

Mathematical Biology - Reaction Diffusion Models and Turing Instability

Stuart Townley

University of Exeter, UK

March 20, 2014



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- When this microscopic movement results in some macroscopic motion of the group we call this a **diffusion process**.
- In order to understand this diffusion via equations let us restrict attention to one spatial dimension (for simplicity)
- Consider a particle moving along the x -axis in a random fashion - let us suppose that in time Δt the particle moves either $+\Delta x$ or $-\Delta x$.

Denote by $p(x, t)$ the probability that a particle released at $x = 0, t = 0$ reaches position x at time t .

- At time $t - \Delta t$ the particle must have been at $x + \Delta x$ or $x - \Delta x$ so that

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- Expanding $p(x, t)$ in a **Taylor Series** we get

$$p(x, t) = \frac{1}{2} \left[\begin{aligned} & p(x, t) - \Delta x \frac{\partial p}{\partial x} - \Delta t \frac{\partial p}{\partial t} + \frac{1}{2}(\Delta x)^2 \frac{\partial^2 p}{\partial x^2} \\ & + (\Delta x)(\Delta t) \frac{\partial^2 p}{\partial x \partial t} + \frac{1}{2}(\Delta t)^2 \frac{\partial^2 p}{\partial t^2} + \dots \end{aligned} \right]$$

$$+ \frac{1}{2} \left[\begin{aligned} & p(x, t) + \Delta x \frac{\partial p}{\partial x} - \Delta t \frac{\partial p}{\partial t} + \frac{1}{2}(\Delta x)^2 \frac{\partial^2 p}{\partial x^2} \\ & - (\Delta x)(\Delta t) \frac{\partial^2 p}{\partial x \partial t} + \frac{1}{2}(\Delta t)^2 \frac{\partial^2 p}{\partial t^2} + \dots \end{aligned} \right]$$

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- Simplifying this we obtain

$$0 = -\Delta t \frac{\partial p}{\partial t} + \frac{1}{2}(\Delta x)^2 \frac{\partial^2 p}{\partial x^2} + \frac{1}{2}(\Delta t)^2 \frac{\partial^2 p}{\partial t^2} + \dots$$

- So

$$\frac{\partial p}{\partial t} = \left(\frac{(\Delta x)^2}{2(\Delta t)} \right) \frac{\partial^2 p}{\partial x^2} + \frac{1}{2}(\Delta t) \frac{\partial^2 p}{\partial t^2} + \dots$$

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- Extensions to higher-dimensions in space and more dependent variables are natural extensions.

- Turing (1952) proposed that under certain circumstances diffusion may act as a **destabilising mechanism**.

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- Let us derive conditions under which this may happen.
- Most **reaction-diffusion systems** of biological interest can be **non dimensionalised** and scaled to take the general form

$$u_t = \gamma f(u, v) + \nabla^2 u \quad v_t = \gamma g(u, v) + d \nabla^2 v \quad (1)$$

[The scale factor γ can obviously be incorporated into the reaction kinetics f and g but we keep it separate for now.]
We typically have two spatial variables x and y and may have more than two dependent variables u and v .

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- Set

$$u = u_0 + \hat{u}, v = v_0 + \hat{v} \text{ with } |\hat{u}|, |\hat{v}| \ll 1$$

Then

$$\begin{aligned} \hat{u}_t &= \gamma[f_u \hat{u} + f_v \hat{v}] \\ \hat{v}_t &= \gamma[g_u \hat{u} + g_v \hat{v}] \end{aligned}$$

where all partial derivatives are evaluated at (u_0, v_0)

- If

$$\underline{w} = \begin{pmatrix} \tilde{u} \\ \tilde{v} \end{pmatrix} \quad \text{then} \quad \underline{w}_t = \gamma \begin{pmatrix} f_u & f_v \\ g_u & g_v \end{pmatrix} \underline{w}$$

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- We look for solutions $\underline{w} \propto e^{\lambda t}$, where λ is an **eigenvalue** of the **linearised matrix**. Then

$$\begin{vmatrix} \gamma f_u - \lambda & \gamma f_v \\ \gamma g_u & \gamma g_v - \lambda \end{vmatrix} = 0 \quad (2)$$

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- For the roots of (2) to have **negative real parts** we require

$$\begin{aligned} f_u + g_v &< 0 & (I) \\ f_u g_v - f_v g_u &> 0 & (II) \end{aligned}$$

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- So, if $\underline{w} = \begin{pmatrix} \tilde{u} \\ \tilde{v} \end{pmatrix}$, then

$$\underline{w}_t = \gamma \begin{pmatrix} f_u & f_v \\ g_u & g_v \end{pmatrix} \underline{w} + D \nabla^2 \underline{w} \quad D = \begin{pmatrix} 1 & 0 \\ 0 & d \end{pmatrix} \quad (3)$$

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- Frequently in **biological applications** zero flux conditions are appropriate (if in a particular application, some other boundary condition is more natural, then the analysis is easily modified).

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- So let \underline{w} be the **time-independent** solution of the eigenvalue problem:

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- Here k is an **eigenvalue** and the corresponding eigenfunctions give us a basis in which to expand a solution.

- If we denote by \underline{w}_k the eigenfunctions of the eigenvalue problem, we seek a solution of the original problem (3) of the form

$$\underline{w}(x, y, t) = \sum_k c_k e^{\lambda_k t} \underline{w}_k(x, y) \quad (4)$$

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- Substituting (4) into (3) and comparing **eigenfunctions** gives

$$\sum_k c_k \lambda_k e^{\lambda_k t} \underline{w}_k = \gamma A \left(\sum_k c_k e^{\lambda_k t} \underline{w}_k \right) + D \nabla^2 \left(\sum_k c_k e^{\lambda_k t} \underline{w}_k \right)$$

where $A = \begin{pmatrix} f_u & f_v \\ g_u & g_v \end{pmatrix}$, the **community matrix** of the reaction part.

- This can be written:

$$\sum_k c_k \lambda_k e^{\lambda_k t} \underline{\mathbf{w}}_k = \gamma A \left(\sum_k c_k e^{\lambda_k t} \underline{\mathbf{w}}_k \right) - D \left(\sum_k c_k e^{\lambda_k t} k^2 \underline{\mathbf{w}}_k \right)$$

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- But $\underline{\mathbf{w}}_k$ are linearly independent.

Hence $\lambda_k \underline{\mathbf{w}}_k = \gamma A \underline{\mathbf{w}}_k - k^2 D \underline{\mathbf{w}}_k$ or

$$(\lambda_k I - \gamma A + k^2 D) \underline{\mathbf{w}}_k = 0.$$

Non-trivial solutions $\lambda = \lambda_k$ exist if

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$$\det(\lambda I - \gamma A + k^2 D) = 0, \quad \text{i.e.}$$

$$\begin{vmatrix} \lambda - \gamma f_u + k^2 & -\gamma f_v \\ -\gamma g_u & \lambda - \gamma g_v + dk^2 \end{vmatrix} = 0$$

- So for non-trivial solutions we require:

$$\lambda^2 + \lambda[k^2(1 + d) - \gamma(f_u + g_v)] + h(k^2) = 0 \quad (5)$$

$$\text{with } h(k^2) = dk^4 - \gamma(df_u + g_v)k^2 + \gamma^2(f_u g_v - f_v g_u)$$

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The former is impossible as we have already required $f_u + g_v < 0$ (condition I)
- Now since $f_u g_v - f_v g_u > 0$ (condition II) $h(k^2)$ can only possibly be negative if

$$df_u + g_v > 0 \quad (III) \quad (\implies d \neq 1 \quad \text{by I})$$

- Now observe that

$$\begin{aligned}h(k^2) &= d \left[k^4 - \frac{\gamma}{d}(df_u + g_v)k^2 + \frac{\gamma^2}{d}(f_u g_v - f_v g_u) \right] \\ &= d \left[\left(k^2 - \frac{\gamma}{2d}(df_u + g_v) \right)^2 + \frac{\gamma^2}{d}(f_u g_v - f_v g_u) \right. \\ &\quad \left. - \frac{\gamma^2}{4d^2}(df_u + g_v)^2 \right]\end{aligned}$$

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- Therefore the minimum value of h occurs at $k^2 = \frac{\gamma}{2d}(df_u + g_v)$. This is the wavenumber of the first mode to become unstable.
- Consequently $h_{\min} = \gamma^2(f_u g_v + f_v g_u) - \frac{\gamma^2}{4d}(df_u + g_v)^2$ and so for instability we need $h_{\min} < 0$, i.e.

$$(df_u + g_v)^2 > 4d(f_u g_v - f_v g_u) \quad (IV)$$

$$((I) \text{ and } (III)) \implies d \neq 1$$

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- By (IV) d_c satisfies

$$(d_c f_u + g_v)^2 = 4d_c(f_u g_v - f_v g_u)$$

and the **wavenumber** of the first **unstable mode** satisfies

$$\begin{aligned} k_{\text{crit}}^2 &= \frac{\gamma}{2d_c}(d_c f_u + g_v) = \frac{\gamma}{2d_c} 2\sqrt{d_c} \sqrt{f_u g_v - f_v g_u} \\ &= \gamma \left[\frac{f_u g_v - f_v g_u}{d_c} \right]^{\frac{1}{2}} \end{aligned}$$

- Consider the **diffusion-driven activator-inhibitor** system

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- For **homogeneous steady solutions** $u = u_0$, $v = v_0$ with

$$\frac{u_0^2}{v_0} = bu_0, \quad u_0^2 = v_0 \implies u_0 = \frac{1}{b} \quad v_0 = \frac{1}{b^2}$$

- Reaction kinetics terms are

$$f = \frac{u^2}{v} - bu \quad g = u^2 - v$$

so

$$\begin{aligned}f_u &= \frac{2u}{v} - b & f_v &= \frac{-u^2}{v^2} \\g_u &= 2u & g_v &= -1\end{aligned}$$

At the steady state

$$f_u = b \quad f_v = -b^2 \quad g_u = \frac{2}{b} \quad g_v = -1$$

- For **stability** in the **absence of diffusion**

$$\left. \begin{array}{l} f_u + g_v < 0 \quad \implies b - 1 < 0 \quad \implies b < 1 \\ f_u g_v - f_u g_v > 0 \quad \implies -b + 2b > 0 \quad \implies b > 0 \end{array} \right\}$$

therefore $0 < b < 1$

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- Diffusion-driven instability** necessitates

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- For **stability** in the **absence of diffusion**

$$\left. \begin{aligned} f_u + g_v < 0 &\implies b - 1 < 0 &\implies b < 1 \\ f_u g_v - f_v g_u > 0 &\implies -b + 2b > 0 &\implies b > 0 \end{aligned} \right\}$$

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$$\implies (db - 1)^2 > 4db$$

$$\text{if } X = db \implies (X - 1)^2 > 4X \implies X^2 - 6X + 1 > 0$$

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- If there exists $P > 0$ so that

$$A_i^T P + P A_i \leq 0, \quad \text{for all } i \in \{1, 2, \dots, n\}, \quad (7)$$

then the quadratic function $V(x) = x^T P x$ is a **Common Lyapunov function** (CLF) for the switching system (6).

- Shorten and Narendra derived necessary and sufficient conditions for the existence of a CLF for a finite number of stable second order systems.
- A pair of 2×2 stable matrices A_1 and A_2 have a common Lyapunov function with strict inequality in (7) if, and only if, the matrices $A_1 A_2^{-1}$ and $A_1 A_2$ have no negative real eigenvalues.

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- We will apply the notion of CLF to the stable matrices A and $-D$ where A is the linearised **reaction matrix** and D is the **diffusion matrix** in a reaction diffusion system.
- Even when one matrix is diagonal, the existence of CLFs is subtle as illustrated by the following example.

- Consider the following stable matrices supposed to arise from linearising a reaction system around a steady state:

$$A_1 = \begin{pmatrix} -1 & 0.2 \\ 0 & -1 \end{pmatrix}, \quad A_2 = \begin{pmatrix} -2 & 6 \\ 0 & -3 \end{pmatrix}, \quad A_3 = \begin{pmatrix} 2 & -1 \\ 8 & -3 \end{pmatrix}$$

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$$P = \begin{pmatrix} 3 & 1 \\ 1 & 5 \end{pmatrix} \quad \text{is a CLF for } A_2 \text{ and } D.$$

- The system

$$\frac{dx}{dt} = Ax$$

is **reactive** i.e. exhibits initial growth, when $A + A^T$ has a positive eigenvalue, equivalently when I is **not** a Lyapunov matrix for A .

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- When I is a Lyapunov function for A then I is a Lyapunov matrix for $A - k^2D$ and so $A - K^2D$ is stable for all k and any diffusion matrix D .
- Therefore DDI implies A is reactive (see Neubert, Caswell and Murray) and reactivity is **necessary** for DDI.

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$$\begin{cases} A^T P + P A < 0 \text{ and} \\ (-D)P + P(-D) < 0 \end{cases} \implies (A - k^2 D)^T P + P(A - k^2 D) < 0$$

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- Whilst simple, this result is **very powerful** in applications. Why? Testing whether pairs of matrices share a CLF is determined using **SEMI-DEFINITE PROGRAMMING** e.g. using `cvx` in Matlab - even in high dimensions!

To load cvx: Check out Steve Boyd at Stanford

```
cvx_setup
```

To run cvx: Key in A and D. Then run:

```
cvx_begin sdp  
variable P(n,n) symmetric  
A'*P+P*A<zeros(n);  
-D'*P-P*D<zeros(n);  
P>=eye(n);  
cvx_end
```



Matlab Code

A simple inhibitor-activator PDE model describing the regenerative growth of Hydra:

$$\begin{cases} \frac{\partial a}{\partial t} = \rho\rho_0 + c_1\rho\frac{a^2}{h} - \mu a + d_1\nabla_x^2 a \\ \frac{\partial h}{\partial t} = c_2\rho' a^2 - \nu h + d_2\nabla_x^2 h. \end{cases}$$

$a(x, t)$ and $h(x, t)$ are the activator and inhibitor concentrations at position x and time t .

The parameters

- Set 1: $c_1 = 0.005$, $c_2 = 0.035$, $d_1 = 0.03$, $d_2 = 0.45$,
 $\rho' = 0.075$ and $\rho = \rho_0 = 3.2$.
- Set 2: $c_1 = 0.05$, $c_2 = 0.025$, $d_1 = 0.03$, $d_2 = 0.45$,
 $\rho' = 0.00075$ and $\rho = \rho_0 = 3.2$

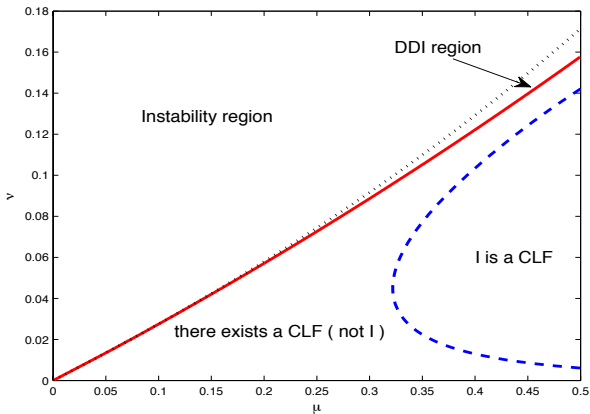


Figure: For Set 1: Parameters (μ, ν) where there is DDI, I is a CLF and there is a CLF.

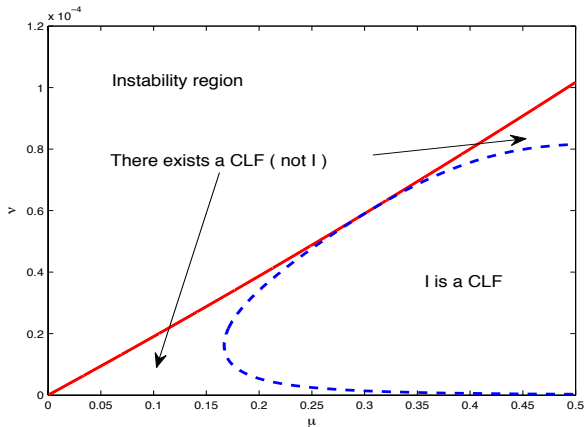


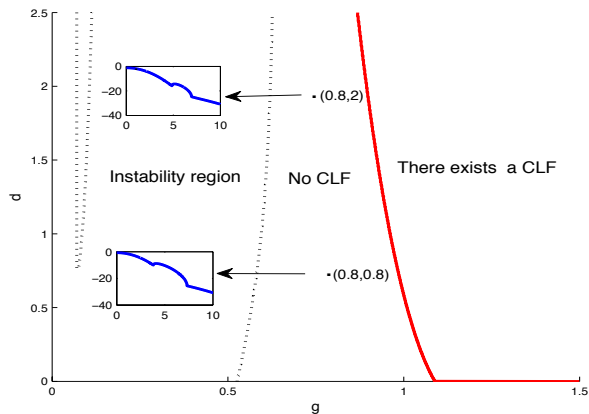
Figure: For Set2: Parameters (μ, ν) where I is a CLF and there is a CLF. Here there is no DDI

Here we consider a three dependent variable model (and so the well known parameter test for DDI does not apply). It describes a spatial model for the interaction of a host (u), a parasite (v) and a hyper-parasite (w).

$$\begin{aligned}\frac{\partial u}{\partial t} &= \tau[u(1 - \frac{u}{K}) - uv] + d_1 \nabla^2 u \\ \frac{\partial v}{\partial t} &= \tau\mu[\frac{uv}{1 + \gamma} - \frac{vw}{1 + \gamma v}] + d_2 \nabla^2 v \\ \frac{\partial w}{\partial t} &= \tau d[v - w] + d_3 \nabla^2 w.\end{aligned}$$

The parameters

$d_1 = 0.02$, $d_2 = 0.2$, $d_3 = 1$, $\mu = 15$, $K = 10$ and $\tau = 1$.



In our set up, indeed in the standard Turing instability framework, D is supposed to be diagonal. However, this is not an essential ingredient of our approach and the CLF-based approach still applies. This is useful for applications where other “movement” mechanisms are invoked.

For example, a common movement mechanism is based on “chemotaxis” which mathematically brings in cross-derivatives. A simple model in which this arises is in the Schnakenberg diffusion-chemotaxis model:

$$\begin{aligned}\frac{\partial u}{\partial t} &= \gamma(a - u + u^2v) + \nabla^2 u - \alpha \nabla \cdot (u \nabla v), \\ \frac{\partial v}{\partial t} &= \gamma(b - u^2v) + d \nabla^2 v\end{aligned}$$

Linearisation around the equilibrium $(a + b, b/(a + b)^2)$ leads to the reaction-diffusion-chemotaxis matrix pencil:

$$A - \|\omega\|^2 D_\alpha,$$

where

$$A = \begin{pmatrix} \frac{b-a}{a+b} & (a+b)^2 \\ \frac{-2b}{a+b} & -(a+b)^2 \end{pmatrix}, \quad D_\alpha = \begin{pmatrix} 1 & -\alpha(a+b) \\ 0 & d \end{pmatrix}.$$

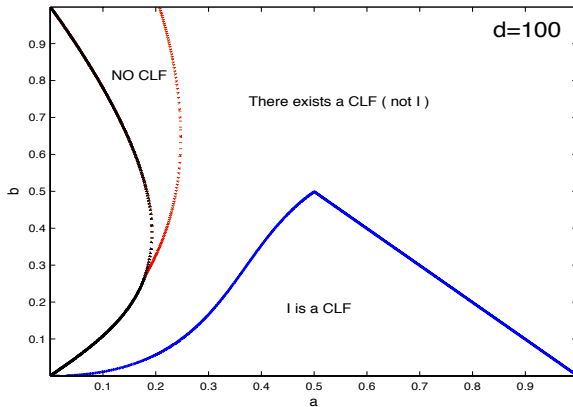


Figure: The parameter used here are $d = 100, \gamma = 1$ and $\alpha = 20$.

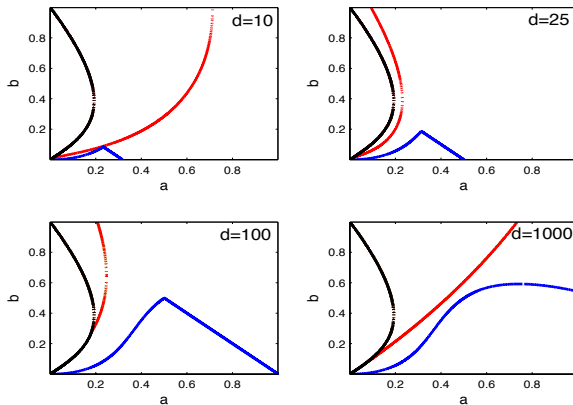


Figure: To the right of the red curve no pattern formation is possible as the diffusion coefficient d is increased: $d = 10, 25, 100$ and 1000 .

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- It provides a more systematic search for parameter domains on which pattern formation is possible compared to ad hoc methods based on computing the dispersion relation for specific parameters
- It is a simple, but powerful, generalisation of the “reactivity is necessary” results of Neubert et al.