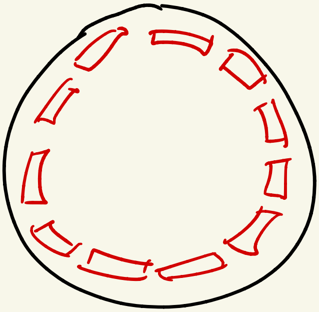
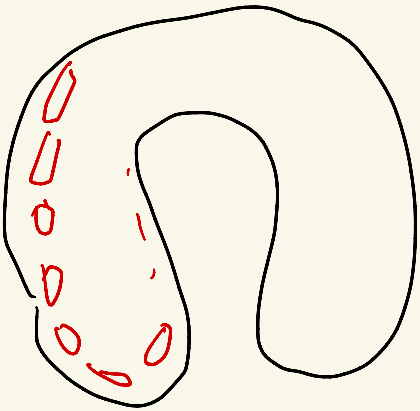
Turing's theory of morphogenesis

Punagrass
11/8/24

Consider a zygote



Gastrulation



Zygote is a sphere of cells

The laws of physics are spherically symmetrical

Q How is symmetry broken in development?

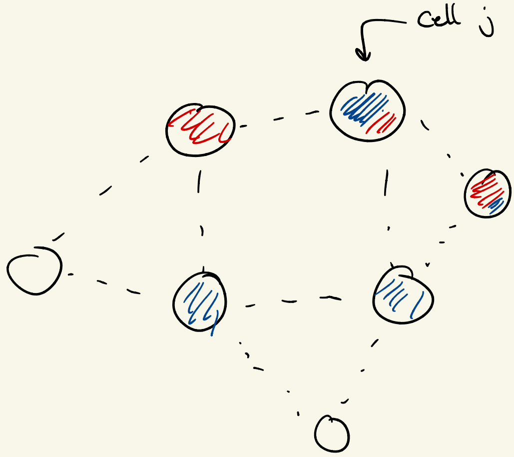
Mathematical model of the zygote

- cells that push, pull, stretch on each other (mechanical forces)

- Chemicals that react w/ each other & diffuse between cells

"In this section a mathematical model of the embryo will be described. This model will be a simplification and an idealization, and consequently a falsification. It is to be hoped that the features retained for discussion are those of greatest importance in the present state of knowledge."

Chemicals u, v are "form producers"



Reaction:

$$\begin{pmatrix} \dot{u}_j \\ \dot{v}_j \end{pmatrix} = f\begin{pmatrix} u_j \\ v_j \end{pmatrix}$$

Diffusion:

Diffusion rate

$$\dot{u}_j = \mu_j \sum_{k \sim j} (u_k - u_j)$$

(makes things spread out)

Ex 1

$$\begin{pmatrix} \dot{u} \\ \dot{v} \end{pmatrix} = \begin{pmatrix} 0 & -1 \\ 1 & 0 \end{pmatrix} \begin{pmatrix} u \\ v \end{pmatrix}$$

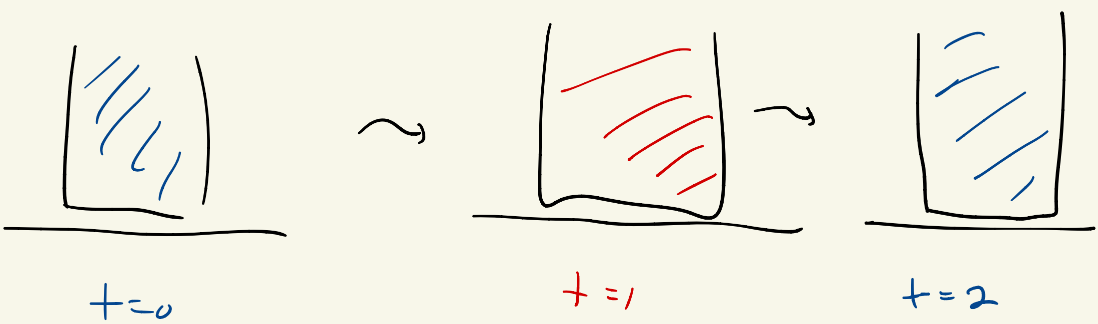
$\dot{u} = -v$ (v is an inhibitor)

$\dot{v} = u$ (u is an activator)

phase

$$u(t) = A\cos(t + t_0)$$

$$v(t) = A\sin(t + t_0)$$



Ex 2

$$\begin{pmatrix} \dot{u} \\ \dot{v} \end{pmatrix} = \begin{pmatrix} 0 & 1 \\ -3 & 4 \end{pmatrix} \begin{pmatrix} u \\ v \end{pmatrix}$$

$\dot{u} = v$ ← Activator

$\dot{v} = -3u + 4v$

inhibitor

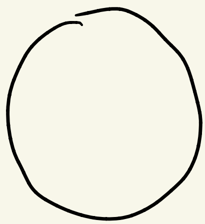
$$\begin{pmatrix} 0 & 1 \\ -3 & 4 \end{pmatrix} v_1 = 3v_1, \qquad v_1 = \begin{pmatrix} 1 \\ 3 \end{pmatrix}$$

$$\begin{pmatrix} 0 & 1 \\ -3 & 4 \end{pmatrix} v_2 = v_2, \qquad v_2 = \begin{pmatrix} 1 \\ 1 \end{pmatrix}$$

$$\begin{pmatrix} u(0) \\ v(0) \end{pmatrix} = \alpha v_1 + \beta v_2 \Rightarrow \begin{pmatrix} u(t) \\ v(t) \end{pmatrix} = e^{3t} \alpha v_1 + e^{t} \beta v_2$$

3 : 1 ratio of u : v (equilibrium ratio)

It doesn't feel like we're closer to answering Q... but let's carry out the analysis.



continuous ring of cells

$x \in [0, 2\pi]$

$u(x,t)$ = concentration of u

$v(x,t)$ = concentration of v

$$\begin{pmatrix} \dot{u} \\ \dot{v} \end{pmatrix} = \underbrace{\begin{pmatrix} \alpha & \beta \\ \gamma & \delta \end{pmatrix} \begin{pmatrix} u \\ v \end{pmatrix}}_{\text{reaction}} + \underbrace{\begin{pmatrix} \nu \Delta u & 0 \\ 0 & \nu \Delta v \end{pmatrix}}_{\text{diffusion}}$$

Fourier series

$$u(x,t) = \sum_{k \in \mathbb{Z}} a_k(t)\, e^{ik\cdot x}$$

$$v(x,t) = \sum_{k \in \mathbb{Z}} b_k(t)\, e^{ik\cdot x}$$

$$\begin{pmatrix} \dot{a}_k \\ \dot{b}_k \end{pmatrix} = \begin{pmatrix} \alpha & \beta \\ \gamma & \delta \end{pmatrix} \begin{pmatrix} a_k \\ b_k \end{pmatrix} - \begin{pmatrix} \mu k^2 a_k & 0 \\ 0 & \nu k^2 b_k \end{pmatrix}$$

$$= \underbrace{\begin{pmatrix} \alpha - \mu k^2 & \beta \\ \gamma & \delta - \nu k^2 \end{pmatrix}}_{R_k} \begin{pmatrix} a_k \\ b_k \end{pmatrix}$$

Let

$\lambda_{max}(k) =$ Maximum real part of eigval of R_k

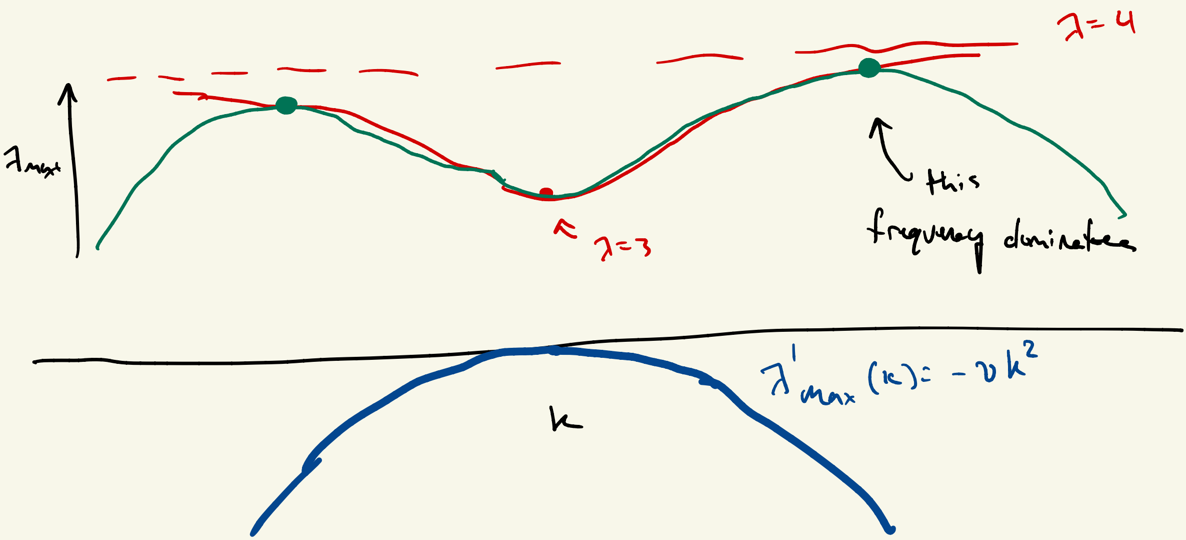
Then typically,

$$\left\| \begin{pmatrix} a_k(t) \\ b_k(t) \end{pmatrix} \right\|_2 \sim e^{\lambda_{max}(k) \cdot t} \left\| \begin{pmatrix} a_k(0) \\ b_k(0) \end{pmatrix} \right\|_2$$

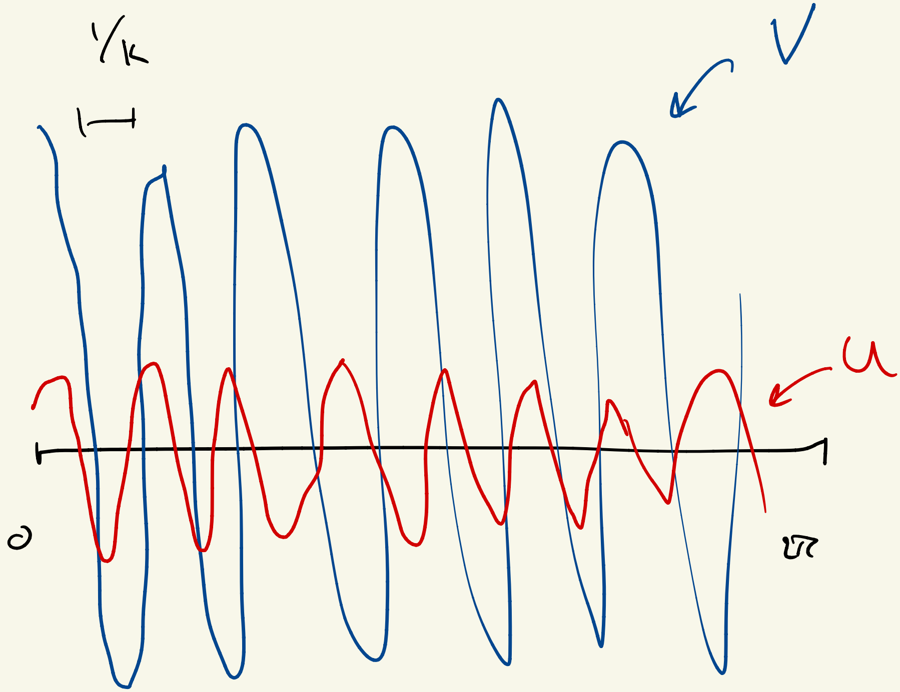
Ex $\quad R_k^{(1)} = \begin{pmatrix} -\mu k^2 & 0 \\ 0 & -\nu k^2 \end{pmatrix} \qquad \mu \geq \nu$

$R_k^{(2)} = \begin{pmatrix} -k^2 & 1 \\ -3 & 4 \end{pmatrix} \qquad \mu = 1, \quad \nu = 0$

$R_k^{(3)} = \begin{pmatrix} -k^2 & 1 \\ -3 & 4 - \varepsilon k^2 \end{pmatrix} \qquad \mu = 1, \quad \nu = \varepsilon$



For activator-inhibitor systems, diffusion can promote more growth

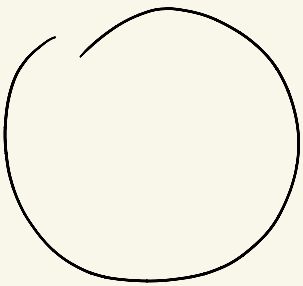


$$\dot{u} = V - k^2$$

$$\dot{V} = -3u + 4V - \varepsilon k^2$$

V makes u, which is instantly destroyed by diffusion

Answer to Q: For some reaction-diffusion systems, the homogeneous state is unstable.

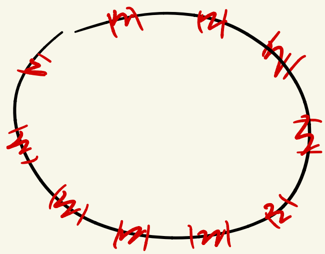


3:1 rat of V : u

both diffuse at rate a.

add more diffusion of u

(homogeneous change)



Turing patterns are a fundamental

PDE phenomena that can be explored

analytically