Pattern formation in Ginzburg-Landau model with lateral inhibition

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Abstract: This work deals with the phenomenology of the Ginzburg-Landau model, taking account on lateral inhibition coupling, to study some pattern formation when the homogenous stationary state is perturbed. The system evolution tends to restore this homogenous state or tends to evolve to a pattern, which is controlled by the lateral inhibition intensity parameter, D, given value. This work contains a linear stability analysis to get the critical value D_0 for the patterns to be formed, and a computational program has been built to check those results and to visualize the patterns.

I. INTRODUCTION.

The spatial pattern formation is an interesting phenomenon occurring when certain systems are driven away from equilibrium. These patterns can be found in different situations and in many types of systems. Examples include patterns in hydrodynamic systems such as the Rayleigh-Bénard convection, Taylor-Couette flow, as well as reactive-diffusive chemical systems, solidification fronts, biological tissues and other cases.

The theoretical starting point for dealing with this phenomenon is usually a set of deterministic equations of "motion", typically in the form of nonlinear partial differential equations. An aim of theory is to describe solutions of the deterministic equations that are likely to be reached starting from typical initial conditions and to persist at long times. For many systems, appropriate starting equations are either not known or too complicated to analyze conveniently. It is thus useful to introduce phenomenological order-parameter models, which lead to good behavior approximation near the point where the homogeneous state symmetry brakes and which may be solved analytically or numerically [1][2].

The present work, focus its attention in biological pattern appearance, in cellular tissue development, when the cells undergo a lateral inhibition interaction between them. This kind of interaction favors different values of certain substance concentration in neighboring cells. This is the opposite situation when diffusive interaction takes place and tends to homogenize the concentration in the cells.

This study considered a cellular tissue as an LxL squared cell lattice where each cell contains an homogeneous concentration, c_{ij}, of certain substance. The Ginzburg-Landau theory has been chosen to establish a simple framework to understand the phenomena and to state a set of differential motion equations for the cell concentration time evolution [3]. This theory was initially thought to explain phase transitions and critical phenomena but it has been proved to be very successfully to understand the pattern appearance in different physical systems.

A program has been built to solve the set of differential equations obtained for the cell-lattice with lateral inhibition in the Ginzburg-Landau theory. It finds numerical solutions, $c_{ij}(t)$, using the Runge-Kutta 4 method when the system is perturbed from his homogeneous steady state. For this perturbation it uses random and different, but close to the steady state, initial conditions in each cell. The goal of the program was to validate the theoretical analysis of the Ginzburg-Landau model to explain the pattern formation and to visualize some of them.

II. THE GINZBURG-LANDAU MODEL.

The Ginzburg-Landau theory (GL) makes an assumption that changes the manner of solving problems on statistical physics. Instead of getting the system's thermodynamics by determining its microscopic Hamiltonian and computing the corresponding partition function, it takes into account that the correlation length is much greater than the microscopic separation. This observation suggests that the system's properties are insensitive to the microscopic details and the point is to avoid dealing with the underlying microscopic structure [4]. For this reason, the GL theory presents a phenomenological approach that only uses macroscopic system variables. But, it has to be said that, instead of dealing with the microscopic details, this approach is only valid close to those states where the order parameter is small.

The theory makes the hypothesis that the free energy can be expanded in powers of the order parameter, c, specific for each system. This order parameter indicates when the system is in a disordered phase or in an ordered one.

For those uniform systems with null external fields, the expansion of the Helmholtz free energy, in powers of the order parameter, can be performed and then only a few terms are needed to understand the macroscopic properties near the transition [5].

In the case of an LxL system, the concentration c_{ij} of a certain substance is the order parameter and each cell is considered as a uniform subsystem. Then, one gets a free energy expansion for each cell in the form:

$$F(c_{ij}) = f_0 + \frac{a}{2}c_{ij}^2 + \frac{\mathrm{b}}{4}c_{ij}^4 , \qquad (1)$$

where f_0, a and b are constants and b is positive.

In terms of the Ginzburg-Landau description, the steady states are those for which the free energy becomes minimal. To minimize the free energy for the whole system the minimization of the free energy in each cell has to be also minimal so the steady states are determined by the condition:

$$\left.\frac{dF(c_{ij})}{dc_{ij}}\right|_{c_{ij}^*} = 0 \;\rightarrow\; ac_{ij}^* + bc_{ij}^{*\,3} = 0 \qquad (2)$$

It is clear to see that the homogeneous state, $c_{ij}^* = 0$ in

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each cell, is always a steady state independently of the a and b given values.

If the system is driven away from the homogeneous steady state, for example applying a field, the condition (2) will be true no longer and the system will evolve to find a new steady state. During the transient, the order parameter is also depending on time, $c_{ij} = c_{ij}(t)$, and it has to be determined from posing and solving the motion equations corresponding to the dynamical situation considered for the studied system.

The starting point for this work is the differential equation obeying a relaxational dynamics to the steady state with diffusive effect occurring for continuous and non-uniform systems. The order parameter, in this general case, depends on the position and on time, $c = c(\vec{r}, t)$, and the considered equation is:

$$\frac{\partial c}{\partial t} = -\Gamma \frac{\partial F}{\partial c} + k\nabla^2 c + \xi(\vec{r}, t) \qquad (3)$$

where the concentration time variation rate is due to three causes reflected in these three terms on the right side of the equation (3).

The first term contains the free energy partial with respect to c, and the kinetic coefficient, Γ. The minus sign appears because a relaxational dynamics is considered and one expects that perturbing the system, from a steady state, would return it to the same state.

The second term takes into account the substance diffusion in each point of the system. The existence of a non-null concentration gradient is responsible for the substance flows appearances that contribute to the concentration time variation rate too. The k constant is called the diffusion coefficient and ∇^2 is the laplacian operator.

Finally, the equation could be supplemented by stochastic terms [1][4] representing thermal noise, $\xi(\vec{r}, t)$, i.e.the fluctuations, but this term is not considered in this work.

A. Dynamic equations for a cell lattice.

Once the dynamical equation for a continuous system has been established, the next step consists in adapt this situation to a discrete LxL cell lattice system.

Firstly, the order parameter has also to be spatial discrete defined. Its position dependence is no longer point dependence in a continuous media, and now it depends on the cell position inside the system:

$$c = c(\vec{r}, t) \rightarrow c_{ij}(t)\,, \qquad (4)$$

where i, j are the cell position index in the lattice and $c_{ij}(t)$ can represent the concentration of certain substance in each cell or the ferromagnet magnetization, etc.

The diffusive term in (3) has also to be redefined to the discrete situation because the laplacian is a continuous field operator. If we take into account that the diffusion phenomenon appears because two neighbor points have different concentrations, one can make a guess and propose a term of the form:

$$k\nabla^2 c(\vec{r}, t) \rightarrow -k(c_{ij}(t) - \bar{c}_{ij}(t)), \qquad (5)$$

where

$$\bar{c}_{ij}(t) = \frac{1}{n}\sum_{<ij>} c_{ij}\,, \qquad (6)$$

is the n first neighbors concentration average of the ij-cell. In this case, *k*, is the lateral activation coefficient and it is positive defined.

With this readaptation of the continuous proposed model into a LxL discrete, non-uniform, and diffusive system, the equivalent dynamic equation (3) for each ij-cell is:

$$\frac{\partial c_{ij}}{\partial t} = -\Gamma \frac{\partial F}{\partial c_{ij}} - k(c_{ij} - \bar{c}_{ij}) + \xi(\vec{r}, t) \qquad (7)$$

where Γ is still called the kinetic coefficient, *k* is the lateral activation coefficient, $k > 0$, and $\xi(\vec{r}, t)$ is a noise term as it was explained before.

B. Diffusion vs Lateral Inhibition.

In section II.A the dynamic equation (3) has been raised considering the existence of diffusive phenomenon in the system. In consequence, a positive signed laplacian term appears in the equation to realize that a diffusive mechanism is favored from high concentration points towards low ones. The diffusion mechanism is the cause of the system evolution to stable states tending to be homogeneous. All cells try to equate their substance concentration with their neighbors.

In the other hand, there exists another mechanism called lateral inhibition mechanism. Under this situation, the system evolution is ruled in a different way and the cells try to differentiate, as much as possible, from their neighbors. It can be understood like a "negative diffusion", in a sense that, this phenomena can be mathematically modeled assuming a diffusive opposite effect and then a negative defined *k* is proposed, $k < 0$.

The dynamic equations set for an LxL system with lateral inhibition mechanism is:

$$\frac{\partial c_{ij}}{\partial t} = -\Gamma \frac{\partial F}{\partial c_{ij}} + D(c_{ij} - \bar{c}_{ij}) + \xi(\vec{r}, t), \qquad (8)$$

where, unlike equation (7), here *D* is the lateral inhibition intensity parameter and is positive defined, > 0 .

For this study, in the dynamic equations set (8), the free energy derivative has been computed taking the expansion (1) with the constant values $a = b = \Gamma = 1$, and no noise term has been considered. This is the simplest case to be solved and to show all its phenomenological content in the pattern formation.

$$\frac{\partial c_{ij}}{\partial t} = -c_{ij} - c_{ij}^3 + D(c_{ij} - \bar{c}_{ij}), \qquad D > 0 \qquad (9)$$

where $\bar{c}_{ij}$ is the first neighbor concentration average of the considered ij-cell as it was defined in the equation (6).

III. 2-d PATTERN FORMATION.

Trying to solve the LxL, nonlinear, coupled, set of partial differential equations to verify if the system stabilizes in a

spatial pattern configuration could not be good idea. It is possible to proceed in an alternative way and obtain interesting results. This way is to assume that a particular pattern is a steady solution of the problem and check if this solution is stable from de equations (9) [3].

A. Chessboard Pattern (4 neighbors 2-d).

This type of pattern can be obtained through a lateral inhibition mechanism where each cell interacts with its 4 first neighbors.

We are considering the chessboard pattern formation when a lateral inhibition mechanism is imposed with the four close neighbors. There exist the chessboard pattern using lateral inhibition with the eight closest neighbors but it has not been seen in this work and then, the analogous analytical result, are not exposed here.

There has been assumed that the chessboard pattern is a steady solution, $\partial c_{ij}/\partial t = 0$, for the set of equations (9), where each cell has taken one of the two possible values: $c_{ij} = c_a$ or $c_{ij} = c_b$. In this case, the 4 neighbor concentration average in each cell, $\bar{c}_{ij}$, is:

$$\begin{aligned} \bar{c}_{ij} &= c_b\,, \quad if \quad c_{ij} = c_a, \\ \bar{c}_{ij} &= c_a\,, \quad if \quad c_{ij} = c_b\,, \end{aligned} \tag{10}$$

Substituting this result in the set of differential equations, one finally finds a system of two nonlinear equations for c_a and c_b which depends on the *D* parameter.

$$\begin{aligned} -c_a - c_a^3 + D(c_a - c_b) &= 0, \\ -c_b - c_b^3 + D(c_b - c_a) &= 0, \end{aligned} \tag{11}$$

A qualitative solution can be found by using a graphic representation method and obtain relevant information about the pattern appearance in the cell lattice. From the first equations (11) one gets $c_b(c_a)$ and from the second $c_a(c_b)$. When these curves are plotted in a c_a *vs* c_b space, see Fig. (1), the points where the curves cut each other are said to be the system solutions.

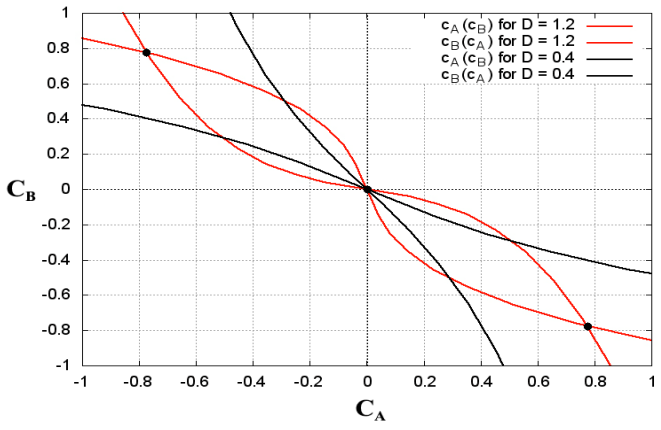

Fig. 1: c_a vs c_b diagram showing system (11) solutions for the two possible situations. The system only presents one real solution (homogeneous) when $D < 0{,}5$ and shows 3 real solutions in the other case

It could be observed that a critical D_0 value exists for the pattern formation ($D > D_0$). It could be recognized because the system has three real solutions, one of them is the homogenous solution $c_a = c_b = 0$, and the other two, $c_a \neq c_b$, are the pattern solutions as the hypothesis was made. Under this critical value ($D < D_0$), there exists only one real solution which corresponds to the homogenous solution and therefore there is no pattern formation in the cell lattice.

Going further, it is possible to assume that, given the equation symmetry observed on (11), then $c_a = -c_b$ is the corresponding pattern concentration solution. Substituting it in the system, one gets:

$$c_a = \pm\sqrt{2D-1}\ , \quad c_b = -c_a \tag{12}$$

The system has real solutions, different from the homogeneous one, when the criticality condition is fulfilled.

$$2D - 1 > 0 \ \rightarrow D > \tfrac{1}{2}\,, \tag{13}$$

Therefore, the chessboard pattern considering lateral inhibition with the four close neighbors appears when $> \frac{1}{2}$.

The corresponding linear stability analysis [6] for the homogeneous fixed point, $c_a^* = c_b^* = 0$, shows that it is no longer a stable point and the chessboard pattern appear from a particular *D* value, when considering lateral inhibitions with the four closest neighbors. In this case, the linear expansion for the displacements close to the fixed point $(c_a^*, c_b^*) = (0{,}0)$ has a jacobian matrix in the form:

$$A = \begin{pmatrix} D-1 & -D \\ -D & D-1 \end{pmatrix}, \tag{14}$$

where its eigenvalues are obtained solving $\det(A - \lambda I) = 0$ and are found to be $\lambda_1 = 2D - 1$ y $\lambda_2 = -1$. The fixed point is meant to be stable while $\lambda_1 < 0$ y $\lambda_2 < 0$ is satisfied. This implies that the homogeneous state is a steady state for $D < \frac{1}{2}$. The same analysis, now taking the pattern solution (12) as a fixed point, gets that the pattern is stable for $D > \frac{1}{2}$. This result means that a little displacement from the homogeneous state when $D > \frac{1}{2}$ ends in a chessboard pattern when the lateral inhibition interaction with the four neighbors is considered.

B. Stripes Patterns (8 neighbors 2-d).

This is the other type of pattern considered. The stripes pattern appears when the lateral inhibition mechanism is the interaction in each cell with its 4 or 8 closest neighbors. As it happened in section A with the chessboard pattern, in this work no stripes pattern has been seen considering a 4 neighbor lateral inhibition interaction, then the analytical results for this case are not exposed here. The present work only accounts for the stripes pattern formation with the eight close neighbors lateral inhibition interaction.

There has been assumed that the stripes pattern is a steady solution, $\partial c_{ij}/\partial t = 0$, in (9) and each cell has one of the two possible concentration values $c_{ij} = c_a$ or $c_{ij} = c_b$. Unlike the

chessboard pattern case, the neighbor's concentration average (6) considering the eight close ones is in this case:

$$\bar{c}_{ij} = \frac{1}{8}(2c_a+6c_b)\,, \quad si \quad c_{ij} = c_a$$
$$\bar{c}_{ij} = \frac{1}{8}(6c_a+2c_b)\,, \quad si \quad c_{ij} = c_b \qquad (14)$$

Substituting it in the differential equation set (9) there is going to be find another system of two equations for c_a and c_b, depending on the D parameter.

$$-c_a - c_a^3 + \frac{3}{4}D(c_a - c_b) = 0,$$
$$-c_b - c_b^3 + \frac{3}{4}D(c_b - c_a) = 0, \qquad (15)$$

and analogously to the chessboard pattern case, plotting the corresponding $c_b(c_a)$ and $c_a(c_b)$ curves, shows that there is also a criticality condition for the stripes pattern formation. Given the symmetry of the equations (15), a solution of the type $c_a = -c_b$ is a system solution. Substituting again in the equations set,:

$$c_a = \pm\sqrt{\frac{3}{2}D - 1}\,, \quad c_b = -c_a \qquad (16)$$

so a stripes pattern appear, when eight neighbors are considered, if $D > \frac{2}{3}$.

The linear stability analysis for the homogeneous steady state gives, in this case, a jacobian matrix:

$$A = \frac{1}{4}\begin{pmatrix} 3D-4 & -3D \\ -3D & 3D-4 \end{pmatrix}, \qquad (17)$$

with the eigenvalues $\lambda_1 = 6D - 4$ y $\lambda_2 = -4$. The stability condition that is required for the fixed point to be stable, imposes, in this case, that the homogeneous state is stable for $D < \frac{2}{3}$. It is, also, verified that the stripes solution fixed point is stable for $D > \frac{2}{3}$. Therefore, a little displacement respect to the homogeneous state would drive away the system to a stripe pattern if $D > \frac{2}{3}$ parameter value is considered.

IV. NUMERICAL RESULTS.

The analytical results found in section III have been verified by numerical simulations.

It solves, numerically, the LxL set of differential equations given in (9), with the four or the eight neighbor concentration average considered term. The aim was to test the starting hypothesis made assuming the Ginzburg-Landau model as a phenomenological approach to the pattern formation phenomena and to verify the conclusions extracted from the analytical results.

In the program, the desired D value can be chosen as a parameter, and a Runge-Kutta 4 method [7] solves $c_{ij}(t_k)$ in each cell, when the cell lattice system is perturbed away from his steady homogeneous state. To take into account this perturbation, the program generates random small displacements in each cell concentration, and they are entered as initial conditions to the set of differential equations to be solved. The concentration evolution in each cell is computed for a set of discrete instants of time $\{t_k\}$ which have been chosen to be equidistant with a time interval step of h, $t_k = t_0 + kh$. The program computes until the concentration in each cell ends in a stationary regime.

The program has been run to test the analytical results, starting from low, D, inhibition parameter values and then increasing them progressively expecting the pattern formation occurs from the predicted critical value, D_0.

The Patterns are shown in Fig. (2), Fig. (3) and Fig. (4):

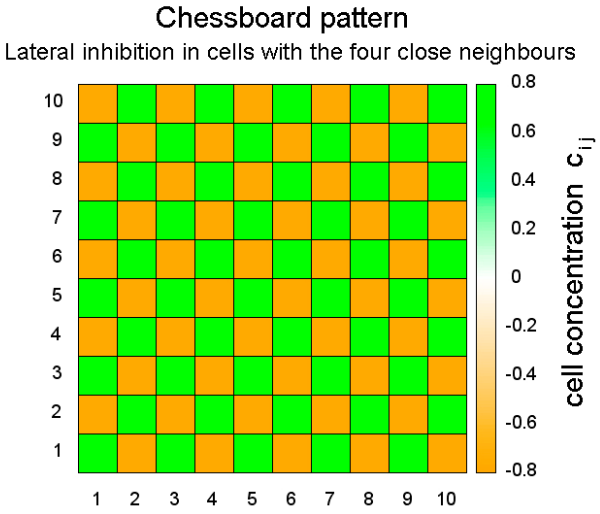

Fig. 2: Chessboard pattern found setting lateral inhibition with the four close neighbors and D = 0.8, when the homogeneous state was perturbed with random initial conditions, -0.01 < $c_{ij}(0)$ < 0.01, and choosing a time step of h = 0.01 for the RK4 method.

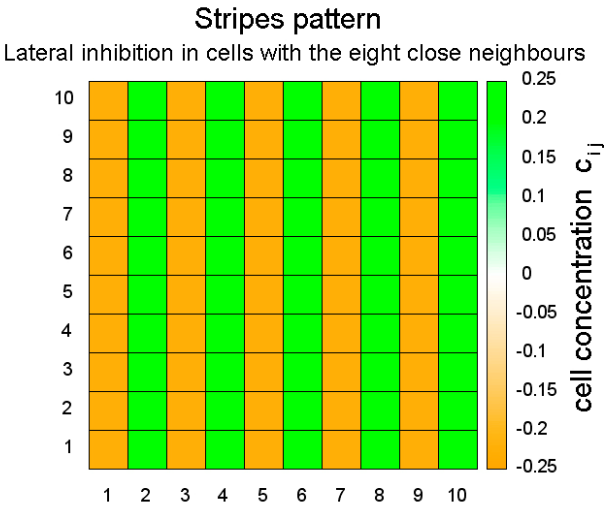

Fig. 3: Stripes pattern found setting lateral inhibition with the eight close neighbors and D = 0.7, when the homogeneous state was perturbed with random initial conditions using the same values as in Fig. (2).

Another interesting result, we were not searching for, came out from simulating results. Sometimes the cell lattice system, being perturbed from the homogeneous state as the same manner as explained before, ended in a different stationary state. For the given D value, it was expected to end in a known pattern but, instead of that, it finally evolved to a different stationary state, not too ordered, where the pattern

started to form. Those stationary states looked like not ordered patterns, maybe disordered ones, but not like completely disordered random configurations Fig. (4). When it happened, the first sensation was that the program wasn't well designed. After revisiting it many times, making computing tests and fixing different initial conditions, it seemed to run correctly and was assumed that the appearance of this kind of patterns was another type of solutions for the set differential equations (9).

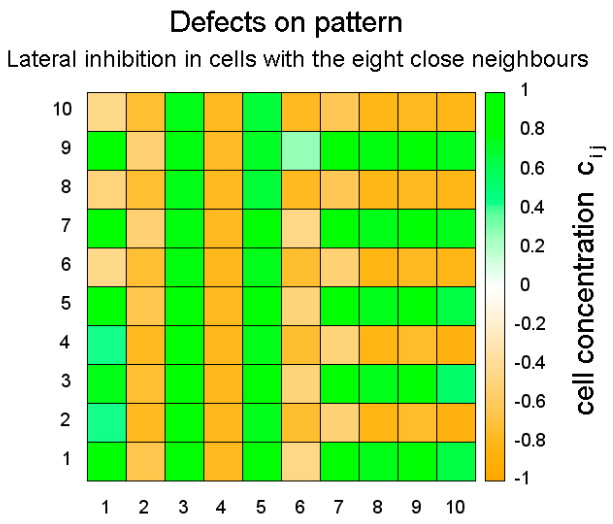

Fig. 4: Stationary pattern found setting lateral inhibition with the eight close neighbors and D = 1.1, when the homogeneous state was perturbed with random initial conditions using the same values as in Fig. (2)..

V. CONCLUSIONS.

The Ginzburg-Landau theory offers a simple model that allows stating a set of dynamical equations for a discrete cell system with lateral inhibition, to explain the phenomenology of the chessboard and stripes pattern formation when the homogeneous state in these systems is perturbed.

The set of the differential equations obtained with the GL model are also analytically treatable and it is possible to obtain some relevant information about the pattern formation.

The first result exposed is that the chessboard and the stripe patterns are effectively stationary states of the system.

Another interesting result comes out from the linear stability analysis. It reveals that for the inhibition intensity parameter values, D, smaller than a critical value, say D_0 , the homogeneous state is a stable state and the system is always returning back when perturbed from it. But, for D values greater than the critical D_0, the homogeneous state becomes unstable and the system evolves to form a pattern.

All these results have been checked with numerical simulations, developed for this aim, and the patterns have been visualized. But this simulations also showed another types of stationary states, which looked like semi ordered ones.

The chosen way to proceed analytically for solving nonlinear equations as (9) is to assume a particular steady solution and verify if that solution fulfill these equations. That is what has been done here with the chessboard and the stripes solution. But nowhere is said that they are the unique solutions. It makes me think that the encountered defects are steady solutions of the equations we couldn't predict because of the difficulty to solve all the cases for a nonlinear set of the differential equations.

For future studies, I'd like to encourage the research of these defects as possible stationary solutions for the Ginzburg-Landau model with lateral inhibition coupling. Interesting answer can be searched for questions like, are they really stationary patterns? Can a very simple defect be designed and assumed as a steady solution of the equations (9) and probe, effectively, that they are stationary solutions? Are they stable or unstable, what happen if one of them is perturbed? Which is the cause that, instead of the expected pattern, one gets a defect for a given D? Taking a pattern and perturbing it, would it be possible to obtain defects as the same way as the homogeneous state is perturbed? To answer these questions numerical simulations could be a good tool to study the phenomenology as the program for this report helped me a lot in understanding the phenomena.

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