Organization and fluctuations in living systems

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Organization and fluctuations in living systems

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The totality is not, as it were, a mere heap, but the whole is something besides the parts.

Aristotle

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Abstract

The formation of structures in living organisms is addressed within the framework of far-from-equilibrium chemical systems using methods of statistical physics, such as kinetic theory and stochastic methods, at an intermediate, mesocopic scale. Three directions are explored. For the purpose of investigating the stochastic elimination of a fast variable, a fast species is eliminated from a nonlinear chemical mechanism. The fluctuations of the slow species using Langevin equations and a master equation are not correctly predicted by the reduced mechanism. The coupling between the fluctuations and the nonlinearities of deterministic dynamics makes the use of the quasi-steady-state approximation delicate when the studied system requires a good control such as in fluorescence correlation spectroscopy (FCS). A submicrometric Turing pattern is simulated in a concentrated system in order to refute certain objections to Turing's model regarding the preservation of proportions in embryos. Assuming an appropriate role of the solvent in the chemical mechanism is sufficient to control the wavelength of the structure by monitoring the concentration of the solution. The results can be exploited to design materials with controlled submicrometric properties in chemical engineering. Following a biomimetic approach, experimental conditions leading to the termination of the Turing structure associated with a decrease of the wavelength are proposed. The sensitivity of the Fisher-Kolmogorov, Petrovsky, Piskunov wave front to small perturbations is used to characterize the effects of the deviation from the dilution limit on diffusion. As a result, the shift of the concentration profiles of two species associated with different diffusion coefficients is a well-adapted criterion to detect perturbations induced by high concentrations. Contrary to the results of a deterministic description, the front speed deduced from the master equation in the dilute case sensitively depends on the diffusion coefficient of the consumed species. In the case of a concentrated solution, the properties of the wave front obtained in the dilute case remain valid but are mitigated by cross-diffusion terms which reduce the impact of different diffusion coefficients.

Streszczenie

Tworzenie struktur w organizmach żywych rozważane jest w ramach odległych od równowagi układów chemicznych przy użyciu metod fizyki statystycznej, takich jak teoria kinetyczna i metody stochastyczne, w pośredniej, mezoskopowej skali. Badane są trzy kierunki. W celu zbadania eliminacji szybkiej zmiennej stochastycznej, wprowadzono szybko reagujący związek do nieliniowego mechanizmu chemicznego. Fluktuacje związku o powolnej dynamice uzyskane za pomocą równań Langevina i równania master nie są prawidłowo przewidywane w mechanizmie zredukowanym. Sprzężenie fluktuacji z nieliniowością dynamiki deterministycznej sprawia, że stosowanie przyblizenia quasi-stacjonarnego jest delikatne, gdy badany układ wymaga dobrej kontroli, np. w spektroskopii korelacji fluorescencyjnej (FCS). Submikrometryczna struktura Turinga jest symulowana w układzie stężonym w celu odrzucenia pewnych zastrzeżeń do modelu Turinga dotyczących zachowania proporcji w zarodkach. Przyjęcie odpowiedniej roli rozpuszczalnika w mechanizmie chemicznym jest wystarczające do kontroli długości fali struktury poprzez monitorowanie stężenia roztworu. Wyniki mogą być wykorzystane do projektowania materiałów o kontrolowanych właściwościach submikrometrycznych w inżynierii chemicznej. Zgodnie z podejściem biomimetycznym, proponowane są warunki doświadczalne prowadzące do zakończenia struktury Turinga związane ze zmniejszeniem długości fali. Wrażliwość frontu fali Fishera-Kolmogorowa, Petrovskiego, Piskunova na małe perturbacje jest wykorzystywana do scharakteryzowania wpływu odchylenia od granicy rozcieńczenia na dyfuzję. W rezultacie, rozsunięcie profili stężeń dwóch składników związanych z różnymi współczynnikami dyfuzji jest kryterium dobrze dostosowanym do wykrywania perturbacji wywołanych przez wysokie stężenia. W przeciwieństwie do wyników opisu deterministycznego, prędkość frontu wyprowadzona z równania master w przypadku rozcieńczonym zależy od współczynnika dyfuzji gatunku konsumowanego. W przypadku roztworu stężonego, właściwości frontu fali uzyskane dla przypadku rozcieńczonego pozostają ważne, ale są łagodzone przez efekty dyfuzji krzyżowej, które zmniejszają wpływ odmiennych współczynników dyfuzji.

Contents

Preamble

Living organisms are fascinating examples of reaction-diffusion systems evolving into self-organized structures through sustained exchanges with the environment. Periodic time oscillations of concentrations, chaotic behaviors, and complex spatial structures are observed in chemical systems maintained far from equilibrium [1, 2, 3, 4].

The formation of Turing patterns and the propagation of a wave front are recognized as playing an essential role in the structuring of living organisms [2]. In 1952, Turing proved that reaction-diffusion processes in initially homogeneous far-from-equilibrium systems may lead to the formation of periodic spatial patterns observed in biology [5]. Zebra stripes and leopard spots are classical illustrations of the contribution of far-from-equilibrium reaction-diffusion systems to the modeling of morphogenesis. Turing's model is now used as a chemical basis for embryo development, e.g. in limb formation and teeth development [6, 7]. Even earlier, in 1937, Fisher built a model describing the propagation of a favored trait in a population. Simultaneously, Kolmogorov, Petrosky, and Piskunov studied the traveling solution of the same equation, further referred to as the FKPP wave front. The information conveyed by a signaling wave front during segmentation is at the base of different models of development [8, 9, 10, 11, 12].

Although associated with chemical mechanisms involving elementary steps between molecules, Turing patterns and FKPP wave fronts were first studied within the framework of a macroscopic approach based on partial differential equations. However, the description of phenomena arising during the early development, when the embryo is composed of a small number of cells, may require approaches at smaller scales. The interplay between fluctuations and nonlinear dynamics is known to induce non intuitive, model-specific behaviors [1, 13, 14]. The description of reaction-diffusion systems at the mesoscopic scale requires stochastic methods introducing random variables but still ignoring the detail of molecular dynamics [15, 16]. The crudest stochastic method used to describe reaction-diffusion systems consists in adding a Langevin force to the deterministic equations and assuming that the probability distribution of the concentrations is Gaussian [13, 14]. The correct description at the mesoscopic scale leads to a master equation relying on the well-founded hypothesis that reactions and diffusion are Markov processes. Reac-

tions are seen as birth and death processes, whereas diffusion is interpreted as jumps between adjacent spatial boxes [1]. Numerical simulations become necessary to describe dynamics at the molecular scale. When the details of electronic reorganization within a molecule can be ignored, classical mechanics is sufficient to describe particle dynamics. Simulations of molecular dynamics involve the computationally expensive deterministic processing of particle displacements and collisions, which could compromise reaching the space and time scales necessary for the emergence of structures in growing systems. In these conditions, it is appealing to consider the smart method intuited and developed by Graeme Bird and known as the direct simulation Monte Carlo (DSMC) [17, 18, 19]. DSMC has been designed to simulate the dynamics of dilute gases and is particularly adapted to space applications [20, 21, 22]. The collisions are efficiently treated through a random procedure known as Monte Carlo. It has been proven [23] that DSMC simulates the Boltzmann equations governing the evolution of the distribution functions for position and velocity of the particles [24]. In addition to following the laws of kinetic theory, DSMC provides stochastic trajectories and correctly simulates the fluctuations in agreement with the master equation [25]. Hence, the direct simulation Monte Carlo method offers an efficient alternative to molecular dynamics and gives access to space and time scales compatible with the simulation of emerging micrometric structures.

In this work, I developed stochastic approaches to far-from-equilibrium structures and focused on Turing patterns and Fisher-Kolmogorov, Petrovsky, and Piskunov wave fronts, both for their relevance in biology and the richness of their behavior from a fundamental point of view. Within this framework, several usual approximations have been revisited. The question of the elimination of a variable, encountered in the study of Turing patterns, incited me to investigate the validity of the widely used steady-state approximation in systems with large fluctuations. I was also led to consider the deviation from the high-dilution limit as a possible way to tune the features of a pattern. Beyond the application to the adaptability of a structure, dealing with concentrated systems prompted me to deepen my knowledge of the cross-diffusion phenomenon and the associated form of Fick's law deduced from irreversible thermodynamics in the linear domain [26]. In parallel, extending both the master equation and the direct simulation Monte Carlo method to concentrated solutions was an attractive challenge.

The manuscript is organized as follows. In the Chapter I, I recall the analytical and numerical methods that I used and adapted to concentrated systems.

The validity of the steady-state approximation in a small chemical system is questioned in Chapter II. In order to investigate to which extent the description of the fluctuations remains correct after elimination of a fast variable, I compared the correlations of concentration fluctuations for two different chemical mechanisms leading to the same reduced

mechanism in which a reactive intermediate species has been omitted. I first drew an analogy between the steady-state approximation and the Born-Oppenheimer approximation and expressed the conditions of validity of the steady-state approximation applied at the macroscopic scale. Then, I developed two stochastic approaches. Using an analytical Langevin approach and simulations of the master equation, I showed that the correlations of concentration fluctuations of the slow species are different depending on whether a fast intermediate species is considered or not in the reaction scheme. In biology, Fluorescence Correlation Spectroscopy (FCS) is widely used to study the dynamics of labeled species, for example to evaluate rate constants when the reaction scheme is supposed to be known [27, 28]. The interpretation of the results requires the comparison of the experimental data with analytical expressions of the correlations. My results point out that, even if it enables the analytical computation of the correlations, a tractable reduced reaction scheme could be misleading. The results have been published in G. Morgado, B. Nowakowski, and A. Lemarchand, Elimination of fast variables in stochastic nonlinear kinetics, Phys. Chem. Chem. Phys. **22**, 20801 (2020) [29].

Chapter III is devoted to Turing patterns. After recalling the basics of Turing structures, I place the subject in the context of morphogenesis. Turing's model relies on a remarkably small number of processes involving two initially homogeneously distributed chemical substances that interact to produce stable patterns. The model involves two chemical species, an activator and an inhibitor. The minimal reaction-diffusion scheme for the emergence of Turing patterns requires the autocatalytic production of the activator and the faster diffusion of the inhibitor [30]: The structure develops through local self-enhancement in conjunction with long-range lateral inhibition [31]. The wavelength of the periodic spatial structure is determined by the reaction rate constants and the diffusion coefficients of the chemical species. Contrary to Taylor vorticies in hydrodynamics, the striking property of Turing patterns is that the wavelength of the structure does not depend on the boundary conditions. The robustness of Turing patterns is a strong feature, but also an argument against them in morphogenesis. Indeed, Turing patterns lack scaling properties: they do not account for size adaptation of the wavelength to the global size of the system. Yet, models of somitogenesis should reflect that the size of the vertebrae is proportional to the size of the embryo [32, 33, 34, 35]. I addressed two points related to the growth of a Turing pattern in a growing system, the question of the scaling properties of a periodic spatial structure and the question of the termination of the structure.

Recently, the Polish-French group proposed to solve the problem of scaling of a Turing pattern at the macroscopic scale by considering the possible perturbations induced by high concentrations of reactants [36]. In these conditions, the variation of the concentration

of the solvent cannot be neglected. The model that the group developed includes the participation of the solvent into the reaction scheme. This third substance introduces an additional variable concentration that can be harnessed to control the behavior of the system. Changing the dilution of the medium makes it possible to tune the wavelength of the emerging Turing pattern. During this PhD, I performed a deeper analysis of the three-variable model at the microscopic scale and examined if the deviation from the high-dilution limit also induces a control of the pattern in small systems. A proof of concept based on simulations of particle dynamics was necessary. To this goal, I considered the direct simulation Monte Carlo (DSMC) method and adapted it to concentrated solutions. The simulations show that doubling the concentration of the solute leads to decreasing the wavelength of the structure by a factor of 2. The results can be considered as a possible interpretation for proportion preservation of embryos in morphogenesis. They can also be used to design materials with controlled submicrometric properties in chemical engineering. The results have been published in G. Morgado, B. Nowakowski, and A. Lemarchand, Scaling of submicrometric Turing patterns in concentrated growing systems, Phys. Rev. E **98**, 032213 (2018) [37] and were presented at the 31st International Symposium on Rarefied Gas Dynamics in Glasgow, in 2018 [38].

The question of the termination of a spatial structure is compelling in morphogenesis: The spine of the vertebrates ends with smaller vertebrae and the fingers with smaller phalanges. Within the framework of Turing patterns, this phenomenon implies both a decrease of the amplitude of the spatial oscillations and a decrease of the wavelength. Deciphering the mechanisms actually controlling the termination of the spine in an embryo is far beyond the scope of this work. The aim was to propose a possible mechanism, inspired by biological structures and compatible with the implementation in a chemical engineering context. The boundary conditions chosen by the group in 2016 [36] to model the growth of the spine behind a freely propagating wave front are well adapted to the design of an artificial spatial structure. I performed a systematic analysis of the effect of all rate constants and diffusion coefficients on the stability and the wavelength of the structure. Interestingly, a monotonous variation of almost any of the dynamical parameters leads to the simultaneous loss of stability of the structure and the decrease of the wavelength. Only the variation of the diffusion coefficient of the activator causes anticorrelated results. Locally varying a rate constant or the diffusion coefficient of the inhibitor in a given chemical system is not straightforward from an experimental point of view. For an easy implementation in chemical engineering, I suggest to impose an appropriate spatial profile for the concentration of the reservoir of inhibitor, resulting in the expected variation of the effective rate constant controlling the injection of the inhibitor in the system and leading to the desired termination of the structure. The results have been published in G. Morgado, L. Signon, B. Nowakowski, and A. Lemarchand, Termination

mechanism of Turing patterns in growing systems, Acta Phys. Pol. B, 50, 1369 (2019) [39].

The results obtained for the model of Turing patterns with a reactive solvent have opened new directions of research. The deviation from the high-dilution limit has an impact on both reaction and diffusion. In the case of Turing patterns, the perturbation of diffusion induced by high concentrations has a negligible effect on the wavelength of the structure. In order to investigate the possible consequences of the perturbation of diffusion in a concentrated reaction-diffusion system, I considered the case of pulled wave fronts, known to be sensitive to even small perturbations [40]. The results dealing with wave fronts are given in Chapter IV. For species with identical diffusion coefficients, the group already showed that an FKPP front is sensitive to the discrete nature of particles [41] and to reaction-induced deviations from partial equilibrium [42]. I proposed an FKPP-based model involving two species A and B engaged in the reaction $A + B \longrightarrow 2\,A$ with different diffusion coeffcients. In a concentrated system, the resulting wave front turns out to be a sensor revealing perturbations of diffusion at the macroscopic scale. Specifically, I showed that the difference of concentrations between the two species A and B at the inflection point of the A profile is a good indicator for diffusion perturbation in concentrated systems. The results have been published in G. Morgado, B. Nowakowski, and A. Lemarchand, Fisher-Kolmogorov-Petrovsky-Piskunov wave front as a sensor of perturbed diffusion in concentrated systems, Phys. Rev. E **99**, 022205 (2019) [43].

Deviations from the high-dilution limit are more prone to happen in small systems, typically in a living cell, where the amplitude of concentration fluctuations are significant. I therefore performed a stochastic analysis of fluctuation effects on an FKPP front with perturbed diffusion in a mesoscopic system. Unexpected results on a more than eighty-year-old problem have been obtained: In a dilute system of small size, the wave front propagates more slowly than expected if species B diffuses faster than species A. In a concentrated system, the results are mitigated by cross-diffusion which reduces the effect of different diffusion coefficients. The results have been published in G. Morgado, B. Nowakowski, and A. Lemarchand, Stochastic approach to Fisher and Kolmogorov, Petrovskii, and Piskunov wave fronts for species with different diffusivities in dilute and concentrated solutions, Physica A **558**, 124954 (2020) [44].

Chapter V contains conclusions.

Chapter I

Methods

This chapter presents different theroretical tools of macroscopic and stochastic descriptions of dynamical systems in chemistry that will be used in later chapters. Mathematical notations are also introduced.

I.1 Chemical kinetics

All considered systems involve reactive species and possibly non reactive species such as the solvent. The steps of a reaction scheme are supposed to be elementary reactions for which the standard laws of kinetics apply. The left-hand side of elementary steps involve one or more molecules. When only one molecule is involved in the left-hand side, the step leads to a *first-order* reaction rate. At the microscopic scale, it usually corresponds to an internal molecular reorganization. When two molecules are involved in the left-hand side, the step leads to a *second-order* reaction rate. At particle scale, it occurs through reactive collisions between two molecules.

It is very unlikely that a collision of more than two molecules occurs. Therefore, we consider that reactions of order higher than two result from the reduction of a set of elementary steps of first and second orders. The assumptions making this reduction possible will be discussed in Sec. II. Each chemical species is assumed to be subject to diffusive transport.

For some systems, we introduce *reservoirs*. A *reservoir* maintains the concentration of a chemical substance constant by instantaneously removing or adding molecules when needed. A *reservoir* is denoted by the letter R in a reaction scheme, and its constant concentration denoted by c_R.

I.1.1 Rate equations

We consider a reaction scheme involving m different steps with n different species $\mathrm{X_i}$. Each step j is associated with a rate constant k_j such that

$$\sum_{i=1}^{n} \alpha_{i,j} \mathrm{X_i} \xrightarrow{k_j} \sum_{i=1}^{n} \beta_{i,j} \mathrm{X_i} \tag{I.1}$$

where $\alpha_{i,j}$ and $\beta_{i,j}$ are possibly vanishing stoichiometric coefficients.

The rate equations for the concentrations c_i of species X_i associated with this reaction scheme are

$$\mathrm{d}_t c_i = \sum_{j=1}^{m} k_j \left[\beta_{i,j} - \alpha_{i,j}\right] \prod_{i'=1}^{n} c_{i'}^{\alpha_{i',j}} \tag{I.2}$$

where the symbol d_t denotes the derivative with respect to time $\dfrac{\mathrm{d}}{\mathrm{d}t}$.

The system state at a given time t is then defined by the vector of concentrations $\mathbf{c} = (c_1(t), c_2(t), ..., c_n(t))$

If the chemical species $\mathrm{X_i}$ is involved in a second or higher-order reaction, the system given in Eq. (I.2) is nonlinear and, in most cases, has no analytical solution.

I.1.2 Reaction-diffusion equation and Fick's law

In addition to the reaction, we introduce diffusive transport. Diffusion tends to homogenize concentrations in an inhomogeneous medium. According to Fick's law, the diffusive flux $\mathbf{j_i}$ of a given chemical species $\mathrm{X_i}$ is proportional to the concentration gradient

$$\mathbf{j}_i = -D_i \nabla c_i \tag{I.3}$$

where D_i is the diffusion coefficient of species $\mathrm{X_i}$. In a reaction-diffusion system, the local variation of concentration c_i of species $\mathrm{X_i}$ is expressed as the sum of a reactive term and a diffusive term, where the latter is given by the divergence of the flux

$$\partial_t c_i = \sum_{j=1}^{m} k_j \left[\beta_{i,j} - \alpha_{i,j}\right] \prod_{i'=1}^{n} c_{i'}^{\alpha_{i',j}} - \nabla \cdot \mathbf{j}_i \tag{I.4}$$

where the symbol ∂_t denotes the partial derivative with respect to time $\dfrac{\partial}{\partial t}$.

In concentrated mixtures involving more than two species, cross-diffusion effects may appear and are discussed in Sec. I.3

Equation (I.4) is valid in a macroscopic approach, in which local fluctuations have been neglected.

I.1.3 Linear stability analysis

In the general case of a homogeneous chemical system, dynamics is governed by a nonlinear system of differential equations for the concentration vector $\mathbf{c} = (c_1, ..., c_n)$

$$\mathrm{d}_t \mathbf{c} = f(\mathbf{c}) \tag{I.5}$$

where f is a vector function characterizing the reaction rates.

The local dynamics around a steady state $\mathbf{c^0} = (c_1^0, ..., c_n^0)$ obeying

$$\mathrm{d}_t c_i^0 = 0, \, \forall i \tag{I.6}$$

can be studied by the linearized dynamics around this state. In order to perform a linear stability analysis, we introduce the small deviation $\delta c_i = c_i - c_i^0$ to the steady state which obeys

$$\mathrm{d}_t \delta\mathbf{c} = \mathbf{M^0} \delta\mathbf{c} \tag{I.7}$$

where $\delta\mathbf{c} = (\delta\mathbf{c_1}, ..., \delta\mathbf{c_n})$ and

$$\mathbf{M^0} = \left(\frac{\partial f(\mathbf{c})}{\partial \mathbf{c}} \right)_{\mathbf{c}=\mathbf{c^0}} \tag{I.8}$$

is the Jacobian matrix for $\mathbf{c} = \mathbf{c}^0$, called the *stability matrix*. Some laws of conservation can be observed and reduce the number of independent variables. We consider that the n variables are all independent. The deviation $\delta\mathbf{c}$ is related to the vector $\gamma = (\gamma_1, ..., \gamma_n)$ in the eigenbasis of $\mathbf{M^0}$ by

$$\delta\mathbf{c} = \mathbf{P}\gamma \tag{I.9}$$

where $\mathbf{P}$ is the change-of-basis matrix. The linear differential equations given in Eq. (I.7) lead to uncoupled equations in the eigenbasis of $\mathbf{M^0}$

$$\mathrm{d}_t \gamma_i = \mu_i \gamma_i \tag{I.10}$$

where μ_i are the eigenvalues of $\mathbf{M^0}$. Equation (I.10) is straightforwardly solved, leading

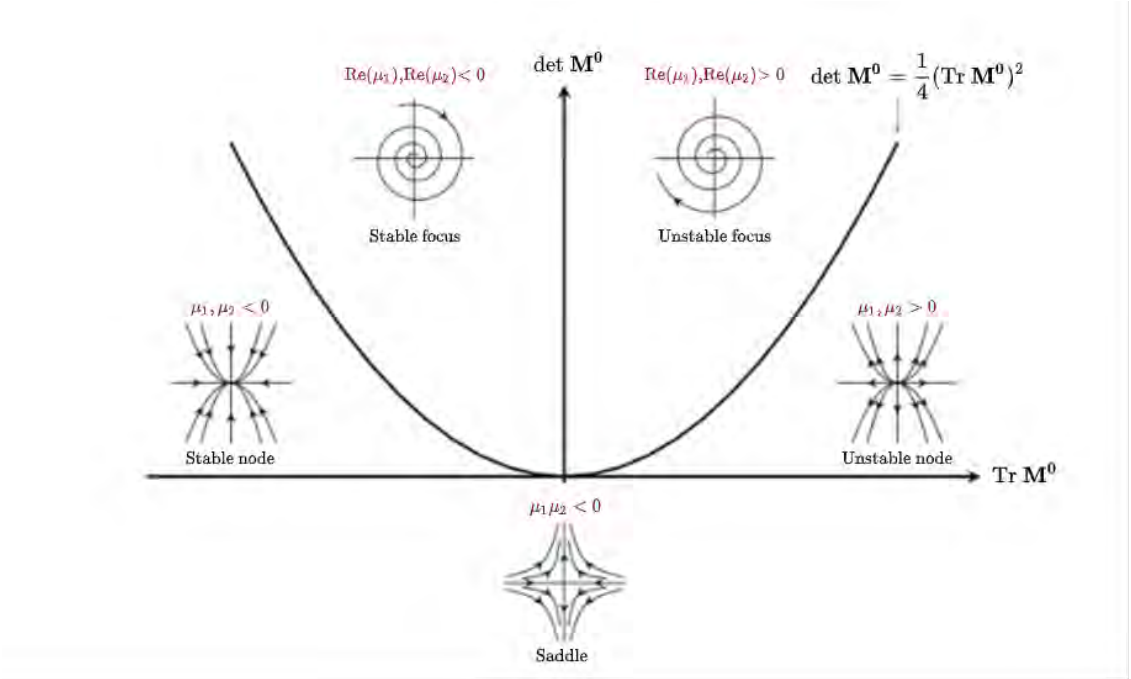


Fig. I.1 *The five typical phase portraits for an $n = 2$ system. [2]*

to

$$\gamma_i = \gamma_i^{\mathrm{ini}} e^{\mu_i t} \tag{I.11}$$

where γ_i^{ini} is the initial value of γ_i.

From Eq. (I.11), it appears that the linear stability of the system is governed by the eigenvalues μ_i. If the real parts of all eigenvalues are negative, then the system eventually converges towards the steady state $\mathbf{c^0}$. The time $\tau_i = 1/|\mathrm{Re}(\mu_i)|$ corresponds to the typical relaxation time in the direction associated with γ_i, as long as the deviation $\delta\mathbf{c}$ is in the linear domain around the steady state $\mathbf{c^0}$.

In Fig. I.1, different phase portraits are presented for an $n = 2$ system. Five typical phase portraits exist: the *stable node* corresponds to two real negative eigenvalues, $\mu_1 < 0$ and $\mu_2 < 0$, the *stable focus* corresponds to two complex-conjugate eigenvalues whose real parts are negative, $\mathrm{Re}(\mu_1) < 0$ and $\mathrm{Re}(\mu_2) < 0$, the *unstable node* corresponds to two real positive eigenvalues, $\mu_1 > 0$ and $\mu_2 > 0$, the *unstable focus* corresponds to two complex-conjugate eigenvalues whose real parts are positive, $\mathrm{Re}(\mu_1) > 0$ and $\mathrm{Re}(\mu_2) > 0$, and the *saddle* corresponds to two real eigenvalues with different signs, $\det \mathbf{M^0} = \mu_1 \mu_2 < 0$.

Finally, substituting Eq. (I.11) for γ_i into Eq. (I.9), we obtain

$$\delta c_i = \sum_j P_{ij} \gamma_j^{\text{ini}} e^{\mu_j t} \tag{I.12}$$

Linear analysis describes local evolution around a steady state within the framework of a macroscopic, deterministic approach. In small systems, close to situations where the dynamics is sensitive to small perturbations, such as bifurcations, a deterministic analysis may be insufficient. A stochastic approach, including the description of the fluctuations at the mesoscopic scale, is then required.
I have used linear stability analyses extended to inhomogeneous systems to study the termination of a Turing structure [39] presented in Sec. III.2.

I.2 Stochastic chemical kinetics

Although chemical dynamics is driven by discrete elementary processes, it is usually sufficient to consider deterministic equations to describe the macroscopic evolution of a chemical system. However, fluctuations may not be negligible in small systems and a stochastic approach may be required [1, 16, 45]. In this section, we introduce two different stochastic descriptions of a chemical system, the chemical Langevin equations [13, 14] and the master equation [1].

I.2.1 Chemical Langevin equations

In this subsection, we introduce a probabilistic approach to a reactive system [46]. We consider the vector of concentrations $\mathbf{c}$ as a vector of random variables. Intuitively, the propensity or transition rate $p_j(\mathbf{c})$ that the j-th step of the reaction occurs in the next time interval $[t, t+dt]$ depends on the order of the step. The probability for a first-order step to occur is proportional to the number of molecules N_i in the system, since each molecule is susceptible to be re-organized

$$\begin{aligned} p_j^I(\mathbf{c})dt = &\text{Probability that a molecule re-organizes itself} \\ &\times \text{Number of molecules } N_i \end{aligned} \tag{I.13}$$

The probability for a second-order step to occur depends on the product of two probabilities

$$\begin{aligned} p_j^{II}(\mathbf{c})dt = &\text{Probability that two given molecules collide} \\ &\times \text{Probability that two colliding molecules react} \\ &\times \text{Number of possible pairs of molecules} \end{aligned} \tag{I.14}$$

According to kinetic theory, the first probability is proportional to the average relative speed and collision cross-section of the two molecules and inversely proportional to the system size Ω. The second probability expresses that reaction occurs if the collision energy exceeds a certain threshold known as activation energy. The product of these two probabilities gives the so-called rate constant introduced in Sec. I.1, except that specific care is needed in order to convert a probability derived from a discrete number of molecules into a proportionality factor that deals with continuous concentrations. Specifically, the conversion introduces as much Ω factors as the order of the reaction.

If concentrations c_i are locally homogeneous, $p_j(\mathbf{c})$ is typically similar to the reactive term in Eq. (I.2) for all reaction orders

$$p_j(\mathbf{c}) \simeq \Omega k_j \prod_{i=1}^{n} c_i^{\alpha_{i,j}} \tag{I.15}$$

During a finite but small time interval $[t, t+\tau]$, the number of reactions $r_j(\mathbf{c}, \tau)$ of step j is a random variable whose mean $\langle r_j \rangle_{t,\tau}$ is deduced from Eq. (I.14)

$$\langle r_j \rangle_{t,\tau} = p_j(\mathbf{c})\tau \tag{I.16}$$

where the concentration $\mathbf{c}$ is evaluated at time t. For the reaction scheme given in Eq. (I.1), the concentration c_i at time $t+\tau$ is given by

$$c_i(t+\tau) = c_i(t) + \frac{1}{\Omega} \sum_{j=1}^{m} (\beta_{i,j} - \alpha_{i,j})\, r_j(\mathbf{c}, \tau) \tag{I.17}$$

Some conditions must be fulfilled for Eqs. (I.16) and (I.17) to hold. On the one hand, τ must be sufficiently small for the variations of concentration between two consecutive time steps to be small. It implies that the propensity given in Eq. (I.14) is constant over the time interval $[t, t+\tau]$. This condition is satisfied if the number of each type of molecules in the system is much larger than 1. On the other hand, τ must be sufficiently large for $r_j(\mathbf{c}, \tau)$ to be substantial, i.e. for the mean number of reactions $\langle r_j \rangle_{t,\tau}$ to be much larger than one. It is not unusual to find systems with sufficiently large numbers of molecules that respect both conditions. Typically, mesoscopic systems are of adequate size for these

two conditions to be satisfied.

It can be argued that each random variable $r_j(\mathbf{c},\tau)$ follows an independent *Poisson* distribution of mean μ. However, the construction of a standard Langevin equation introduces independent first and second cumulants of the probability distribution of $\mathbf{c}$. Using the condition that the system contains a large amount of molecules, each *Poisson* random variable $r_j(\mathbf{c},\tau)$ can be approximated by a normal random variable $\mathcal{N}(\mu,\sigma^2)$ of same mean μ and variance σ^2. The linear combination theorem for normal distributions

$$\mathcal{N}(\mu,\sigma^2) = \mu + \sigma\mathcal{N}(0,1) \tag{I.18}$$

and Eq. (I.16) allow us to write Eq. (I.17) into the form

$$c_i(t+\tau) = c_i(t) + \frac{1}{\Omega}\sum_{j=1}^{m}(\beta_{i,j}-\alpha_{i,j})\left[p_j(\mathbf{c})\tau + (p_j(\mathbf{c})\tau)^{1/2}\mathcal{N}(0,1)\right] \tag{I.19}$$

Considering the time τ as an infinitesimal time interval $\mathrm{d}t$ that respects the conditions mentioned above and using Eq. (I.15), we write Eq. (I.19) as a *chemical Langevin equation*

$$\frac{\mathrm{d}c_i}{\mathrm{d}t} = \sum_{j=1}^{m} k_j(\beta_{i,j}-\alpha_{i,j})\prod_{i'=1}^{n} c_{i'}^{\alpha_{i',j}} + \sum_{j=1}^{m}(\beta_{i,j}-\alpha_{i,j})\left[k_j\prod_{i'=1}^{n} c_{i'}^{\alpha_{i',j}}\right]^{1/2}\xi_j(t) \tag{I.20}$$

with independent Gaussian white noises $\xi_j(t)$

$$\begin{aligned}\langle\xi_j(t)\rangle &= 0\\ \langle\xi_j(t)\xi_{j'}(t')\rangle &= \delta_{j,j'}\delta(t-t')\end{aligned} \tag{I.21}$$

In Eq. (I.20), the first term is the deterministic rate equation given in Eq. (I.2) and the second term is a noise term denoted by η_i. The noise η_i is written as the sum of the noises $\eta_{i,j}$ associated with the reaction steps j involving the chemical species $\mathrm{X_i}$

$$\eta_i(t) = \sum_{j=1}^{m}\eta_{i,j}(t) = \sum_{j=1}^{m}(\beta_{i,j}-\alpha_{i,j})\left[k_j\prod_{i'=1}^{n} c_{i'}^{\alpha_{i',j}}\right]^{1/2}\xi_j(t) \tag{I.22}$$

The variances and covariances of the noises $\langle\eta_i(t)\eta_j(t')\rangle$ are given by

$$\langle\eta_i(t)\eta_j(t')\rangle = \left[\sum_{j'=1}^{m} k_{j'}(\beta_{i,j'}-\alpha_{i,j'})(\beta_{j,j'}-\alpha_{j,j'})\prod_{i'=1}^{n} c_{i'}^{\alpha_{i',j'}}\right]\delta(t-t') \tag{I.23}$$

I have used the Langevin approach in the study of the stochastic elimination of fast variables [29] presented in Sec. II.

I.2.2 Master equation

a) Reactive-only system

Although a Langevin approach is a good start, it requires some assumptions on the size of the system and the nature of the fluctuations. The master equation offers a better description of a system at a mesoscopic scale [1, 14, 47]. We consider that the system has a given probability $P(\{\Phi\}, t)$ to be in a given state

$$\{\Phi\} = \{N_1, N_2, ..., N_n\} \tag{I.24}$$

at time t. The system state is described by the discrete numbers N_i of molecules of each chemical species X_i. During a finite time interval $[t, t+\tau]$, the probability of finding the system in a given state $\{\Phi\}$ evolves according to all possible reactions. The reactions are assumed to be Markov processes. Consequently, the probability $P(\{\Phi\}, t+\tau)$ for the system to be in state $\{\Phi\}$ at time $t+\tau$ only depends on system state at time t and the transition rates or propensities between all states at time t and the state $\{\Phi\}$ at time $t+\tau$

$$\begin{aligned} P(\{\Phi\}, t+\tau) =& P(\{\Phi\}, t) \times \text{Probability to remain in the state } \{\Phi\} \\ &+ \sum_{\{\Phi'\}} [P(\{\Phi'\}, t) \times \text{Probability to jump from state } \{\Phi'\} \text{ to state } \{\Phi\}] \end{aligned} \tag{I.25}$$

The probability of leaving a given state is the sum of the probabilities to go from that state to any other one. The probability to remain in a given state is simply (1− Probability of leaving that state). If we note $T(\{\Phi\} \to \{\Phi'\})$ the transition rate from state $\{\Phi\}$ to state $\{\Phi'\}$, Eq. (I.25) can be written as

$$P(\{\Phi\}, t+\tau) - P(\{\Phi\}, t) = \sum_{\{\Phi'\}} [P(\{\Phi'\}, t) \times T(\{\Phi'\} \to \{\Phi\}) - P(\{\Phi\}, t) \times T(\{\Phi\} \to \{\Phi'\})] \tag{I.26}$$

Intuitively, the probability of leaving the current state $\{\Phi\}$ is the probability that one reaction occurs in the time interval $[t, t+\tau]$, as in Eq. (I.14). Therefore, we use the same assumption as in Eq. (I.15) but with discrete numbers of molecules

$$\sum_{\{\Phi'\}} T(\{\Phi\} \to \{\Phi'\}) = \sum_{j=1}^{m} p_j \tau = \sum_{j=1}^{m} k_j \prod_{i'=1}^{n} A_{\alpha_{i',j}}^{N_{i'}} \tau \tag{I.27}$$

where we made explicit the number of possible pairs of molecules

$$A_{\alpha_{i',j}}^{N_{i'}} = \frac{N_{i'}!}{(N_{i'} - \alpha_{i',j})!} \tag{I.28}$$

Finally, assuming that the time τ is sufficiently small to be considered as an infinitesimal time interval dt and using Eqs. (I.26) and (I.27), we write the *master equation* for a homogeneous reactive system

$$\partial_t P(\{\Phi\},t) = \sum_{j=1}^{m} k_j \left[\prod_{i'=1}^{n} A_{\alpha_{i',j}}^{N_{i'}-(\alpha_{i',j}-\beta_{i',j})} P(\{\Phi'_j\},t) - \prod_{i'=1}^{n} A_{\alpha_{i',j}}^{N_{i'}} P(\{\Phi\},t) \right] \tag{I.29}$$

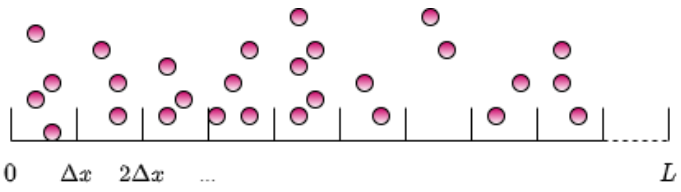
where the state $\{\Phi'_j\}$ is the state that evolves into the state $\{\Phi\}$ after one elementary reaction j.

b) With diffusion

In order to take diffusion into account in a master equation, we introduce at least one space dimension and the transition rates describing the diffusive processes. For any reaction-diffusion system, the master equation can be divided into two terms

$$\partial_t P(\{\Phi\},t) = \partial_t P(\{\Phi\},t)|_{\text{reaction}} + \partial_t P(\{\Phi\},t)|_{\text{diffusion}} \tag{I.30}$$

where the first term accounts for the reactive processes described in Eq. (I.29) and the second term accounts for the diffusive processes. For the sake of simplicity, we assume that there are N molecules of only one chemical species X. The system is a one-dimensional array of length L, divided into ℓ boxes of length $\Delta x = \dfrac{L}{\ell}$



where each box is considered homogeneous. We use periodic boundary conditions. The number of molecules in each box i is denoted by $N(i,t)$. The state of the system is given by

$$\{\Phi\} = \{N(1,t), N(2,t), ..., N(i,t), ..., N(\ell,t)\} \tag{I.31}$$

Similarly to Eq. (I.26), the probability to leave the state $\{\Phi\}$ during a time interval $[t, t+\tau]$ is equal to the probability that a single molecule of the system jumps from its current box to a neighboring one [1, 14]. Assuming that boxes are independent, the probability to leave the state $\{\Phi\}$ can be written as the sum of all probabilities in each box for one

molecule to jump

$$\text{Prob. to leave state } \{\Phi\} = \sum_{\{\Phi'\}} T(\{\Phi\} \to \{\Phi'\}) \tag{I.32}$$

$$= \sum_{i=1}^{\ell} \text{Prob. that one molecule leaves box } i \tag{I.33}$$

The probability to remain in the state $\{\Phi\}$ is then simply (1-Probability to leave state $\{\Phi\}$). Hence, we only need to determine the probability that a molecule leaves a box i. This probability is given by the propensity d_i that one molecule leaves the box i

$$d_i dt = (\text{Probability that the molecule jumps to the left} \tag{I.34}$$

$$+\text{Probability that the molecule jumps to the right}) \tag{I.35}$$

$$\times \text{Number of molecules in the box } i \tag{I.36}$$

According to kinetic theory, the probability for a molecule to go left or right is proportional to the square root of temperature [14]. The Einstein relation gives the relation between the macroscopic diffusion coefficient of Eq. (I.3) and temperature. Typically, in large systems, the diffusive flux between two cells is related to the propensity d_i. We have

$$d_i \simeq \frac{2D}{\Delta x^2} N(i,t) \tag{I.37}$$

where D is the diffusion coefficient of the chemical species X. Using this approximation, we write the diffusion term of Eq. (I.30) for a single species in the form

$$\partial_t P(\{\Phi\},t)|_{\text{diffusion}} = \frac{D}{\Delta x^2} \sum_{i=1}^{\ell} (N_i + 1) \left[P(\{N(i-1,t)-1, N(i,t)+1\} + P(\{N(i,t)+1, N(i+1,t)-1\} \right.$$

$$\left. - 2N_i P(\{\Phi\},t) \right. \tag{I.38}$$

where only the number of molecules differing from $N(i,t)$ in cell i are made explicit.

I have used a master equation approach in the study of the stochastic elimination of a fast variable [29] presented in Sec. II and in the analysis of fluctuation effects of an FKPP wave front [44] presented in Sec. IV.2.2.

I.3 Concentrated solution

Usually, in solutions, solvent particles are nonreactive and in large excess compared to reactants. Hereafter, a solution is said highly diluted when the local solvent concentration is arguably constant. Considering the high-dilution limit ensures that the diffusion

coefficient of all reactants and the concentration of the solvent are constant. Hence, in the case of a reactive solvent, its concentration can be included into the rate constants of the corresponding reactions. However, small systems may be crowded, which invalidates the approximation of a large amount of solvent. The study of the effects of a deviation from the high-dilution limit in small systems is therefore necessary.

I.3.1 High-dilution limit

We present the effect of the deviation from the high-dilution limit on the reaction-diffusion dynamics using a simple example. We consider the Verhulst model [48]

$$\mathrm{A} + \mathrm{S} \xrightarrow{k} 2\,\mathrm{S} \tag{I.39}$$

where A is a reactive species and S a reactive solvent. In the absence of hypothesis on the relative orders of magnitude of the concentrations c_A and c_S of species A and S, the rate equation for A is

$$\mathrm{d}_t c_A = -k c_A c_S \tag{I.40}$$

The total concentration c^{tot} of chemical species

$$c^{\mathrm{tot}} = c_A + c_S \tag{I.41}$$

is constant according to Eq. (I.39). Therefore, we can eliminate Eq. (I.40)'s dependency on c_S

$$\mathrm{d}_t c_A = -k c^{\mathrm{tot}} c_A \left(1 - \frac{c_A}{c^{\mathrm{tot}}}\right) \tag{I.42}$$

and recognize the logistic function. The solution of Eq. (I.42) is

$$c_A(t) = \frac{c^{\mathrm{tot}} c_A^{\mathrm{ini}} e^{-k c^{\mathrm{tot}} t}}{c^{\mathrm{tot}} + c_A^{\mathrm{ini}} (e^{-k c^{\mathrm{tot}} t} - 1)} \tag{I.43}$$

where c_A^{ini} is the initial value of c_A.
However, if the reaction scheme involves more steps and is more complex, the associated rate equations may not be solvable. In this case, it is possible to assume that the concentration of solvent c_S is much larger than the concentration of reactants. Consequently, c_S is considered constant and the reaction step becomes a lower-order reaction

$$\mathrm{A} \xrightarrow{k_S} 2\,\mathrm{S} \tag{I.44}$$

where the modified rate constant k_S is given by

$$k_S = kc_S \tag{I.45}$$

This approximation is what we call the *high-dilution limit*. Our aim is to characterize the deviation from the high-dilution limit. Thus, we define the parameter

$$\delta = \frac{\sum\limits_{i \neq S} c_i^0}{c^{\text{tot}}} = 1 - \frac{c_S^0}{c^{\text{tot}}} \tag{I.46}$$

that represents the ratio of the sum of the concentrations c_i^0 of all non-solvent reactants evaluated at a steady state and the total concentration. When δ tends to 0, the solvent is in large excess with respect to the other species and the high-dilution approximation is valid. On the contrary, when δ increases, the deviation from the high-dilution limit increases, and the previous assumption fails. This parameter is defined at a homogeneous stationary state such that it remains constant even if the system exhibits spatial structures such as Turing patterns. If the system exhibits multiple stationary states, the parameter is defined according to the stable homogeneous stationary state of interest.

I.3.2 Modified Fick's law in a concentrated solution

According to Fick's law applied to a dilute system, the diffusive flux of one species is proportional to the gradient of its concentration. The associated diffusion coefficient is derived from kinetic theory according to the characteristics of the species. In a concentrated solution, the concentration of one species has an impact on the diffusion of another species and cross-diffusion terms must be considered. We consider a concentrated solution of species A and B. The solvent S is still considered in excess but not in great excess, so that we are confronted with a ternary mixture of A, B, and S particles [36].

In a highly diluted solution, the center of mass of the solvent and the center of mass of the system are typically the same. However, we expect that, in a concentrated system, the two centers of mass are different. The idea is to exploit the frame of the solvent in which Fick's law takes a simpler form [26, 36]. The flux of species X=A,B in the frame of the solvent is

$$\mathbf{j}_X^S = c_X(\mathbf{u}_X - \mathbf{u}_S) \tag{I.47}$$

where $\mathbf{u}_X$ is the velocity of the center of mass of species X in the frame of the system.

By definition, the flux of the solvent vanishes in the frame of the solvent

$$\mathbf{j}_S^S = 0 \tag{I.48}$$

The fluxes in the frame of the solvent can be expressed in terms of the fluxes in the frame of the system using Eq. (I.47)

$$\mathbf{j}_X^S = c_X(\mathbf{u}_X - \mathbf{u} + \mathbf{u} - \mathbf{u}_S) \tag{I.49}$$

$$= \mathbf{j}_X - \frac{c_X}{c_S}\mathbf{j}_S \tag{I.50}$$

which gives, using the law of conservation $c^{\text{tot}} = c_A + c_B + c_S$ and Eq. (I.48)

$$\mathbf{j}_A = \left(1 - \frac{c_A}{c^{\text{tot}}}\right)\mathbf{j}_A^S - \frac{c_A}{c^{\text{tot}}}\mathbf{j}_B^S \tag{I.51}$$

$$\mathbf{j}_B = -\frac{c_B}{c^{\text{tot}}}\mathbf{j}_A^S + \left(1 - \frac{c_B}{c^{\text{tot}}}\right)\mathbf{j}_B^S \tag{I.52}$$

Next step consists in using Fick's law relating the fluxes in the frame of the solvent and the concentration gradients. Within the framework of linear irreversible thermodynamics, the entropy production per unit mass due to isothermal diffusion is given by

$$\sigma = \frac{1}{T}\sum_{X=A,B,S} \mathbf{j}_X \cdot (-\nabla_T \mu_X) \tag{I.53}$$

where T is the temperature, ∇_T the spatial gradient at constant temperature, and μ_X the chemical potential of species X. Assuming that the deviation from the high-dilution limit remains sufficiently small, the chemical potential for a given species is the same as in an ideal solution

$$\mu_X = \mu_X^0 + k_B T \log \frac{c_X}{c^{\text{tot}}} \tag{I.54}$$

where μ_i^0 is the standard chemical potential of species X and k_B is the Boltzmann constant. At constant pressure and temperature, the Gibbs-Duhem equation states that

$$\sum_{X=A,B,S} c_X \cdot (-\nabla_T \mu_X) = 0 \tag{I.55}$$

Using Eqs. (I.48) and (I.55), we write Eq. (I.53) in the form

$$\sigma = \frac{1}{T} \sum_{X=A,B,S} c_X(\mathbf{u}_X - \mathbf{u}_S + \mathbf{u}_S - \mathbf{u}) \cdot (-\nabla_T \mu_X) \tag{I.56}$$

$$= \frac{1}{T} \sum_{X=A,B} \mathbf{j}_X^S \cdot (-\nabla_T \mu_X) \tag{I.57}$$

By introducing phenomenological coefficients Ω_{XY} to write linear relationships between fluxes and forces

$$\mathbf{j}_X^S = \sum_{Y=A,B} \Omega_{XY}(-\nabla_T \mu_Y) \tag{I.58}$$

and using Eq. (I.54), we obtain the Fick's law in the frame of the solvent

$$\mathbf{j}_X^S = \sum_{Y=A,B} D_{XY}^S(-\nabla c_Y) \tag{I.59}$$

where D_{XY}^S are diffusion coefficients. However, even in a concentrated solution the notion of solvent keeps some relevance. Although the variation of the concentration of the solvent cannot be ignored, the concentrations of A and B are significantly smaller than the concentration of the solvent S. In these conditions, the vast majority of the binary collisions involve at least one S solvent particle. Hence, diffusion of species X=A,B is mainly imposed by the collisions between X and the solvent S while the impact of the collisions between A and B is negligible. We therefore admit that D_{XY}^S is negligible for X≠Y and we denote D_{XX}^S by D_X^S, for X=A,B. Consequently, Eq. (I.59) becomes

$$\mathbf{j}_X^S = D_X^S(-\nabla c_X) \text{ with X=A,B} \tag{I.60}$$

so that the flux of X in the frame of the solvent only depends on the concentration of X. Finally, the modified Fick's law in the frame of the system that accounts for the deviation from the high-dilution limit in a ternary mixture is given by

$$\mathbf{j}_A = -\left(1 - \frac{c_A}{c^{\text{tot}}}\right) D_A^S \nabla c_A + \frac{c_A}{c^{\text{tot}}} D_B^S \nabla c_B \tag{I.61}$$

$$\mathbf{j}_B = \frac{c_B}{c^{\text{tot}}} D_A^S \nabla c_A - \left(1 - \frac{c_B}{c^{\text{tot}}}\right) D_B^S \nabla c_B \tag{I.62}$$

$$\tag{I.63}$$

which can also be written under the matrix form

$$\begin{pmatrix} \mathbf{j}_A \\ \mathbf{j}_B \end{pmatrix} = \begin{pmatrix} \left(1 - \frac{c_A}{c^{\text{tot}}}\right) & -\frac{c_A}{c^{\text{tot}}} \\ -\frac{c_B}{c^{\text{tot}}} & \left(1 - \frac{c_B}{c^{\text{tot}}}\right) \end{pmatrix} \begin{pmatrix} -D_A^S \nabla c_A \\ -D_B^S \nabla c_B \end{pmatrix} \tag{I.64}$$

I have used the modified Fick's law to study the effect of the deviation from the high-dilution limit in Sec. IV.2.

I.4 Numerical methods

I.4.1 Gillespie algorithm

In the general case, the master equation presented in Eq. (I.29) is not solvable. Nevertheless, it is possible to generate a stochastic trajectory using the Gillespie algorithm [49]. Gillespie uses a kinetic Monte Carlo procedure to directly simulate the reaction and diffusion processes and solve the master equation. The general formulation of the algorithm contains several steps, which are presented hereafter.

a) Reactive-only system

We consider the reaction scheme presented in Eq. (I.1) and the associated master equation given in Eq. (I.29). Each reaction step j has a certain probability to occur within a random time interval $[t, t+\tau]$. During this time interval, the propensity p_j that the next elementary reaction is a reaction j is given by Eq. (I.14), with the same assumptions as for Eq. (I.27)

$$p_j = k_j \prod_{i'=1}^{n} A_{\alpha_{i',j}}^{N_{i'}} \tag{I.65}$$

Thus, the propensity p_0 that any reaction occurs is the sum of all propensities p_j of the m steps

$$p_0 = \sum_{j=1}^{m} p_j \tag{I.66}$$

If the time interval $[t, t+\tau]$ is split into infinitesimal intervals dt

then the probability $P_{\oslash}(\tau)$ that no reaction occurs in the time interval $[t, t+\tau]$ is equal

to

$$P_{\oslash}(\tau) = \lim_{dt\to 0}(1 - p_0 dt)^{\frac{\tau}{dt}} = e^{-p_0\tau} \tag{I.67}$$

Therefore, the probability P_0 that *at least* one reaction occurs is

$$P_0 = 1 - e^{-p_0\tau} \tag{I.68}$$

implying that the probability distribution of random reaction time τ is

$$p(\tau) = \partial_\tau P_0 = p_0 e^{-p_0\tau} \tag{I.69}$$

The random reaction time τ is exponentially distributed with mean

$$\langle\tau\rangle = \frac{1}{p_0} \tag{I.70}$$

The first step of the simulation is the initialization of all numbers of molecules, rate constants of the reaction, and the random number generators. Then, in the second step, we generate a random time interval according to Eq. (I.69) and select a random elementary reaction proportionally to its propensity using Eq. (I.66). In the third step, we update the number of molecules according to the reaction that occurred and increase the time step by the randomly generated reaction time. Finally, we go back to the second step where we generate a new random reaction time and a new elementary reaction. Eventually, the simulation stops when the number of reactants has reached zero or the simulation time has run out.

b) With diffusion

When diffusion processes are involved, the Gillespie algorithm can be easily adapted. We now consider the system described by Eq. (I.30). During a random time interval $[t, t+\tau]$, the propensity d_i^{X} that a molecule X leaves the box i is given by Eq. (I.37)

$$d_i^{\mathrm{X}} = d_i^{\mathrm{X}}|_{\mathrm{left}} + d_i^{\mathrm{X}}|_{\mathrm{right}} \simeq \frac{2D_X}{\Delta x^2} N_X(i,t) \tag{I.71}$$

where $d_i^{\mathrm{X}}|_{\mathrm{left}}$ and $d_i^{\mathrm{X}}|_{\mathrm{right}}$ denote the propensity that a molecule X in the box i jumps to the left or to the right, respectively. *A priori*, these two propensities are equal. The propensity d_0 that any molecule leaves its box is

$$d_0 = \sum_X \sum_{i=1}^{\ell} d_i^{\mathrm{X}} \tag{I.72}$$

which can be added to the propensity given by Eq. (I.66). Then, we adapt the second step of the algorithm such that a random elementary process (reaction or diffusion) is selected proportionaly to its propensity.

I have used Gillespie algorithm in the study of the elimination of a fast variable [ ] presented in Sec. II and the study of an FKPP wave front in a concentrated system [ ] presented in Sec. IV.2.2.

I.4.2 Direct Simulation Monte Carlo method

a) Concept

The Direct Simulation Monte Carlo method (DSMC), developed by Graeme Bird in the 60's, is a numerical method used to compute molecular gas flows in aerodynamics [, ,]. It has been successfully extended to include reactive mechanisms and can be used to simulate highly diluted solutions. The method relies on a kinetic Monte Carlo algorithm which generates stochastic trajectories of particles and amounts to a direct simulation of the Boltzmann equations including fluctuations. Particles are hard spheres of mass m and radius r with continuous positions and velocities. Initial positions of the particles, compatible with the macroscopic initial conditions for the concentrations, are randomly chosen. The initial velocities are sampled according to a Maxwellian distribution with $k_BT = 1$. During a time step, positions are updated according to the velocities. The main feature of DSMC is to treat collisions statistically. The space is discretized into cells of length Δx, where particles are susceptible to collide only with particles inside the same cell. According to the collision integral of the Boltzmann equation, the probability of collision of two particles is proportional to their relative velocity [ ]. The "No Time Counter" (NTC) algorithm [,] derives an integer upper bound to the maximum number of collisions to be performed during the time step. An acceptance-rejection method is then used to test whether a collision between two randomly chosen particles in a box is accepted or not. The collisions are considered elastic from the mechanical point of view and the final relative velocity of the colliding pair is determined according to isotropic scattering.

During a collision, a chemical reaction may happen. The reaction occurs with a probability proportional to the corresponding rate constant determined by a steric factor ρ_{AB} and an activation energy E_A. According to kinetic theory, in a binary mixture of A and B species, the collision frequency is given by

$$Z_{\mathrm{AB}} = c_{\mathrm{A}} c_{\mathrm{B}} \sigma_{\mathrm{AB}} \sqrt{\frac{8 k_B T}{\pi \mu_{\mathrm{AB}}}} \tag{I.73}$$

where σ_{AB} is the cross-section of the collision and $\mu_{\mathrm{AB}} = \dfrac{m_A m_B}{m_A + m_B}$ is the reduced mass of the reactants. Only the fraction of encounters that has a relative kinetic energy greater than the activation energy E_A of the reaction reacts. Therefore, the rate of the reaction is

$$v_{\mathrm{AB}} = Z_{\mathrm{AB}} \rho_{\mathrm{AB}} \exp\left(-\frac{E_A}{RT}\right) \tag{I.74}$$

If we compare this result to Eq. (I.2), where the rate of a binary reaction is $v_{\mathrm{AB}} = k_j c_A c_B$, the expression of the rate constant as a result of kinetic theory is

$$k_{\mathrm{AB}} = \rho_{\mathrm{AB}} \sigma_{\mathrm{AB}} \sqrt{\frac{8 k_B T}{\pi \mu_{\mathrm{AB}}}} \exp\left(-\frac{E_A}{RT}\right) \tag{I.75}$$

In the simulations that we performed, it is assumed that the activation energy of all reactions is equal to 0 and that no reaction is endothermic or exothermic. Therefore, the temperature is constant and homogeneous in all simulations. The cross-section of the collisions between two molecules A and B is given by

$$\sigma_{\mathrm{AB}} = \pi (r_{\mathrm{A}} + r_{\mathrm{B}})^2 \tag{I.76}$$

for all collisions considered. The procedure used to obtain desired diffusion coefficients is also derived from kinetic theory. In a binary mixture, the diffusion coefficients of both A and B particles are equal and given by

$$D_{\mathrm{A}} = D_{\mathrm{B}} = D_{\mathrm{AB}} \simeq \frac{3}{8(c_{\mathrm{A}} + c_{\mathrm{B}})(r_{\mathrm{A}} + r_{\mathrm{B}})^2} \sqrt{\frac{k_B T}{\pi \mu_{\mathrm{AB}}}} \tag{I.77}$$

In this expression, the diffusion coefficient depends on the local concentration $c_{\mathrm{A}} + c_{\mathrm{B}}$. However, diffusion coefficients are assumed to be constant in space and time in Eq. (I.4). This hypothesis requires that no particle is created *ex nihilo* or destroyed, and that exchanges with the exterior (such as *reservoirs*) do not radically change the local concentration. Therefore, we make sure that the concentration $c_{\mathrm{A}} + c_{\mathrm{B}}$ is arguably constant in the simulation. Another condition for collisions to be correctly simulated is that the cell length Δx is smaller than the mean free path of colliding particles

$$\ell = \frac{1}{\sqrt{2} c^{\mathrm{tot}} \pi (r_A + r_B)^2} \tag{I.78}$$

In highly diluted solutions, the excess of solvent makes this condition hard to fulfill while keeping reasonable computation times. The condition can be relaxed if the mean gradients of concentration between two neighboring cells are typically smaller that the amplitude

of the concentration fluctuations.
I have used the DSMC method to simulate species with different diffusion coefficients and Turing structures in a concentrated system [37]. The results are presented in Sec. III.3.

b) Third-order reaction

In the article [37] presented in Chapter III, we consider a ternary mixture of A, B, and S species where one step of the reactive mechanism is a third-order reaction. The difficulty was to adapt the DSMC algorithm to correctly simulate a third-order reaction. The issue has been solved as follows by M. Mareschal *et al.* [51] and already used by the group [52]. The reaction

$$2\,\mathrm{A} + \mathrm{B} \xrightarrow{k} 3\,\mathrm{A} \tag{I.79}$$

is split into two second-order reactions

$$\mathrm{A} + \mathrm{B} \xrightarrow{k_1=k} \mathrm{AB} \tag{I.80}$$

$$\mathrm{AB} + \mathrm{A} \xrightarrow{k_2\to\infty} 3\,\mathrm{A} \tag{I.81}$$

where the first reaction occurs with the same rate constant k as the third-order reaction and the second reaction is supposed instantaneous. The simulations reproduce the third-order reaction given in Eq. (I.79) as follows. When a binary collision between a particle A and a particle B is accepted in a given spatial box, a complex AB is supposed to be formed. A third particle is randomly chosen in the same spatial box. If it is an A particle, the AB complex is immediately transformed into two A particles. Hence, according to Eq. (I.75) and the probability $\frac{c_A}{c^{tot}}$ of picking a particle A, the rate constant k obeys

$$k = \frac{4(r_\mathrm{A} + r_\mathrm{B})^2}{c^\mathrm{tot}}\sqrt{\pi k_B T} \propto \frac{1}{c^\mathrm{tot}} \tag{I.82}$$

with $\mu_{AB} = E_A = \rho_{AB} = 1$. Due to the proportionality to $1/c^\mathrm{tot}$, the rate constant k depends on the deviation δ from the high-dilution limit from Eq. (I.46).

c) Diffusion in a ternary mixture

Observing a Turing structure requires the simulation of sufficiently different diffusion coefficients for the activator and the inhibitor. As already mentioned, the diffusion coefficients of the two components are identical in a binary mixture. The solvent, introduced to study concentrated solutions, advantageously plays the role of the third kind of particles with respect to diffusion. The problem of tuning the diffusion coefficients in the simulation of a ternary mixture has already been addressed by the group [53] and I recall the main lines

of the method. Qualitatively, faster diffusion of the inhibitor is obtained by considering particles of the same mass but different diameters. In a ternary mixture of A, B, and S [54], the fluxes of matter $\mathbf{j}_A$, $\mathbf{j}_B$, and $\mathbf{j}_S$ are expressed as

$$\mathbf{j}_X = D'_{XY}\partial_x c_Y + D'_{XZ}\partial_x c_Z \tag{I.83}$$

for $X, Y, Z = A, B, R$, where the three-component diffusion coefficients D'_{AB}, D'_{AS}, and D'_{BS} are derived from the two-component diffusion coefficients D_{AB}, D_{AS}, and D_{BS} from Eq. (I.77)

$$D'_{XY} = D_{XY}\left[1 + \frac{c_Z(D_{XZ} - D_{XY})}{c_X D_{YZ} + c_Y D_{XZ} + c_Z D_{XY}}\right] \tag{I.84}$$

The presence of the concentrations in the expression of the diffusion coefficients may imply non desired space-dependent diffusivities. However, considering

$$c_S D'_{AB} \gg c_A D'_{BS} + c_B D'_{AS} \tag{I.85}$$

$$c_S \gg c_A \tag{I.86}$$

$$c_S \gg c_B \tag{I.87}$$

and using Eq. (I.84) leads to

$$D'_{AB} \simeq D'_{AS} \simeq D_{AS} \tag{I.88}$$

$$D'_{BA} \simeq D'_{BS} \simeq D_{BS} \tag{I.89}$$

which, combined with Eq. (I.83) for $c^{\text{tot}} = c_A + c_B + c_S$ constant, gives

$$\mathbf{j}_A = -D_{AS}\partial_x c_A \tag{I.90}$$

$$\mathbf{j}_B = -D_{BS}\partial_x c_B \tag{I.91}$$

Thus, when the solvent is sufficiently in excess, the diffusion coefficients of A and B species are the same as in a binary mixture of A and S particles and B and S particles, respectively. Intuitively, in a system with S particles in excess, the proportion of collisions involving no S particles is negligible. Hence, we assume that the diffusive mechanism of A and B particles is dominated by their interaction with the S particles. For the sake of simplicity, we write

$$D_A \simeq D_{AS} \tag{I.92}$$

$$D_B \simeq D_{BS} \tag{I.93}$$

In Eq. (I.77), the diffusion coefficient depends on the local concentration of the two species involved in the diffusive process. In Chapter. III, we study Turing structures with spatial oscillations of the concentrations, which undermines the hypothesis of constant diffusion coefficients. In order to derive appropriate diameters for the different types of particles [53], we consider spatial averages of the concentrations. Then, writing $d = \frac{D_B}{D_A}$ and $m_A = m_B$, and using Eq. (I.77), we get

$$r_B = \frac{r_A + (1 - \sqrt{d'})r_S}{\sqrt{d'}} \tag{I.94}$$

where $d' = \frac{d(c_S + c_A)}{c_R + c_B} \simeq d$. As r_B must be positive, we obtain the condition

$$r_A > (\sqrt{d'} - 1)r_S \tag{I.95}$$

If this last condition is satisfied with a small margin, then

$$r_B \ll r_A \tag{I.96}$$

and $D_B \gg D_A$ as desired.
Finally, introducing Eq. (I.95) into Eq. (I.85), we obtain the condition on the concentration of solvent S for the proper simulation of the diffusion coefficients

$$c_S \gg \sqrt{(dc_A + c_B)(c_A + c_B)} \left(1 - \frac{1}{\sqrt{d'}}\right) \tag{I.97}$$

Chapter II

Stochastic approach to the steady-state approximation

The usual adiabatic elimination often encountered in chemistry is the steady-state approximation, consisting in eliminating a fast concentration. In a complex mechanism, identifying a fast concentration is not straightforward [55, 56, 57, 58, 59, 60]. A linear analysis may be locally performed and requires linearizing the rate equations, computing the eigenvalues, and using the change-of-basis matrix to relate the concentrations and the eigenmodes. The relationships between the eigenvalues and the rate constants may not be trivial and the knowledge of the rate constants is not always sufficient to identify a fast variable at first glance.

II.1 Context

We give an example of steady-state approximation in a simple case involving two elementary steps with rate constants of different orders of magnitude, sufficient to generate a fast concentration. The example also illustrates how third-order steps may be obtained by reduction of a mechanism containing second-order steps.

We consider a reaction scheme involving two elementary steps and four species A, B, C, and D

$$\begin{aligned} \mathrm{A} + \mathrm{B} &\xrightarrow{\varepsilon k} \mathrm{C} \\ \mathrm{A} + \mathrm{C} &\xrightarrow{k} 2\,\mathrm{D} \end{aligned} \tag{II.1}$$

The first step is supposed to be much slower than the second one, i.e. the parameter ε obeys $\varepsilon \ll 1$. The quantities $c_A + c_C + c_D$ and $c_A - 2c_B - c_C$ are conserved and dynamics involves two independent variables. It is however simpler to keep the three variables c_A,

c_B, and c_C. The rate equations are given by

$$\mathrm{d}_t c_A = -\varepsilon k c_A c_B - k c_A c_C \tag{II.2}$$

$$\mathrm{d}_t c_B = \varepsilon k c_A c_B \tag{II.3}$$

$$\mathrm{d}_t c_C = \varepsilon k c_A c_B - k c_A c_C \tag{II.4}$$

Introducing a new time scale $\tau = \varepsilon t$, expanding the concentrations into power series of ε, and using Eq. (II.4) at zeroth order, we deduce that $c_C^{(0)} = 0$. Consequently, we have

$$\mathrm{d}_\tau c_C^{(0)} = k c_A^{(0)} (c_B^{(0)} - c_C^{(1)}) = 0 \tag{II.5}$$

which implies $c_C^{(1)} = c_B^{(0)}$. Finally, Eqs. (II.2) and (II.3) lead to

$$\mathrm{d}_\tau c_A^{(0)} = -2 k c_A(0) c_B(0) \tag{II.6}$$

$$\mathrm{d}_\tau c_B^{(0)} = -k c_A(0) c_B(0) \tag{II.7}$$

which corresponds to the rate equations associated with a third-order reaction

$$2\,\mathrm{A} + \mathrm{B} \xrightarrow{\varepsilon k} 2\,\mathrm{D} \tag{II.8}$$

The reaction between nitrogen monoxide and chlorine

$$2\,\mathrm{NO} + \mathrm{Cl_2} \longrightarrow 2\,\mathrm{NOCl} \tag{II.9}$$

illustrates the reduced mechanism given in Eq. (II.8). The mechanism proposed in Eq. (II.1) does not rely on any chemical considerations and is only one possible two-step mechanism compatible with the reaction between nitrogen monoxide and chlorine.

II.2 Summary of the results

In the previous example, the dynamics of the system is described at a macroscopic scale. The nonlinearities of the deterministic dynamics and the large fluctuations reached in small systems are known to interact [61, 62, 63] and make the elimination of fast concentrations a nontrivial problem in stochastic systems [58, 64, 65]. In biological experiments, Fluorescence Correlation Spectroscopy (FCS) [66] is widely used to study the dynamics of labeled species, for example, to evaluate rate constants when the reaction scheme is supposed to be known. The interpretation of the results requires the comparison of the experimental data with analytical expressions of the correlations of concentration fluctuations for the reaction scheme of interest. However, reaction schemes in biology often

involve hundreds of steps and the computation of the correlations is not tractable before a reduction of the mechanism. Defining the scope of fast concentration elimination in stochastic nonlinear dynamics is therefore essential to interpret FCS results. Similarly, the reduction of a mechanism may lead to nonpolynomial nonlinearities, as exemplified by the reduced Michaelis–Menten scheme. The conclusions that could be derived from the stochastic analysis of the reduced Michaelis–Menten model may differ from the direct analysis of the complete scheme [67]. In order to analyze the consequences of mechanism reduction, I consider a minimal chemical model involving two species of variable concentrations capable of evolving into a Turing pattern. Then, the two-variable model is assumed to be the reduction of two different three-variable models. The problem is to determine if the correlations of fluctuations in the three-variable models are correctly predicted by the two-variable model, in the limit where the reduction of deterministic dynamics is valid. I developed an analytical approach based on chemical Langevin equations linearized around the steady state of interest as presented in Sec. I.2.1. Following the method applied in references [61, 62, 63] to characterize the asymmetry of time cross-correlations in far-from-equilibrium systems, I determined the expressions of the correlations of concentration fluctuations in the two- and three-variable models. In parallel, I performed simulations of the corresponding master equations (see Sec. I.2.2) using Gillespie algorithm according to the procedure given in Sec. I.4.1. The weaknesses of the Langevin approach in the description of the internal fluctuations in a nonlinear chemical system have been highlighted [68]. The master equation approach has proven that the two-variable model does not correctly predict the fluctuations in the three-variable systems. We concluded that the coupling between the fluctuations and the nonlinearities of deterministic dynamics makes the use of the steady-state approximation delicate when the studied system requires a good control of the fluctuations. The predictions of the correlations based on a reduced mechanism must be considered with special care when preventing hazards in explosive phenomena, modeling pattern formation in biology, or dealing with small systems in which variances of fluctuations are detected as in fluorescence correlation spectroscopy [65, 69].

II.3 Publication

The results are published in the article “Elimination of fast variables in stochastic nonlinear kinetics”, G. Morgado, B. Nowakowski, and A. Lemarchand, *Phys. Chem. Chem. Phys.*, **22**, 20801-20814 (2020) [29].

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Elimination of fast variables in stochastic nonlinear kinetics

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A reduced chemical scheme involving a small number of variables is often sufficient to account for the deterministic evolution of the concentration of the main species contributing to a reaction. However, its predictions are questionable in small systems used, for example, in fluorescence correlation spectroscopy (FCS) or in explosive systems involving strong nonlinearities such as autocatalytic steps. We make precise dynamical criteria defining the validity domain of the quasi-steady-state approximation and the elimination of a fast concentration in deterministic dynamics. Designing two different three-variable models converging toward the same two-variable model, we show that the variances and covariance of the fluctuations of the slow variables are not correctly predicted using the two-variable model, even in the limit of a large system size. The most striking weaknesses of the reduced scheme are figured out in mesoscaled systems containing a small number of molecules. The results of two stochastic approaches are compared and the shortcomings of the Langevin equations with respect to the master equation are pointed out. We conclude that the description of the fluctuations and their coupling with nonlinearities of deterministic dynamics escape reduced chemical schemes.

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Chapter III

Turing patterns

In 1952, Alan Turing presents one of his later most famous works [5]. He proposes a mathematical analysis of reaction-diffusion systems that may exhibit periodic spatial structures from an initially homogeneous state. The discovery of time oscillations in a chemical reaction was made in the 50s by the Russian biochemist B. Belousov, while looking for a non-organic analog to the Krebs cycle [70]. A young chemist, A. Zhabotinsky, became famous in the 60s for the work he devoted to this reaction with the observation of spatial structures and chemical wave fronts [71]. Nowadays, the tradition associates their two names to designate this complex reaction. Experimental evidence of Turing type nonequilibrium chemical patterns has been provided in 1990 by the group of De Kepper [72].

III.1 Emergence of a Turing pattern

Turing patterns (or Turing structures) only appear in out-of-equilibrium systems, therefore relying on the outside environment to maintain the pattern. Initial conditions and parameters such as the kinetic rate constants and the diffusion coefficients of the reactive species are also crucial for the existence and the shape of the pattern. The patterns appear when an inhomogeneous perturbation arises in a homogeneous stationary state. One of the simplest systems that exhibits Turing patterns is the Gray-Scott model [73], which involves two reactive species A and B in a third-order autocatalytic reaction

$$\mathrm{A} \xrightarrow{k_1} \mathrm{R_A} \tag{III.1}$$

$$2\,\mathrm{A} + \mathrm{B} \xrightarrow{k_2} 3\,\mathrm{A} \tag{III.2}$$

$$\mathrm{B} \underset{k_{-3}^*}{\overset{k_3}{\rightleftharpoons}} \mathrm{R_B} \tag{III.3}$$

where R_A and R_B are *reservoirs* of particles A and B, respectively. The associated reaction-diffusion equations are

$$\partial_t c_A = -k_1 c_A + k_2 c_A^2 c_B + D_A \partial_x^2 c_A \tag{III.4}$$

$$\partial_t c_B = -k_2 c_A^2 c_B - k_3 c_B + k_{-3} + D_B \partial_x^2 c_B \tag{III.5}$$

where $k_{-3} = k^*_{-3} c_{R_B}$ with c_{R_B} constant. The system possesses three stationary states. The steady state

$$c_A^0 = 0 \tag{III.6}$$

$$c_B^0 = \frac{k_{-3}}{k_3} \tag{III.7}$$

corresponds to the absence of A particles and is obviously stable according to the chemical scheme given in Eqs. (III.1-III.3). The two other states are derived from Eqs. (III.4) and (III.5)

$$c_A^{\pm} = \frac{k_{-3} \pm \sqrt{k_{-3}^2 - 4\dfrac{k_1^2 k_3}{k_2}}}{2k_1} \tag{III.8}$$

$$c_B^{\pm} = \frac{k_{-3} - k_1 c_A^{\pm}}{k_3} = \frac{k_{-3} \mp \sqrt{k_{-3}^2 - 4\dfrac{k_1^2 k_3}{k_2}}}{2k_3} \tag{III.9}$$

By performing a linear stability analysis, as presented in Sec. I.1.3, we show that the state (c_A^+, c_B^+) is stable towards homogeneous perturbations whereas (c_A^-, c_B^-) is unstable. Knowing that Turing patterns emerge from inhomogeneous perturbations, we consider the evolution of a local inhomogeneous perturbation $\delta\mathbf{c} = (\delta c_A, \delta c_B)$ around the state (c_A^+, c_B^+). According to Eqs.(III.4) and (III.5) and in the framework of a linear approach, the Fourier transform of the perturbation

$$\delta\tilde{\mathbf{c}} = \frac{1}{\sqrt{2\pi}} \int \mathrm{d}x \delta c \cdot e^{-iqx} \tag{III.10}$$

obeys

$$\partial_t \delta\widetilde{c_A} = -k_1 \delta\widetilde{c_A} + k_2 \left(2c_A^+ c_B^+ \delta\widetilde{c_A} + {c_A^+}^2 \delta\widetilde{c_B}\right) - q^2 D_A \delta\widetilde{c_A} \tag{III.11}$$

$$\partial_t \delta\widetilde{c_B} = -k_2 \left(2c_A^+ c_B^+ \delta\widetilde{c_A} + c_A^2 \delta\widetilde{c_B}\right) - k_3 \delta\widetilde{c_B} - q^2 D_B \delta\widetilde{c_B} \tag{III.12}$$

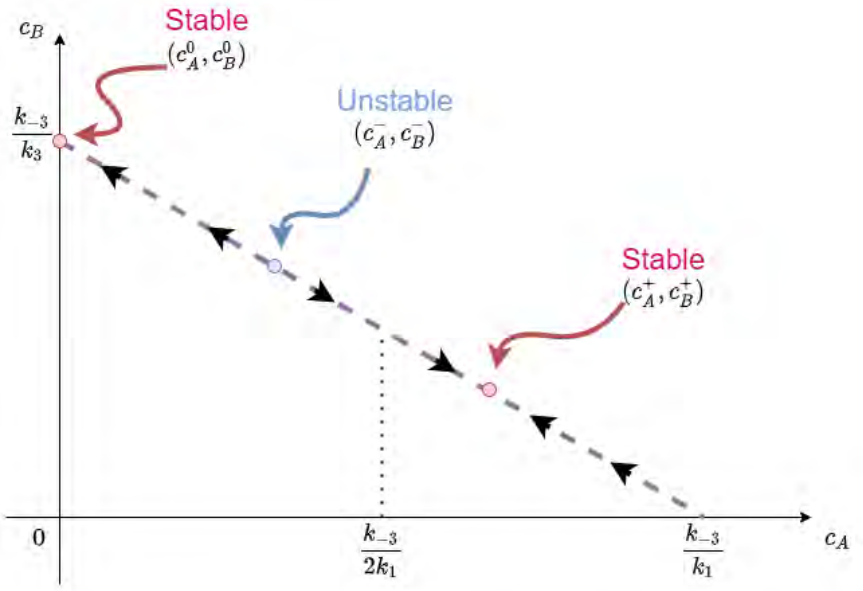

Fig. III.1 *Stationary states of the model given in Eqs. (III.1-III.3)* in the space of concentrations (c_A, c_B)

from which we obtain the stability matrix

$$\mathbf{M} = \begin{pmatrix} m_{11} - q^2 D_A & m_{21} \\ m_{12} & m_{22} - q^2 D_B \end{pmatrix} \tag{III.13}$$

where

$$m_{11} = -k_1 + 2k_2 c_A^+ c_B^+ \tag{III.14}$$

$$m_{21} = k_2 {c_A^+}^2 \tag{III.15}$$

$$m_{12} = -2k_2 c_A^+ c_B^+ \tag{III.16}$$

$$m_{22} = -k_2 {c_A^+}^2 - k_3 \tag{III.17}$$

The two eigenvalues of the stability matrix are

$$\mu_\pm = \frac{1}{2}\left[m_{11} + m_{22} - q^2(D_A + D_B) \pm \sqrt{[(m_{11} - m_{22}) - q^2(D_A - D_B)]^2 + 4m_{21}m_{12}}\right] \tag{III.18}$$

The steady state (c_A^+, c_B^+) is unstable if the real part of one eigenvalue is positive. We look for the Fourier mode $q_{\max}$ that maximizes the largest eigenvalue μ_+

$$q_{\max} = \sqrt{\frac{m_{11} - m_{22}}{D_A - D_B} - \frac{D_A + D_B}{D_A - D_B}\sqrt{\frac{-m_{12}m_{21}}{D_A D_B}}} \tag{III.19}$$

If the value $\mu_+(q_{\max})$ is positive, then the inhomogeneous perturbation grows and a Turing pattern emerges. The pattern consists of sinusoidal oscillations of A and B concentrations with the wavelength

$$\lambda = \frac{2\pi}{q_{\max}} \tag{III.20}$$

Equation (III.19) is valid for any reaction mechanism involving two chemical species susceptible to evolve into a Turing pattern. We can therefore express general conditions for the emergence of Turing patterns. First, we remark that if the two diffusion coefficients are equal, i.e. $D_A = D_B$, then Eq. (III.19) diverges and no Turing pattern can emerge. Second, the wavelength depends only on the rate constants and the diffusion coefficients, and not on the boundary conditions of the system. This makes the Turing pattern independent of the size of the system, at least at the macroscopic scale [74, 75, 76].

III.2 Termination mechanism of Turing patterns

III.2.1 Context

Models of periodic spatial patterns usually involve infinite systems or periodic boundary conditions [77, 78, 79]. However, in morphogenesis, the question of the termination of a structure arises [80, 81]. Specifically, the spine of the vertebrates ends with smaller vertebrae. In the framework of Turing patterns, this phenomenon implies both a decrease of the amplitude of the spatial oscillations and a decrease of the wavelength. Deciphering the mechanisms controlling the termination of the spine in an embryo is far beyond the scope of this work. Our aim is to propose a possible mechanism at the macroscopic scale, inspired by biological structures and compatible within a chemical engineering context. The boundary conditions chosen by the group in 2016 [36] to model the growth of the spine are well adapted to the design of an artificial spatial structure. In the model of reference [36], the Turing pattern develops behind a wave front propagating from left to right. Neumann or second-type boundary conditions are chosen at the left boundary at which the derivative of the concentration with respect to the spatial coordinate x vanishes. The emerging Turing pattern will therefore possess an extremum at the left boundary. A free boundary is imposed at the right, i.e. the system grows freely in this direction, so

that the propagation of the wave front to the right is not perturbed. The right part of the Turing pattern, located behind the front, is free and not affected by the boundaries.

III.2.2 Summary of the results

As explained in Sec. III.1, the stability of the Turing pattern is related to the eigenvalues of the stability matrix around the homogeneous steady state. A real, positive eigenvalue μ_+ corresponds to an unstable homogeneous steady state and a stable Turing structure. As μ_+ tends to 0, the amplitude of the spatial oscillations decreases. Destabilization is reached when $\mu_+ = 0$. Using Eqs. (III.18) and (III.20), I performed a systematic analysis of the effect of all rate constants and diffusion coefficients of the model given in Eqs. (III.4) and (III.5) on the eigenvalue μ_+ and the wavelength of the structure λ. Interestingly, a monotonous variation of almost any of the dynamical parameters leads to the desired behavior. In particular, either the increase or the decrease of a rate constant leads to the simultaneous loss of stability of the structure and the decrease of its wavelength. Only the variation of the diffusion coefficient D_A of the activator causes anti-correlated results, i.e. a decrease of the oscillation amplitude and an increase of the wavelength. For a given chemical system, locally varying a rate constant or the diffusion coefficient D_B of the inhibitor is not straightforward in the framework of chemical engineering. For an easy implementation, I suggest to impose an appropriate spatial profile for the concentration of the reservoir $\mathrm{R_B}$, resulting in the increase of the effective rate constant $k_{-3}R_B$ of the process given in Eq. (III.3) and the desired termination of the structure.

III.2.3 Publication

The results are published in the article "Termination mechanism of Turing patterns in growing systems", G. Morgado, L. Signon, B. Nowakowski, and A. Lemarchand, Acta Phys. Pol. B, **50**, 1369 (2019) [39].

TERMINATION MECHANISMS OF TURING PATTERNS IN GROWING SYSTEMS

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The question of the termination of a periodic spatial structure of Turing-type in a growing system is addressed in a chemical engineering perspective and a biomimetic approach. The effects of the dynamical parameters on the stability and the wavelength of the structure are analytically studied and used to propose experimental conditions for which a Turing pattern stops by itself with a decreasing wavelength. The proposed mechanism is successfully checked by the numerical integration of the equations governing the dynamics of the activator and the inhibitor. We conclude that a local increase of the concentration of the reservoir which controls the injection rate of the inhibitor into the system can be used to achieve the appropriate termination of a Turing pattern.

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1. Introduction

During embryonic development, segmented structures of the body such as the spine and the digits are formed by the production of repeated elements. Since the seminal work of Turing [1] accounting for the formation of biological pattern in the framework of reaction–diffusion models, experimental evidences of Turing structures have been given in chemistry [2–4] and biology [5, 6]. Recent years have witnessed a growing number of papers where reaction–diffusion principles are proposed to model the formation of biological periodic spatial structures [7–13]. Following Turing, a

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two-component chemical system composed of an autocatalytically-produced activator by consumption of an inhibitor that diffuses faster may produce periodic spatial structures such as stripes in one-dimensional (1D) systems and hexagons in 2D. In other words, a Turing pattern emerges by local self-activation and lateral inhibition [14]. The concepts developed to model living systems provide a source of inspiration in chemical engineering [15–22]. However, standard models of Turing patterns generate structures in infinite systems and the question of the termination of a striped structure in a finite system arises in a perspective of biomimetism in material science. Specifically, it is desirable to find experimentally achievable conditions creating a finite-size structure, whose growth stops by itself with decreasing oscillation amplitude and respects the decrease of the wavelength during the termination process. To this aim, we use an as simple as possible reaction–diffusion model [23] admitting a Turing structure developing behind a propagating wave front and examine the effect of all parameters on both the stability and the wavelength of the structure [5, 22]. We already used a stochastic approach to a Turing pattern [23] and showed that, contrary to intuition, the internal fluctuations may have a constructive effect and stabilize the structure outside the domain of stability predicted by a deterministic description. Here, we adopt a macroscopic approach. Our goal is to select suitable conditions from this systematic approach and to propose termination mechanisms compatible with processing in chemical engineering.

The paper is organized as follows. In Section 2, a reaction–diffusion model involving local activation and long-range inhibition is presented. An analytical stability condition and the wavelength expression of the Turing pattern are given. The influence of the parameters of the model on the stability and the wavelength of the pattern is studied in Section 3. The analysis of the results leads to the selection of a user-friendly termination mechanism in the framework of chemical engineering. The analytical predictions regarding stability and wavelength are compared to numerical results for the chosen mechanism. Section 4 contains conclusions. The possibility that the different mechanisms exhibited could be found as termination scenarios in morphogenesis is raised.

2. Model

We consider the following reaction mechanism inspired from the Schnakenberg model [24] and the Gray–Scott model [25]:

$$\mathrm{A} \xrightarrow{k_1} \mathrm{R}_1\,, \tag{1}$$

$$2\mathrm{A} + \mathrm{B} \xrightarrow{k_2} 3\mathrm{A}\,, \tag{2}$$

$$\mathrm{B} \underset{k_{-3}}{\overset{k_3}{\rightleftharpoons}} \mathrm{R}_2\,, \tag{3}$$

where R_1 and R_2 are reservoirs. The concentrations R_1 and R_2 of the reservoirs are assumed to be constant in time. The reaction given in Eq. (2) autocatalytically produces species A and consumes species B. Due to the ability of accelerating its own production, species A is called an activator whereas species B, which is consumed by the same process, is called an inhibitor. The macroscopic dynamics of the system is governed by two partial differential equations [9, 23]

$$\frac{\partial A}{\partial t} = -k_1 A + k_2 A^2 B + D_A \frac{\partial^2 A}{\partial x^2}\,, \tag{4}$$

$$\frac{\partial B}{\partial t} = k_{-3} R_2 - k_3 B - k_2 A^2 B + D_B \frac{\partial^2 B}{\partial x^2} \tag{5}$$

for the concentrations A and B of the activator and the inhibitor supposed to have different diffusion coefficients D_A and D_B. For appropriate rate constant values, such that

$$\Delta = (k_{-3}R_2)^2 - 4k_1^2 k_3/k_2 \geq 0\,, \tag{6}$$

the system admits two steady states ($A_0 = 0, B_0 = k_{-3}R_2/k_3$) and

$$A_\mathrm{T} = \frac{k_{-3}R_2 + \sqrt{\Delta}}{2k_1}\,, \tag{7}$$

$$B_\mathrm{T} = \frac{k_{-3}R_2 - \sqrt{\Delta}}{2k_3} \tag{8}$$

that are stable with respect to homogeneous perturbations. The index T stands for Turing. A linear stability analysis of Eqs. (4) and (5) reveals that the steady state $(A_\mathrm{T}, B_\mathrm{T})$ can be destabilized by inhomogeneous perturbations [3, 5, 9, 23]. The Fourier transforms $A_q(t) = \int_{-\infty}^{\infty} A(x,t)e^{-iqx}\mathrm{d}x$ and $B_q(t) = \int_{-\infty}^{\infty} B(x,t)e^{-iqx}\mathrm{d}x$, where q is the Fourier mode, are introduced. In the Fourier space, the linear stability operator M is given by

$$M = \begin{pmatrix} k_1 - D_A q^2 & k_2 A_\mathrm{T}^2 \\ -2k_1 & -\frac{k_2 k_{-3} R_2}{k_1} A_\mathrm{T} - D_B q^2 \end{pmatrix}. \tag{9}$$

The eigenvalues of the matrix M obey the characteristic equation $\mu^2+\alpha\mu+\beta=0$, with $\alpha = k_1 - \frac{k_2 k_{-3} R_2}{k_1} A_{\mathrm{T}} - (D_A+D_B)q^2$ and $\beta = 2k_1^2 A_{\mathrm{T}}/B_{\mathrm{T}} - (k_1 - D_A q^2)(k_{-3}R_2/B_{\mathrm{T}} + D_B q^2)$. The Turing structure develops if the largest eigenvalue

$$\mu = \frac{1}{2}\left(k_1 - \frac{k_2 k_{-3} R_2}{k_1} A_{\mathrm{T}} - (D_A + D_B)q^2 + \sqrt{\left(k_1 + \frac{k_2 k_{-3} R_2}{k_1} A_{\mathrm{T}} + (D_B - D_A)q^2\right)^2 - 8k_1 k_2 A_{\mathrm{T}}^2}\right) \tag{10}$$

is real and positive [3, 5]. Indeed, a system of differential equations, linearized around a homogeneous steady state, is easily solved by diagonalizing the linear operator. Then, the solution is a linear combination of eigenmodes which exponentially depend on time according to the corresponding eigenvalues. A term associated with a real, positive eigenvalue grows in time, leading to trajectories in the concentration space that move away from the fixed point [5]. In the studied system, the destabilization of the steady state occurs in favor of a Turing pattern. Equation (10) imposes conditions on the parameter values. In particular, the diffusion coefficient D_B of the inhibitor B must be sufficiently larger than the diffusion coefficient D_A of the activator A: The destabilization of the homogeneous steady state $(A_{\mathrm{T}}, B_{\mathrm{T}})$ requires local self-activation, ensured by the autocatalytic production of the activator through the reaction given in Eq. (2), as well as long-range inhibition, due to the larger diffusion coefficient of the inhibitor. The mode $q_{\max}$, which maximizes the eigenvalue μ, is the most unstable Fourier mode

$$q_{\max} = \sqrt{\frac{A_{\mathrm{T}}(D_A+D_B)\sqrt{2k_1k_2D_A/D_B} - k_1 - k_2k_{-3}R_2A_{\mathrm{T}}/k_1}{D_B - D_A}}\,. \tag{11}$$

In order to account for the termination of the Turing pattern in a growing system, including the fact that the structure ends with a gradually shorter spatial oscillation, we need to find conditions for which the structure tends to lose its stability while its wavelength decreases. The wavelength of the periodic structure is given by

$$\lambda = \frac{2\pi}{q_{\max}}\,. \tag{12}$$

The Turing structure becomes unstable as the value of the largest eigenvalue vanishes for the mode $q_{\max}$ associated with the maximum of μ

$$\mu_{\max} = \frac{1}{2}\left(k_1 - \frac{k_2 k_{-3} R_2}{k_1} A_{\mathrm{T}} - (D_A + D_B) q_{\max}^2 + \sqrt{\left(k_1 + \frac{k_2 k_{-3} R_2}{k_1} A_{\mathrm{T}} + (D_B - D_A) q_{\max}^2\right)^2 - 8 k_1 k_2 A_{\mathrm{T}}^2}\right) \quad (13)$$

with $q_{\max}$ given in Eq. (11). Figure 1 illustrates the behavior of $\mu_{\max}$ for parameter values associated with a stable Turing pattern with $\mu_{\max} > 0$. It is also shown that it is sufficient to increase the value of $k_{-3}R_2$ to shift the curve $\mu(q^2)$ down and lose the stability of the Turing pattern.

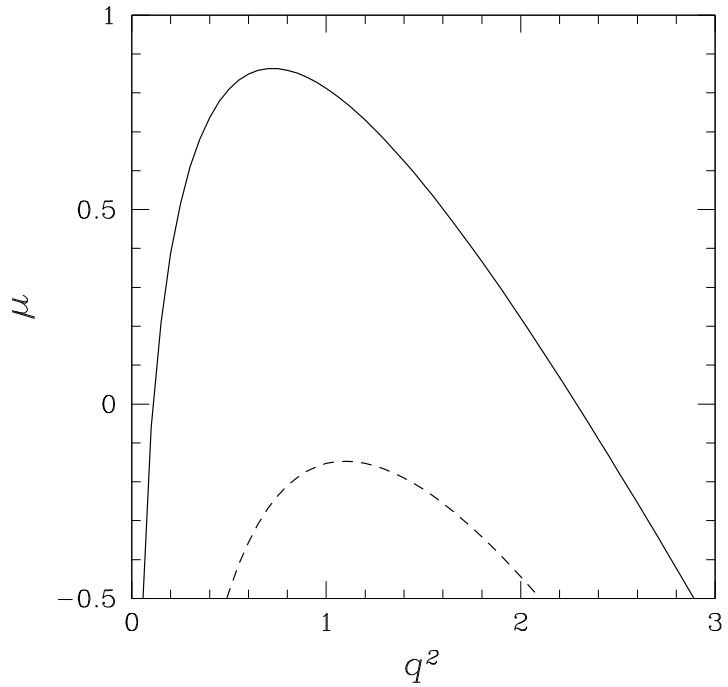

Fig. 1. The largest eigenvalue μ of the linear operator M *versus* square of Fourier mode q^2. Solid line: $k_{-3}R_2 = 8.76$. Dashed line: $k_{-3}R_2 = 10$. Other parameter values: $k_1 = 2.92$, $k_2 = 1$, $k_3 = 2.19$, $D_A = 1$, $D_B = 10$.

In the next section, we investigate the behavior of λ and $\mu_{\max}$ as each parameter controlling dynamics varies. Specifically, we aim at identifying diffusion coefficients or rate constants whose variation leads both to a decrease of the wavelength and a destabilization of the Turing structure, *i.e.* negative values for the maximum of the eigenvalue.

3. Results

The concentration R_2 of the inhibitor reservoir is first assumed to be homogeneous. Figures 2 and 3 show the variations of the wavelength λ and the maximum value $\mu_{\max}$ of the eigenvalue with one of the diffusion

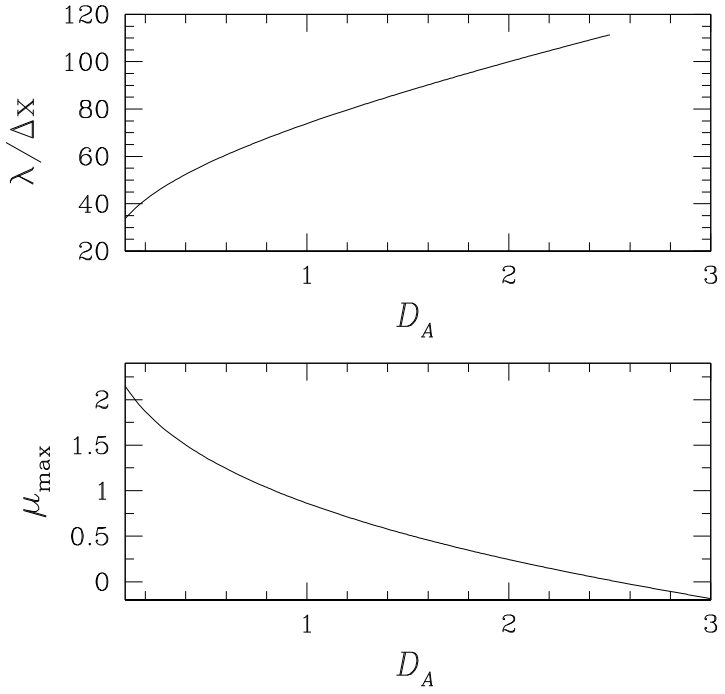

Fig. 2. Top: Scaled wavelength $\lambda/\Delta x$ of the Turing pattern *versus* diffusion coefficient D_A of species A. Bottom: Maximum value $\mu_{\max}$ of the largest eigenvalue of the linear operator M *versus* D_A. Parameter values: $k_1 = 2.92$, $k_2 = 1$, $k_3 = 2.19$, $k_{-3}R_2 = 8.76$, $D_B = 10$, $\Delta x = 0.1$.

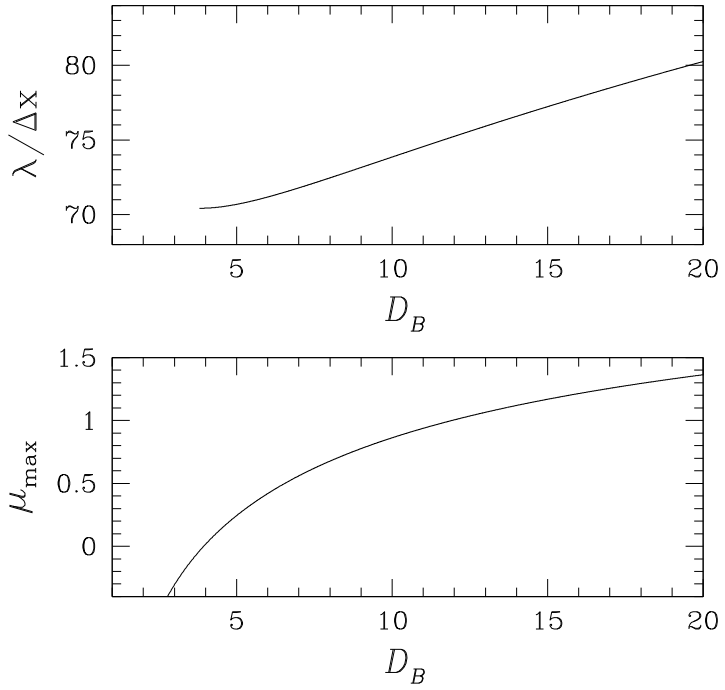

Fig. 3. Top: Scaled wavelength $\lambda/\Delta x$ of the Turing pattern *versus* diffusion coefficient D_B of species B. Bottom: Maximum value $\mu_{\max}$ of the largest eigenvalue of the linear operator M *versus* D_B. Parameter values: $k_1 = 2.92$, $k_2 = 1$, $k_3 = 2.19$, $k_{-3}R_2 = 8.76$, $D_A = 1$, $\Delta x = 0.1$.

coefficients, the other parameters being constant. The results are deduced from Eqs. (11) and (12) for λ and Eq. (13) for $\mu_{\max}$, the expressions of the steady state $(A_{\mathrm{T}}, B_{\mathrm{T}})$ being given in Eqs. (7) and (8). To facilitate the comparison with the numerical integration of Eqs. (4) and (5) that will be performed in the following, the wavelength is given in a number of spatial cells of length $\Delta x = 0.1$. As shown in Fig. 2, the decrease in the maximum value $\mu_{\max}$ of the eigenvalue as the diffusion coefficient D_A of species A increases is accompanied by an increase of the wavelength λ: The loss of stability of the Turing structure occurs with an increase of the spatial period. We conclude that a variation of the diffusion coefficient D_A cannot be argued as a justification of the termination process. The behavior with respect to the diffusion coefficient D_B of species B is different. The simultaneous loss of stability of the structure and the decrease of the wavelength are observed in Fig. 3 as D_B decreases: The diffusion coefficient D_B of species B can be considered as a suitable parameter in the search for a termination model.

Figures 4–7 show the variations of the wavelength λ and the maximum value $\mu_{\max}$ of the eigenvalue with rate constants. The variations of λ are given in a bounded interval of rate constant values, in which the Turing pattern is stable. At one of the endpoints of the interval, the eigenvalue $\mu_{\max}$ vanishes and at the other endpoint, the condition of existence of the steady

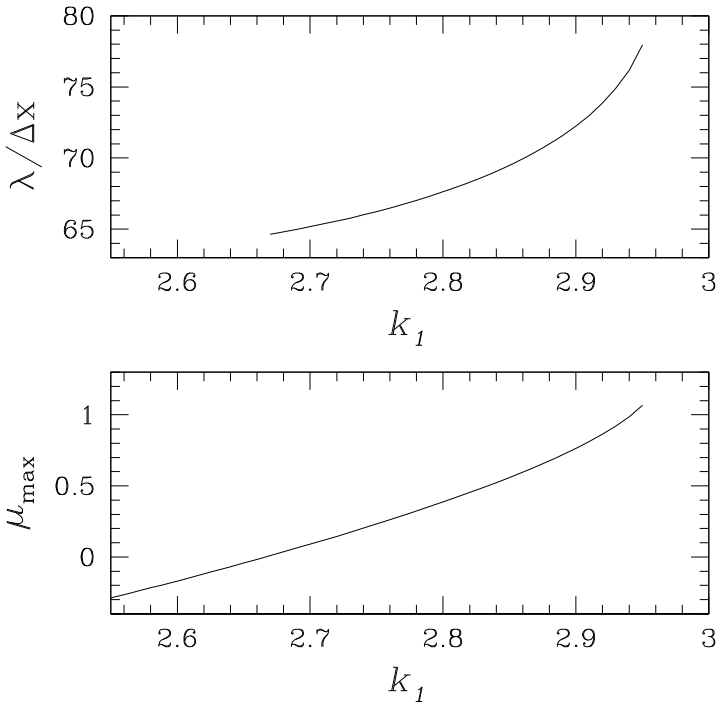

Fig. 4. Top: Scaled wavelength $\lambda/\Delta x$ of the Turing pattern *versus* rate constant k_1 of the chemical reaction given in Eq. (1). Bottom: Maximum value $\mu_{\max}$ of the largest eigenvalue of the linear operator M *versus* k_1. Parameter values: $k_2 = 1$, $k_3 = 2.19$, $k_{-3}R_2 = 8.76$, $D_A = 1$, $D_B = 10$, $\Delta x = 0.1$.

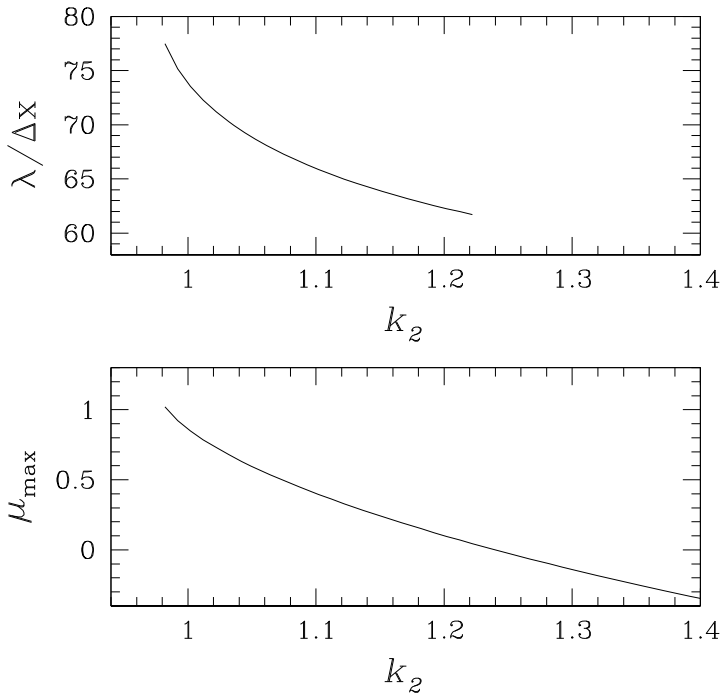

Fig. 5. Top: Scaled wavelength $\lambda/\Delta x$ of the Turing pattern *versus* rate constant k_2 of the chemical reaction given in Eq. (2). Bottom: Maximum value $\mu_{\max}$ of the largest eigenvalue of the linear operator M *versus* k_2. Parameter values: $k_1 = 2.92$, $k_3 = 2.19$, $k_{-3}R_2 = 8.76$, $D_A = 1$, $D_B = 10$, $\Delta x = 0.1$.

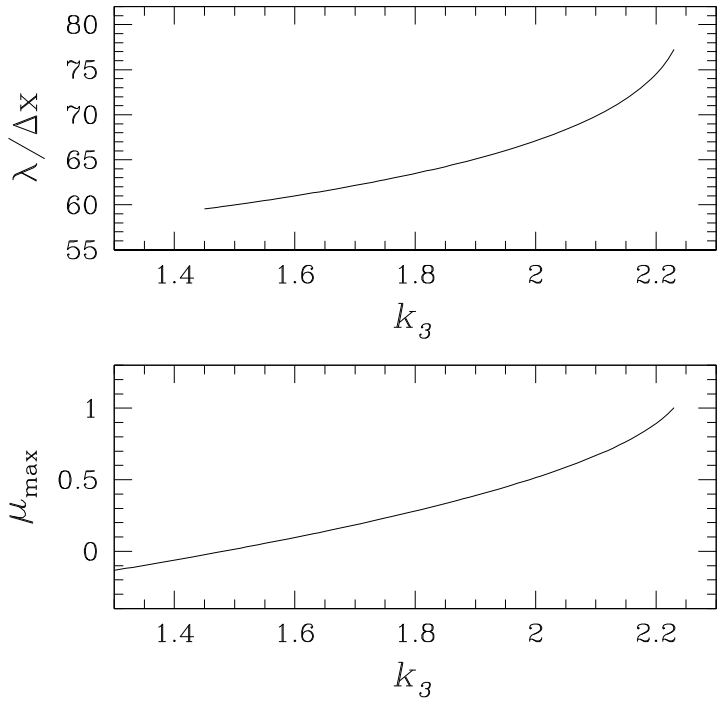

Fig. 6. Top: Scaled wavelength $\lambda/\Delta x$ of the Turing pattern *versus* rate constant k_3 of the forward chemical reaction given in Eq. (3). Bottom: Maximum value $\mu_{\max}$ of the largest eigenvalue of the linear operator M *versus* k_3. Parameter values: $k_1 = 2.92$, $k_2 = 1$, $k_{-3}R_2 = 8.76$, $D_A = 1$, $D_B = 10$, $\Delta x = 0.1$.

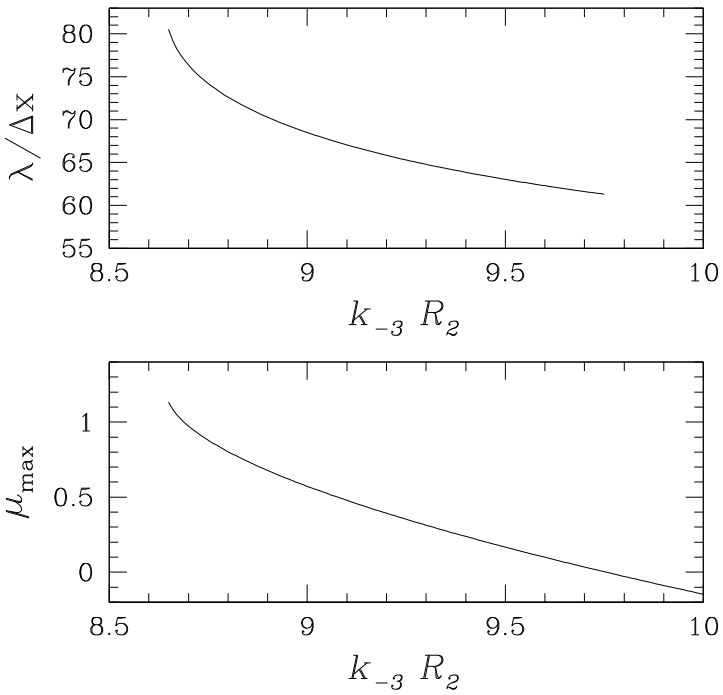

Fig. 7. Top: Scaled wavelength $\lambda/\Delta x$ of the Turing pattern *versus* rate constant $k_{-3}R_2$ of the backward chemical reaction given in Eq. (3). Bottom: Maximum value $\mu_{\max}$ of the largest eigenvalue of the linear operator M *versus* $k_{-3}R_2$. Parameter values: $k_1 = 2.92$, $k_2 = 1$, $k_3 = 2.19$, $D_A = 1$, $D_B = 10$, $\Delta x = 0.1$.

state $(A_{\mathrm{T}}, B_{\mathrm{T}})$ given in Eq. (6) is no longer satisfied. The two desired behaviors, *i.e.* the decrease of both λ and $\mu_{\max}$, are observed as k_1 decreases, k_2 increases, k_3 decreases, and $k_{-3}R_2$ increases. For an assumed homogeneous concentration R_2 of the reservoir, the variations of λ and $\mu_{\max}$ with R_2 are analogous to the variations with $k_{-3}R_2$. According to the chemical reaction given in Eq. (1), decreasing the rate constant k_1 tends to increase the concentration of species A. Following Eq. (2), increasing the rate constant k_2 of the autocatalytic step tends to increase the concentration of species A and decrease the concentration of species B. This last result seems to be inconsistent with the consequences drawn from the decrease in k_3 or the increase in $k_{-3}R_2$, which result in increasing the concentration of species B according to Eq. (3). However, we already stated that increasing B through soliciting the reservoir R_2 results in consuming species B faster by the autocatalytic step given in Eq. (2) [9, 26]. In particular, we observed that introducing a local source of species B leads to the nonintuitive local decrease of B concentration. Hence, all the variations of the rate constants that lead to a loss of stability of the Turing pattern are eventually associated with an increase of A concentration and a decrease of B concentration.

The diffusion coefficients and the rate constants characterize dynamics and are intrinsic to the reaction–diffusion system. Nevertheless, it is always possible to imagine spatial variations of the dynamical parameters. Well-chosen variations of the diffusion coefficient D_B of the inhibitor and each of the four rate constants of the chemical mechanism could be *a priori* used to build a termination model. In the framework of the application to developmental biology, steric hindrance and molecular crowding in the tail of an embryo may be invoked to justify the decrease of the diffusion coefficients. In chemical engineering, a local increase of temperature could be used to induce a local increase of the rate constants. However, a local increase of molecular crowding or temperature is susceptible to simultaneously affect several dynamical parameters [13, 22, 27–32]. Whereas a decrease of D_B is desired to destabilize the Turing pattern, while decreasing its wavelength, a simultaneous decrease of D_A would be detrimental. Similarly, an increase of k_2 and k_{-3} due to temperature increase could be satisfying but the joint decrease of k_1 and k_3 could blur the effect on the Turing structure. The simplest way to imagine the control of a targeted parameter leading to the desired behavior is to impose well-chosen spatial variations of the reservoir concentration R_2. Indeed, the product $k_{-3}R_2$ plays the role of an apparent rate constant for the backward reaction given in Eq. (3) that can be fixed at will in chemical engineering in the case of a single dynamical system with uniquely defined intrinsic parameters.

According to Fig. 7, increasing R_2 tends to destabilize the Turing pattern and decrease its wavelength. We examine if the results deduced from a stability analysis can be used in a dynamical approach. The results of the numerical integration of Eqs. (4) and (5) for a homogeneous concentration R_2 and a piecewise linear profile are given in Fig. 8. The initial condition is a step function between the steady state $(A_\mathrm{T}, B_\mathrm{T})$ in the first 10 cells on the left and the steady state (A_0, B_0) in the remaining cells. The initial total number of cells is set at $n_0 = 610$. Introducing the cell label $i = x/\Delta x$, where Δx is the cell length, and the discrete time $s = t/\Delta t$, where Δt is the time step, we choose

$$A(i, s = 0) = A_\mathrm{T}\,, \qquad B(i, s = 0) = B_\mathrm{T}\,, \qquad \text{for} \qquad 1 \le i \le 10\,, \tag{14}$$

$$A(i, s = 0) = A_0\,, \qquad B(s, s = 0) = B_0\,, \qquad \text{for} \qquad 11 \le i \le n_0\,. \tag{15}$$

To account for the growth of the system and simultaneously avoid boundary effects that may alter the wavelength of the structure [16], we impose a fixed boundary on the left and a free growing end on the right [9, 23, 26]. For parameter values for which the steady state $(A_\mathrm{T}, B_\mathrm{T})$ is unstable with respect to inhomogeneous perturbations, a Turing pattern develops after the passage of a chemical wave front. More precisely, according to Eqs. (4) and (5) and

due to the no-flux boundary conditions applied on the left boundary, the concentrations in the first cell obey

$$\begin{aligned} A(1,s+1) &= A(1,s) - k_1\Delta t A(1,s) + k_2\Delta t A(1,s)^2 B(1,s) \\ &\quad + D_A \frac{\Delta t}{(\Delta x)^2}(A(2,s) - A(1,s))\,, \end{aligned} \tag{16}$$

$$\begin{aligned} B(1,s+1) &= B(1,s) + k_{-3}R_2\Delta t - k_3\Delta t B(1,s) - k_2\Delta t A(1,s)^2 B(1,s) \\ &\quad + D_B \frac{\Delta t}{(\Delta x)^2}(B(2,s) - B(1,s)) \end{aligned} \tag{17}$$

so that both $A(1,s)$ and $B(1,s)$ are extremum of the Turing pattern in the first spatial cell $i = 1$.

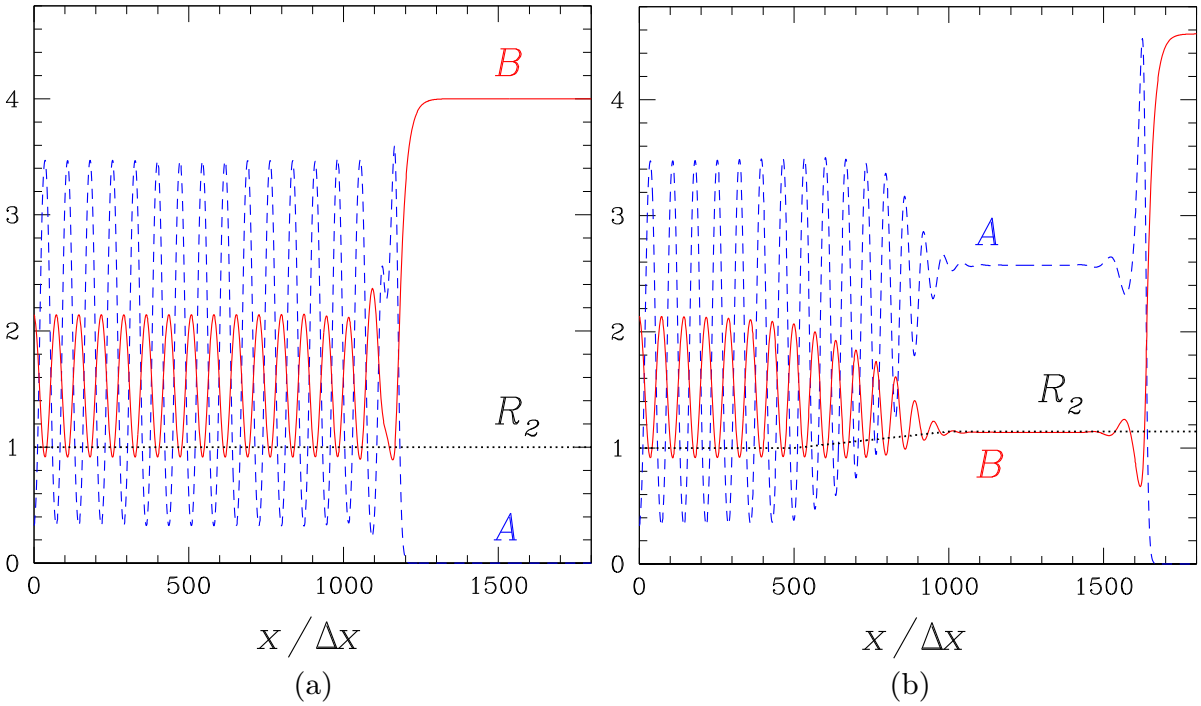

Fig. 8. Spatial profiles deduced from the numerical integration of Eqs. (4) and (5) for $k_1 = 2.92$, $k_2 = 1$, $k_3 = 2.19$, $k_{-3} = 8.76$, $D_A = 1$, $D_B = 10$, $\Delta t = 10^{-4}$, $t_{\text{end}}/\Delta t = 2000000$, $\Delta x = 0.1$. Black dotted line: Imposed concentration R_2 of the reservoir. (a) Homogeneous concentration $R_2 = 1$, (b) Piecewise linear R_2 profile. Gray/blue dashed line: Concentration of species A *versus* cell label $x/\Delta x$. Black/red solid line: Concentration of species B *versus* cell label $x/\Delta x$.

Spatial cells are added to the right end of the system at the front speed to counterbalance the progression of the wave front and mimic system growth: At all the discrete times s for which the concentration $B(n-600,s)$ of species B in the $n-600$ cell becomes smaller than $0.99B_0$, the total number n of cells is increased by 1. Provided that the front propagates at a speed smaller than $\Delta x/\Delta t$, this protocol ensures that a layer of about 600 cells

remains in the stationary state (A_0, B_0) on the right of the system, so that the propagation of the front is not significantly affected by the finite size of the system. To draw Fig. 8 (b), we have chosen the parameter values given in the caption of Fig. 1 and imposed $k_{-3} = 8.76$ for the following spatial profile for the concentration R_2 of the inhibitor reservoir:

$$R_2 = 1\,, \qquad \text{for} \quad 1 \leq i < 500\,, \tag{18}$$

$$R_2 = 2.83 \times 10^{-4} i + 0.858\,, \qquad \text{for} \quad 500 \leq i < 1000\,, \tag{19}$$

$$R_2 = 1.14\,, \qquad \text{for} \quad 1000 \leq i\,. \tag{20}$$

The simulation is stopped at time t_{end} for which the wave front has passed cell $i = 1000$. It is worth noting that the Turing pattern is unchanged for larger values of the final integration time. Then, only the position of the concentration gradients associated with the traveling wave evolve in time but the Turing structure has stopped growing and remains in a steady state with a fixed number of wavelengths. As desired, the increase of the concentration R_2 leads to the termination of the Turing structure.

As illustrated in Fig. 7, the Turing structure is expected to be stable in the range of $1 \leq i < 500$ for which $k_{-3}R_2 = 8.76$ and unstable in the range of $i \geq 1000$ for which $k_{-3}R_2 = 10$. More precisely, according to Eq. (13), the maximum of the eigenvalue $\mu_{\max}$ vanishes for $k_{-3}R_2 = 9.75$, *i.e.* $R_2 = 1.11$ for $k_{-3} = 8.76$, which occurs in spatial cell $i = 900$. Hence, the Turing pattern is predicted to be stable in the range of $0 \leq i < 900$ and unstable beyond this domain. The results shown in Fig. 8 (b) confirm the analytical predictions. The amplitude of the spatial oscillations decreases between $i \simeq 500$ and $i \simeq 1000$. The system is in a steady state in the range of $1000 \leq i < 1500$.

The increase of R_2 not only destabilizes the Turing structure but also modifies the steady state values and the propagation speed of the wave front. The comparison between Figs. 8 (a) and 8 (b) shows that, as R_2 increases, the wave front propagates faster, A_{T} increases, B_{T} decreases and B_0 increases. As a consequence of the variation of A_{T} and B_{T}, the oscillations of A and B concentrations are not symmetrical in the range of $500 \leq i < 900$. The decrease of the wavelength predicted in Fig. 7 is more difficult to check by a qualitative analysis. Using the numerical results illustrated in Fig. 8 (b), we evaluate the local wavelength by computing the number of cells between two minima of the A concentration profile. The results are given in Fig. 9 and compared to the analytical prediction deduced from Eqs. (11) and (12). The agreement between the numerical and analytical results is very satisfying in the range of $600 \leq i < 900$. Oscillations of very small amplitude are observed in Fig. 8 (b) in the range of $900 \leq i < 1000$, proving that a very damped Turing structure remains in a small area where instability was

predicted. The wavelength of the structure in the range of $1 \leq i < 500$ is slightly affected by the increase of R_2 from cell $i = 500$ but the deviation from the analytical prediction is only 2.5 percent. This small difference is related to the linear approximation used in wavelength evaluation that neglects non-linear terms that may be more important for large structures. Interestingly, the wavelength is sensitively decreased in the expected area in which the concentration of the reservoir R_2 increases: As shown in Fig. 9, the wavelength is reduced from 72 spatial cells to less than 61, before the structure disappears. We conclude that an increase in the concentration of the reservoir R_2 related to the inhibitor B is sufficient to account for the destabilization of the Turing pattern associated with a decrease of the wavelength. As anticipated by the results given in Fig. 7, according to which an increase of R_2 decreases the wavelength λ and leads to a negative eigenvalue $\mu_{\max}$ around (A_T, B_T), we suggest that an appropriate spatial variation of R_2 can be used in chemical engineering to stabilize the homogeneous steady state and induce a termination of the Turing pattern in a growing system.

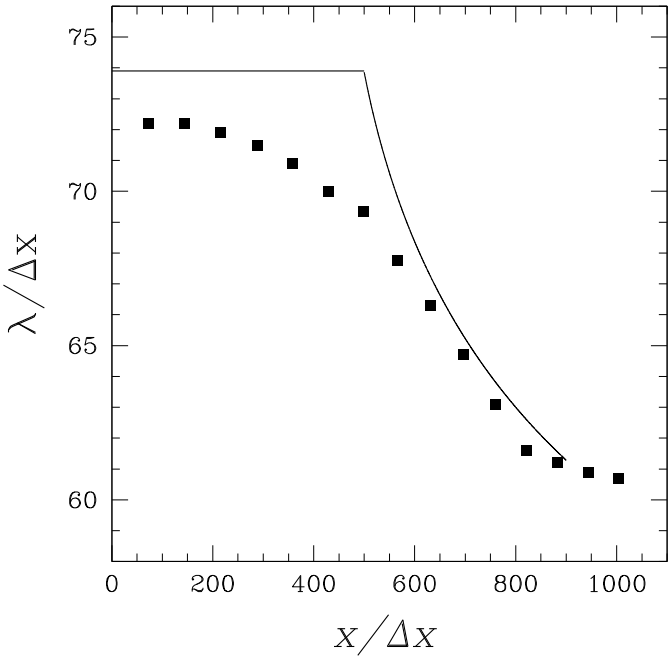

Fig. 9. Spatial variation of the scaled wavelength $\lambda/\Delta x$ of the Turing pattern *versus* cell label $x/\Delta x$ for the parameter values given in the caption of Fig. 8 (b). Symbols: Results deduced from the numerical integration of Eqs. (4) and (5). Solid line: Analytical prediction given in Eq. (12).

4. Conclusion

In a biomimetic approach, we have addressed the question of the termination of a Turing structure in a growing system. A free boundary is imposed at the growing part, which ensures that the wavelength of the pat-

tern is not perturbed by fixed boundary conditions. After deriving analytical expressions for the stability condition and the wavelength of the structure, we perform a systematic analysis of the effect of all dynamical parameters on the pattern. Apart from the variation of the diffusion coefficient of the activator, a well-chosen variation of the dynamical parameters leads to the desired behavior, *i.e.* the simultaneous loss of stability and the decrease of the wavelength. In particular, an increase of the effective rate constant $k_{-3}R_2$, where k_{-3} is the rate constant of the reaction injecting the inhibitor from the reservoir at the concentration R_2, is associated with a destabilization of the Turing pattern accompanied by a decrease of the wavelength.

Imposing a spatial variation of the concentration of the reservoir R_2 turns out to be an appropriate protocol for chemical engineering. However, the proposed procedure imposes the total length of the structure but not its number of wavelengths. In the framework of developmental biology, for example in the case of the growth of the digits or the spine of the vertebrates, the termination process has to respect the total number of segments for a possible variation in the length of the global structure. Therefore, it is necessary to imagine that the system itself is able to count the number of already formed segments and to trigger the variation of a parameter leading to smaller subsequently formed segments. If the concept of the Turing structure is kept in the formation of biological patterns, the presented results could be used to suggest such relevant parameters. The local increase of the rate constant k_{-3} that would be activated when a given number of segments has already been formed can be straightforwardly proposed. Similarly, the local increase of the rate constant k_2 controlling the autocatalytic production of the activator or the local decrease of the rate constant k_1 or k_3, associated with the absorption of the activator or the inhibitor by reservoirs, would lead to the desired phenomenon. The local decrease of the diffusion coefficient of the inhibitor offers an alternative. The nature of the mechanism that would trigger such a response of the system when a given number of segments has been created remains an open question.

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III.3 Scaling of Turing patterns

III.3.1 Summary of the results

The lack of adaptability to the global size of the system is topical [82, 83, 84, 85, 86, 87, 88] and one of the main objections against Turing-based models in morphogenesis. Specifically, in somitogenesis, it is expected that vertebra size adapts to the size of the embryo. Just before my arrival in the group, B. Nowakowski and A. Lemarchand introduced a model, inspired by the Schnakenberg model [89] and the Gray-Scott model [73] capable of addressing this issue at the macroscopic scale [36]. They proposed to address the problem in the context of molecular crowding, known to lead to non-negligible effects on the chemical mechanism [90, 91, 92, 93, 94, 95]. They considered a concentrated system in which the variations of the concentration of the solvent cannot be neglected and admitted that the reaction scheme presented in Eqs. (III.1-III.3) is modified as follows

$$\mathrm{A} + \mathrm{S} \xrightarrow{k_1} \mathrm{R_A} \tag{III.21}$$

$$2\,\mathrm{A} + \mathrm{B} \xrightarrow{k_2} 3\,\mathrm{A} \tag{III.22}$$

$$\mathrm{B} + \mathrm{S} \underset{k_{-3}}{\overset{k_3}{\rightleftharpoons}} \mathrm{R_B} \tag{III.23}$$

They solved the partial differential equations governing the evolution of the concentrations and proved that the wavelength of the Turing pattern can be controlled by the deviation from the high-dilution limit, roughly defined as the ratio $(c_A + c_B)/c_S$ of the solute concentration and the solvent concentration.

The deviation from the high-dilution limit is more prevalent in smaller systems such as biological cells. The challenge I faced was to adapt the model to simulations of particle dynamics based on the direct simulation Monte Carlo method presented in Sec. I.4.2. Even if the number of particles in the system varies, one of the constraints of the simulations is to keep the total number of simulated particles constant, in order to check the absence of bias in the total momentum and kinetic energy. It may imply the creation of ghost particles that slow down the simulation. The scheme given in Eqs. (III.21-III.23) does not conserve the number of particles and involves reservoir particles that are also time consuming.

I proposed to solve the problem using the following scheme

$$\begin{aligned} \mathrm{A} + \mathrm{S} &\xrightarrow{k_1} 2\,\mathrm{S} \\ 2\,\mathrm{A} + \mathrm{B} &\xrightarrow{k_2} 3\,\mathrm{A} \\ \mathrm{B} + \mathrm{S} &\xrightarrow{k_3} 2\,\mathrm{S} \end{aligned} \tag{III.24}$$

$$\begin{cases} \mathrm{R_B} \xrightarrow{k_{-3}} \mathrm{B} \\ \mathrm{S} \longrightarrow \mathrm{R_S} \end{cases} \tag{III.25}$$

in which the solvent particles play the role of particles of the reservoirs $\mathrm{R_B}$ and $\mathrm{R_S}$. In other words, when the process given in Eq. (III.25) occurs in a given spatial box, the particle B is created with the velocity and the position of a randomly chosen particle S of the same box. At the same time, the particle S disappears exactly at the same constant rate k_{-3} as the particle B is created. The step cannot be written $\mathrm{S} \xrightarrow{k_{-3}} \mathrm{B}$, because it would introduce a term $k_{-3}S$ in the rate equation of B instead of the constant term k_{-3}. I performed DSMC simulations of a reactive ternary mixture of A, B, and S particles with different diameters in order to reproduce different diffusion coefficients as presented in Sec. I.4.2. My results show that the wavelength of Turing patterns can be tuned at the submicrometric scale by controlling the total concentration, i.e. the deviation from the high-dilution limit. More precisely, doubling the concentration of the solute decreases the wavelength of the structure by a factor of 2. The results can be considered as a possible interpretation for proportion preservation of embryos in morphogenesis. We suggest that they could be used to design biomimetic materials with controlled submicrometric properties in chemical engineering.

III.3.2 Publication

The results are published in the article “Scaling of submicrometric Turing patterns in concentrated growing systems”, G. Morgado, B. Nowakowski, and A. Lemarchand, Phys. Rev. E, **98**, 032213 (2018) [37].

Scaling of submicrometric Turing patterns in concentrated growing systems

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The wavelength of a periodic spatial structure of Turing type is an intrinsic property of the considered reaction-diffusion dynamics and we address the question of its control at the microscopic scale for given dynamical parameters. The direct simulation Monte Carlo method, initially introduced to simulate particle dynamics in rarefied gases, is adapted to the simulation of concentrated solutions. We perform simulations of a submicrometric Turing pattern with appropriate boundary conditions and show that taking into account the role of the solvent in the chemical mechanism allows us to control the wavelength of the structure. Typically, doubling the concentration of the solute leads to decreasing the wavelength by two. The results could be used to design materials with controlled submicrometric properties in chemical engineering. They could also be considered as a possible interpretation of proportion preservation of embryos in morphogenesis.

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Chapter IV

Fisher-Kolmogorov-Petrovsky-Piskunov front

For more than eighty years, the Fisher-Kolmogorov-Petrovsky-Piskunov (FKPP) wave front has been providing new puzzles to researchers in dynamical systems theory and statistical physics. Within the framework of a deterministic description, corrections to the asymptotic propagation speed have been determined depending on the steepness of the initial condition first by Bramson [96, 97], then by Ebert and Saarloos [98], and currently by Brunet and Derrida [99, 100]. The role of fluctuations on the propagation speed has been first numerically detected using Langevin equations [101, 102], a master equation, DSMC and molecular dynamics simulations [103] The analytical stochastic description of FKKP fronts continues to be developed [104]. My contribution to the subject differs by taking into account different diffusion coefficients for the two reacting species.

IV.1 State of the art for identical diffusion coefficients

The FKPP model generalizes the Verhulst model, presented in Eq. (I.39),

$$\mathrm{A} + \mathrm{B} \xrightarrow{k} 2\,\mathrm{A} \tag{IV.1}$$

to inhomogeneous systems. For species A and B with the same diffusion coefficient D, the rate equations are written

$$\partial_t c_A = k c_A c_B + D\partial_x^2 c_A \tag{IV.2}$$

$$\partial_t c_B = -k c_A c_B + D\partial_x^2 c_B \tag{IV.3}$$

According to Eq. (IV.1), the quantity $c^{\mathrm{tot}} = c_A + c_B$ is conserved, leading to the single

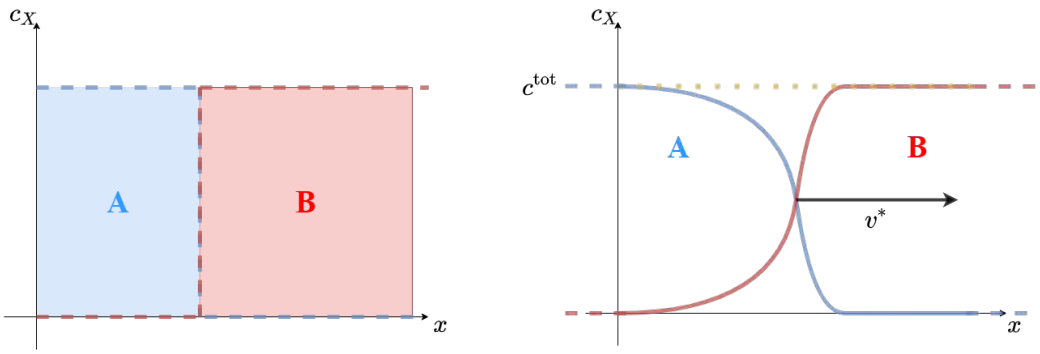

Fig. IV.1 *Left: Concentrations of A and B species vs. space coordinate x at time $t = 0$. Right: Concentrations of A and B species vs. space coordinate x when $t \to \infty$. The wave travels with a stationary velocity v^*.*

rate equation

$$\partial_t c_A = k c^{\text{tot}} c_A \left(1 - \frac{c_A}{c^{\text{tot}}}\right) + D\partial_x^2 c_A \tag{IV.4}$$

This equation exhibits traveling wave solutions, here between the unstable steady state $c_A = 0$ and the stable steady state $c_A = c^{\text{tot}}$.

IV.1.1 Minimum velocity v^*

The specific properties of an FKPP front can be qualitatively understood as follows. The unstability of the stationary state $c_A = 0$ makes the leading edge of the front sensitive to perturbations. From a theoretical point of view, the properties of the leading edge in which the concentration c_A is small can be studied within the framework of a linearized analysis. The front is "pulled" by the leading edge and the propagation speed does not depend on the nonlinearities of the dynamics.

The propagation speed v of the front is derived from the linearized version of Eqs. (IV.4) around the unstable state $(c_A = 0, c_B = c^{\text{tot}})$ in the moving frame $\zeta = x - vt$

$$-v\frac{\mathrm{d}c_A}{\mathrm{d}\zeta} = k c^{\text{tot}} c_A + D\frac{\mathrm{d}^2 c_A}{\mathrm{d}\zeta^2} \tag{IV.5}$$

Provided that the profile c_A follows an exponential form in the leading edge

$$c_A \simeq e^{-\gamma\zeta} \tag{IV.6}$$

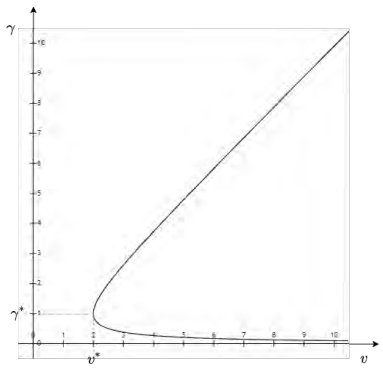

Fig. IV.2 *Diagram representing the two branches* $\gamma_+(v)$ *and* $\gamma_-(v)$ *for* $k = c^{tot} = D = 1$.

where γ depends on v, Eq. (IV.5) leads to a second-order polynomial

$$D\gamma^2 - v\gamma + kc^{\text{tot}} = 0 \tag{IV.7}$$

with real solutions

$$\gamma_\pm = \frac{v \pm \sqrt{v^2 - 4kc^{tot}D}}{2D} \tag{IV.8}$$

if $v^2 - 4kc^{tot}D \geq 0$.
For sufficiently steep initial conditions, in particular for the step function shown in Fig. IV.1, the wave front converges towards a stationary profile that travels at the minimum speed v^* [105]. According to Eq. (IV.8), the minimum speed v^* is given by

$$v^* = 2\sqrt{kc^{tot}D} \tag{IV.9}$$

Figure IV.2 shows the two branches $\gamma_+(v)$ and $\gamma_-(v)$. The minimum speed v^* corresponds to the meeting point $\gamma_+(v^*) = \gamma_-(v^*)$ of the two branches.

IV.1.2 Cutoff effect

In 1997, Brunet and Derrida showed that the introduction of a cutoff in the leading edge of the front significantly reduces the minimal velocity of the front. In this section, I recall the main lines of the demonstration [106]. If a cutoff ε is introduced in the reaction term of Eq. (IV.1), the rate equation for concentration c_A is

$$\partial_t c_A = kc^{\text{tot}} c_A \left(1 - \frac{c_A}{c^{\text{tot}}}\right) \Theta\left(\frac{c_A}{c^{\text{tot}}} - \varepsilon\right) + D\partial_x^2 c_A \tag{IV.10}$$

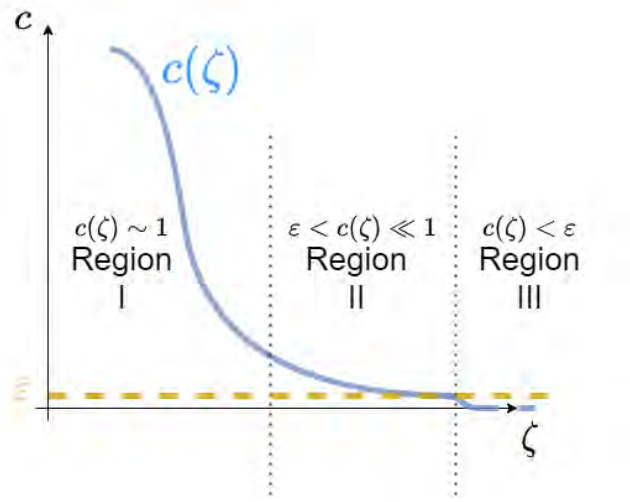

Fig. IV.3 *The three regions introduced by Brunet and Derrida [106] in the leading edge of an FKPP wave front with a cutoff ε.*

where $\Theta(x)$ is the Heaviside step function. Introducing the scale variables

$$c = \frac{c_A}{c^{\mathrm{tot}}} \tag{IV.11}$$

$$x' = \sqrt{\frac{kc^{\mathrm{tot}}}{D}}x \tag{IV.12}$$

$$t' = k(c^{\mathrm{tot}})^2 t \tag{IV.13}$$

and the coordinate $\zeta = x' - vt'$ in the moving frame, and looking for stationary solutions $c(\zeta)$, we find

$$vc' + c'' + c(1-c)\Theta(c-\varepsilon) = 0 \tag{IV.14}$$

Denoting the velocity v_ε of the front with a cutoff, Brunet and Derrida introduce the shift Δ with respect to the minimum velocity

$$\Delta = v^* - v_\varepsilon \tag{IV.15}$$

As shown in Fig. IV.3, three different regions can be defined in the leading edge: In region I, c is of order 1, in region II $\varepsilon < c \ll 1$, and in region III $c < \varepsilon$. In region I, the front is not significantly affected by the cutoff and the differential equation is expected to be the same as Eq. (IV.5). In region II, the concentration c is negligible with respect to 1 and the nonlinear term c^2 can be neglected compared to the linear term. In region III, the reaction term vanishes due to the Heaviside funtion.

It reads

$$\begin{cases} \text{Region I} & v^* c' + c'' + c = 0 \\ \text{Region II} & v_\varepsilon c' + c'' + c = 0 \\ \text{Region III} & v_\varepsilon c' + c'' = 0 \end{cases} \tag{IV.16}$$

These three second-order linear differential equations can be solved. The main issue is to build a continuous, derivable solution at the boundaries of the different regions. Denoting γ^* and $\gamma_r \pm i\gamma_i$ the solutions of Eq. (IV.8) for v^* and v_ε respectively yields

$$\begin{cases} \text{Region I} & c_I(\zeta) \simeq C_I \zeta e^{-\gamma^* \zeta} \\ \text{Region II} & c_{II}(\zeta) \simeq C_{II} e^{-\gamma_r \zeta} \sin\left(\gamma_i \zeta + C'_{II}\right) \\ \text{Region III} & c_{III}(\zeta) \simeq \varepsilon e^{-v_\varepsilon (\zeta - \zeta_0)} \end{cases} \tag{IV.17}$$

where C_I, C_{II}, C'_{II}, and ζ_0 are constants that can be derived from the boundary conditions. Between the regions I and II, the boundary condition imposes

$$C_I \zeta e^{-(\gamma^* - \gamma_r)\zeta} = C_{II} \sin\left(\gamma_i \zeta + C'_{II}\right) \tag{IV.18}$$

On the one hand, it is expected that, according to Eq. (IV.15), the difference $\gamma^* - \gamma_r$ is of order Δ. On the other hand, Eq. (IV.8) shows that γ_i is of order $\Delta^{1/2}$. Therefore, imposing $C'_{II} = 0$ at the leading order in $\Delta^{1/2}$ yields

$$C_I = C_{II} \gamma_i \tag{IV.19}$$

Between regions II and III, the concentration is equal to the cutoff ε and $\zeta = \zeta_0$. The conditions of continuity and derivability of the function $c(\zeta)$ are given by

$$\begin{cases} C_I e^{-\gamma_r \zeta_0} \sin\left(\gamma_i \zeta_0\right) = \varepsilon \gamma_i \\ C_I e^{-\gamma_r \zeta_0} \left[-\gamma_r \sin\left(\gamma_i \zeta_0\right) + \gamma_i \cos\left(\gamma_i \zeta_0\right)\right] = -v_\varepsilon \varepsilon \gamma_i \end{cases} \tag{IV.20}$$

Combining these two equations gives

$$v_\varepsilon = \gamma_r - \frac{\gamma_i}{\tan(\gamma_i \zeta_0)} \tag{IV.21}$$

Intuitively, the difference Δ is expected to be small, i.e. $\gamma_r \simeq \gamma^* = 1$ and $v_\varepsilon \simeq v^* = 2$. Therefore, it is possible to write

$$\tan(\gamma_i \zeta_0) \simeq -\gamma_i \tag{IV.22}$$

which is ensured only if $\gamma_i \zeta_0 \simeq \pi + \gamma_i$. Introducing this last assumption in Eq. (IV.20) and assuming that $\zeta_0 \gg 1$ leads to

$$\zeta_0 \simeq -\frac{\ln \varepsilon}{\gamma^*} \tag{IV.23}$$

$$\gamma_i \simeq \frac{\pi}{\zeta_0 - 1} \simeq \frac{\pi}{\zeta_0} \simeq \frac{\pi \gamma^*}{|\ln \varepsilon|} \tag{IV.24}$$

Brunet and Derrida expand v_ε into power series of γ_i,

$$v_\varepsilon \simeq v(\gamma^* \pm i\gamma_i) \simeq v(\gamma^*) - \frac{1}{2} v''(\gamma^*) \gamma_i^2 \tag{IV.25}$$

and find that the shift in velocity due to the cutoff obeys

$$\Delta \simeq \frac{v''(\gamma^*) \pi^2 \gamma^{*2}}{2(\ln \varepsilon)^2} \tag{IV.26}$$

For the same parameter values as in Fig. IV.2, the shift is of order $\frac{\pi^2}{2(\ln \varepsilon)^2}$. The introduction of a cutoff in the deterministic equation has been shown to correctly reproduce the effect of fluctuations in different stochastic systems that can be associated with Eq. (IV.4) in the macroscopic limit. In particular, branching Brownian motion [107] and the reaction-diffusion master equation associated with the scheme $\mathrm{A} + \mathrm{B} \longrightarrow 2\,\mathrm{A}$ [103] both lead to corrections of the propagation speed obeying Eq. (IV.26). Qualitatively, the discrete nature of the random variables in the two considered stochastic approaches implies the existence of a rightmost particle, which plays the role of a cutoff in the leading edge of the front.

IV.2 Results for different diffusion coefficients

IV.2.1 Deterministic description

a) High-dilution limit

The result given in Eq. (IV.9) is obtained for $D_A = D_B$. I address the more general case $D_A \neq D_B$, which implies that the quantity $c_A + c_B$ is not constant. It is to be noted that the deterministic model with different diffusion coefficients cannot straightforwardly be associated with elementary diffusion processes at the particle scale. Indeed, in a binary mixture, the diffusion coefficients of the two species are identical as shown in Eq. (I.77). A ternary mixture involving a solvent S in addition to A and B species offers a possible microsocopic picture of a model with $D_A \neq D_B$., as shown in Sec. I.3.2. The excess of solvent with respect to the solute implies that the collisions between S and A particles,

on the one hand, and S and B particles, on the other hand, determine the diffusion coefficients of A and B, respectively. Therefore, we introduce a solvent S that allows the diffusion coefficients of A and B species to be different. The rate equations are

$$\partial_t c_A = k c_A c_B + D_A \partial_x^2 c_A \tag{IV.27}$$

$$\partial_t c_B = -k c_A c_B + D_B \partial_x^2 c_B \tag{IV.28}$$

Linearizing the equations in the moving frame $\zeta = x - vt$ around $(c_A = 0, c_B = c^0)$ leads to

$$-v\partial_\zeta c_A = k c^0 c_A + D_A \partial_\zeta^2 c_A \tag{IV.29}$$

$$-v\partial_\zeta c_B = -k c^0 c_A + D_B \partial_\zeta^2 c_B \tag{IV.30}$$

where c^0 is the boundary value of c_B on the right side of the system, According to Eq. (IV.29), c_A does not depend on c_B, which means that the same procedure as $D_A = D_B$ can be applied. We conclude that the minimum velocity of the front is given by

$$v^* = 2\sqrt{k c^0 D_A} \tag{IV.31}$$

for all D_B. Intuitively, the leading edge asymptotically tends to the state $(0, c^0)$, for any given value of D_B. The propagation speed of pulled fronts being imposed by the leading edge, it is not surprising that the velocity does not depend on D_B.

In the high-dilution limit, the challenge was to find properties of the front profile susceptible to be affected by the difference of diffusion coefficients between species A and B. The linearization of the Eqs. (IV.27) and (IV.28) does not help in achieving this objective. I worked to develop an analytical approach, important to test the quality of the numerical results for possibly small perturbations of front properties. I focused on an expansion method proposed by Murray to give an estimation of the profile width of an unperturbed FKPP front [2]. The idea implemented by Murray is to consider $1/v^2$ as a small parameter. Clearly, the quality of the expansion is not excellent, $v*$ being equal to 2 for the scaled variables given in Eqs. (IV.11-IV.13). As a consequence, the first-order expansion delivered results valid in a small interval of D_B close to the value set for D_A and I was obliged to determine the second-order corrections. According to the approach of Murray, it was legitimate to first consider whether the width of the front would be affected by different diffusion coefficients for A and B. Even if the width is perturbed, the effect remains small. By examining the results of the numerical integration of Eqs. (IV.27) and (IV.28), I then stated that the vertical shift between the profiles of A and B could be a good candidate. I proposed to use what I called the height h between the A and B profiles, defined as the difference $c_A(\zeta = 0) - c_B(\zeta = 0)$, where the origin $\zeta = 0$ of the

moving frame is set at $c_A(\zeta = 0) = c^{tot}/2$. The results are very satisfying. The height h changes sign for $D_A = D_B$ and reaches more than 5% of c^{tot} in the investigated range of D_B smaller than D_A and more than -25% of c^{tot} for values of D_B larger than D_A.

b) Concentrated system

The results I obtained in the dilute case were very encouraging regarding the initial goal of using the FKPP front as an indicator of diffusion perturbation in a concentrated system. I therefore considered the modified rate equations associated with the FKPP model

$$\partial_t c_A = k c_A c_B + D_A \partial_x \left[\left(1 - \frac{c_A}{c^{\text{tot}}} \right) \partial_x c_A \right] - D_B \partial_x \left(\frac{c_A}{c^{\text{tot}}} \partial_x c_B \right) \tag{IV.32}$$

$$\partial_t c_B = -k c_A c_B + D_B \partial_x \left[\left(1 - \frac{c_B}{c^{\text{tot}}} \right) \partial_x c_B \right] - D_A \partial_x \left(\frac{c_B}{c^{\text{tot}}} \partial_x c_A \right) \tag{IV.33}$$

obtained from Eqs. (IV.27) and (IV.28) by taking into account the modified Fick's law given in Eqs. (I.61) and (I.62). The same procedure than in Eqs.(IV.29) and (IV.30) is applied, but the minimal velocity of the front remains the same as in Eq. (IV.31). My initial motivation for studying the propagation of an FKPP front was to exploit its sensitivity to small perturbations in order to use the front as a sensor of the perturbation of diffusion induced by high concentrations. From this point of view, this result, which states that the propagation speed does not depend neither on the diffusion coefficient of species B nor the concentration of the system, is disappointing. However, the results that I obtained within the framework of a stochastic description based on a master equation, with the introduction of a cutoff, interestingly challenges the result given in Eq. (IV.31).

I used the same expansion technique as in the dilute case to determine analytical expressions of the width and the height in the concentrated case. The results were confirmed by the numerical solutions of Eqs (IV.32) and (IV.33). The height h proved to be a good criterion to reveal the perturbation of diffusion in a concentrated system. The high-concentration-induced correction to the height monotonically decreases as D_B increases and remains larger that 5% for $D_B = 20D_A$. Values of D_B smaller than D_A lead to high-concentration-induced corrections to the height of more than 25%. However, this good score is partly due to the intrinsically small values of h in the range $D_B \leq D_A$. In particular, it should not be forgotten that h vanishes for $D_B = D_A$ and cannot be used in this specific case.

To conclude, the experimental determination of the vertical shift h between the profiles of the two species at the origin of the moving frame and the comparison with the expected value in the high-dilution limit should provide a satisfying test of high-concentration-induced perturbation of diffusion, more accurate in the range $2D_A \leq D_B \leq 20D_A$.

c) Publication

The results about the deterministic approach to the perturbation of an FKPP front for different diffusion coefficients in the dilute and concentrated cases are published in "Fisher-Kolmogorov-Petroskii-Piskunov wave front as a sensor of perturbed diffusion in concentrated systems", G. Morgado, B. Nowakowski, and A. Lemarchand, Phys. Rev. E, **99**, 022205 (2019) [43]

Fisher-Kolmogorov-Petrovskii-Piskunov wave front as a sensor of perturbed diffusion in concentrated systems

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The sensitivity to perturbations of the Fisher and Kolmogorov, Petrovskii, Piskunov front is used to find a quantity revealing perturbations of diffusion in a concentrated solution of two chemical species with different diffusivities. The deterministic dynamics includes cross-diffusion terms due to the deviation from the dilution limit. The behaviors of the front speed, the shift between the concentration profiles of the two species, and the width of the reactive zone are investigated, both analytically and numerically. The shift between the two profiles turns out to be a well-adapted criterion presenting noticeable variations with the deviation from the dilution limit in a wide range of parameter values.

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IV.2.2 Stochastic description

The results I obtained in Sec. IV.2.1 within the framework of a deterministic description show that introducing different diffusion coefficients $D_A \neq D_B$ does not modify the wave-front speed.

The contribution of a stochastic description involving discrete random variables, as is the case for a master equation, is specially valuable. Using Gillespie algorithm recalled in Sec.I.4.1, I performed simulations of the master equation associated with the reaction A+B $\longrightarrow$ 2 A and $D_A \neq D_B$. The results are qualitatively different from the results of the deterministic description. The master equation predicts that the propagation speed of the front is sensitively decreased if species B diffuses faster than species A. Typically, the front speed is reduced by 22% for $D_B = 16D_A$. This result can be qualitatively interpreted as follows. The fast diffusion of particles B quickly brings them to the vicinity of A particles where they are consumed by the autocatalytic reaction. Contrary to intuition, a large value of D_B leads to a smoother B profile. Hence, the rightmost particle A is surrounded by a smaller number of particles B than in the case $D_B \leq D_A$ and the front propagates more slowly.

From a theoretical point of view, this result is the most striking contribution of my PhD work. It is rewarding to bring out a new result on a problem that is more than 80 years old.

Using a deterministic analogy inspired from the cutoff approach of Brunet and Derrida, I consider Eqs. (IV.27) and (IV.28) in which a cutoff ϵ is introduced

$$\partial_t c_A = k c_A c_B \Theta(\frac{c_A}{c^{\rm tot}} - \varepsilon) + D_A \partial_x^2 c_A \tag{IV.34}$$

$$\partial_t c_B = -k c_A c_B \Theta(\frac{c_A}{c^{\rm tot}} - \varepsilon) + D_B \partial_x^2 c_B \tag{IV.35}$$

The linear analysis leads to a correction to front speed obeying Eq. (IV.26) which does not account for the behavior at large D_B. The problem is nonlinear and the linear cutoff approach presented in Sec. IV.1.2 fails. As suggested in Fig. IV.4, I conjecture that, for $D_B > D_A$, the leading edge of the A profile sees a smaller concentration of B than for $D_B \leq D_A$, leading to the empirical formula

$$v_\varepsilon = 2\sqrt{2 c_{B_\varepsilon} D_A}\left(1 - \frac{\pi^2}{2(\ln \varepsilon)^2}\right) \tag{IV.36}$$

where the B concentration c_{B_ϵ} at the abscissa x_ϵ for which $c_A(x_\epsilon)/c^{tot} = \epsilon$ is deduced from the numerical integration of the deterministic equations.

The results of the master equation satisfactorily agree with the empirical formula in which, according to reference [103], the cutoff ϵ is evaluated by the inverse of the

number of particles in the reactive interface. Despite intensive efforts and trials involving many methods, I could not derive an analytical prediction of the correction to the front speed for $D_B > D_A$. Using the perturbative approach in power of $1/v^2$ developed in the deterministic case as explained in Sec. IV.2.1 does not help as the nonlinear effect of D_B is lost when Eqs. (IV.34) and (IV.35) are linearized. Deducing the variance $\langle c_A c_B \rangle$ from a Langevin approach as in Sec. II is of no use because it involves continuous variables and even misses the linear cutoff effect. Applying the Hamilton-Jacobi technique to solve the master equation [108, 109] is also not successful. The effect of fast diffusion of the consumed species on the propagation speed that I numerically evidenced opens new perspectives in the fundamental description of Fisher - Kolmogorov, Petrovsky and Piskunov wave fronts.

a) Concentrated system

In a stochastic description using a master equation, diffusion is a jump process from one spatial cell to an adjacent cell. In a dilute system, the diffusion rate of a given species only depends on the number of particles of that species in the departure cell. The main difficulty in the master equation approach to a concentrated system is the definition of the transition rates including cross-diffusion.

I considered the master equation given in Eq. (I.30) and wrote the associated diffusion term as

$$\begin{aligned}\partial_t P(\{\Phi\},t)|_{\text{diffusion}} = \sum_i [&T^-_{N_A(i)+1} P(\{N_A(i-1)-1, N_A(i)+1\}) \\ &+ T^+_{N_A(i)+1} P(\{N_A(i)+1, N_A(i+1)-1\}) \\ &+ T^-_{N_B(i)+1} P(\{N_B(i-1)-1, N_B(i)+1\}) \\ &+ T^+_{N_B(i)+1} P(\{N_B(i)+1, N_B(i+1)-1\})] \end{aligned} \tag{IV.37}$$

where $T^{\pm}_{N_X(i)}$ are the transition rates associated with the jump of a particle X=A,B from cell i containing $N_X(i)$ particles to the left (-) or the right (+), respectively. The transition rates must be compatible with the macroscopic diffusion fluxes given in Eqs. (I.61) and (I.62). Consequently, $T^{\pm}_{N_X(i)}$ has a nontrivial dependence on the particle numbers of the two species in both the departure and arrival cells.

In order to propose an appropriate expression of $T^{\pm}_{N_X(i)}$, I introduced a discrete flux $j_X(i+1/2)$ at the interface between the cells i and $i+1$ and related it to the difference of transition rates to the left and to the right. Using Eqs. (I.61) and (I.62) and replacing $\partial_x c_X$ by $\dfrac{N_X(i+1)-N_X(i)}{\Omega \Delta x}$ where Ω stands for the volume of a single cell, I assigned

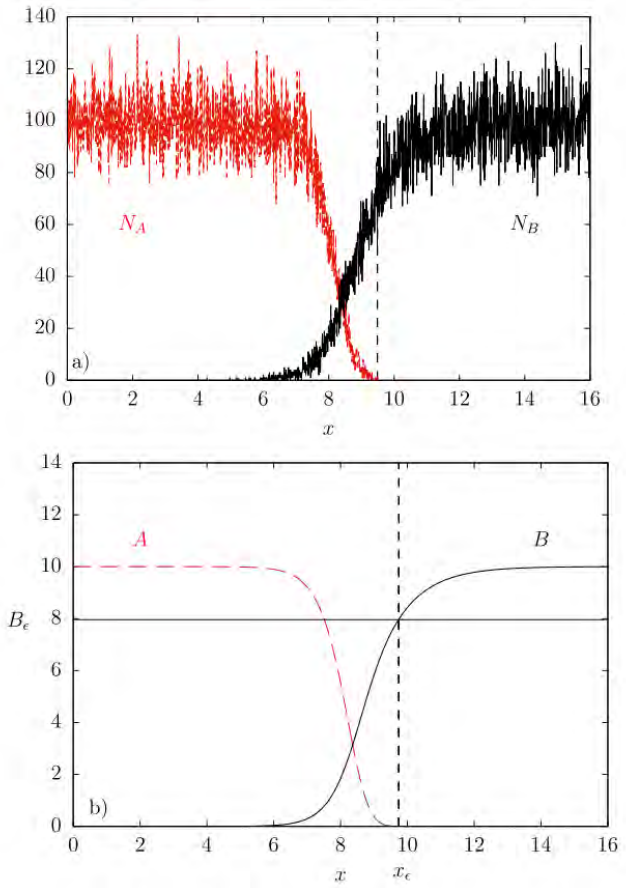

Fig. IV.4 *(a) Numbers N_A of particles A (red dashed line) and N_B of particles B (black solid line) versus spatial coordinate x deduced from simulation of the master equation for $D_A = 1$, $D_B = 16$ (other parameter values given in reference [44]). The vertical dashed line indicates the rightmost cell occupied by A particles. (b) Concentrations c_A of species A (red dashed line) and c_B of species B (black solid line) versus spatial coordinate x deduced from numerical integration of the deterministic equations in the presence of a cutoff ϵ. The vertical dashed line indicates the abscissa x_ϵ for which the scaled A concentration $c_A(x_\epsilon)/c^{tot}$ reaches the cutoff value ϵ. The horizontal line indicates the value c_{B_ϵ} of B concentration at the abscissa x_ϵ.*

well-chosen terms of the flux $j_X(i+1/2)$ to the transition rates to the left and to the right

$$T^{\pm}_{N_A(i)} = \frac{D_A}{\Delta x^2} N_A(i) - \frac{N_A(i \pm 1/2)}{\Omega c^{\mathrm{tot}} \Delta x^2} [D_A N_A(i) - D_B N_B(i \pm 1)] \tag{IV.38}$$

$$T^{\pm}_{N_B(i)} = \frac{D_B}{\Delta x^2} N_B(i) - \frac{N_B(i \pm 1/2)}{\Omega c^{\mathrm{tot}} \Delta x^2} [D_B N_B(i) - D_A N_A(i \pm 1)] \tag{IV.39}$$

in order to ensure that $T^{\pm}_{N_X(i)}$ is positive or equal to zero for any number of particles.

The expression of $T^{\pm}_{N_X(i)}$ depends on the number of particles $N_X(i+1/2)$ at the interface between two cells. Various definitions of this number of particles may be proposed. I checked that different definitions, all ensuring that the transition rate vanishes when the departure cell is empty, lead to similar results.
Simulations of the resulting master equation using Gillespie algorithm have been performed for different values of the diffusion coefficient D_B of species B. I found that the decrease of the propagation speed of the front observed as D_B increases is mitigated by cross-diffusion which reduces the impact of different diffusion coefficients.

b) Publication

In addition to evidencing fluctuation effects on front speed, which constitutes the major result, I characterized profile width W and height h in the stochastic approach, in both the dilute and concentrated cases. The results about W and h are closer to what could be expected after the deterministic study [43]. All my results about the stochastic approach to FKPP fronts are published in the article "Stochastic approach to Fisher and Kolmogorov, Petrovskii, and Piskunov wave fronts for species with different diffusivities in dilute and concentrated solutions", G. Morgado, B. Nowakowski, and A. Lemarchand, Physica A, **558**, 124954 (2020) [44].

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Stochastic approach to Fisher and Kolmogorov, Petrovskii, and Piskunov wave fronts for species with different diffusivities in dilute and concentrated solutions

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ABSTRACT

A wave front of Fisher and Kolmogorov, Petrovskii, and Piskunov type involving two species A and B with different diffusion coefficients D_A and D_B is studied using a master equation approach in dilute and concentrated solutions. Species A and B are supposed to be engaged in the autocatalytic reaction A+B $\rightarrow$ 2A. Contrary to the results of a deterministic description the front speed deduced from the master equation in the dilute case sensitively depends on the diffusion coefficient of species B. A linear analysis of the deterministic equations with a cutoff in the reactive term cannot explain the decrease of the front speed observed for $D_B > D_A$. In the case of a concentrated solution, the transition rates associated with cross-diffusion are derived from the corresponding diffusion fluxes. The properties of the wave front obtained in the dilute case remain valid but are mitigated by cross-diffusion which reduces the impact of different diffusion coefficients.

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Conclusion

In this work, I have been concerned with the formation of structures in living organisms. I chose to describe biological systems at an intermediate, mesocopic scale, using methods of statistical physics, such as kinetic theory and stochastic methods. My contribution to the stochastic elimination of fast variables in the framework of chemical kinetics [29] has illustrated the complex interplay between nonlinear deterministic dynamics and fluctuations. Specifically, I have shown that the linearized Langevin equations used to analytically compute the correlations of concentration fluctuations around steady values do not correctly capture the behavior of the system, in particular close to bifurcations. As a perspective, with the aim of developing an improved analytical approach, I suggest to consider the procedure proposed by Roberts and collaborators [110, 111, 112, 113] to derive stochastic normal forms valid in the vicinity of the center manifold. Roberts *et al.* assign orders of magnitude to the different terms of the evolution equations, in particular the Langevin forces. They derive approximate equations for the slow variables, describing the dynamics on the center manifold up to the desired order. The technique generalizes the ideas developed by Arnold to derive deterministic normal forms [114]. The treatment of the vicinity of a bifurcation is naturally included in the method and simply consists in including small terms related to the bifurcation parameter in the expansion procedure. It is to be noted that the expansion leads to non trivial noise terms involving convolution integrals of exponential terms and Langevin forces, which introduce memory noise terms in the reduced stochastic dynamics. Higher order terms of the expansion even yield nonlinear noise combinations between a Langevin force and a convolution integral of an exponential function and a Langevin force, which shows how complex the stochastic elimination of fast variables is [110]. The quality of the approach, i.e. the order at which the expansion can be troncated, could be checked by numerical integration of the Langevin equations, using the Euler-Maruyama method with Itô interpretation of the multiplicative noise [115]. The great advantage of the numerical integration of the Langevin equations would be to facilitate the comparison with the simulation of the master equation. As proved in the study of time asymmetry of correlation functions in far-from-equilibrium conditions in a bistable system [63], in oscillating systems close to a Hopf bifurcation [63, 62] and a saddle-node

infinite period bifurcation [63], it is however probable that the Langevin approach, although including multiplicative noise terms and all the nonlinearities of the dynamics, will not be sufficient to capture the subtleties of the interaction between fluctuations and deterministic nonlinearities. In general, the non Gaussian character of chemical noise intrinsically invalidates the Langevin approach. It is especially true in the intricate case of the stochastic elimination of fast variables. The correct description of concentration fluctuations is essential to predict the behavior of many systems that are sensitive to perturbations, in particular due to explosive behavior, the vicinity of a bifurcation, the existence of many simultaneously stable states or simply because they are small [116]. Hence, combustion hazards, pattern formation in developmental biology including Turing structures and Fisher - Kolmogorov, Petrovsky, Piskunov (FKPP) wave fronts require stochastic analyses.
The simulations of a submicrometric Turing pattern in a concentrated system I performed refute certain objections to Turing's model regarding the preservation of proportions in embryos. Assuming an appropriate role of the solvent in the chemical mechanism is sufficient to control the wavelength of the structure by monitoring the concentration of the solution. A significant decrease of the wavelength is obtained in a more concentrated solution for the considered chemical scheme. The adaptation of the size of the structure to the size of the embryo then follows from the hypothesis that a smaller embryo has greater concentrations of morphogens, imposed by the mother and not by the size of the embryo. In this respect, small embryos lead to a crowded environment [117, 118, 119]. The results can be exploited to design materials with controlled submicrometric properties in chemical engineering [120, 121, 122, 123]. Following a biomimetic approach, I proposed experimental conditions, compatible with the requirements of chemical engineering, to observe the termination of a Turing structure in a growing system. Among the different parameters playing on the stability of the pattern and the value of the wavelength, I selected the concentration of the reservoir which sets the injection rate of the inhibitor into the system for its easy control in the region where the experimentalist wishes the structure to stop.

I also characterized the effect of concentrated solutions on another spatio-temporal structure, often encountered in biology, a Fisher - Kolmogorov, Petrovsky, Piskunov (FKPP) wave front, used to model the propagation of a virus or a favorable genetic trait in a population. I focused on the modification of diffusion due to high concentrations. Beyond the description of concentrated solutions, I was led to consider reactive species with different diffusion coefficients. Performing simulations of the master equation, I obtained a nice result stating that an FKPP front is slowed down when the consumed species diffuses faster than the autocatalytically produced species. The analytical description of this phenomenon, using a nonlinear cutoff approach, is certainly a reasonable perspec-

tive. The consequences of high concentrations on biological structures deserves further attention. The results show that, using particle dynamics simulations, it is possible to check the validity of macroscopic models at the submicrometric scale. The new directions explored in the field of chemical engineering, as part of a biomimetic approach, could encourage experimentalists to design model systems for testing the main influence of high concentrations on organized behaviors.

The results obtained during my PhD led me to formulate some general ideas about the modeling of structures in biology and prompted me to revisit how the vision of biological patterns had evolved over the last century and the beginning of 21st century. Morphogenesis is an important part of developmental biology. Axial segmentation and the formation of periodic patterns are observed in invertebrates such as insects and crustaceans as well as in vertebrate embryos. The striking analogies between biological structures and the patterns that spontaneously emerge in far-from-equilibrium chemical systems logically incited theoreticians to use models of chemical kinetics to study biological phenomena. Experimental evidence of periodic spatial structures in a reaction-diffusion system, without the contribution of physical phenomena such as gravity and mechanical instabilities, was given in 1990 [72], long after the corresponding model was proposed by Turing in 1952. Previously, it had taken even more time to apply the concepts of dynamical systems, developed by mathematicians such as Henri Poincaré around 1900, to the description of far-from-equilibrium nonlinear phenomena in uniform systems. The temporal organization in homogeneous chemical systems, from periodic oscillations to chaos, has been interpreted in the context of dynamical systems theory in the 70s, first from a theoretical point of view, in particular in the group of the Nobel prize Ilya Prigogine in Brussels. Then, in the 80s, the Belousov–Zhabotinsky (BZ) reaction has been extensively studied. With the development and mastery of continuously stirred tank reactors (CSTRs) ensuring far-from-equilibrium conditions, the BZ reaction proved to provide an ideal experimental example of dynamical systems exhibiting all the different types of bifurcations and scenarios to chaos [124, 125, 126, 127, 128]. Application to biology arrived later and, at the very beginning of the 2000s, the concept of systems biology was introduced. It is indeed tempting to apply the notions of the theory of dynamical systems to model certain biological phenomena. Living systems are typically maintained far from equilibrium by exchanges of energy and matter with the environment and spontaneously evolve into organized structures.

Two antagonistic views, known as holism and reductionism, are usually adopted to study chemical systems and provide disjointed information. On the one hand, holism proposes a global approach to a system and neglects the discrete nature of matter. After a modeling effort to identify essential mechanisms and extract a small number of dynamical variables, the system is described at the macroscopic scale. It is then possible to

write differential equations governing the evolution of a homogeneous system and partial differential equations in the case of an inhomogeneous system. The nonlinearities of the equations determine the behavior of the system, depending on the parameter values and the involved bifurcations. A global, general classification of some biological phenomena can be obtained within the framework of such a deterministic, macroscopic analysis. Such a description ignores the fluctuations of the macroscopic variables that are induced by the microscopic dynamics of a huge number of elementary constituents. This global approach can be misleading in systems of small size like the systems typically studied in developmental biology. The role of fluctuations on the macroscopic behavior of a system is also significant, even in a large system, close to bifurcations [29] or for marginally stable solutions such as FKPP fronts [44].

On the other hand, reductionism focuses on the atomistic or molecular scale. However, the huge number of particles prompts the use of numerical simulations. The evolution of wave functions or particle positions and velocities, dictated by fundamental interactions according to quantum or classical mechanics, can then be followed. Even with the latest generation of computers, it is still extremely long to reach the space and time scales necessary to observe the formation of macroscopic patterns using ab-initio simulations, density functional theory, and even molecular dynamics. Moreover, the connection between changing a parameter characterizing atomistic interactions and changing a macroscopic property of a structure is not firmly established. The numerical simulations at the microscopic scale may provide empirical knowledge but it remains difficult to build qualitative relationships between the molecular structure and the macroscopic properties of the system. Reductionism gives access to the specific properties of a given system but the prediction of the behavior of a system showing a small difference in the microscopic characteristics often fails. Generalization within a reductionist approach is delicate.

In order to bridge the gap between the two remote microscopic and macroscopic scales, I chose to develop a description at the mesoscopic scale, which presents the advantage of accounting for the fluctuations as well as providing a general framework to develop analytical approaches. The strength of statistical physics is to propose a probabilistic description of a system composed of a large number of components. Microscopic features of molecules such as their atomic components, their chemical functions, and their structure are not explicitly taken into account by the stochastic description, which retains some consequences of these microscopic properties at the mesoscopic scale and take them into account in a coarse-grained manner. In particular, the notion of stochastic trajectory includes dissipation and irreversibility but with a more refined approach than the macroscopic description. Specifically, microscopic reversibility with respect to time reversal is lost in a master equation approach [61, 62, 63] but the production of entropy may decrease along a stochastic trajectory. The fluctuation theorem demonstrated by Galavotti

and Cohen makes precise the probability that such an event occurs [129, 130, 131, 132]. Writing a master equation associated with a given system, for example to account for cross-diffusion in a concentrated system [44], already represents an effort of modeling, i.e. an effort to extract ingredients from the microscopic scale that are essential to describe the phenomenon of interest at the mesoscopic scale. Approximating a master equation by Langevin equations makes it possible to derive analytical expressions that better point out the discontinuities in the properties induced by bifurcations [29]. From a general point of view, the analytical approaches made available by statistical physics offer the possibility to better « understand » complex phenomena. They at least guide the intuition and make it possible to guess the behavior of an unknown system having some points in common with the one previously studied.

The categorization of a given description into a holistic approach or a reductionist approach is not always clear. Specifically, the stochastic description using Langevin equations is obtained by adding a noise term to the deterministic equations, which includes a part of the microscopic complexity into the equations. In this respect, the description by Langevin equations lies between the two approaches.

Kinetic theory offers another interesting view by considering both deterministic macroscopic behavior and intrinsic probabilistic behavior of matter: It looks at the evolution of the distributions of the position and velocity of the particles. In particular, collision integrals govern the evolution of particle velocities. I have illustrated how kinetic theory is able to make the link between the elastic and reactive collisions between hard spheres and macroscopic parameters such as diffusion coefficients and rate constants [37]. The need for considering a mixture of at least three different species to obtain different diffusion coefficients for two reactants becomes obvious in kinetic theory whereas it is hidden in the two partial differential equations governing the macroscopic evolution of the concentrations of the two reactants [37]. As a conclusion, I would like to point out the value of describing a biological system on a mesoscopic scale in order to extract minimal ingredients, decipher mechanisms, and obtain some analytical results guiding intuition and understanding [133, 134, 135, 136]. However, the master equation and the kinetic equations are not usually solvable without strong approximations. It is of primer importance to check the validity of the analytical results. In this respect, both approaches benefit from the possibility to perform direct simulations of the equations using kinetic Monte Carlo simulations. Gillespie algorithm simulates stochastic trajectories obeying the master equation and the direct simulation Monte Carlo method (DSMC) introduced by Bird is a direct simulation of the kinetic equations including fluctuations. In a DSMC simulation, a particle represents thousands of true molecules [18], is assimilated to a hard sphere, and its collisions are randomly treated in an approximate way. Under these assumptions, particle dynamics is simulated up to thousand times faster than using molecular dynamics,

which allows us to simulate Turing patterns in a reasonable computation time, even in a concentrated system [37]. Finally, it is worthwhile to notice that the efficient simulation tools provided by kinetic Monte Carlo algorithms, that I first applied to materials science, specifically to the submicrometric simulation of gypsum crystallization [137, 138], are particularly well adapted to the simulations of biological submicrometric systems, which gives an idea of the potential of such methods.

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