Turing Patterns: How Development Take Shape

A concise tutorial on biological motivation, reaction–diffusion mathematics, simulation, and classical models

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1 Part 1 — Biological Motivation

1.1 Development as spatial organization

Figure 1: Patterns and Forms in Biological Development.

A developing organism must generate positional information. Cells need to determine where they are, which identity to adopt, and how to organize with neighboring cells. This produces repeated structures, pigmentation patterns, and complex tissue architectures.

The central question is:

How does a developing organism generate spatial information?

The genome provides molecular instructions, but not a literal map of every final cell position. Spatial order can instead emerge through **self-organization**: simple local interactions produce global structure.

1.2 Turing's idea

In 1952, Alan Turing proposed that pattern can emerge from the interaction of:

- **Reaction**: molecules regulate local production and degradation.
- **Diffusion**: molecules move through space.

Individually, reaction is local and diffusion smooths differences. Together, they can produce spontaneous spatial organization.

$$\text{local interactions} + \text{differential movement} \longrightarrow \text{emergent pattern}$$

1.3 Activator–inhibitor logic

A minimal conceptual system contains:

- an **activator** that amplifies a local signal,
- an **inhibitor** that suppresses activation and spreads farther.

This gives the classic principle:

$$\boxed{\text{short-range activation} + \text{long-range inhibition}}$$

Diffusion usually erases gradients. Turing's insight was that, in a coupled system with unequal diffusion rates, diffusion can destabilize a uniform state rather than restore it.

Biological patterns do not always require a pre-existing blueprint. Spatial information can emerge from local molecular interactions coupled to transport.

2 Part 2 — Reaction–Diffusion Mathematics

2.1 Reaction

A reaction describes local molecular change:

$$\frac{\partial u}{\partial t} = f(u),$$

where u is concentration and $f(u)$ combines production, degradation, activation, and inhibition. Reaction alone has no spatial term.

2.2 Diffusion

Diffusion is described by:

$$\frac{\partial u}{\partial t} = D\nabla^2 u,$$

where D is the diffusion coefficient and $\nabla^2 u$ is the Laplacian.
The Laplacian compares a point with its neighborhood:

$$\nabla^2 u = \frac{\partial^2 u}{\partial x^2} + \frac{\partial^2 u}{\partial y^2}.$$

A local maximum tends to decrease; a local minimum tends to increase. Diffusion therefore smooths spatial variation.

2.3 Reaction plus diffusion

For one component:

$$\frac{\partial u}{\partial t} = f(u) + D_u\nabla^2 u.$$

For two interacting components:

$$\frac{\partial u}{\partial t} = f(u, v) + D_u\nabla^2 u,$$

$$\frac{\partial v}{\partial t} = g(u, v) + D_v\nabla^2 v.$$

Here:

- $f(u, v)$ and $g(u, v)$ describe local interactions,
- $D_u\nabla^2 u$ and $D_v\nabla^2 v$ describe transport.

2.4 Diffusion-driven instability

A classical Turing system begins near a homogeneous steady state:

$$f(u^*, v^*) = 0, \qquad g(u^*, v^*) = 0.$$

The reaction system is stable without diffusion. A small spatial perturbation is then introduced. Under suitable kinetics and differential diffusion, selected spatial modes grow.

uniform state → small perturbation → local amplification → spatial pattern

A common activator–inhibitor condition is:

$$D_v > D_u,$$

although unequal diffusion alone is not sufficient. The reaction Jacobian, diffusion coefficients, parameters, boundary conditions, and domain size must all be compatible with instability.

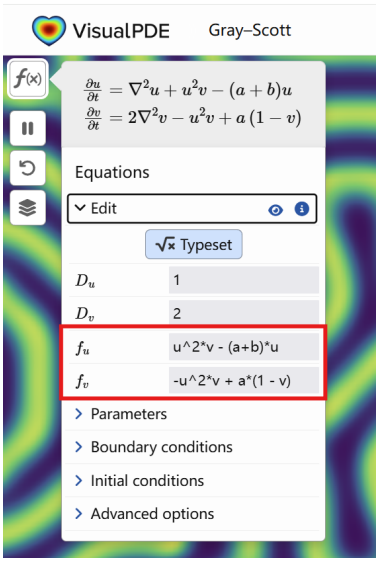
3 Part 3 — Build Your First Turing Model

Task 1 — Build a reaction–diffusion system

Construct, step by step:

- single-molecule diffusion,
- two-molecule diffusion,
- positive feedback,
- an activator–inhibitor system.

Use Python in a Jupyter Notebook or implement the equations in VisualPDE(recommend). The website: https://visualpde.com/sim/ This simulator is initially the Gray–Scott Model. You can edit the equations in the f(x) panel at the top right corner to visualize different reaction–diffusion simulations.



This section adds one mechanism at a time.

Caution: Parameter tuning requires care. Some parameter combinations may lead to numerical instability or runaway growth! You may consult AI to identify suitable parameter ranges for exploration.

3.1 Numerical setup

On a square grid, a five-point approximation is:

$$\nabla^2 u_{i,j} \approx u_{i+1,j} + u_{i-1,j} + u_{i,j+1} + u_{i,j-1} - 4u_{i,j}.$$

Euler time integration gives:

$$u^{n+1} = u^n + \Delta t \left(D_u \nabla^2 u^n + f(u^n, v^n) \right).$$

The same update applies to v.

3.2 Step 1: Diffusion — molecules move through space

The simplest spatial process is diffusion.

For one molecule u:

$$\boxed{\frac{\partial u}{\partial t} = D_u \nabla^2 u}$$

where D_u is the diffusion coefficient.

The Laplacian describes the difference between the concentration at one point and its neighbors.

A local concentration peak will gradually spread:

$$\text{high concentration} \rightarrow \text{lower concentration}$$

Therefore:

Diffusion smooths spatial differences.

Diffusion alone cannot create spatial patterns because it always drives the system toward uniformity.

3.3 Step 2: Two molecules diffuse independently

Now consider two molecular species:

$$u(x, y, t), \qquad v(x, y, t)$$

with different diffusion coefficients:

$$\frac{\partial u}{\partial t} = D_u \nabla^2 u,$$

$$\frac{\partial v}{\partial t} = D_v \nabla^2 v.$$

For example:

$$D_v > D_u$$

means that v spreads faster than u.

Although the two molecules have different spatial ranges, they do not interact.

Different diffusion rates alone are not sufficient to generate patterns.

A mechanism is required to amplify spatial differences.

3.4 Step 3: Add autocatalytic activation

A key idea in biological pattern formation is positive feedback.

A simple chemical reaction can be written as:

$$2U + V \to 3U$$

According to the mass-action principle, the reaction rate is:

$$r = u^2 v.$$

This means that existing u molecules promote the production of more u.

The corresponding model is:

$$\boxed{\frac{\partial u}{\partial t} = D_u \nabla^2 u + u^2 v}$$

$$\boxed{\frac{\partial v}{\partial t} = D_v \nabla^2 v - u^2 v}$$

The term:

$$u^2 v$$

has two roles:

- It increases u through autocatalytic activation.
- It consumes v as a reaction resource.

A small fluctuation can therefore be amplified:

$$\text{small fluctuation} \to \text{local amplification}.$$

However, activation alone cannot generate stable spatial organization.

Positive feedback amplifies signals, but a stabilizing mechanism is still required.

3.5 Step 4: Add production and degradation — the Schnakenberg model

Real biological systems usually contain continuous production and degradation.

We therefore add:

- constant production of u: $+a$,
- degradation of u: $-u$,
- constant production of v: $+b$.

The model becomes:

$$\boxed{\frac{\partial u}{\partial t} = D_u \nabla^2 u + a - u + u^2 v}$$

$$\boxed{\frac{\partial v}{\partial t} = D_v \nabla^2 v + b - u^2 v}$$

This is the Schnakenberg reaction–diffusion model.
The reaction terms are:

$$\boxed{f(u,v) = a - u + u^2 v}$$

$$\boxed{g(u,v) = b - u^2 v}$$

The nonlinear term $u^2 v$ represents autocatalytic production of u coupled with consumption of v.

A classical Turing instability requires:

1. a homogeneous steady state,
2. stability of that state without diffusion,
3. a small spatial perturbation,
4. diffusion-driven growth of selected modes.

$$\boxed{\text{reaction} + \text{diffusion} + \text{instability} \longrightarrow \text{spatial pattern}}$$

Different models share this framework. Their main difference lies in $f(u,v)$ and $g(u,v)$.

3.6 Minimal Python implementation

```
import numpy as np

def laplacian(z):
    return (
        np.roll(z, 1, axis=0)
        + np.roll(z, -1, axis=0)
        + np.roll(z, 1, axis=1)
        + np.roll(z, -1, axis=1)
        - 4.0 * z
    )

def simulate_schnakenberg(
    size=100, steps=12000,
    Du=1.0, Dv=40.0,
    a=0.1, b=0.9,
    dt=0.002, seed=4
):
    rng = np.random.default_rng(seed)

    u_star = a + b
    v_star = b / (a + b)**2

    u = u_star + 0.01*rng.standard_normal((size, size))
    v = v_star + 0.01*rng.standard_normal((size, size))

    for _ in range(steps):
        f = a - u + u**2*v
        g = b - u**2*v

        u += dt*(Du*laplacian(u) + f)
        v += dt*(Dv*laplacian(v) + g)

    return u, v
```

Task 2 — Explore parameter space

Vary diffusion coefficients and reaction parameters in your Python or in VisualPDE. Record:

- whether a pattern forms,
- spot or stripe morphology,
- characteristic spacing,
- time to pattern formation,
- a possible biological interpretation.

4 Part 4 — Classical Reaction–Diffusion Models

4.1 Why are there many models?

A reaction–diffusion model is a simplified mechanistic hypothesis. Different reaction functions can represent autocatalysis, inhibition, substrate depletion, external supply, degradation, or saturation.

There is no universally best model. A model is useful when its assumptions match the biological or physical question.

4.2 A unified framework of Turing patterns

All two-component reaction–diffusion models can be written as:

$$\boxed{\frac{\partial u}{\partial t} = D_u \nabla^2 u + f(u,v)}$$

$$\boxed{\frac{\partial v}{\partial t} = D_v \nabla^2 v + g(u,v)}$$

4.3 Schnakenberg model

$$f(u,v) = a - u + u^2 v, \qquad g(u,v) = b - u^2 v.$$

Mechanism: constant supply, removal of u, and autocatalytic conversion coupled to depletion of v.

Typical use: a compact model for classical diffusion-driven instability.

Typical behavior: stationary spots, stripes, and mixed patterns.

4.4 Gierer–Meinhardt model

One common form is:

$$f(u,v) = \rho_u \frac{u^2}{v} - \mu_u u + \sigma_u,$$

$$g(u,v) = \rho_v u^2 - \mu_v v + \sigma_v.$$

Mechanism: u self-activates, promotes production of v, and is suppressed by v. Usually $D_v \gg D_u$.

Typical use: developmental patterning, organizers, and morphogen-based systems.

For numerical work, replace v by $v + \varepsilon$ in the denominator.

4.5 Gray–Scott model

$$f(u,v) = -uv^2 + F(1-u),$$

$$g(u,v) = uv^2 - (F+k)v.$$

The core reaction is:

$$U + 2V \to 3V.$$

Mechanism: substrate feed, nonlinear conversion, and removal.
Typical use: open chemical systems and computational pattern exploration.
Typical behavior: spots, replication, labyrinths, waves, and dynamic patterns. Not every Gray–Scott pattern is a classical stationary Turing pattern.

4.6 Brusselator model

$$f(u,v) = A - (B+1)u + u^2 v,$$

$$g(u,v) = Bu - u^2 v.$$

Mechanism: input, conversion, and nonlinear autocatalysis.
Typical use: theoretical studies of chemical oscillations and pattern-forming instability.
Typical behavior: uniform states, oscillations, waves, and Turing patterns.

4.7 Minimal saturating activator–inhibitor model

$$f(u,v) = \alpha \frac{u^2}{K^2 + u^2} - \gamma uv - \mu_u u,$$

$$g(u,v) = \beta u - \mu_v v.$$

Mechanism: bounded self-activation, inhibitor production, inhibition, and degradation.
Typical use: a teaching model for local activation and long-range inhibition.

4.8 Model comparison

Model	Main mechanism	Interpretation	Common behavior
Schnakenberg	Autocatalysis and substrate depletion	Idealized mass-action network	Stationary spots and stripes
Gierer–Meinhardt	Activator–inhibitor feedback	Short-range activation and long-range inhibition	Localized peaks and periodic patterns
Gray–Scott	Feed, conversion, and removal	Open chemical system	Static and dynamic complex patterns
Brusselator	Autocatalytic chemical kinetics	Idealized oscillatory chemistry	Oscillations, waves, and Turing patterns
Saturating activator–inhibitor	Bounded activation and inhibition	Simplified regulatory network	Spatial competition

The diffusion terms describe transport. The reaction functions $f(u,v)$ and $g(u,v)$ encode the mechanistic hypothesis.

Task 3 — Compare classical models

Simulate several models, such as Schnakenberg, Gierer–Meinhardt, Gray–Scott, and Brusselator. Compare their assumptions, pattern morphology, strengths, and limitations. Use Python in a Jupyter Notebook or implement the equations in VisualPDE, then Vary diffusion coefficients and reaction parameters. Just same as Task 1 Task 2.

When selecting or designing a model, ask:

1. What activates what?
2. What inhibits what?
3. Is production linear, cooperative, or saturating?
4. Are components supplied or removed externally?
5. Which component moves faster?
6. Does the model represent a specific pathway or a general mechanism?

Optional Tasks

Pattern challenge

Try to generate patterns resembling:

- leopard spots,
- zebra stripes,
- fish-like pigmentation,
- labyrinths or fingerprints.

Document the model and parameter set used.

Mars Mission — Design your own model

A new morphogen system has been discovered on Mars. No model exists.
Design your own $f(u, v)$ and $g(u, v)$:

- state the biological assumptions,
- simulate the system,
- test whether patterns are stable,
- compare the behavior with a classical model.

There is no single correct answer.

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