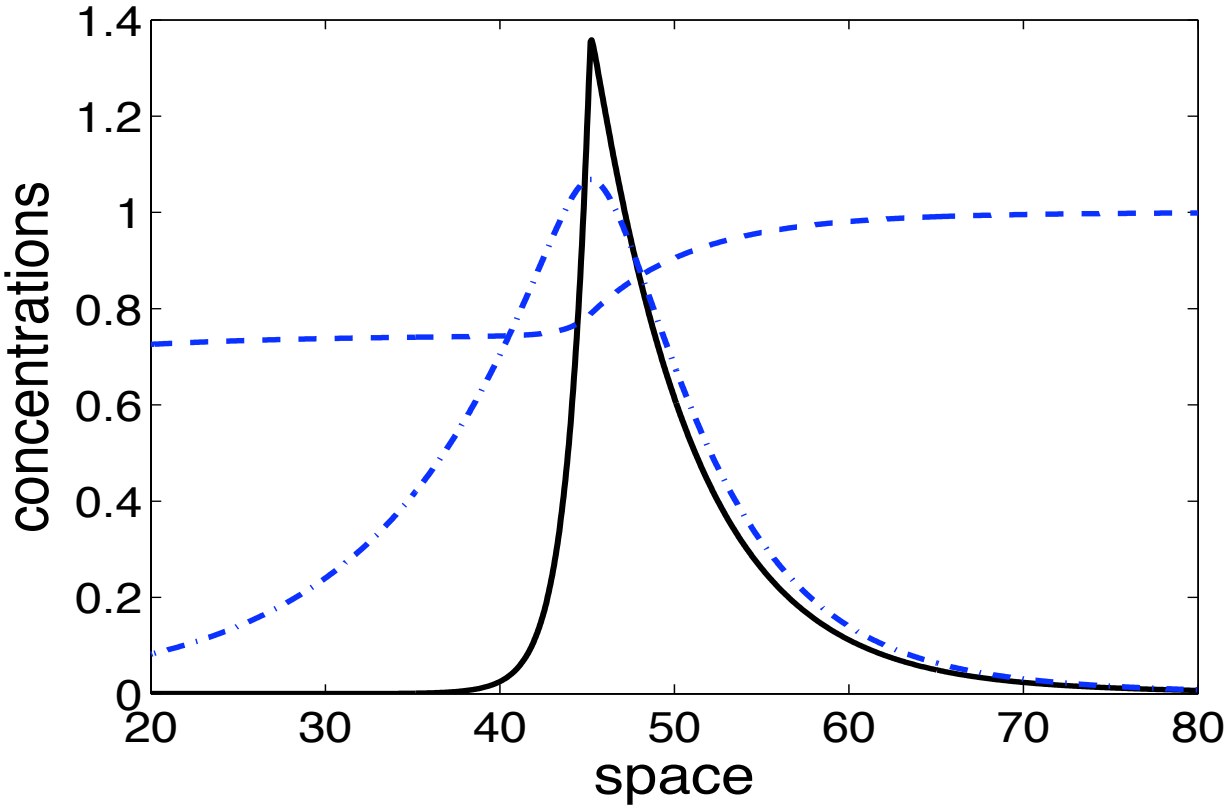
$$\partial_t \rho - \underbrace{D_\rho \Delta \rho}_{\textit{diffusion}} + \underbrace{\nabla \cdot (\rho u_S + \rho u_N)}_{\textit{chemotactic flux}} = 0$$

$$u_S = - \int_{v \in V} v \psi \left(v \cdot \nabla S \right) \frac{dv}{|V|}$$

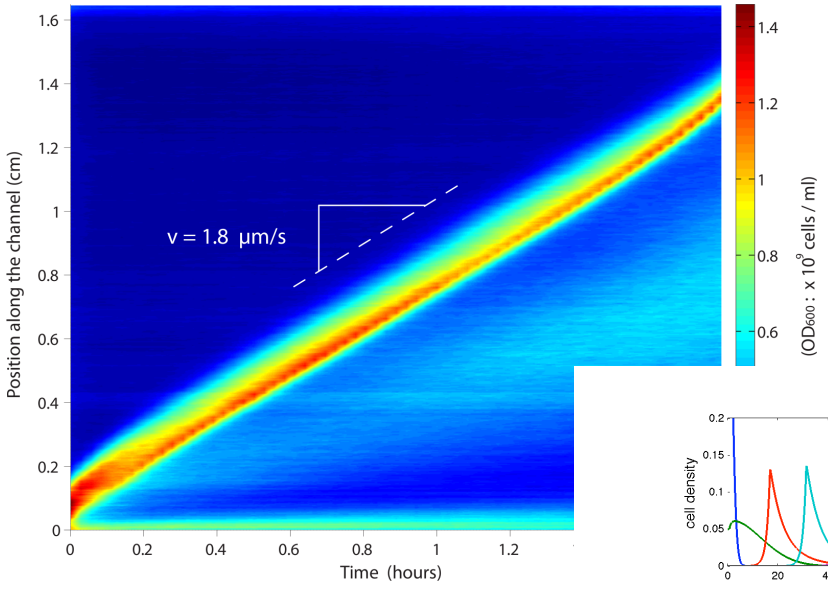
In the case of a stiff response function $\psi = \mathrm{Heaviside}$:

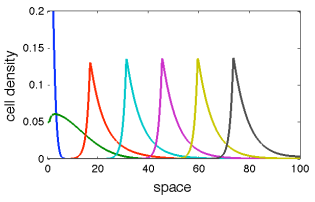
$$u_S = \chi s \frac{\nabla S}{|\nabla S|}$$

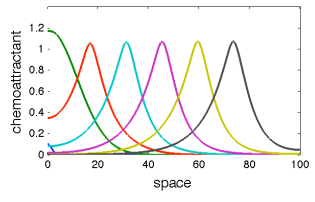
Numerical evidence for traveling pulses

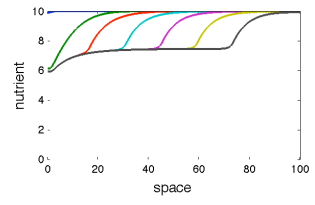


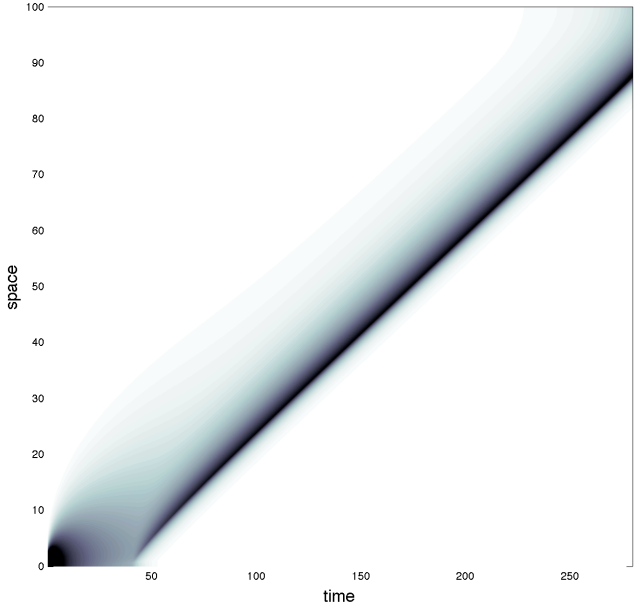
Numerical evidence, ctd.



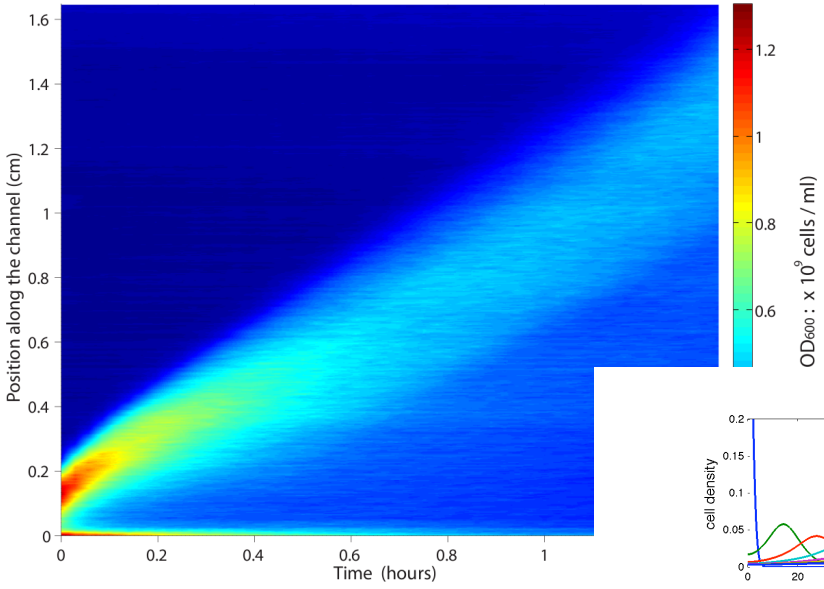


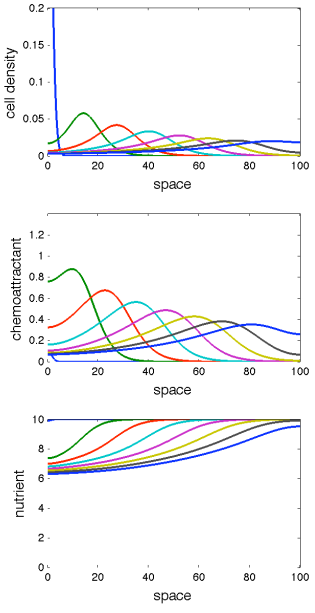


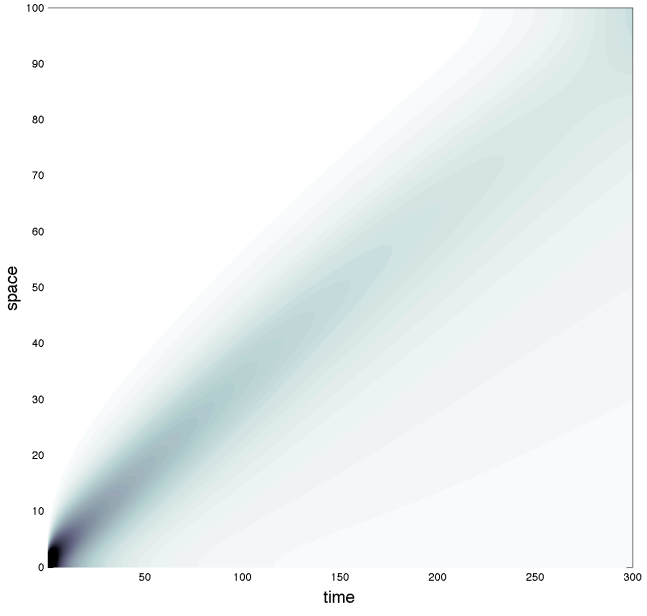




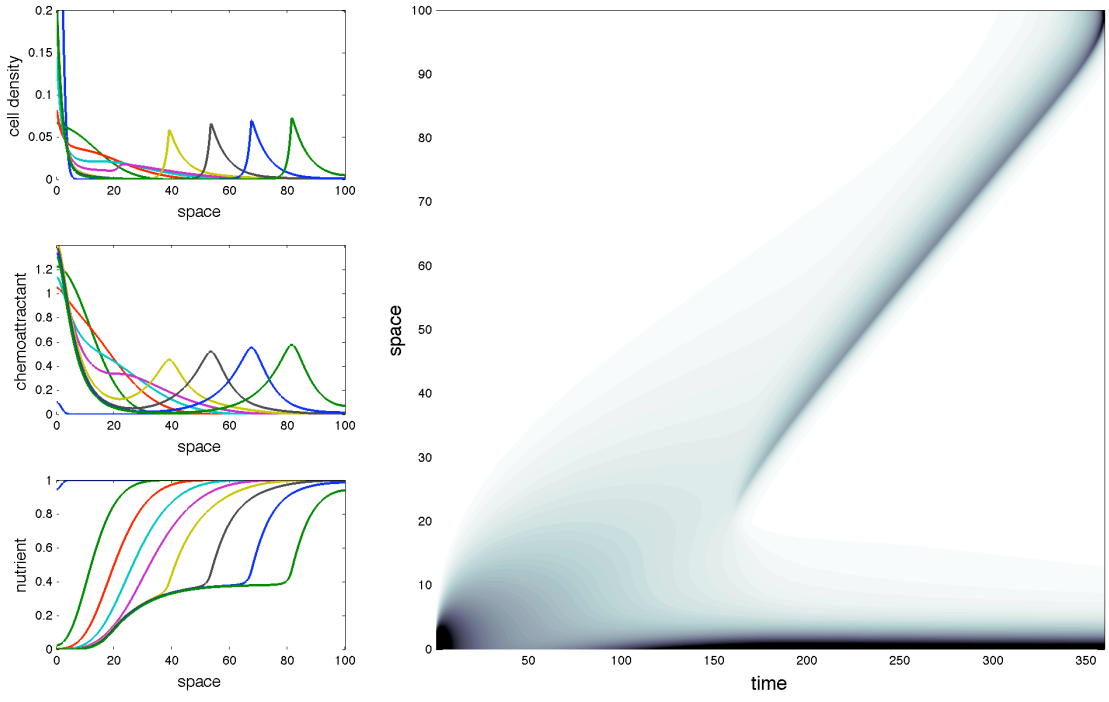
Numerical evidence, ctd.







Numerical evidence, ctd.



Limited nutrient: coexistence of a stationary state and a traveling pulse

Some quantitative features

In the case of a stiff response function $\psi = \mathrm{Heaviside}$, we obtain a formula for the speed of the pulse:

$$\chi_N - \sigma = \chi_S \frac{\sigma}{\sqrt{4 D_S \alpha + \sigma^2}} .$$

The profile is a combination of two exponential tails.

$$\rho(z) = \begin{cases} \rho_0 \exp\left(\lambda^- z\right) , & z < 0 \\ \rho_0 \exp\left(\lambda^+ z\right) , & z > 0 \end{cases}$$

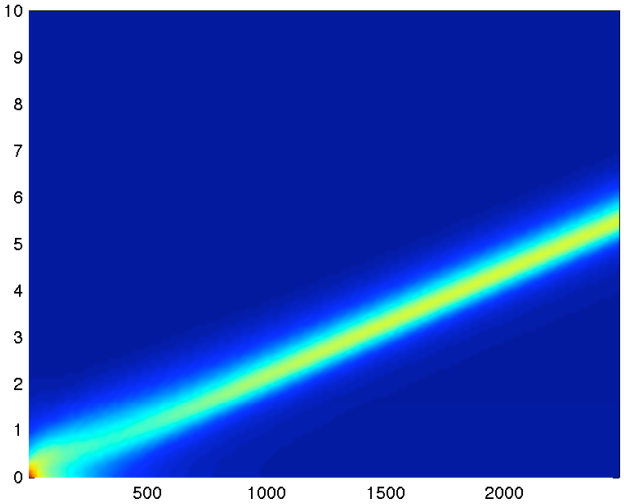
Asymmetry of the profile is given by:

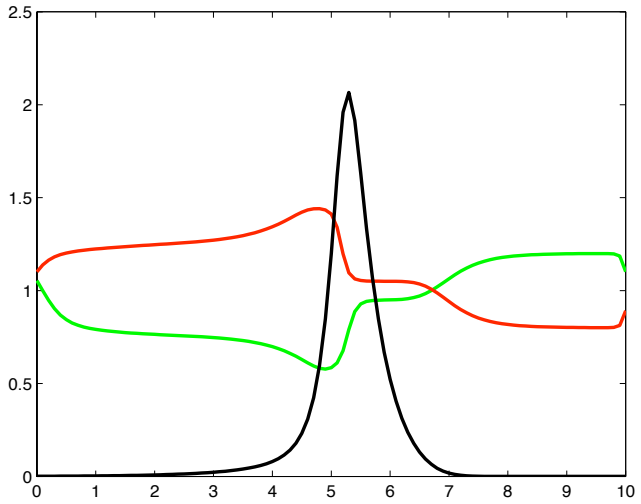
$$\frac{\lambda^-}{|\lambda^+|} = \frac{\sqrt{4 D_S \alpha + \sigma^2} + \sigma}{\sqrt{4 D_S \alpha + \sigma^2} - \sigma} .$$

Therefore it is strongly asymmetric when $\sigma \gg 2\sqrt{D_S \alpha}$ (speed of chemical diffusion).

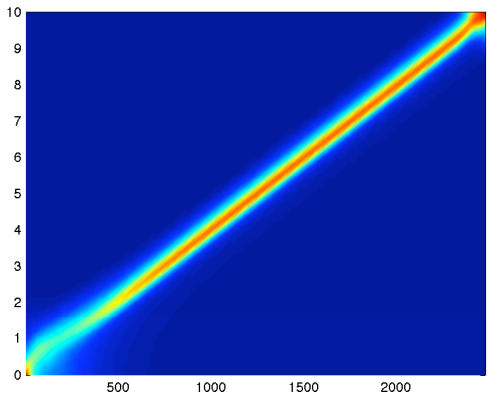
Traveling kinetic pulses

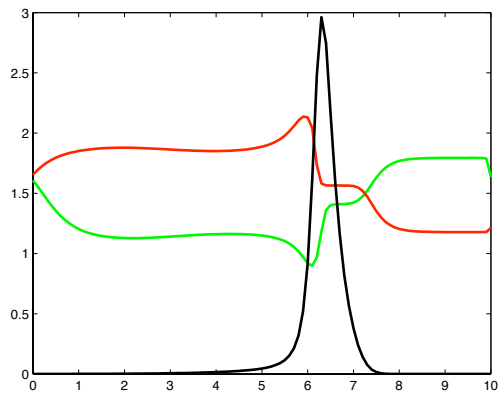
In fact... The diffusion scaling is not valid in some experimental setting. Traveling waves are likely to exist at the kinetic level too.





Future: test micro effects such as angular diffusion during tumbling.





Conclusions

- There is a hierarchy of mathematical models for collective cell motion (micro-, meso-, macroscopic).
- The appropriate choice relies on a compromise between accuracy of description and simplicity of formulation.
- The ODA kinetic model is suitable for bacterial motion. It is possible to derive simplified model (of parabolic types) which are better adapted than the usual ones.
- Existence of stable traveling pulses is linked to the stationary chemotaxis problem (without nutrient).

Thank you for your attention!