

A new PDE model of bacterial aggregation

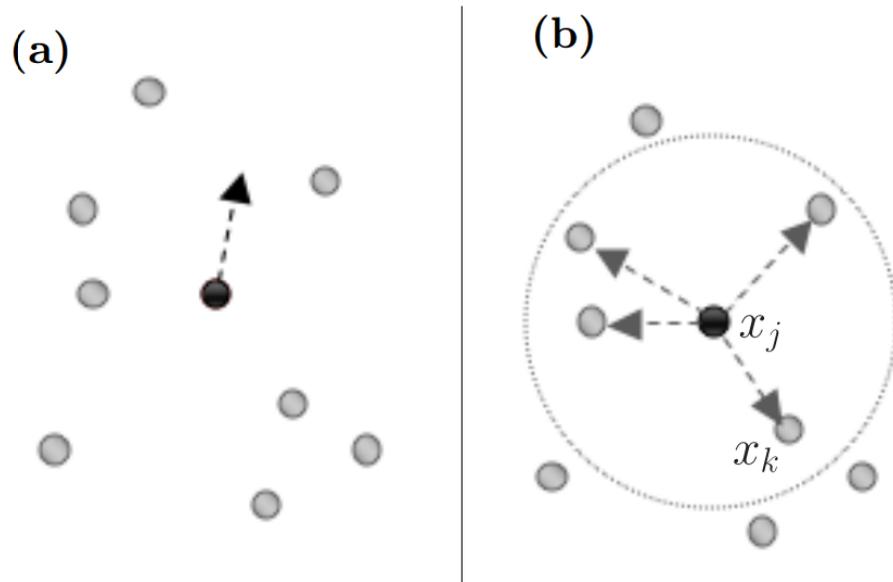
Theodore Kolokolnikov

Joint work with Paul-Christopher Chavy-Waddy

Dalhousie University

Galante-Wisen-Bhaya-Levy model (agent-based):

- Each bacteria has position x_j and a direction d_j . Bacteria move at some **fixed speed**.
- Bacteria switches its direction at a certain **switching rate**.
 - When choosing new direction, the bacteria picks at random another bacteria within its **sensing radius**, and then orients itself to move towards it.



- Aggregations form as switching rate is increased.

- Pseudocode:

```
for t=0:dt:1000
```

```
  for j=1:n % cycle through each bacteria
```

```
    if rand < switching_rate*dt
```

```
      Pick a random bacteria  $x_k$  within sensing_radius of  $x_j$ 
```

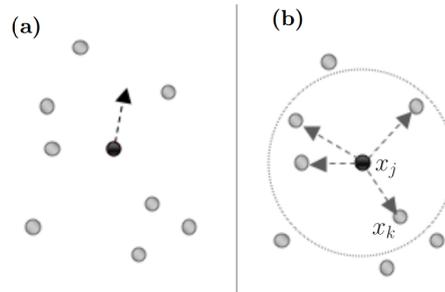
```
      Update orientation:  $d_j = (x_k - x_j) / |x_k - x_j|$ 
```

```
    end
```

```
  end
```

```
  x=x+d*speed*dt
```

```
end
```



- Movie: switching rate = 3
- Movie: switching rate = 2
- Movie: switching rate = 0.5

One-dimensional ODE lattice model (Galante-Levy)

- Each bacteria is oriented either left or right. Denote average densities by L_j, R_j for lattice points $j = 1 \dots n$.
- At each time-step:
 - Bacteria either moves to an adjacent cell according to its current orientation with rate a
 - Or it switches orientation with rate c
- ODE lattice model on n bins:

$$\frac{dR_j}{dt} = aR_{j-1} - (a + c)R_j + cU_{j-1}\eta_{j-1}^+ \quad (1a)$$

$$\frac{dL_j}{dt} = aL_{j+1} - (a + c)L_j + cU_{j+1}\eta_{j+1}^- \quad (1b)$$

$$U_j = L_j + R_j, \quad (1c)$$

$$\eta_j^\pm = \frac{\sum_{k=1}^d U_{j\pm k}}{\sum_{k=1}^d (U_{j+k} + U_{j-k})}. \quad (1d)$$

- Simulation of ODE model
 - Uniform state: [movie: a=1, c=1.9](#)
 - Aggregations form: [movie: a=1, c=2.2](#)

Symmetrization

- Let

$$V_j = R_{j+1} + L_{j-1}; \quad U_j = R_j + L_j. \quad (2)$$

- The model becomes:

$$\begin{aligned} \frac{dU_j}{dt} &= a(U_{j-1} + U_{j+1} - V_j) - (a + c)U_j + c(U_{j-1}\eta_{j-1}^+ + U_{j+1}\eta_{j+1}^-) \\ \frac{dV_j}{dt} &= (a + c)(U_j - V_j) \\ \eta_j^\pm &= \frac{\sum_{k=1}^d U_{j\pm k}}{\sum_{k=1}^d (U_{j+k} + U_{j-k})}. \end{aligned} \quad (3)$$

- $U_j = R_j + L_j$ is the **total** bacteria in bin j ;
- $V_j = R_{j+1} + L_{j-1}$ represents the density of bacteria near bin j that is **diffusing away** from bin j .
- At the steady state, the total density is the same as the diffusing density.
- **Simplified model:** suppose that $V_j \sim U_j$, then

$$\boxed{\frac{dU_j}{dt} = a(U_{j-1} + U_{j+1}) - (2a + c)U_j + c(U_{j-1}\eta_{j-1}^+ + U_{j+1}\eta_{j+1}^-)} \quad (4)$$

Stability of the homogeneous state

The model

$$\frac{dU_j}{dt} = a(U_{j-1} + U_{j+1}) - (2a + c)U_j + c(U_{j-1}\eta_{j-1}^+ + U_{j+1}\eta_{j+1}^-)$$

has admits a homogeneous state $U_j = U$. Linearize around it:

$$U_j(t) = U + \phi_j e^{\lambda t}$$

Then

$$\begin{aligned} \lambda \phi_j &= \left(a + \frac{c}{2} + \frac{c}{4d} \right) (\phi_{j-1} + \phi_{j+1}) - \left(2a + c - \frac{c}{2d} \right) \phi_j \\ &\quad - \frac{c}{4d} (\phi_{j+d} + \phi_{j-d} + \phi_{j+d+1} + \phi_{j-d-1}) \end{aligned}$$

Ansatz:

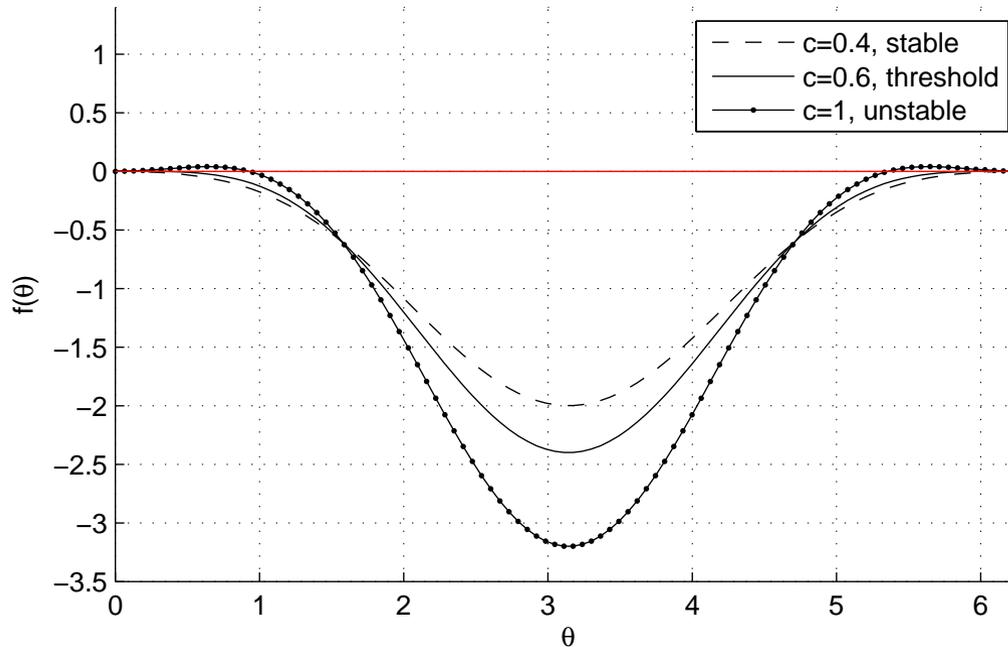
$$\phi_j = \phi e^{\lambda t} e^{\frac{2\pi m j i}{n}}; \quad m = 0 \dots n - 1$$

$$\lambda = f\left(\frac{2\pi m}{n}\right), \quad m = 0 \dots n - 1,$$

$$f(\theta) = (2a + c)(\cos(\theta) - 1) + \frac{c}{2d}(1 + \cos(\theta) - \cos(d\theta) - \cos((d+1)\theta))$$

$$f(\theta) = (2a + c) (\cos(\theta) - 1) + \frac{c}{2d} (1 + \cos(\theta) - \cos(d\theta) - \cos((d+1)\theta))$$

a=0.3, d=1



- $f(0) = 0$, $f'(0) = 0$,
- Can be shown that $f(\theta) \leq 0$ for all θ iff $f''(0) = -2a + dc < 0$,
- **Homogeneous state is stable if $c < c_0$; unstable if $c > c_0$, where**

$$c_0 = 2a/d.$$

Continuum limit

$$\frac{dU_j}{dt} = a(U_{j-1} + U_{j+1}) - (2a + c)U_j + c(U_{j-1}\eta_{j-1}^+ + U_{j+1}\eta_{j+1}^-)$$

- Let $U_j(t) = u(x, t)$ so that $U_{j+k}(t) = u(x + kh, t)$
- Expanding up to $O(h^2)$, we get:

$$u_t = -h^2 \left(c \frac{d}{2} - a \right) u_{xx}$$

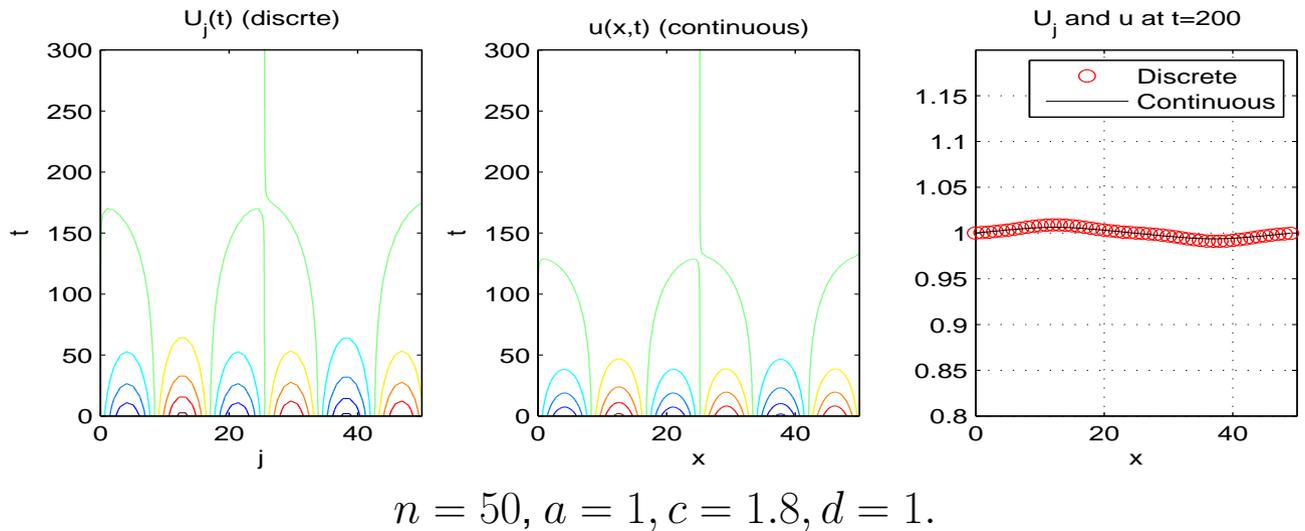
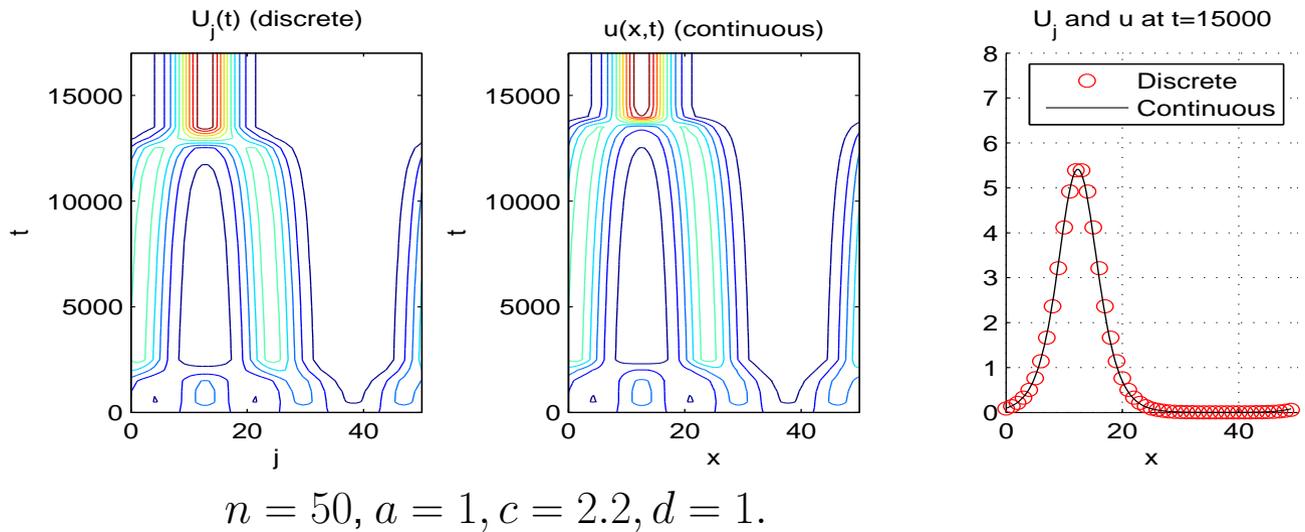
- This recovers the linear stability threshold $c \frac{d}{2} - a = 0$.

- Expanding to $O(h^4)$ we get:

$$u_t = -Au_{xx} - Bu_{xxxx} + C \left(\frac{u_x u_{xx}}{u} \right)_x, \quad v_t = (a + c)(u - v);$$

$$A = h^2 \left(c \frac{d}{2} - a \right); \quad B = \frac{h^4}{12} \left(\frac{c}{2} [1 + d(d^2 + 2d + 3)] - a \right);$$

$$C = \frac{h^4}{24} c (2d + 1)(d + 1)^2.$$



- Suppose that $c\frac{d}{2} - a > 0$ (i.e. homogeneous state unstable). Scale $x = \hat{x} (B/A)^{1/2}$; $t = \hat{t}BA^{-2}$. After dropping the hats we then obtain

$$\boxed{u_t = -u_{xx} - u_{xxxx} + \alpha \left(\frac{u_x u_{xx}}{u} \right)_x} \quad (5)$$

where

$$\alpha := \frac{c(2d+1)(d+1)^2}{(c[1+d(d^2+2d+3)] - 2a)}. \quad (6)$$

Inhomogeneous steady state

$$u_t = -u_{xx} - u_{xxxx} + \alpha \left(\frac{u_x u_{xx}}{u} \right)_x$$

Set $u_t = 0$ and assume u decays at ∞ :

$$0 = -u_x - u_{xxx} + \alpha \frac{u_x u_{xx}}{u}. \quad (7a)$$

Because of scaling symmetry $u \rightarrow \lambda u$, we get a reduction of order:

$$u = \exp(v); \quad v_x = z$$
$$z'' + z + (3 - \alpha)zz' + (1 - \alpha)z^3, \quad z = u_x/u.$$

Write it as:

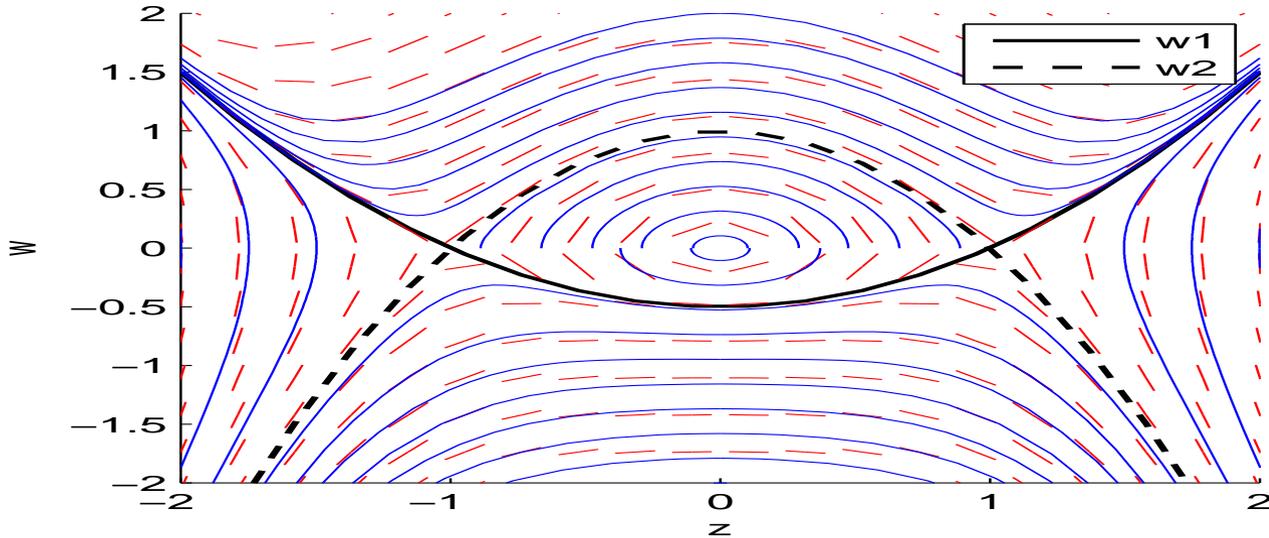
$$\frac{dz}{dx} = w; \quad (8)$$

$$\frac{dw}{dx} = -z + (\alpha - 3)zw + (1 - \alpha)z^3. \quad (9)$$

Get 1st order Abel ODE:

$$\frac{dw}{dz} = \frac{-z}{w} - (3 - \alpha)z - (1 - \alpha)\frac{z^3}{w}. \quad (10)$$

Phase portarat:



The two saddles are connected by heteroclinic orbits of the form of a parabola. So try **Ansatz:**

$$w = Az^2 + B.$$

There are two solutions:

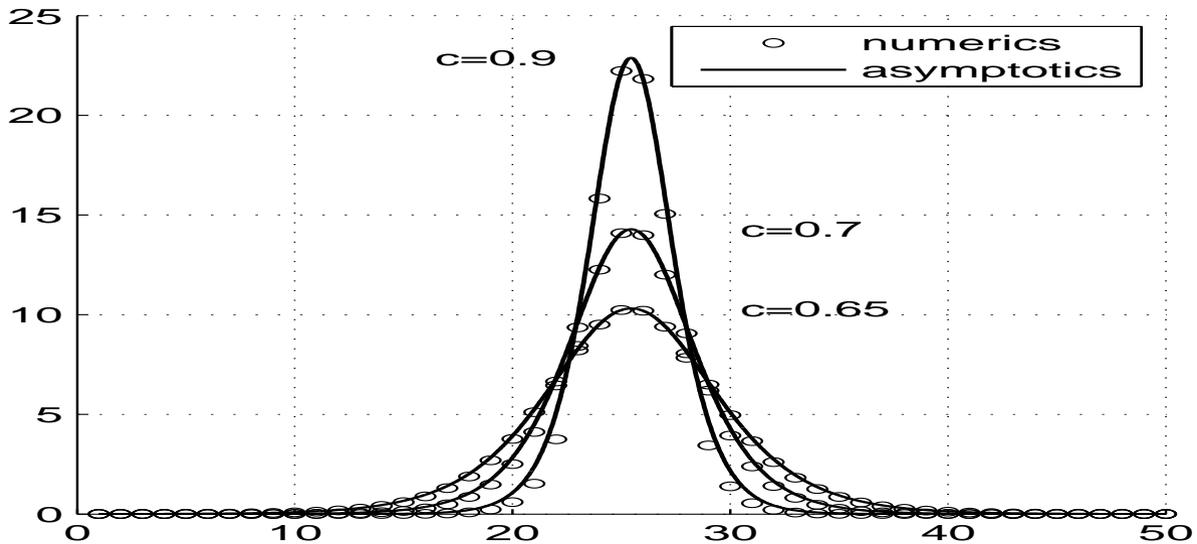
$$w_1 = \frac{(\alpha - 1)z^2 - 1}{2}; \quad w_2 = -z^2 + \frac{1}{\alpha - 1}.$$

Substitute $w = w_1$ into (9) yields

$$\frac{dz}{dx} = \frac{(\alpha - 1)z^2 - 1}{2} \quad (11)$$

Solve it and unwind the transformations to get

$$u(x) = C \left[\operatorname{sech} \left(\frac{\sqrt{\alpha-1}}{2} x \right) \right]^{\frac{2}{\alpha-1}}. \quad (12)$$



Conclusions

- We derived a novel PDE model of bacterial aggregation:

$$u_t = -u_{xx} - u_{xxxx} + \alpha \left(\frac{u_x u_{xx}}{u} \right)_x$$

- Explicit spike profile:
$$u(x) = C \left[\operatorname{sech} \left(\frac{\sqrt{\alpha-1}}{2} x \right) \right]^{\frac{2}{\alpha-1}} .$$

- Open questions:

- Structural stability?
- Metastability?

- Preprint is available for download from my website:

<http://www.mathstat.dal.ca/~tkolokol/bacteria.pdf>

Thank you! Any questions?