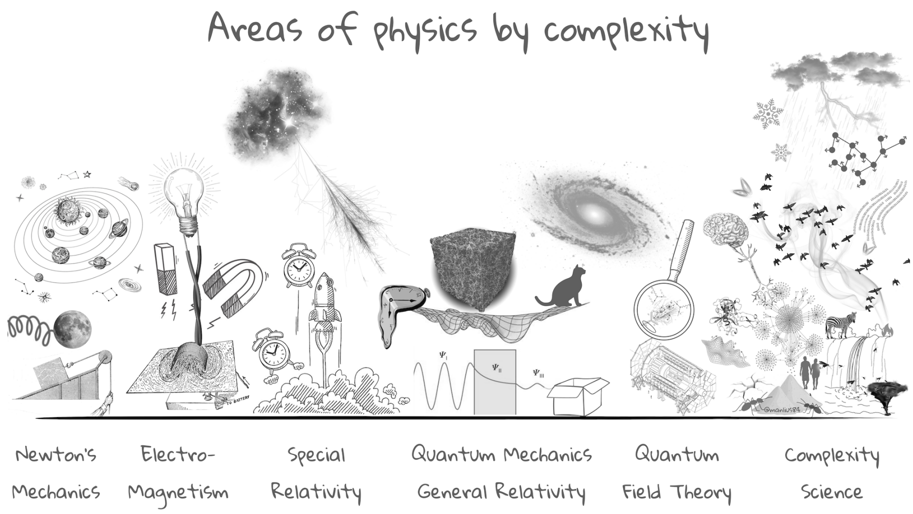
Final Report

Physics of Complex Networks: Structure and Dynamics

Università degli Studi di Padova



Project # 18: Turing Patterns

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1.1 | Task Description

The goal of this task is to analyze a reaction-diffusion (Turing) dynamics on networks, with specific suggestion to replicate the results found in [3].

A system governed by a reaction-diffusion mechanism can exibit pattern emergence when perturbed from an initial linearly stable equilibrium state. The conditions for pattern initiation are found through linear stability analysis. The subsequent evolution of the pattern is non-linear and eventually results in a steady state (that can be either stationary or time dependent).

The authors of [3] described mathematically and with simulations both the pattern initiation and its subsequent non-linear evolution to the steady state. In order to keep the workload manageable for this project, I made the choice to focus only on **pattern initiation**, but do it in full mathematical detail.

1.2 | General Conditions for Diffusion-Driven Instability

Detailed Derivation of the above stated facts

1.3 | Results of the Simulations

2 | Appendix

2.1 | Turing Patterns in a continuous medium

This section contains an elementary introduction to reaction-diffusion systems for pattern formation.

An activator- inhibitor system is described by the following set of equations:

$$\begin{cases} \frac{\partial}{\partial t}u(\mathbf{x},t) = f(u,v) + D_{\text{act}}\nabla^2 u(\mathbf{x},t) \\ \frac{\partial}{\partial t}v(\mathbf{x},t) = g(u,v) + D_{\text{inh}}\nabla^2 v(\mathbf{x},t) \end{cases} \tag{2.1}$$

where $u(\mathbf{x},\, t)$ is the local density of the activator and $v(\mathbf{x},\, t)$ is the local density of the inhibitor. D_u and D_v are the diffusion coefficients of the ligands or morphogens. The reactions are encoded in the functions $f(u,\, v)$ and $g(u,\, v)$. There are several choices for $f(u,\, v)$ and $g(u,\, v)$ that are able to generate patterns. Among the most studied are the Schnakenberg (1979) and the Gieger-Meinhardt (1972) kinetics (see [2]). Whatever kinetics we might choose, it needs to meet the following basic requirements:

1. Existence of a homogeneous, linearly stable equilibrium $(\overline{u},\, \overline{v})$ in absence of diffusion:

$$\begin{pmatrix} u(\mathbf{x},\, t) \\ v(\mathbf{x},\, t) \end{pmatrix} = \begin{pmatrix} \overline{u} \\ \overline{v} \end{pmatrix} \quad \text{where} \quad f(\overline{u}\,, \overline{v}) = g(\overline{u}\,, \overline{v}) = 0 \quad \text{and, given that}$$

$$J_F(\overline{u}\,, \overline{v}) := \begin{pmatrix} f_u & f_v \\ g_u & g_v \end{pmatrix}, \quad \begin{cases} \operatorname{tr}(J_F) = f_u + g_v < 0 \\ \det(J_F) = f_u \cdot g_v f_v \cdot g_u > 0 \end{cases} \quad \text{(linear stability)}$$

2. Correct behaviour in the neighborhood of the fixed point $(\overline{u},\, \overline{v})$:

3. Diffusion-Driven Instability

Qualitatively, those functions should describe the following facts:

- the activator u enhances its own production and the production of the inhibitor v;

- the inhibitor v suppresses the production of both the activator u and itself,

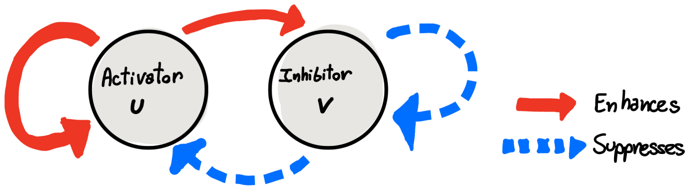


Figure 2.1: A state diagram of the reactions

Mathematically, these conditions translate to the following relations on the partial derivatives:

$$\begin{cases} \frac{\partial f}{\partial u} > 0\,, & \frac{\partial f}{\partial v} < 0 \\ \frac{\partial g}{\partial u} > 0\,, & \frac{\partial g}{\partial v} < 0 \end{cases}$$

It is required that, in absence of diffusion, a uniform stationary state exists, i.e. $(\overline{u}\,,\overline{v})$ where $f(\overline{u}\,,\overline{v}) = g(\overline{u}\,,\overline{v}) = 0$.

$$\rightarrow \begin{pmatrix} u(\mathbf{x},t) \\ v(\mathbf{x},t) \end{pmatrix} = \begin{pmatrix} \overline{u} \\ \overline{v} \end{pmatrix} \quad \forall\, \mathbf{x},\, t$$

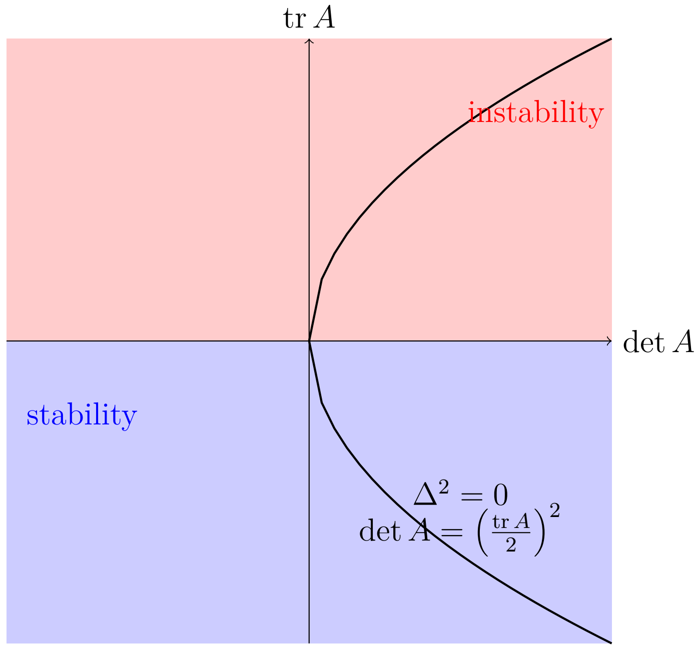
Also, it is required that this equilibrium is linearly stable under the effect of small perturbations. Indeed, the key idea of the Turing model is that the instability is driven by diffusion, and appears only above a certain threshold function of the diffusion parameters.

The linear stability requirement is satisfied if the jacobian matrix of $F(u,v) = (f(u,v), g(u,v))$ evaluated at the fixed point $(\overline{u}\,,\overline{v})$, $J_F(\overline{u}, \overline{v})$, has all eigenvalues with negative real parts $\mathcal{R}e(\lambda_i) < 0$. Say

$$J_F(\overline{u}\,,\overline{v}) := \begin{pmatrix} f_u & f_v \\ g_u & g_v \end{pmatrix}$$

Then

$$Re\{\lambda_i\} < 0 \iff J_F(\overline{u}\,,\overline{v}) < 0 \quad \text{(neg. def.)} \iff \begin{cases} \mathrm{tr}(J_F) < 0 \\ \det(J_F) > 0 \end{cases} \iff \begin{cases} f_u + g_v < 0 \\ f_u \cdot g_v - f_v \cdot g_u > 0 \end{cases}$$


tr A
instability
det A
stability
$\Delta^2 = 0$
$\det A = \left(\frac{\operatorname{tr} A}{2}\right)^2$

[2]

3 | Bibliography

[1] Mark A. Lewis Yingfei Yi Arianna Bianchi, Thomas Hillen. *The Dynamics of Biological Systems*. Mathematics of Planet Earth. Springer Cham, 2019. doi: 10.1007/978-3-030-22583-4.

[2] J. D. Murray. *Mathematical Biology II*. Interdisciplinary Applied Mathematics. Springer New York, NY, 3 edition, 2003. doi: 10.1007/b98869.

[3] Mikhailov A. Nakao, H. Turing patterns in network-organized activator–inhibitor systems. *Nature Phys*, 2010. doi: 10.1038/nphys1651.

[4] Takashi Miura Shigeru Kondo. Reaction-diffusion model as a framework for understanding biological pattern formation. *Science*, 2010. doi: 10.1126/science.1179047.

A guide to the bibliography

This assignment specifically focuses on Turing patterns in *networks*, with recommendation to replicate the findings presented in [3].

However, for someone unfamiliar with Turing patterns, a few preliminary read may be necessary. Article [4], targeted at biologists, offers an intuitive overview of the concept with minimal mathematical details. To delve deeper into the mathematical foundations, [2, *Chapter 2: Spatial Pattern Formation with Reaction Diffusion Systems*] provides a comprehensive and detailed explanation of Turing Patterns in a continuous medium. Another valuable resource is [1, *Chapter 7: The Turing Model for Biological Pattern Formation*], which, while shorter than Murray's chapter, still offers insightful observations.