



# Interactions of Solitary Modes in Models of Bacterial Chemotaxis

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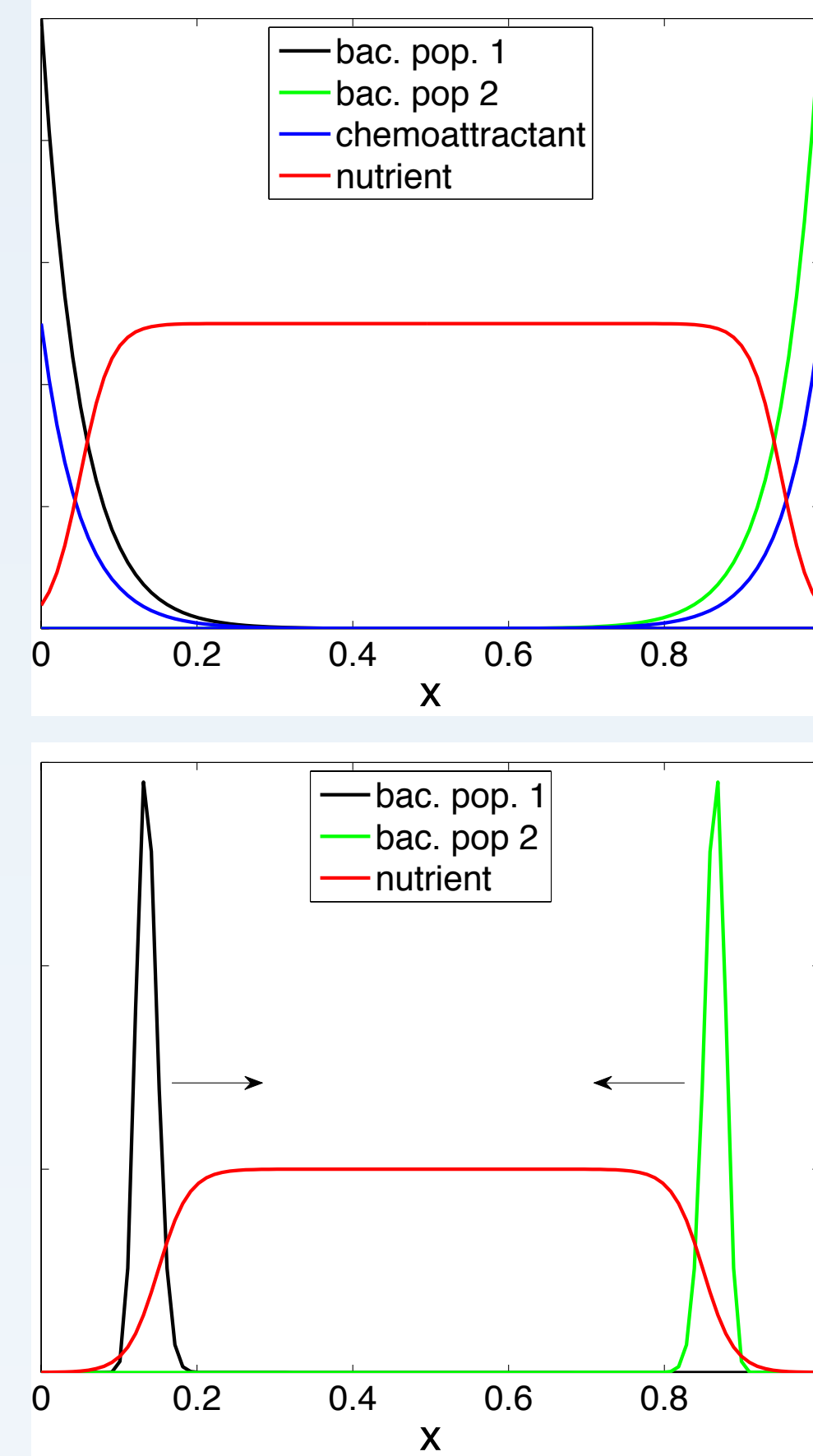
## Experimental Overview

*E. coli* is an example of a bacterial species that moves by chemical sensing, or chemotaxis.

The bacteria produce an attractant to which they are attracted.

The Salman lab ran the following experiment:

- Two identical populations of *E. coli* were placed on opposite ends of a long plate containing a densely and uniformly distributed nutrient.
- Both populations consume the nutrient while moving as a traveling pulses toward the center of the plate
- Upon collision, three different outcomes are observed:
  - The bacteria collide, combine, and diffuse out.
  - The bacteria collide, combine, and move left or right as a single population.
  - The bacteria never collide, but instead move back toward their initial side before collision takes place.



**Question:** Given that the experimental setup is nearly identical in each trial, what causes the different outcomes?

## Model

We use an adaptation of the classic Keller-Segel model for bacterial chemotaxis with the following assumptions:

- All quantities are suspended in a liquid medium and therefore diffuse.
- The chemotactic sensitivity decreases as a function of the available chemoattractant and nutrient.
- Any growth in the bacterial population is negligible.
- No flux on the boundaries.

With these assumptions, we derive the following model:

$$\begin{aligned} \frac{\partial b_1}{\partial t} &= D_b \frac{\partial^2 b_1}{\partial x^2} - \chi_a \frac{\partial}{\partial x} \left[ \frac{b_1}{(1+\alpha a)^2} \frac{\partial a}{\partial x} \right] - \chi_c \frac{\partial}{\partial x} \left[ \frac{b_1}{(1+\gamma c)^2} \frac{\partial c}{\partial x} \right] \\ \frac{\partial b_2}{\partial t} &= D_b \frac{\partial^2 b_2}{\partial x^2} - \chi_a \frac{\partial}{\partial x} \left[ \frac{b_2}{(1+\alpha a)^2} \frac{\partial a}{\partial x} \right] - \chi_c \frac{\partial}{\partial x} \left[ \frac{b_2}{(1+\gamma c)^2} \frac{\partial c}{\partial x} \right] \\ \frac{\partial a}{\partial t} &= D_a \frac{\partial^2 a}{\partial x^2} + r(b_1 + b_2) - \mu a \\ \frac{\partial c}{\partial t} &= D_c \frac{\partial^2 c}{\partial x^2} - \beta(b_1 + b_2)c \end{aligned}$$

$b_i$  - bacterial population  $i$   
 $a$  - attractant  
 $c$  - nutrient ("chow")

$$\left. \frac{\partial b_{1,2}}{\partial x} \right|_{x=0,1} = \left. \frac{\partial a}{\partial x} \right|_{x=0,1} = \left. \frac{\partial c}{\partial x} \right|_{x=0,1} = 0$$

$$b_{1,2}(x, 0) = f_{1,2}(x), \quad a(x, 0) = g(x), \quad c(x, 0) = h(x)$$

## Existence of Bump Solution

We first determine conditions on the total bacterial population size such that a bump solution exists.

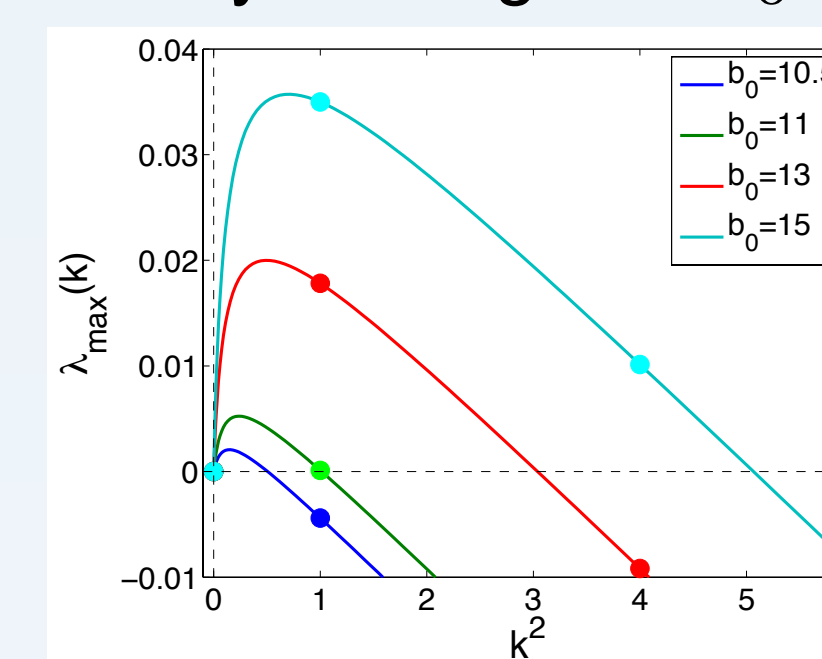
Consider the reduced, one bacterial population system in the absence of the nutrient:

$$\begin{aligned} 0 &= D_b \frac{\partial^2 b}{\partial x^2} - \chi_a \frac{\partial}{\partial x} \left[ \frac{b}{(1+\alpha a)^2} \frac{\partial a}{\partial x} \right] \\ 0 &= D_a \frac{\partial^2 a}{\partial x^2} + r b - \mu a \end{aligned} \quad (1)$$

The system admits constant solution  $b = b_0$ ,  $a_0 = \frac{r}{\mu} b_0$  for any nonnegative  $b_0$ .

This uniform state is unstable if either eigenvalue of the Jacobian  $J$  is positive for any  $k$ .

$$J = \begin{pmatrix} -(k\pi)^2 D_b & \frac{(k\pi)^2 \chi_a b_0}{(1+\alpha a_0)^2} \\ r & -(k\pi)^2 D_a - \mu \end{pmatrix}$$

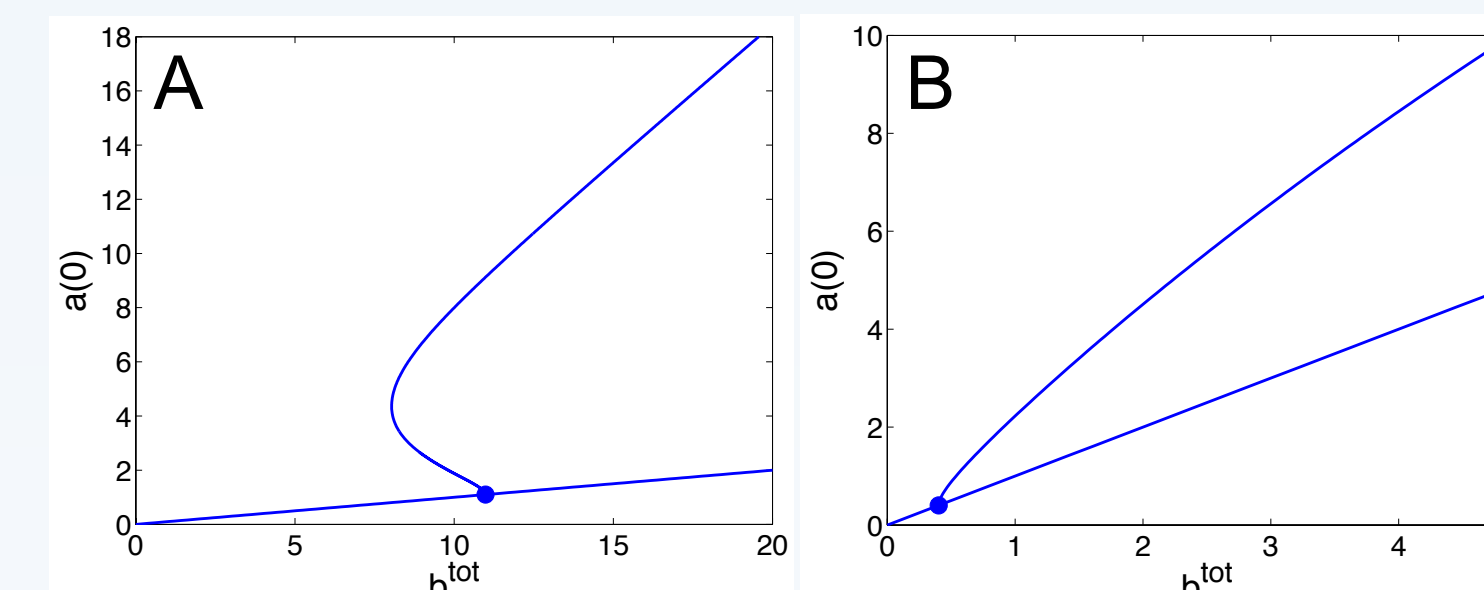


If the uniform state is unstable, we expect a bump solution to exist; that is, non-constant solutions of system (1) with no-flux boundary conditions.

We find the bump solutions by numerically solving a boundary value problem, then continuing the solution in the parameter  $b^{tot}$ , the total amount of bacteria.

The continuation reveals a critical  $b^{tot}$ , at which bump solutions bifurcate from the uniform state:

- Subcritical bifurcation:** local bistability between uniform state and bump solution is expected
- Supercritical bifurcation:** no bistability



## Normal Form Analysis

We analytically classify the criticality of the bifurcation through normal form analysis.

To introduce our bifurcation parameter explicitly into the system, we make the

change of variables  $B = b/b^{tot}$ , where  $b^{tot} = \int_0^1 b(x) dx$ :

$$\begin{aligned} 0 &= D_b \frac{\partial^2 B}{\partial x^2} - \chi_a \frac{\partial}{\partial x} \left[ \frac{B}{(1+\alpha a)^2} \frac{\partial a}{\partial x} \right] \\ 0 &= D_a \frac{\partial^2 a}{\partial x^2} + r b^{tot} B - \mu a \end{aligned}$$

We perturb off of the critical uniform solution and collect same-order terms to get

$$\begin{aligned} \mathcal{O}(\epsilon) \quad \mathcal{L}(B_1, a_1) &= \begin{pmatrix} 0 \\ -r b_1^{tot} \end{pmatrix} & B &= 1 + B_1 \epsilon + B_2 \epsilon^2 + B_3 \epsilon^3 + \mathcal{O}(\epsilon^4) \\ & & a &= a_0 + a_1 \epsilon + a_2 \epsilon^2 + a_3 \epsilon^3 + \mathcal{O}(\epsilon^4) \\ \mathcal{O}(\epsilon^2) \quad \mathcal{L}(B_2, a_2) &= \begin{pmatrix} \chi_a \frac{\partial}{\partial x} \left[ \frac{-2\alpha a_1}{(1+\alpha a_0)^3} + \frac{B_1}{(1+\alpha a_0)^2} \right] \frac{\partial a_1}{\partial x} \\ -r b_2^{tot} \end{pmatrix} & b^{tot} &= b_0^{tot} + b_1^{tot} \epsilon + b_2^{tot} \epsilon^2 + b_3^{tot} \epsilon^3 + \mathcal{O}(\epsilon^4) \end{aligned}$$

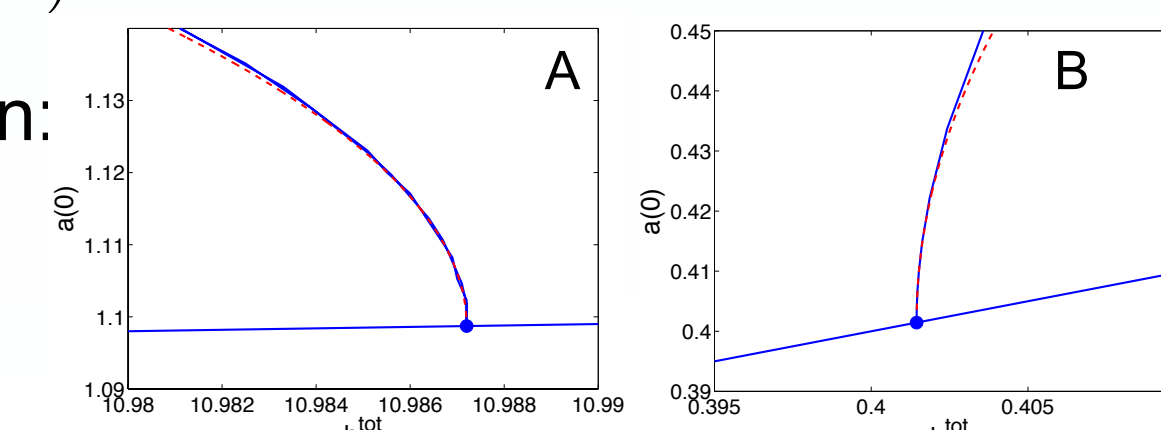
$$\mathcal{O}(\epsilon^3) \quad \mathcal{L}(B_3, a_3) = \begin{pmatrix} \chi_a \frac{\partial}{\partial x} \left[ \frac{-2\alpha a_1}{(1+\alpha a_0)^3} + \frac{B_1}{(1+\alpha a_0)^2} \right] \frac{\partial a_2}{\partial x} + \left( \frac{-2\alpha(a_2 + a_1 B_1)}{(1+\alpha a_0)^3} + \frac{3\alpha^2 a_1^2}{(1+\alpha a_0)^4} + \frac{B_2}{(1+\alpha a_0)^2} \right) \frac{\partial a_1}{\partial x} \\ -r b_3^{tot} B_1 - r b_3^{tot} \end{pmatrix}$$

where  $\mathcal{L}(B, a) = \begin{pmatrix} D_b \frac{\partial^2 B}{\partial x^2} & -\chi_a \frac{\partial}{\partial x} \left[ \frac{B}{(1+\alpha a)^2} \frac{\partial a}{\partial x} \right] \\ r b^{tot} B & D_a \frac{\partial^2 a}{\partial x^2} - \mu a \end{pmatrix}$ .

Recursively solving these equations and applying the Fredholm Alternative Theorem yields the bifurcation equation  $\Lambda b_2^{tot} L - L^3 = 0$ , where  $\Lambda$  is a function of model parameters and  $a = a_0 + L \cos(\pi x) \epsilon + \mathcal{O}(\epsilon^2) = a_0 + \sqrt{\Lambda b_2^{tot}} \cos(\pi x) \epsilon + \mathcal{O}(\epsilon^2)$

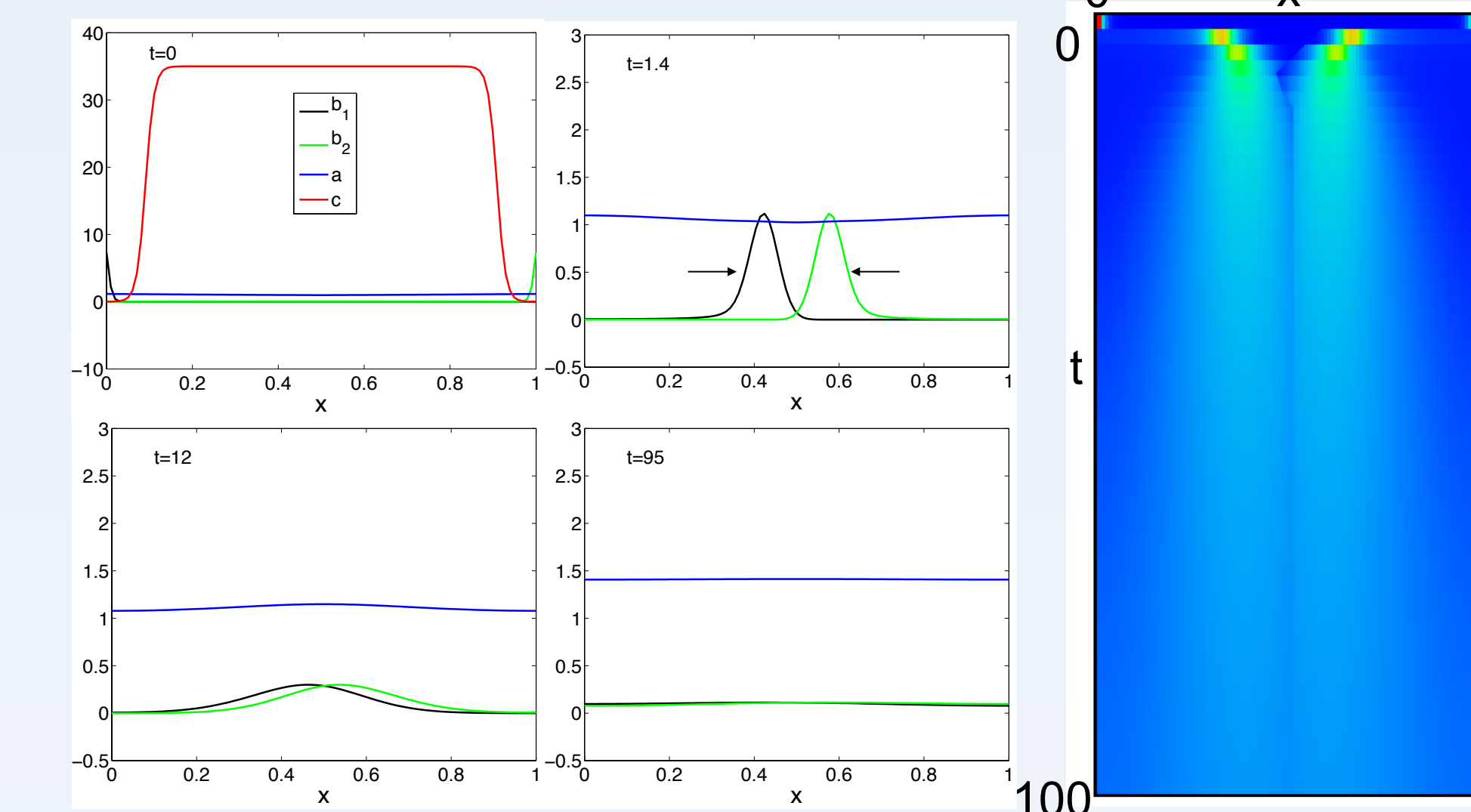
The sign of  $\Lambda$  determines the criticality of the bifurcation:

- If  $\Lambda < 0$ , the bifurcation is subcritical.
- If  $\Lambda > 0$ , the bifurcation is supercritical.



## Simulations

**Case 1. Bacteria combine and diffuse.**

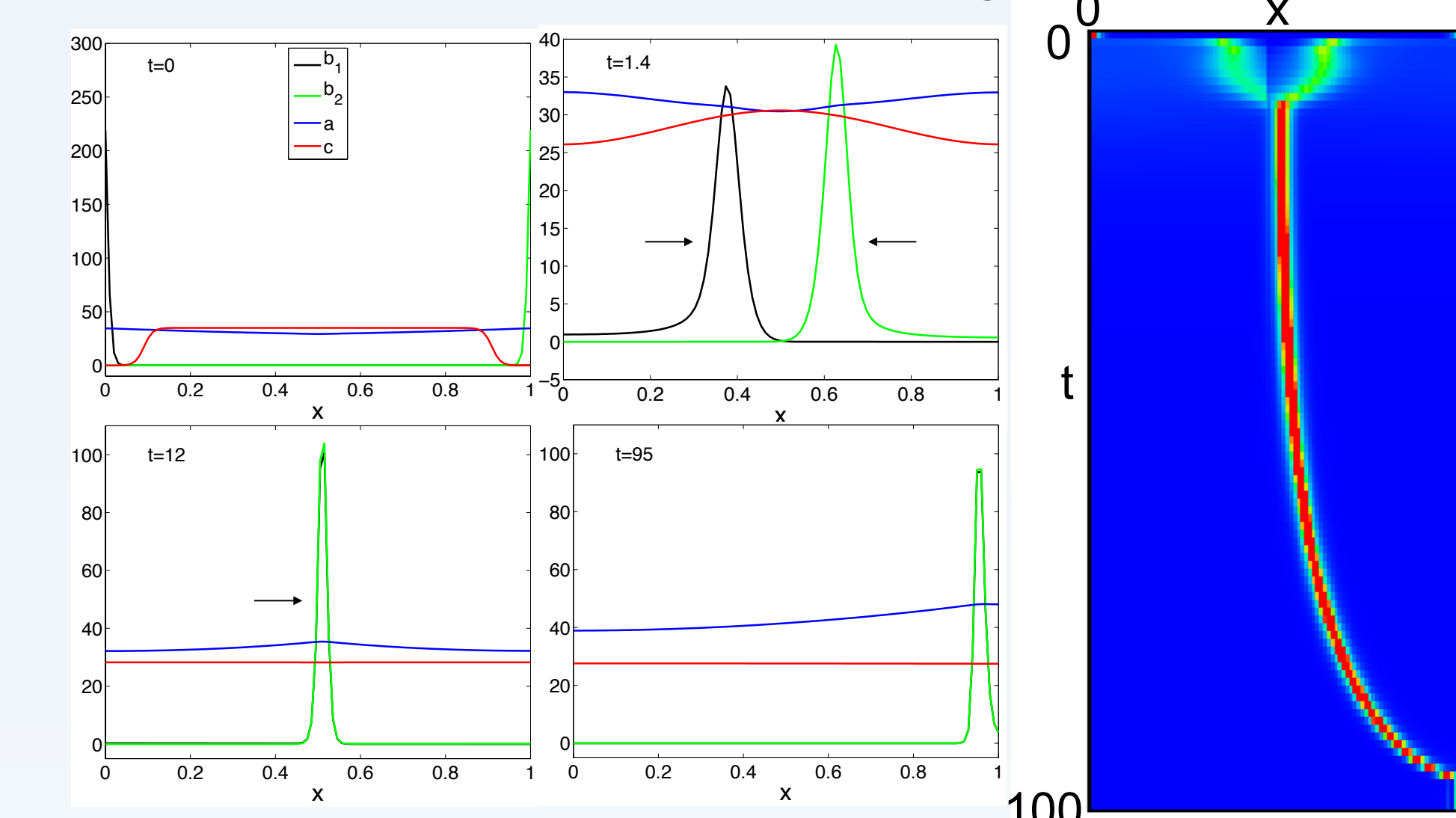


If the bacterial population is sufficiently small, the uniform state is stable.

Upon collision, the two populations combine and diffuse as a single population.

In general, the critical  $b^{tot}$  value at which the uniform state loses stability is a function of model parameters.

**Case 2. Bacteria combine and move right.**

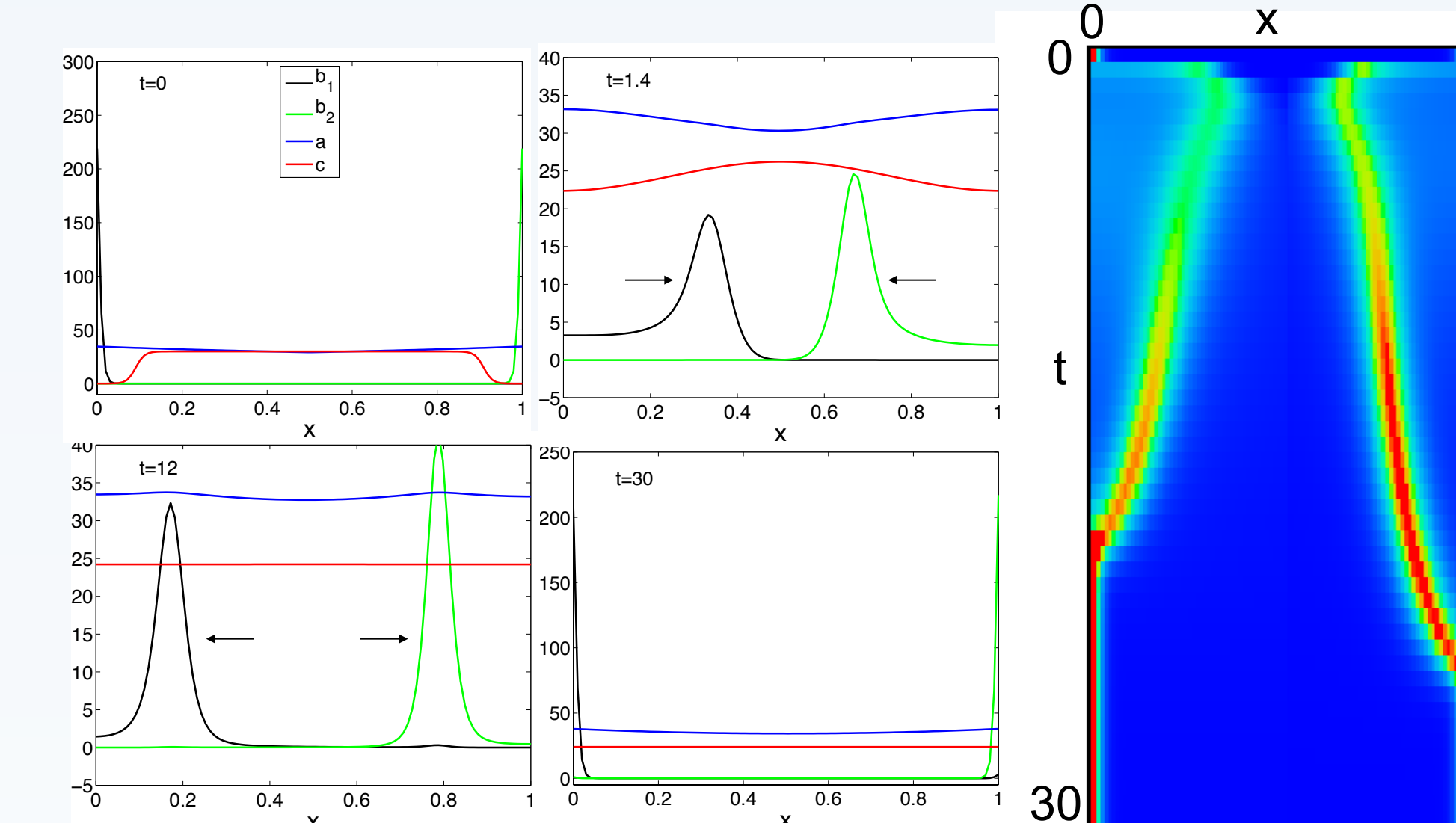


For sufficiently large  $b^{tot}$ , the uniform solution loses stability and the bump solution becomes stable.

Here, a sufficiently strong chemotactic attraction to the nutrient allows both populations to meet and combine.

In general, the outcome depends heavily on the diffusivity of the nutrient and the relative chemotactic sensitivities to the attractant and nutrient.

**Case 3. Bacteria never combine, turn around.**



Here, a smaller amount of available nutrient causes the two populations to turn around before collision.

In general, faster diffusion of the nutrient or a stronger relative chemotactic attraction to the attractant than to the nutrient can cause the same qualitative outcome.

## Future Work: Wave Speed

Starting from the bump solution, the bacteria move as a traveling pulse across the plate once the nutrient  $c$  is introduced.

We assume the dynamics of and due to  $c$  are slow near the bump solution.

Making the traveling wave ansatz  $z = x + \nu t$ , the system becomes

$$\begin{aligned} \epsilon \nu b_z &= D_b b_{zz} - \chi_a \frac{\partial}{\partial z} \left[ \frac{b}{(1+\alpha a)^2} \frac{\partial a}{\partial z} \right] - \epsilon \chi_c \frac{\partial}{\partial z} \left[ \frac{b}{(1+\gamma c)^2} \frac{\partial c}{\partial z} \right] \\ \epsilon \nu a_z &= D_a a_{zz} + r b - \mu a \\ \epsilon \nu c_z &= \epsilon D_c c_{zz} - \epsilon \beta b \end{aligned}$$

The linear part should have a nonzero nullspace, and if so the Fredholm Alternative Theorem will determine  $\nu$ .

## References

- T. Hillen and K. J. Painter, A user's guide to PDE models for chemotaxis. *J. Math. Biol.* 58, 183-217 (2009).
- H. Salman, et al, Solitary modes of bacterial culture in a temperature gradient. *PRL.* 97, 118101 (2006).