IEEE Access
Multidisciplinary | Rapid Review | Open Access Journal

SPECIAL SECTION ON INTELLIGENT SYSTEMS FOR THE INTERNET OF THINGS

Received October 23, 2017, accepted November 13, 2017, date of publication December 6, 2017,
date of current version February 28, 2018.

Digital Object Identifier 10.1109/ACCESS.2017.2780324

A Semi-Automatic Numerical Algorithm for Turing Patterns Formation in a Reaction-Diffusion Model

ROSANNA CAMPAGNA[1], SALVATORE CUOMO[2], FRANCESCO GIANNINO[1], GERARDO SEVERINO[1], AND GERARDO TORALDO[2]

[1]Department of Agricultural Sciences, University of Naples Federico II, 80138 Naples, Italy
[2]Department of Mathematics and Applications, University of Naples Federico II, 80138 Naples, Italy

Corresponding authors: Rosanna Campagna (rosanna.campagna@unina.it) and Salvatore Cuomo (salvatore.cuomo@unina.it)

This work was supported by the System dynamics modeling of microbial cell cultures (MOD_CELL_DEV) Project—Programma di finanziamento della ricerca di Ateneo 2015, University of Naples Federico II.

ABSTRACT The Turing pattern formation is modeled by *reaction-diffusion* (RD) type *partial differential equations*, and it plays a crucial role in ecological studies. Big data analytics and suitable frameworks to manage and predict structures and configurations are mandatory. The processing and resolution procedures of mathematical models relies upon numerical schemes, and concurrently upon the related automated algorithms. Starting from a RD model for vegetation patterns, we propose a semi-automatic algorithm based on a smart numerical criterion for observing ecological reliable results. Numerical experiments are carried out in the case of spot's formations.

INDEX TERMS Vegetation turing patterns, finite difference methods, Internet of Things.

I. INTRODUCTION

The availability of modeling frameworks to investigate biological and environmental phenomena is of paramount importance for predicting purposes. The huge amount of data from the real world also requires techniques and tools to extract, manage and properly classify information. The *Internet of Things* (IoT) system of connecting machines and sensors is a useful tool for reading the real world. In fact, by extracting information from a large number of data acquired in biological as well as environmental contexts, one gains physical insights on the processes at stake, and can forecast at different temporal/spatial scales. The basis of these approaches is the automation of the processing and resolution procedures of mathematical models that describe the real world. The Turing pattern formation is mathematically modelled by RD-type PDEs. Most of the early studies on Turing patterns dealt with chemical RD-systems. The fundamental concept introduced by Turing was that, in order to be stable (steady), states have to be diffusion-free. To the contrary, diffusion favors the emergence of unstable and spatially heterogeneous patterns [1]. The pattern formation dynamics generally occurs due to the interaction of two (or more) chemicals. This is generally modelled by a system of nonlinear PDEs.

The are many studies relating biological processes to Turing patterns via RD models. Due to the nonlinear nature of the overall mathematical problem, it is generally very hard getting an analytical solution. Thus, in the majority of the real world situations, one must resort to numerical methods. Nevertheless, there is a relatively limited number of studies on the matter, the importance of the problem at stake, notwithstanding. The widely adopted numerical schemes for RD models are the *finite difference* (FD) [2], and finite element methods [3]. More recently, discontinuous Galerkin finite element methods [4] have become increasingly popular, as well. Finally, implicit-explicit schemes have been also used, especially in conjunction with spectral methods in Fluidmechanics [5]. One of the first example arising Turing instability is from the Brusselator model [6]. The unique feature of such a problem is that it enables one getting analytical solutions which lend themselves as benchmark to validate more involved numerical schemes [7]–[10]. The same is for the Schnakenberg model [11], representing a simplified version of the previous one [12], [13]. A detailed analysis about the time-integration schemes, and numerical results can be found in [12] and [13]. Finally, a generalization of the previous models, accounting for the spatial pattern's distribution, was provided by Gray-Scott [14]. Implicit-explicit schemes to describe pattern formation arising from such a model can be found in [15]. Besides the numerical approaches, RD-type models related to Turing's patterns have been

tackled by means of the cellular automata models [16]. Such an approach could be used to develop a counterpart to simulate both the Brusselator's model and that of Gray-Scott [17].

In this paper we present a numerical (FD) approach for a RD model describing the vegetation patterns' formation as determined by the interactions between biomass evolution, water availability and toxicity in plant-soil feedback [18]. It is shown that our algorithm leads to a simple stability criterion avoiding numerical artifacts. In particular, such a criterion serves as a tool to be (consciously) used in the integration scheme in order to avoid meaningless results [19]. The paper is organized as follows. In the section II we present the RD model giving rise to the vegetation patterns formation; in section III we focus on the numerical solution by a FD scheme, and the accuracy *vs* stability of the numerical model. Section IV exploits the algorithmic into details; conclusions are outlined in the Section V.

II. THE MATHEMATICAL MODEL AND THE DISCRETIZED SCHEME

We consider the numerical solution of the following system of nonlinear PDEs [18]:

$$\frac{\partial B}{\partial t} = D_B \Delta B + G_B(B, W, T), \tag{1a}$$

$$\frac{\partial W}{\partial t} = D_W \Delta W + G_W(B, W), \tag{1b}$$

$$\frac{\partial T}{\partial t} = T[Bqs - (k + wp)] + qdB, \tag{1c}$$

where B, W, T are the specific (per unit surface) biomass, water, and toxic compounds. The coefficients $D_B, D_W \in \mathbb{R}^+$ accounts for the diffusion of the biomass and water, respectively, whereas the nonlinear reaction terms G_B and G_W are defined as:

$$\begin{aligned} G_B(B, W, T) &= cB^2W - (d + sT)B, \\ G_W(B, W) &= p - rB^2W - lW. \end{aligned} \tag{2}$$

The positive parameters appearing into (2) are chosen either in accordance with [20], [21] or selected from within an order-of-magnitude feasibility range. More precisely, p is the rain intensitiy, k is the rate of decay of toxicity, and s is the sensitivity of the plants to the toxicity (see [18, Table 1] for further details). Equations (1a)–(1c) are defined on a bounded domain $\Omega \subset \mathbb{R}^2$, and are subjected to zero Neumann-type boundary conditions along the boundary $\partial\Omega$ of the domain. The initial conditions are:

$$B(x, y, 0) = B_0, \quad W(x, y, 0) = W_0, \quad T(x, y, 0) = 0, \tag{3}$$

for $(x, y) \in \Omega$. A FD scheme on a regular grid in Cartesian coordinates provides an approximation of the solution over a finite number of grid points $\{z_{i,j}\}$, s.t. $z_{i,j} = (i\Delta x, j\Delta y)$ $i = 0, \ldots, N_x - 1$, $j = 0, \ldots, N_y - 1$, with $\Delta x := \frac{x_{max}}{N_x - 1}$ and $\Delta y := \frac{y_{max}}{N_y - 1}$ the grid mesh-sizes. If a temporal grid is defined as $\tau^k := k\Delta t$, $k = 0, \ldots, M$, with temporal step-size $\Delta t := \frac{t_{max}}{M}$, the scheme provides an approximation, say $u^k_{i,j}$, at $z_{i,j}$ and time step τ^k.

Let $u^k_{i,j}$ be the approximation of B, W and T at $z_{i,j}$ and time step τ^k. For the eqs (1a)–(1b) we apply a FD scheme forward in time and centered (second order) in the space, whereas (1c) is solved by a first order accurate forward Euler scheme. We then define a weight average scheme can be defined for the two PDEs, that is based on a convex (θ-type) combination of the spatial terms of the forward/backward difference methods. We set $D \equiv D_B = D_W$ in (1a)–(1b), so that it yields

$$\begin{aligned} u^{k+1}_{i,j} - u^k_{i,j} = D\mu[&\theta_1(\Delta y^2 \cdot \delta_x^2 u^{k+1}_{i,j} + \Delta x^2 \cdot \delta_y^2 u^{k+1}_{i,j}) + \\ &+ (1 - \theta_1)(\Delta y^2 \cdot \delta_x^2 u^k_{i,j} + \Delta x^2 \cdot \delta_y^2 u^k_{i,j})] + \\ &+ \Delta t[\theta_2 g^{k+1} + (1 - \theta_2) g^k] \end{aligned} \tag{4}$$

$\forall (i, j)$, $i = 1, \ldots, N_x$, $j = 1, \ldots, N_y$, being

$$\begin{aligned} \delta_x^2 u^k_{i,j} &= u^k_{i+1,j} - 2u^k_{i,j} + u^k_{i-1,j}, \\ \delta_y^2 u^k_{i,j} &= u^k_{i,j+1} - 2u^k_{i,j} + u^k_{i,j-1}, \end{aligned}$$

whereas g^k is the non linear term at the time level τ^k, and

$$\mu = \frac{\Delta t}{\Delta x^2 \Delta y^2}. \tag{5}$$

To investigate the Turing pattern formation, it is sufficient to assume $\theta_2 = 0$ (explicit scheme).

III. A SEMI-AUTOMATIC ALGORITHM FOR VEGETATION TURING PATTERNS

With $\theta := \theta_1$, we re-write (4) into matrix form as $AX = Y$, being A, X and Y a $3N_xN_y \times 3N_xN_y$ matrix, and $3N_xN_y \times N_xN_y$ matrices, respectively. Such matrices are defined as:

$$A = \begin{pmatrix} A_B & 0 & 0 \\ 0 & A_W & 0 \\ 0 & 0 & I_{N_x \times N_y} \end{pmatrix},$$

$$X = \begin{pmatrix} X_B^{k+1} \\ X_W^{k+1} \\ X_T^{k+1} \end{pmatrix},$$

$$Y = \begin{pmatrix} Y_B^k \\ Y_W^k \\ Y_T^k \end{pmatrix},$$

where A_B and A_W are square sparse, pentadiagonal, non-symmetric, positive definite, diagonally dominant, and banded (width N_x) matrices of $N_x \times N_y$-order; $I_{N_x \times N_y}$ is the unit matrix of order $N_x \times N_y$. By setting

$$\begin{aligned} R_1 &:= \frac{\theta \Delta t D_B}{(\Delta x)^2}, \quad R_2 := \frac{\theta \Delta t D_B}{(\Delta y)^2}, \\ r_1 &:= \frac{(1 - \theta)\Delta t D_B}{(\Delta x)^2}, \quad r_2 := \frac{(1 - \theta)\Delta t D_B}{(\Delta y)^2}, \end{aligned} \tag{6}$$

and

$$\begin{aligned} S_1 &:= \frac{\theta \Delta t D_W}{(\Delta x)^2}, \quad S_2 := \frac{\theta \Delta t D_W}{(\Delta y)^2}, \\ s_1 &:= \frac{(1 - \theta)\Delta t D_W}{(\Delta x)^2}, \quad s_2 := \frac{(1 - \theta)\Delta t D_W}{(\Delta y)^2}. \end{aligned} \tag{7}$$

$(k > 0)$, the (i, j)-th elements of A_B and A_W are respectively:

$$(1 + 2R_1 + 2R_2)b_{i,j}^{k+1} - R_1\left(b_{i+1,j}^{k+1} + b_{i-1,j}^{k+1}\right) + \\ - R_2\left(b_{i,j-1}^{k+1} + b_{i,j+1}^{k+1}\right) \quad (8)$$

and

$$(1 + 2S_1 + 2S_2)w_{i,j}^{k+1} - S_1\left(w_{i+1,j}^{k+1} + w_{i-1,j}^{k+1}\right) + \\ - S_2\left(w_{i,j-1}^{k+1} + w_{i,j+1}^{k+1}\right) \quad (9)$$

$(i = 0, \ldots, N_x - 1, j = 0, \ldots, N_y - 1$ and $k = 0, \ldots, M)$. Likewise, the Y-bocks are

$$\begin{aligned} Y_B^k &= b_{i,j}^k + \Delta t\left[c{b_{i,j}^k}^2 w_{i,j}^k - (d + st_{i,j}^k)b_{i,j}^k\right] + \\ &+ r_1\left(b_{i+1,j}^k - 2b_{i,j}^k + b_{i-1,j}^k\right) + \\ &+ r_2\left(b_{i,j-1}^k - 2b_{i,j}^k + b_{i,j+1}^k\right) \\ Y_W^k &= w_{i,j}^k + \Delta t\left[p - r{b_{i,j}^k}^2 w_{i,j}^k - lw_{i,j}^k\right] \\ &+ s_1\left(w_{i+1,j}^k - 2w_{i,j}^k + w_{i-1,j}^k\right) + \\ &+ s_2\left(w_{i,j-1}^k - 2w_{i,j}^k + w_{i,j+1}^k\right) \end{aligned} \quad (10)$$

and

$$Y_T^k = t_{i,j}^k + \Delta t\left[q(d + st_{i,j}^k)b_{i,j}^k - (k + wp)t_{i,j}^k\right]$$

$(i = 0, \ldots, N_x - 1, j = 0, \ldots, N_y - 1)$. The parameter θ allows to swap the numerical scheme, that is $\theta = 0$ provides explicit (forward in time) FD, $\theta = 1/2$ corresponds to the Crank-Nicolson scheme, whereas $\theta = 1$ a fully implicit (backward in time) Euler scheme. The explicit scheme has second-order convergence in the space, and a first order accuracy in time. It is conditionally stable, and the *Courant-Friedrichs-Lewy (CFL)* condition is:

$$\exists\, c > 0 \;:\; \Delta t \le c\Delta x^2.$$

For the numerical approximation (4), the CFL writes as

$$\exists\, c > 0 \;:\; \Delta t \le \frac{c}{2D}\frac{\Delta x^2 \Delta y^2}{\Delta x^2 + \Delta y^2}. \quad (11)$$

Given this, we aim at:

(1) keeping low the truncation error;
(2) containing the round-off error propagation, and therefore the sneaky numerical artefacts which can arise when $D\mu(\Delta x^2 + \Delta y^2) \to 0$.

IV. RESULTS

Due to the block diagonal form and the constant coefficients of A_B, A_W and $I_{N_x \times N_y}$, we solve w.r.t. B, W and T independently at each time level. Each system is solved (see Table 1) by the *generalized minimal residual iterative method* (GMRES). With the parameter values listed in the Table 1 of [18], simulations were performed on a $N_x \times N_y = 100$x100 square lattice with $x_{max} = 50$, and $y_{max} = 50$. The initial conditions are $B_0 = 0.2$ kg/m^2 in $N_0 = 5000$ randomly selected elements, and $B_0 = 0$ in the remaining nodes, $W_0 = 40$ kg/m^2 and $T_0 = 0$ at all points. Moreover we fix $p = 0.8$ and we run the simulations along $t_{max} = 20000$ days. We set $\theta = 0$ and

$$\Phi = \frac{c}{2D}\frac{\Delta x^2 \Delta y^2}{\Delta x^2 + \Delta y^2}$$

in the (11), with $c = 1$ and

$$\frac{1}{D} = \min\left\{\frac{1}{DB}, \frac{1}{DW}\right\}.$$

Table 2 summarizes the results obtained for different values of Δt, $\Delta x = \Delta y$ and Φ; a brief description follows.

Test case *condition satisfied*: $\Delta t < \Phi$

case 1) Let be $\Delta t = 0.05$, $\Delta x = \Delta y = 0.5$, $\Phi = 0.0797$. The condition (11) is satisfied and we assume the computed solution B_{ref} as a reference. The last column of Table 2 refers to the maximum error in the solution, w.r.t. B_{ref}. In the Fig.1 (up row) we have depicted the temporal evolution of the biomass-density, whereas the temporal evolution of biomass density, averaged over the lattice is represented in the Fig. 2 (left). The response of plants to toxicity negative feedback ($s = 0.2$) combined with a high toxicity decay rate ($k = 0.2$), gives rise (after about 12 minutes) to stable patterns.

Test cases *condition not satisfied*: $\Delta t > \Phi$

In the Table 2 we have summarized also the results obtained on failing the condition (11), both by increasing Δt and decreasing Φ:

case 2) Let be $\Delta t = 0.05$, $\Delta x = \Delta y = 0.38$, $\Phi = 0.0469$. A reduction of $\Delta x = \Delta y$, does not let Φ to overcome Δt, and concurrently the condition (11))

TABLE 1. Semi-automatic algorithm for turing pattern.

Require: *Set input values* {under hypothesis (11)}
for $k = 1 : t_{max}$ **do**
  Computation of ${Y_B}^k$ by $D_B, c, d, s, \Delta t, r_1, r_2$
  Computation of ${Y_W}^k$ by $D_W, p, r, \Delta t, s_1, s_2$
  Computation of ${Y_T}^k$ by $\Delta t, q, d, s, w, k, p$
  Solve $A_B[X_B^{k+1}] = {Y_B}^k$ $\{call\ GMRES\}$
  Solve $A_W[X_W^{k+1}] = {Y_W}^k$ $\{call\ GMRES\}$
  Solve $I_{N_x \times N_y}[X_T^{k+1}] = {Y_T}^k$ $\{T$ updating$\}$
end for
return

TABLE 2. Numerical results.

case num.	(11) satisfied	Δt	$\frac{\Delta x}{\Delta y}$	Φ	$\|B - B_{ref}\|_\infty$
1)	**yes**	**0.05**	**0.5**	**0.079**	-
2)	*no*	0.05	0.38	0.046	GMRES tol. not satisfied
3)	*no*	0.08	0.5	0.079	4.8115e+01
4)	*no*	0.09	0.5	0.079	numerically singular matrices
5)	*no*	0.1	0.5	0.079	numerically singular matrices

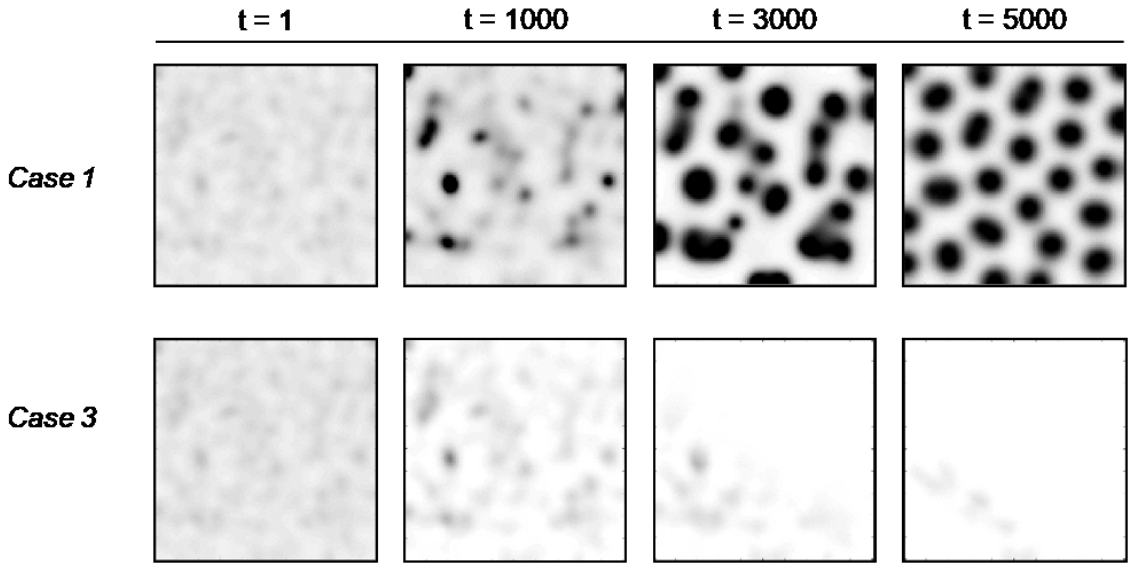


FIGURE 1. The temporal evolution of biomass density: case 1) in Table 2, with $\Delta t = 0.05$, $\Delta x = \Delta y = 0.5$, $\Phi = 0.0797$ (up); case 3) in Table 2, with $\Delta t = 0.08$, $\Delta x = \Delta y = 0.5$, $\Phi = 0.0797$ (down).

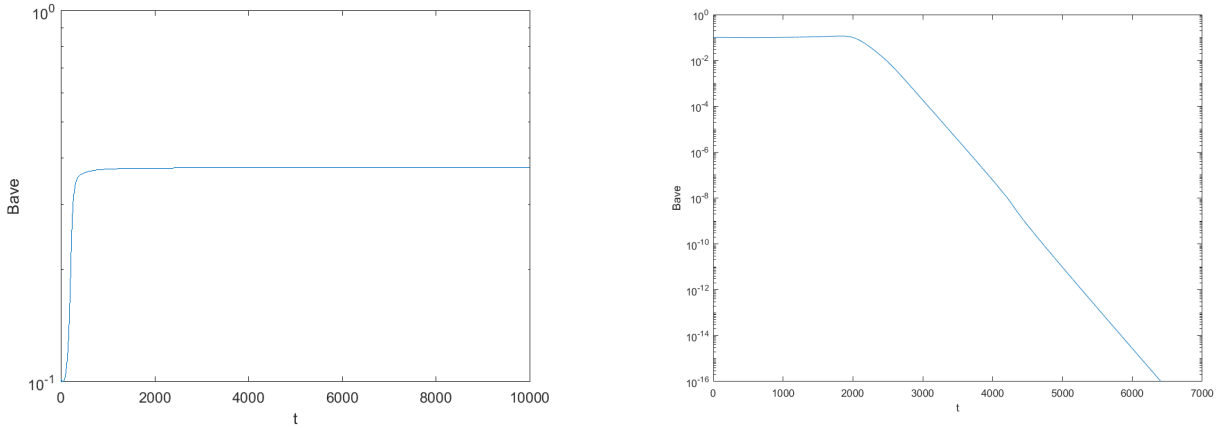


FIGURE 2. The temporal evolution of mean biomass density in case 1) (left) and case 3) (right). In this last case, the mean value decreases fast toward zero in less than 7000 time steps.

is violated. With the parameters values listed in the first line of the Table 2, GMRES (without restart and in the default number equal to 10 iterations) doesn't satisfy the prescribed tolerances $\epsilon \in \{10^{-6}, 10^{-4}, 10^{-2}\}$; the execution is interrupt since the solver GMRES doesn't converge.

case 3) Let $\Delta t = 0.08$, $\Delta x = \Delta y = 0.5$, $\Phi = 0.0797$. By increasing Δt w.r.t. Φ, the computed values move away from the reference values, according to the absolute error in the last column. In Fig.1 (down) some spots represent the biomass evolution when the condition (11) is violated. *The disappearance of the pattern formation after about 10 seconds, is due to the amplification of the round-off errors through the time stepping, and it demonstrates that also a small perturbation in the amplification factor can lead to an unreliable solution.* The Fig.2 (right) shows how the mean value of the biomass vanishes (in about 7000 time steps).

case 4), 5) Let us assume that $\Delta t = 0.09$ and $\Delta t = 0.1$, with $\Delta x = \Delta y = 0.5$ and $\Phi = 0.0797$. An increase of Δt renders the iteration matrices (quasi)-singular, such that no solution can be achieved.

V. CONCLUSIONS

The IoT systems can be viewed as a glass for reading the real world, granting the process and producing a huge amount of data. The automation of the processing and resolution procedures of mathematical models describing the real world is mandatory to get insights on the physics underlying the biological/environmental processes.

In the present paper we have developed a numerical scheme for a particular RD model describing the formation and evolution of the vegetation pattern. The numerical

scheme relies upon a semi-automatic algorithm based on a stability criterion, that limits the amplification error in the computed solution. Simulations show that, when the criterion is satisfied, the numerical scheme converges towards a reliable solution.

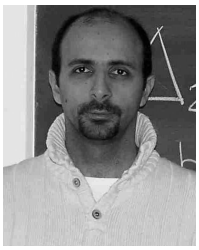
REFERENCES

[1] A. M. Turing, "The chemical basis of morphogenesis," *Phil. Trans. Roy. Soc. London B, Biolog. Sci.*, vol. 237, no. 641, pp. 37–72, 1952.
[2] C. V. Pao, "Numerical solutions of reaction–diffusion equations with nonlocal boundary conditions," *J. Comput. Appl. Math.*, vol. 136, no. 1, pp. 227–243, 2001.
[3] C. Johnson, *Numerical Solution of Partial Differential Equations by the Finite Element Method*. Cambridge, U.K.: Cambridge Univ. Press, 1988.
[4] J. Zhu, Y.-T. Zhang, S. A. Newman, and M. Alber, "Application of discontinuous galerkin methods for reaction-diffusion systems in developmental biology," *J. Sci. Comput.*, vol. 40, no. 1, pp. 391–418, 2009.
[5] S. J. Ruuth, "Implicit-explicit methods for reaction-diffusion problems in pattern formation," *J. Math. Biol.*, vol. 34, no. 2, pp. 148–176, 1995.
[6] I. Prigogine and R. Lefever, "Symmetry breaking instabilities in dissipative systems. II," *J. Chem. Phys.*, vol. 48, pp. 1695–1700, Feb. 1968.
[7] S. A. Manaa, R. K. Saeed, and F. H. Easif, "Numerical solution of brusselator model by finite difference method," *J. Appl. Sci. Res.*, vol. 6, no. 11, pp. 1632–1646, 2010.
[8] Z. U. A. Zafar, K. Rehan, M. Mushtaq, and M. Rafiq, "Numerical treatment for nonlinear brusselator chemical model," *J. Differ. Equ. Appl.*, vol. 23, no. 3, pp. 521–538, 2017.
[9] R. Mittal and R. Jiwari, "Numerical solution of two-dimensional reaction-diffusion brusselator system," *Appl. Math. Comput.*, vol. 217, no. 12, pp. 5404–5415, 2011.
[10] R. C. Mittal and R. Rohila, "Numerical simulation of reaction-diffusion systems by modified cubic b-spline differential quadrature method," *Chaos, Solitons Fractals*, vol. 92, pp. 9–19, Nov. 2016.
[11] J. Schnakenberg, "Simple chemical reaction systems with limit cycle behaviour," *J. Theor. Biol.*, vol. 81, no. 3, pp. 389–400, 1979.
[12] I. Sgura, B. Bozzini, and D. Lacitignola, "Numerical approximation of Turing patterns in electrodeposition by ADI methods," *J. Comput. Appl. Math.*, vol. 236, no. 16, pp. 4132–4147, 2012.
[13] R. Zhang, X. Yu, J. Zhu, and A. F. Loula, "Direct discontinuous Galerkin method for nonlinear reaction–diffusion systems in pattern formation," *Appl. Math. Model.*, vol. 38, no. 5, pp. 1612–1621, 2014.
[14] P. Gray and S. K. Scott, "Autocatalytic reactions in the isothermal, continuous stirred tank reactor: Oscillations and instabilities in the system $A + 2B \longrightarrow 3B$; $B \longrightarrow C$," *Chem. Eng. Sci.*, vol. 39, no. 6, pp. 1087–1097, 1984.
[15] K. Zhang, J. C.-F. Wong, and R. Zhang, "Second-order implicit-explicit scheme for the gray-scott model," *J. Comput. Appl. Math.*, vol. 213, no. 2, pp. 559–581, 2008.
[16] C. P. Graván and R. Lahoz-Beltra, "Evolving morphogenetic fields in the zebra skin pattern based on Turing's morphogen hypothesis," *Int. J. Appl. Math. Comput. Sci.*, vol. 14, no. 3, pp. 351–361, 2004.
[17] J. E. Pearson, "Complex patterns in a simple system," *Science*, vol. 261, no. 5118, pp. 189–192, 1993.
[18] A. Marasco *et al.*, "Vegetation pattern formation due to interactions between water availability and toxicity in plant–soil feedback," *Bull. Math. Biol.*, vol. 76, no. 11, pp. 2866–2883, 2014.
[19] R. Seppelt and O. Richter, "'It was an artefact not the result': A note on systems dynamic model development tools," *Environ. Model. Softw.*, vol. 20, no. 12, pp. 1543–1548, 2005.
[20] C. Klausmeier, "Regular and irregular patterns in semiarid vegetation," *Science*, vol. 284, no. 5421, pp. 1826–1828, 1999.
[21] F. Cartenì, A. Marasco, G. Bonanomi, S. Mazzoleni, M. Rietkerk, and F. Giannino, "Negative plant soil feedback explaining ring formation in clonal plants," *J. Theor. Biol.*, vol. 313, pp. 153–161, Nov. 2012.
[22] K. W. Morton and D. F. Mayers, *Numerical Solution of Partial Differential Equations: An Introduction*. New York, NY, USA: Cambridge Univ. Press, 2005.
[23] A. Quarteroni, *Numerical Models for Differential Problems*, 2nd ed. Cham, Switzerland: Springer, 2013.
[24] G. Smith, *Numerical Solution of Partial Differential Equations: Finite Difference Methods*. Oxford, U.K.: Oxford Univ. Press, 1985.

ROSANNA CAMPAGNA is currently with the Department of Agricultural Sciences, University of Naples Federico II. She was involved in the software design for scientific computing and numerical methods for PDEs and related applications, including the biological-environmental modeling, and the management of water systems. Her research activity is concerned with the development and the analysis of numerical methods and computational approaches for the identification and parameter estimation of applied models. Theoretical and computational results are concerned with numerical methods for inverse problems, such as the Laplace transform inversion and the image restoration.

SALVATORE CUOMO is currently with the Department of Mathematics and Applications "R. Caccioppoli," University of Naples Federico II. He was involved in the numerical problems in several application fields, including e-health and engineering. His research activity is concerned with the inverse problems, numerical methods, and scientific computing algorithms. He is a member of several international and national research projects.

FRANCESCO GIANNINO is currently with the Department of Agricultural Sciences, University of Naples Federico II. His research interest is mainly devoted to the design, development, and analysis of mathematical models in biology. His methodological and computational aspects have been considered for several different applications. His research has been carried out in the frame of several international projects and collaborations with European research groups, which are leaders in the area of biology modeling.



GERARDO SEVERINO is currently with the Department of Agricultural Sciences, University of Naples Federico II. His research activity is concerned with the theory of flow and transport in heterogeneous porous formations; up-scaling of hydraulic properties; hydraulics of wells in randomly heterogeneous aquifers; soil hydrology; stochastic differential equations; inverse modeling. He is a member of several international and national research projects. He serves as an Associate Editor for numerous leading journals, and he has several ongoing research cooperations with both national and international academic institutions.

GERARDO TORALDO is currently with the Department of Mathematics and Applications "R. Caccioppoli," University of Naples Federico II, where he is currently a Full Professor in numerical analysis. He was involved in several application fields, including agro-food technologies and biological modeling, and management of water systems. His research activity concerned with the design, theoretical analysis, and implementation of algorithms for nonlinear optimization.