Turing-like patterns in an asymmetric dynamic Ising model

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To investigate novel aspects of pattern formation in spin systems, we propose a mapping between reactive concentrations in a reaction-diffusion system and spin orientations in a dynamic multiple-spin Ising model. This specifically designed Ising model has asymmetric short-range interactions and several spin types coexisting at a site. The model is able to produce spatial patterns observed in reaction diffusion systems including Turing structures, showing that long-range interactions are not necessary to get such patterns in Ising models. While we used the example of genetic regulation during embryo-genesis to build our model, it can be used to study the behavior of other complex systems of interacting agents.

Introduction.— The mechanisms underlying global pattern formation from local interactions are studied in many fields of physics, chemistry and biology \[ \text{[13]} \]. Ising spins on lattices are simple discrete agents that can form patterns such as +1 or −1 spins domains. On the other hand, other widespread patterning models use continuous variables such as the concentrations of chemical species in reaction-diffusion systems. This models can lead to the formation of other complex patterns such as Turing striped patterns \[ \text{[4]} \]. Few Ising models can also lead to the formation of Turing patterns. They combine ferromagnetic nearest neighbor interactions with anti-ferromagnetic long-range interactions found for instance in ultra-thin magnetic films \[ \text{[5–6]} \]. Long-range interactions (i.e. decreasing with the distance as a power law \[ 1/r^\alpha \text{[7]} \]) are considered as a necessary condition for the formation of Turing-like patterns such as mazes or bubbles with a typical width of several lattice constants. Short-range interactions can only lead to ferromagnetic (all spins up or down) or anti-ferromagnetic (alternating up and down spins) states. In the presence of frustration, one-site large stripes can occur \[ \text{[8]} \]. In this letter, we construct a dynamic short-range Ising model presenting all the patterns of reaction-diffusion models, including Turing patterns, showing that long-range interactions are not necessary.

In 1952, Alan Turing proposed his reaction diffusion model to account for pattern formation in one of his most emblematic example: the embryo-genesis. In an embryo, each cell possesses the same set of genes, but the spatio-temporal patterning of their expression allow tissues and organs differentiation. \[ \text{Turing patterns usually involve two chemical species, called here a and b, and necessitate three main ingredients: an auto-catalysis of a, an asymmetry in reciprocal interactions (i.e. a enhances the formation of b while b penalizes the formation of a), and a quantitative difference in their diffusion coefficients. These rules lead chemical species to self-organize in space with a typical wave length that depends only on the parameters. Beside these self-organized patterns \[ \text{[9–11]} \] suggested by Turing, embryo-genesis provides examples of externally-driven patterns that are pre-formed at large scales, for instance by chemical gradients in the case of the Drosophila’s fertilized egg \[ \text{[12–13]} \]. These gradients activate specific genes in different locations of the embryo and these gene’s products subsequently act on other genes in a combinatorial manner. In the current view, the spatial regulation of gene expression in developing embryos is explained by combinations of these two different and complementary classes of scenarios \[ \text{[14]} \]. Various models implementing these two classes of scenarios have been proposed, either based on differential equations or cellular automata \[ \text{[15]} \]. Recently, an Ising model \[ \text{[16]} \] has also been developed to model gene patterning during embryo-genesis. Each spin corresponds to a gene that can be in one of the two states: active or inactive. Each site represent a nucleus and can contain several spins/genes. The spatial proximity between nucle does the interaction lattice (non null couplings), while coupling values defines the interaction network between spin/genes. These couplings are a simplification of the molecular mechanisms at work: gene transcription in RNA, RNA translation in proteins and protein diffusion to neighboring cells where they can modify transcrip tion rate of other genes. While being different from more detailed reaction-diffusion models, this Ising model features the most important ingredient of such models: short range interactions between spin/genes. Based on this similarity, we also placed ourselves in this context to build an extended version of the Ising model \[ \text{[16]} \], implementing asymmetric interactions between spin types, that could lead to Turing patterns.

In this letter, we first introduce a minimal and discretized model of a Stochastic Reaction Diffusion Automaton (SRDA) as a reference model. Then we construct our Asymmetric Dynamic Ising Model (ADIM) and establish a mapping between the ADIM and the SRDA. From this mapping we show that the ADIM can reproduce the variety of patterns of a reaction-diffusion system and thus that short-range interactions can lead to the formation of Turing-like patterns in Ising models.

Reaction Diffusion Automaton (RDA).— Reaction diffusion models describe the evolution in time and space of the concentrations \( c = (c_a, c_b, \ldots) \) of \( n_s \) chemical species
a, b, . . . undergoing two processes: diffusion, associated to diffusion coefficients $D_a, D_b, \ldots$ and local reactions $R_a(c, g), R_b(c, g), \ldots$ resulting in the creation of units of $a, b, \ldots$ per time unit, where $g$ is a possible external gradient forcing the system. The continuous space and time equations are for each specie $a$ of the form:

$$\partial_t c_a = D_a \nabla^2 c_a + R_a(c, g)$$

(1)

As a discrete automaton, here is the probabilistic automaton on a 1D lattice. The vector $c_i(t) = (c_{ia}(t), c_{ib}(t), \ldots)$ contains the concentrations of the $n$ considered species on each lattice site $i$ at discrete time $t$. The external gradient $g$ prescribed time-independent additional specie $g_i$ on site $i$. Each time step is divided in three substeps. The first one ($t \to t'$) is the production event: each concentration is incremented by 1 with probability:

$$P_{\text{prod}}^{ia} = \frac{1}{1 + e^{-u_a(c_i, g_i)}}$$

(2)

It is a common usage to model gene regulation by sigmoidal functions. This exact form has been used for *Drosophila* development modeling[17]. We choose

$$u_a(c_i, g_i) = \sum_b (\phi_{ba} c_{ib}) + \kappa_a g_i - \theta_0$$

(3)

where the $\phi_{ba}$ are the reaction constants between species (the sum is over all species, including $a$ itself), $\kappa_a$ represents the effects of the gradient $g$ on specie $a$ and $\theta_0$ is an activation threshold common to all species.

The second event ($t' \to t''$) is diffusion, approximated by a Gaussian kernel $G_{\sigma_a}$ of standard deviation $\sigma_a$ and mean value 0:

$$c_{ia}(t'') = \sum_{|j-i|<2\sigma_a} G_{\sigma_a}(|j-i|) c_{j,a}(t')$$

(4)

The third event ($t'' \to t+1$) is degradation, assumed to occur at the same rate $\varepsilon$ for all specie:

$$c_{ia}(t+1) = \varepsilon c_{ia}(t'')$$

(5)

where $0 < \varepsilon < 1$.

To represent the steady states, concentrations are normalized by $c_{\max} = \frac{1}{1 + \varepsilon}$, so $c^* = \frac{c}{c_{\max}}$ is comprised between 0 and 1.

As described in the introduction, two classes of patterns can emerge from our model: gradient-induced patterning (Fig 1-i) and Turing instabilities (Fig 1-ii). The two types of mechanisms can be combined (Fig 1-iii) leading to the appearance of hybrid patterns[14].

**Asymmetric Dynamic Ising Model (ADIM).—** The classical Ising model has been created in 1920[13] as a toy model describing ferromagnetism. The spins are bivalued (usually $S_i = \pm 1$, but here, we equivalently choose $S_i = 0, 1$). They are placed on a lattice and interact with their nearest neighbors with an interaction constant $J > 0$ that tends to align them. In the presence of a space-dependent magnetic field $h_i$, the energy of the system is:

$$E = -J \sum_{i,j} S_i \cdot S_j - \sum_i h_i S_i$$

(6)

where $\partial_i$ contains the nearest neighbors of site $i$.

The first step to map our reaction-diffusion automaton is to design a multiple-spin Ising model, similarly to [16]. To each site $i$ of the lattice, we associate $n$ spin types corresponding to the different genes $a, b, \ldots$. $S_i$ becomes a vector $S_i = (s_{ia}, s_{ib}, \ldots)$ of components 0 or 1. The concentration of the SRDA now corresponds to the average value of the spin, named magnetization. Each spin type interacts with all other spin types including itself. We thus rewrite $J$ as a matrix $J$ whose coefficient $J_{ab}$ represents the interactions between $a$-spins and $b$-spins. To mimic the gradient effect on the different genes, $h_i$ is supposed to be coupled differently to each spin-type and we introduce a coupling vector $K = (k_a, k_b, \ldots)$, where $k_a$ represents the effect of $h_i$ on the $a$-spins. Eq (6) becomes:

$$E = -\sum_{i,j} S_i^t J S_j - \sum_i h_i K S_i$$

(7)

To get patterns typical for reaction-diffusion phenomena, we also introduce spin type dependent interaction range $r_a$. An $a$-spin now acts on its neighboring sites up to a distance $r_a$, including itself. We denote by $\partial_i r_a$ this set of spins (e.g. $\partial_i r_a = [i - r_a : i + r_a]$ on a 1D chain). The interaction parameters are re-scaled using the volume $V_{\partial_i r_a}$, which is the number of sites in $\partial_i r_a$ (e.g. $V_{\partial_i r_a} = 2r_a + 1$ in 1D).

We notice that only the average values $\bar{J}_{ab} = \frac{\sum_{i,j} J_{ab}}{V_{\partial_i r_a}}$ are important in the determination of the equilibrium state.
of Eq (7), obtained at finite temperature $T \neq 0$ using e.g. the Metropolis algorithm [19]. However, the matrix $\bar{J}$ needs to be effectively asymmetric to reproduce the asymmetry of the reaction constants $\phi_{ab}$ leading to the formation of interesting patterns. We thus take a step further from [16] by implementing parallel dynamics in our model, similarly to kinetic asymmetric Ising models [20] [21], making it a non-equilibrium model.

At each time step $t$, we calculate an effective field $h_{ia}^{\text{eff}}(t)$ influencing the $s_{ia}$ spin:

$$h_{ia}^{\text{eff}}(t) = \sum_b \left( \frac{J_{ba}}{V_{\partial_b}} \sum_{j \in \partial_b} s_{jb}(t) \right) + k_a h_t - h_0.$$  

where we introduce $h_0$ an homogeneous external gradient.

All spins are then updated to give the configuration at time $t+1$ according to the following probability distribution:

$$P(s_{ia}(t+1)) = \frac{e^{-\beta h_{ia}^{\text{eff}}(t)s_{ia}(t+1)}}{2 \cosh(\beta h_{ia}^{\text{eff}}(t))},$$

where $\beta = 1/T$. The temperature $T$ accounts for the noisiness of the system.

Models comparison.— The SRDA and ADIM are both governed by Markovian dynamics and share important features: asymmetry in the coupling matrices and locality of the interactions. In the ADIM however, local reactions and transport are merged in nearest neighbors interactions. Still, many parameters appear to have similar roles: $\bar{J}$ and $\Phi$, $k$ and $\kappa$, $h_0$ and $\theta_0$, and $r$ and $\sigma$, as presented Table I. Two parameters are nevertheless model specific: the degradation rate $\varepsilon$ and the temperature $T$.

We wish to investigate the similarity in patterns that can be obtained by confronting the two models. We study the case $n_a = 1$, which corresponds to a classical Ising model under a space-dependent external field. We fix $T = 1$ in the ADIM since this temperature gives the most direct equivalence with Eq (2) (see Supp. Mat.). For the sake of simplicity, we fix $r_a = \sigma_a = 1$ so that interactions are only between nearest neighbors and we chose the space-dependent external field to be linear. In this conditions, we show by a calculation using the homogeneous solutions in mean-field approximation (see Supp. Mat.) that the value of degradation that gives the best mapping between interaction parameters in both models is $\varepsilon_{\text{opt}} = 0.5$.

Fig 2-a-d presents the mean concentration $\langle c^a \rangle$ and the magnetization $M$ of the patterns obtained by the SRDA and ADIM in the planes $(\phi_{aa}, \kappa_a)$ and $(J_{aa}, k_a)$ with $h_0 = \theta_0 = 1$. They represent the fraction of space and time where respectively $a$ is being produced or spins $s_a$ are up. For all probed regions of the parameter space, very similar patterns are observed for both the ADIM and the SRDA. Two broad zones of $\langle c^a \rangle = M = 1$ and $\langle c^a \rangle = M = 0$ correspond to full activation (Fig 2-a) and full inhibition (Fig 2-d). Transition between these two states can be done either through the formation and displacement of a sharp boundary (Fig 2-d), corresponding to strong inhibition by the external gradient and auto-

| TABLE I. Correspondence between parameters |
|-------------------------------------------|
| **SRDA** | **ADIM** |
| --- | --- |
| Diffusion constant | $\sigma$ | $r$ |
| Reaction constant | $\phi$ | $\bar{J}$ |
| Reaction constant | $\kappa$ | $k$ |
| Activation threshold | $\theta_0$ | $h_0$ |
| Degradation | $\varepsilon = 0.5$ | |
| Noise | $T = 1$ | Temperature |
FIG. 3. (a) 2D ADIM simulations on 128x128 periodic boxes with $h_0 = 1$, $r_a = 1$, $r_b = 5$, $J_{aa} = 13$, $J_{bb} = 0$, $J_{ab}$ and $J_{ba}$ varying, and $T = 1$. Dark red corresponds to $s_a = 1$ and pink to $s_a = 0$. A variety of Turing-like patterns is observed. (b) Pseudo order parameter $\Lambda$ as a function of temperature for “maze” ($\star$) and “bubbles” ($\bullet$) patterns issued from (a). (c) Snapshots at different temperatures of these same patterns.

activation, or by the appearance and intensification of a smooth gradient-like pattern (Fig 2-♦), corresponding to a gradient activation balanced by a null or very low auto-inhibition.

Yet, the sharpness of the ■-pattern is different in both models. Intuitively this sharpness depends on the correlation length of the system and thus the difference in parameters causes an increase in the correlation lengths and a decrease of the border sharpness. It is therefore possible to choose a value for $r_a$ for which the slope exactly matches the slope obtained for any given value of $\sigma_a$ (see Supp. Mat. for more discussion on this matter).

**Turing patterns in the ADIM.**— In light of these similarities between SRDA and ADIM in the case $n_s = 1$, we now look at the case $n_s = 2$ with no external gradient and try to reproduce Turing patterns. To investigate a richer variety of Turing patterns, we also switch to 2D with periodic boundary conditions. A main feature enabling Turing instabilities in reaction diffusion models is the difference of diffusion coefficients for both species. Likewise, the ratio $r_b/r_a$, where $a$ is the activator spin-type and $b$ is the inhibitor spin-type, need to be great enough to form stripes patterns of spin orientations (see Supp.Mat.). 2D patterns as a function of the interactions $J_{ab} > 0$ and $J_{ba} < 0$ are presented in Fig 3-a for $r_a = 1$ and $r_b = 5$. A subtle trade-off between these two values gives rise to different types of patterns, including “maze” $\star$ and “bubbles” $\bullet$.

We next investigate the effect of temperature on the stability of these patterns. In long-range interacting Ising models at equilibrium, phase transitions between smectic, nematic or liquid phases can occur when $T$ varies [22]. Here, the various patterns do not break any symmetry and no such phase transition can occur. However, there is a typical width of the ribbons, or distance between the bubbles. This length leads to the definition of a pseudo order parameter $\Lambda$ (see Supp. Mat.). Fig 3-b shows $\Lambda$ for different system sizes versus the temperature. A dynamic crossover occurs at different temperatures between a patterned and a disordered phase. These temperatures do not depend on the lattice size, thus excluding potential confounding finite size effects. The order parameter also gives us a measure of the typical length of the patterns $L_\Lambda$. Here for $r_a = 1$ and $r_b = 5$ we have $L_\Lambda \approx 8$ lattice spacings, but one can tune this typical length by modifying the ratio $r_b/r_a$ (see Supp.Mat. for a complete description).

In the Ising model, temperature reflects thermal noise, whereas in a reaction diffusion system, noise is related to the number of molecules: a lower number leads to larger relative fluctuations in the local concentrations. Molecular dynamics studies point out the importance of fluctuations for the emergence of Turing patterns [23]. Our results on the stability of patterns with temperature suggest on the other hand that if the number of molecules becomes too small (corresponding to high temperatures, hence high fluctuations) the patterns could disappear.

To conclude, using an embryo-genesis-inspired mapping with a reaction-diffusion model, we have constructed the ADIM, a short-range out-of-equilibrium Ising model giving rise to Turing patterns of typical length scale several lattice spacings. Such Turing patterns had previously only been observed in long-range Ising models. While interesting on a theoretical level, our mapping between the reaction diffusion and Ising models can also be useful to extrapolate specific features of a model on the other one and vice versa.

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Supplemental Materials: Turing-like patterns in a asymmetric dynamic Ising model

NUMERICAL METHODS

ADIM— The system is composed of $N_S$ sites. On each site is associated $n_s$ spin types. Parallel dynamics is implemented as follows.

We initialize the system at $t = 0$ by randomly attributing a value 0 or 1 at each of the $n_s \times N_S$ spins. At each time step $t$ we calculate the effective field $h_{ia}^{\text{eff}}(t)$ for each $a$-type spin on each site $i$:

$$h_{ia}^{\text{eff}}(t) = \sum_b \left( \frac{J_{ba}}{V_{\text{eff}} b} \sum_{j \in \partial h_i} s_{jb}(t) \right) + k_a h_i - h_0,$$  \hspace{1cm} (S1)

where $J_{ba}$ is the action of $b$-spins on $a$-spins, $h_i$ the value of the space dependent external magnetic field at site $i$, $k_a$ the coupling between $h$ and $a$-type spins and $h_0$ a global external field. $\partial h_i$ designates the nearest neighbors of spin $s_{ib}$, defined by the interaction range $r_b$ for $b$-spin type such as $\partial h_b = \{ j, |j-i| < r_b \}$ and $V_{\text{eff}} = \text{Card}(\partial h_i)$.

We calculate the corresponding Boltzmann probabilities:

$$P(s_{ia}(t+1) = 1) = \frac{e^{\beta h_{ia}^{\text{eff}}(t)}}{2 \cosh(\beta h_{ia}^{\text{eff}}(t))},$$  \hspace{1cm} (S2)

where $\beta = T^{-1}$ is the inverse temperature.

In 1D, the simulation runs at a fixed temperature $T$. In 2D, the stationary state is calculated using a simulated annealing (SA) to avoid freezing in configurations with long relaxation times. Cooling strategy is exponential:

$$T_{SA}(t) = T_0 \times a^t,$$  \hspace{1cm} (S3)

with $0 < a < 1$.

The spins at time $t+1$ are simultaneously chosen according to these probabilities. The operation is repeated during $n_t$ time steps, and in case of SA, $a$ is chosen so that $T_{SA}(n_t) = T$, ie $a = \left( \frac{T_0}{T} \right)^{n_t^{-1}}$. Then the simulation is pursued and recorded for $n_{\text{rec}}$ time steps. Finally $\langle s_{ia} \rangle$ is obtained by averaging over the $n_{\text{rec}}$ recorded configurations. Typically, $n_t = 250$ and $n_{\text{rec}} = 50$.

SRDA— The system is composed of $N_S$ sites at which is associated $n_s$ specie concentrations $c_a$. Each concentration is randomly chosen at $t = 0$ between 0 and 1. Each time step is subdivided in 3 events as presented in the main text.

This is repeated for $n_t$ time steps to reach the stationary state. Then each concentration is normalized by $c_{\text{max}}$ to obtain $0 < c_{\text{ia}} < 1$. Typically, $n_t = 200$.

In both models, the boundary conditions are set to reflecting in the case 1D to have gradient-dependent patterns. In the 2D ADIM, we choose periodic boundary conditions.

DETERMINATION OF $\varepsilon_{\text{opt}}$ USING HOMOGENEOUS STATIONARY SOLUTIONS

We use here the homogeneous steady state solutions in mean-field approximation for both models to establish a relationship between parameters in the case of one specie $a$ ($n_s = 1$), and more specifically to find the optimal value $\varepsilon_{\text{opt}}$ for which both model lead to the same patterns for equal network parameters.

ADIM— The mean-field approximation for the ADIM is (see Eq. [8]):

$$\langle s_{ia} \rangle = \frac{1}{1 + e^{-\beta h_{ia}^{\text{eff}}(t)}}.$$  \hspace{1cm} (S4)

For only one spin type $a$ ($n_s = 1$):

$$\langle s_{ia} \rangle = \frac{1}{1 + e^{-\beta [J_{aa}(s_{ia}) + k_a h_i - h_0]}},$$  \hspace{1cm} (S5)

Since we consider a homogeneous state and we are in 1D, $\sum_{j \in \partial a_a} \langle s_{ja} \rangle = (2r_a + 1) \langle s_{ia} \rangle$ and $V_{\text{eff}} = 2r_a + 1$, leading to:

$$\langle s_{ia} \rangle = \frac{1}{1 + e^{-\beta [J_{aa}(s_{ia}) + k_a h_i - h_0]}},$$  \hspace{1cm} (S6)

SRDA— In the mean-field approximation for the SRDA model, we average over several realizations of time evolution for each time step. Thus, we replace the probabilistic increment of the production step (Eq (2)) by a deterministic one:

$$c_{ia}(t') = c_{ia}(t) + \frac{1}{1 + e^{-u_a(c_{ia},g)}}.$$  \hspace{1cm} (S7)

By combining this new equation to the two other events (diffusion (Eq (4)) and degradation (Eq (5))), we get:

$$c_{ia}(t+1) = \varepsilon \left[ \sum_{|j-i|<2r_a} G_{\sigma_a}(|j-i|) c_{ja}(t) + \frac{1}{1 + e^{-u_a(c_{ia},g)}} \right].$$  \hspace{1cm} (S8)

In the classical PDE reaction-diffusion approach as defined in Eq (1), searching for an homogeneous steady state equates to look for the solution of $R_a(c,g) = 0$ since $\partial_t c_a = 0$ (steady state) and $\nabla^2 c_a = 0$ (homogeneous). In our SRDA, the homogeneity translates in $\forall j c_{ja}(t) = c_{ia}(t)$, and using the fact that $\sum_{r<2r} G_{\sigma_a}(r) = 1$, we obtain:

$$\sum_{|j-i|<2r_a} G_{\sigma_a}(|j-i|) c_{ja}(t) + \frac{1}{1 + e^{-u_a(c_{ia},g)}} = c_{ia}(t')$$  \hspace{1cm} (S9)

which leads to a simplification of Eq (S8):

$$c_{ia}(t+1) = \varepsilon \left[ c_{ia}(t) + \frac{1}{1 + e^{-u_a(c_{ia},g)}} \right].$$  \hspace{1cm} (S10)
FIG. S1. Correspondence between $r_a$ using the sharp-boundary pattern introduced in main text (see Fig 2). (a) Increasing the spatial parameters $\sigma_a$ and $r_a$ decreases the boundary sharpness. (b) Quantitative evaluation of the sharpness by fitting the boundary interface by an affine function. (c) $\sigma_a$ and $r_a$ as a function of the measured sharpness are fitted by power laws $y = \frac{1}{\varepsilon}$. For any given sharpness, $\sigma_a^{\text{fit}}$ and $r_a^{\text{fit}}$ can be calculated using these fits. (d) $r_a^{\text{fit}}$ as a function of $\sigma_a^{\text{fit}}$.

Being at steady-state $c_{ia}(t+1) = c_{ia}(t)$, and using $c_{\text{max}} = \frac{1}{1+\varepsilon}$, we retrieve $c^*$:

$$c_{ia}^* = \frac{1}{1 + e^{-\varepsilon(a_i - G_i)}} \quad (S11)$$

For $n_s = 1$:

$$c_{ia}^* = \frac{1}{1 + e^{\left[\frac{\varepsilon}{a_i} - 1\right]}} \quad (S12)$$

Optimal mapping value of $\varepsilon$—Eq (S12) and Eq (S14) are combined to search for the solution of $\langle s_{ia} \rangle = c_{ia}^*$, leading to:

$$\beta [J_{aa} \langle s_{ja} \rangle + k_a h_i - h_0] = \frac{\varepsilon}{1 - \varepsilon} c_{ia}^* + \kappa_a g_i - \theta_0. \quad (S13)$$

For $\beta = T^{-1} = 1$, identical network parameters ($J_{aa} = \phi_{aa}$, $k_a = \kappa_a$ and $h_0 = \theta_0$) and under the same external gradient ($h_i = g_i$), we get:

$$\langle s_{ia} \rangle = \frac{\varepsilon}{1 - \varepsilon} c_{ia}^*. \quad (S14)$$

Finally, we obtain the optimal degradation parameter $\varepsilon$ for which both models gives equivalent homogeneous steady-state for equivalent parameters, as presented in the results of the main content of this letter Fig 2:

$$\varepsilon = 0.5 \quad (S15)$$

EQUIVALENCE BETWEEN $\sigma_a$ AND $r_a$

To evaluate the correspondence between $\sigma_a$ in the SRDA and $r_a$ in the ADIM we use the sharp boundary pattern presented in the main text for $n_s = 1$ under a linear external gradient. This pattern appear when the spin/gene activates itself but is repressed by the gradient ($J_{aa} = 7$ and $k_a = -5$). As seen in the main text and shown again in Fig S1a, as $\sigma_a$ or $r_a$ increases, the sharpness of the boundary decreases. We first measure this sharpness by fitting the boundary interface ($0.2 < c_{ia}^* \langle s_{ia} \rangle < 0.8$) by a affine function of the position (Fig S1b). The slope defines the sharpness of the boundary. Both the diffusion constant $\sigma_a$ and the interaction range $r_a$ as a function of sharpness are fitted by power laws $y = \frac{1}{\varepsilon}$. From these fits we calculated $\sigma_a^{\text{fit}}$ and $r_a^{\text{fit}}$ for any given sharpness and plotting $r_a^{\text{fit}}$ as a function of $\sigma_a^{\text{fit}}$ gives us a equivalence between $r_a$ and $\sigma_a$ (Fig S1d).

ANALYSIS OF 2D PATTERNS

To study the 2D patterns obtained with our ADIM, we use their 2D Fourier Transforms (FT). Fig S2a and c represent these Fourier transforms at different temperatures for the "maze" and "bubbles" patterns studied in the main text. These patterns have one characteristic length and it results in a circular distribution of wave vectors in the reciprocal space. We compute for each radius $q$ the mean intensity $\lambda(q)$ of the FT in the corresponding circle. Fig S2b and d show the curves $\lambda(q)$ for the different temperatures studied. From this, we define the order parameter used in the main text as the peak value of these curves $\Lambda = \max(\lambda(q))$.

The corresponding length in the direct space $L_A$ is the value to the typical length of the pattern. It depends on the ratio $r_b/r_a$ between the interaction ranges of the "inhibitor" spin-type and the "activator" spin-type. Fig S3a show the "maze" pattern with $r_a = 1$ and different values of $r_b$ and the corresponding FT. $L_A$ is calculated for different ratio $r_b/r_a$ (Fig S3b). In order for a pattern to form, $r_b$ needs to be great enough, here $r_b \geq 3$. $L_A$ is linearly increasing as the ratio $r_b/r_a$ is increasing. Thus the typical length of the patterns can be chosen by tuning the values of $r_b$ and $r_a$. 
FIG. S2. (a), (c): (i) Snapshots of patterns in 128 $\times$ 128 periodic square boxes for $T = 0.5, 1, 2, 3$ for respectively "maze" and "bubbles" patterns introduced in main text (Dark red corresponds to $s_a = 1$ and pink to $s_a = 0$) and (ii) 2D Fourier transforms of these patterns averaged on $n = 100$ independent simulations. (b), (d): Mean value $\lambda(q)$ of the FT over circles of radius $q$ over different temperatures between 0 and 3. The peak value of this distribution gives us the order parameter $\Lambda$. The corresponding length in direct space $L_\Lambda$ is the characteristic length of the pattern.

FIG. S3. (a): (i) 128 $\times$ 128 zoomed snapshots of the "maze" pattern of 512 $\times$ 512 periodic square boxes simulations with $r_a = 1$ and for $r_b = 1, 5, 10, 20$ (Dark red corresponds to $s_a = 1$ and pink to $s_a = 0$) and (ii) the correspondent 2D Fourier Transforms averaged on $n = 20$ independent simulations. (b) The value of the typical length $L_\Lambda$ of the patterns as a function of the ratio $r_b/r_a$. 