Chapter 28
Chemical Coupling of Phase Oscillators

Ricardo Luiz Viana and Pedro Haerter

Abstract A general theory is presented for the coupling among nonlinear oscillators mediated by a diffusing chemical substance. We extend a model originally developed by Kuramoto, who supposed that the diffusion characteristic time is much shorter than the oscillator main period, such that diffusion occurs very fast. We eliminate this constraint and consider diffusion to have an arbitrary characteristic time, by solving exactly the diffusion equation using suitable Green functions. We present results for phase and frequency synchronization of chemically coupled phase oscillators in different geometries.

Keywords Phase oscillators · Coupling · Synchronization · Order parameter

28.1 Introduction

In many problems of physical and biological interest we consider nonlinear oscillators (active cells) whose interaction is mediated by a chemical substance which is secreted and absorbed by the cells, and diffuses along the inter-cellular medium [1]. Moreover, the rate of secretion can depend on the cell dynamics, as well as the rate of absorption. In this way the dynamics of the cells are effectively coupled by the diffusing chemical substance, leading to a non-local coupling type.

This kind of chemical coupling has been mathematically described by a reaction-diffusion model by Kuramoto leading to non-local couplings [2]. In this model the state variables of each oscillator influence the secretion of a chemical substance obeying a diffusion equation. The rate of absorption depends on the local concentration of this substance at each cell position. The spatio-temporal dynamics of such non-locally coupled systems is extremely rich, giving rise to phenomena like power-law

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spatial correlations [3], chimeras [4], Turing-Hopf mixed mode solutions [5], noisy on-off intermittency with multi-scaling properties [6], noise-induced transition to turbulence [7], and phase turbulence [8].

Besides the interesting dynamical features of such model, it has been used to describe neuronal networks of non-locally coupled Hodgkin-Huxley equations with excitatory and inhibitory coupling [9], the transition to bursting synchronization in neuronal networks [10], the interaction among biological clock cells of the suprachiasmatic nucleus [11]. In the latter example it is thought that the synchronization of clock cells is due to their interaction mediated by γ-aminobutyric acid (GABA) or other neurotransmitters [12, 13]. The transition to synchronization of networks of generic phase oscillators with coupling mediated by a rapidly diffusing substance has been investigated in detail by numerical [14] and analytical methods [15].

In the original version of the Kuramoto reduction the diffusion characteristic time is much shorter than the oscillator main period, such that diffusion occurs very fast, i.e. the system achieves instantaneously a stationary concentration of the diffusing chemical [2]. However, this model cannot be properly applied if the diffusion time is comparable or is much bigger than the oscillator period. In this case one has to consider the diffusion equation and the corresponding Green function. In this paper we solved the diffusion equation for cases in one, two and three dimension, with and without boundary conditions. The resulting interaction kernels can be of interest for modeling of physico-chemical and biological problems in which the coupling among oscillators is mediated by a slowly diffusing substance.

We consider that the dynamical behavior of each "cell" is described by a phase oscillator with average period T, such that we can model physico-chemical and biological problems in which the interaction is mediated by a substance with typical diffusion time $\sim T$, for example. This seems to be the case in many problems of chemotaxis, which is the ability of cells to move along the direction of concentration gradients of signaling chemicals [16].

One of the most investigated organisms with respect to the chemotactic response is the amoeba *Dictyostelium*. In the absence of food the *Dictyostelium* cells release signal molecules into their environment, such that they can find other cells and move to create clusters [17]. During this process, about 10^5 *Dictyostelium* cells release the chemoattractant cyclic adenosine monophosphate (cAMP) every 6 min during periods reaching 5 to 6 hours after starvation [17]. This suggests that the diffusion is very slow compared with internal rhythms of the individual cells.

There are many biological problems in which the relevant oscillator periods are relatively long, like the problem of synchronization of menstrual cycles (with a period of 28 days for humans) investigated in many works by McClintock and co-workers [18]: women that live together synchronize their menstrual cycles. This synchronization is thought to be mediated by airborne chemosignals called pheromones that diffuse in the atmosphere, such that there must be a common air supply.

This paper is organized as follows: in Sect. 28.2 we present the coupling model based on the solution of a reaction-diffusion equation governing the interaction among cell oscillators. In Sect. 28.3 we show the Green's functions in free space in one, two, and three dimensions. The case of finite domains (Dirichlet bound-

ary condition) is considered in Sect. 28.4. Section 28.5 presents some systems of coupled phase oscillators, and a discussion on their synchronization properties. Our Conclusions are left to the final Section.

28.2 Coupling Model

In the following we will deal with two classes of vectors, which are represented with a different notation: (i) positions $\mathbf{r}$ in a d-dimensional Euclidean space, in which the oscillators are embedded; (ii) state variables $\mathbf{X} = (X_1, X_2, \ldots X_M)^T$ in a M-dimensional phase space of the dynamical variables characterizing the state of the system at a given time t (Fig. 28.1). There are N oscillator cells located at discrete positions $\mathbf{r}_j$, where $j = 1, 2, \cdots N$, in the d-dimensional Euclidean space; and $\mathbf{X}_j$ is the state variable for each oscillator, whose time evolution is governed by the autonomous vector field $\mathbf{F}(\mathbf{X}_j)$. The systems are not necessarily identical, though, for they can have slightly different parameters.

We suppose that the time evolution is affected by the local concentration of a chemical, denoted as $A(\mathbf{r}, t)$, in the form

$$\frac{d\mathbf{X}_j}{dt} = \mathbf{F}(\mathbf{X}_j) + K\, A(\mathbf{r}_j, t), \qquad (j = 1, 2, \ldots N), \tag{28.1}$$

meaning that each oscillator absorbs the chemical which is secreted by all other oscillators and diffuses in the inter-oscillator medium. The parameter $K > 0$ measures the intensity of the coupling. In the following we suppose that all variables, including spatial coordinates and time, have been adequately normalized, being thus nondimensional.

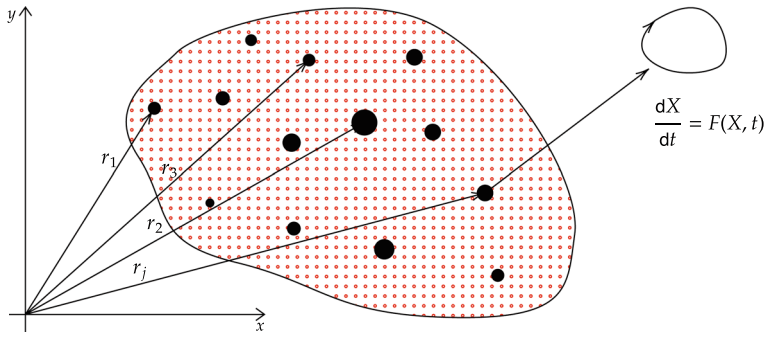


Fig. 28.1 A system of chemically coupled pointlike phase oscillators

The chemical concentration satisfies a diffusion equation of the form

$$\frac{\partial A(\mathbf{r},t)}{\partial t} + \eta\, A(\mathbf{r},t) - D\,\nabla^2 A(\mathbf{r},t) = \sum_{k=1}^{N} h(\mathbf{X}_k(t))\,\delta(\mathbf{r}-\mathbf{r}_k), \tag{28.2}$$

where η is a phenomenological damping parameter (representing the chemical degradation of the mediating substance) and D is a diffusion coefficient. The diffusion equation above has a source term h which depends on the oscillator state at the discrete positions $\mathbf{r}_j$ they occupy. This means that each oscillator secretes the chemical with a rate depending on the current value of its own state variable.

In Kuramoto reduction it is assumed that the diffusion is so fast, compared with the oscillator period, that we may set $\dot{A} \approx 0$, such that the concentration relaxes to a stationary value (adiabatic elimination) [2–4]. This is justifiable if the diffusion time τ_c is much less than the dominant oscillator period T. Let ℓ be the characteristic length of the system: from the diffusion equation we can estimate the diffusion time as $\tau_c \sim \ell^2/D$, where D is the diffusion coefficient. Hence Kuramoto reduction is valid provided $\tau_c \ll T$ or $T \gg \ell^2/D$.

On the other hand, Kuramoto reduction will be no longer valid if the timescales T and τ_c are comparable, which can occur either if the coupling is slow or the oscillator dynamics is fast (high-frequency phenomena). In this case we have to solve the non-homogeneous diffusion Eq. (28.2) using Green's function method. In the general case, for a finite domain $\mathcal{D}$, there is a surface $\partial\mathcal{D}$ on which we have to specify suitable boundary conditions. One such example is absorbing boundary conditions (Dirichlet), for which the concentration vanishes on $\partial\mathcal{D}$, i.e. $A(\mathbf{r} \in \partial\mathcal{D}, t) = 0$. Moreover we must specify the initial conditions, e.g. with a uniform initial concentration over $\mathcal{D}$. For simplicity we suppose that initially there is no substance in the domain: $A(\mathbf{r} \in \mathcal{D}, t = 0) = 0$.

The Green's function $G(\mathbf{r}, t|\mathbf{r}', t')$ satisfies the equation

$$\frac{\partial G}{\partial t} + \eta G - D\,\nabla^2 G = \delta(\mathbf{r}-\mathbf{r}')\,\delta(t-t'), \tag{28.3}$$

with the following boundary and initial conditions

$$G(\mathbf{r} \in \partial\mathcal{D}, t|\mathbf{r}', t') = 0, \qquad G(\mathbf{r}, t=0|\mathbf{r}'; t') = 0, \tag{28.4}$$

respectively. We also impose the causality condition $G(\mathbf{r}, t|\mathbf{r}'; t') = 0$, if $t < t'$. It follows that the Green's function has the symmetry property

$$G(\mathbf{r}, t|\mathbf{r}', t') = G(\mathbf{r}', -t'|\mathbf{r}, -t).$$

On multiplying (28.2) by $G(\mathbf{r}, t|\mathbf{r}', t')$ and (28.3) by $A(\mathbf{r}', t')$, subtracting the two, integrating over primed volume and primed time t', and applying the second Green's formula, we obtain a solution to the inhomogeneous diffusion equation for absorbing boundary conditions and vanishing initial concentration

$$A(\mathbf{r},t) = \sum_{k=1}^{N} \int_0^{t^+} dt'\, h(\mathbf{X}_k(t'))\, G(\mathbf{r},t|\mathbf{r}_k,t'). \tag{28.5}$$

Inserting this expression into Eq. (28.6) gives a system of integro-differential equations for the dynamical variables $\mathbf{X}_j(t)$.

$$\frac{d\mathbf{X}_j}{dt} = \mathbf{F}(\mathbf{X}_j) + K \sum_{k=1}^{N} \int_0^{t^+} dt'\, h(\mathbf{X}_k(t'))\, G(\mathbf{r}_j,t|\mathbf{r}_k,t'), \qquad (j = 1,2,\ldots N). \tag{28.6}$$

The key difficulty here is that the coupling term depends not only on the current system state, *but on all its history over time*. Hence, even a numerical approach is considerably more complicated than for a system of coupled differential equations.

28.3 Green Functions in Free Space

We begin by the simplest case in which there are no bounding surfaces, i.e. the domain is the entire space (this is equivalent to making the surface $\partial\mathcal{D}$ "going to infinity"), where the boundary condition is $A(|\mathbf{r}| \to \infty, t) = 0$. The Green's function of the diffusion problem in the d-dimensional free space is obtained by solving (28.3) using Fourier transforms, and reads

$$G_d(\mathbf{r},t|\mathbf{r}_k,t') = \frac{\Theta(t-t')\, e^{-\eta(t-t')}}{(2\pi)^d} \int d^d\mathbf{k}\, e^{i\mathbf{k}\cdot(\mathbf{r}-\mathbf{r}_k)-Dk^2(t-t')}, \tag{28.7}$$

where Θ is the Heaviside unit-step function. For $d = 1$ the Green function (28.7) is

$$G_1(x,t|x_k,t') = \frac{\Theta(t-t')}{\sqrt{4\pi D(t-t')}}\, e^{-\eta(t-t')} \exp\left[-\frac{(x-x_k)^2}{4D(t-t')}\right], \tag{28.8}$$

whereas for two and three dimensions, it reads

$$G_2(\mathbf{r},t|\mathbf{r}_k,t') = \frac{\Theta(t-t')e^{-\eta(t-t')}}{4\pi D(t-t')} \exp\left[-\frac{(x-x_k)^2+(y-y_k)^2}{4D(t-t')}\right], \tag{28.9}$$

$$G_3(\mathbf{r},t|\mathbf{r}_k,t') = \frac{\Theta(t-t')e^{-\eta(t-t')}}{[4\pi D(t-t')]^{3/2}} \exp\left[-\frac{(x-x_k)^2+(y-y_k)^2+(z-z_k)^2}{4D(t-t')}\right], \tag{28.10}$$

It is useful to define an interaction kernel as the time integral of the Green function

$$\sigma_d(\mathbf{r},\mathbf{r}_k;t) = \int_0^{t^+} dt'\, G_d(\mathbf{r},t|\mathbf{r}_k,t'), \tag{28.11}$$

such that, for the one-dimensional case, it is given by

$$\sigma_1(x, x_k, t) = \int_0^{t^+} dt' \frac{e^{-\eta(t-t')}}{\sqrt{4\pi D(t-t')}} \exp\left[-\frac{(x-x_k)^2}{4D(t-t')}\right], \tag{28.12}$$

which becomes, after a change of variables,

$$\sigma_1(x, x_k, t) = \frac{x - x_k}{4D\sqrt{\pi}} \int_{u_1}^{\infty} du \, \frac{e^{-u-a_1/u}}{u^{3/2}}, \tag{28.13}$$

where

$$a_1 = \frac{\eta(x-x_k)^2}{4D} = \left\{\frac{\gamma(x-x_k)}{2}\right\}^2, \qquad u_1 = \frac{(x-x_k)^2}{4Dt}, \tag{28.14}$$

and we defined a coupling length

$$\gamma = \sqrt{\frac{\eta}{D}}. \tag{28.15}$$

For the two-dimensional case the interaction kernel is

$$\sigma_2(\mathbf{r}, \mathbf{r}_k; t) = \frac{1}{4\pi D} \int_{u_2}^{\infty} \frac{du}{u} \, e^{-u-a_2/u}, \tag{28.16}$$

where

$$a_2 = \frac{\eta[(x-x_k)^2 + (y-y_k)^2]}{4D} = \left|\frac{\gamma(\mathbf{r}-\mathbf{r}_k)}{2}\right|^2, \qquad u_2 = \frac{|\mathbf{r}-\mathbf{r}_k|^2}{4Dt}, \tag{28.17}$$

and, similarly, the kernel in three-dimensions is

$$\sigma_3(\mathbf{r}, \mathbf{r}_k; t) = -\frac{1}{4D\pi^{3/2}} \frac{1}{|\mathbf{r}-\mathbf{r}_k|} \int_{u_3}^{\infty} \frac{du}{\sqrt{u}} \exp\left(-u - \frac{a_3}{u}\right), \tag{28.18}$$

where

$$a_3 = \frac{\eta}{4D}|\mathbf{r}-\mathbf{r}_k|^2, \qquad u_3 = \frac{|\mathbf{r}-\mathbf{r}_k|^2}{4Dt}. \tag{28.19}$$

If the diffusion time is much smaller than the characteristic time of the system we can suppose that the diffusion is practically instantaneous, i.e. the chemical concentration relaxes immediately to its equilibrium value $\dot{A}_E = 0$. In this limit the diffusion equation no longer involves the time explicitly:

$$\eta\, A_E(\mathbf{r}) - D\,\nabla^2 A_E(\mathbf{r}) = \sum_{k=1}^{N} h(\mathbf{X}_k)\,\delta(\mathbf{r}-\mathbf{r}_k), \tag{28.20}$$

such that the equilibrium concentration, with the same boundary and initial conditions of the general case, is given by

$$A_E(\mathbf{r}) = \sum_{k=1}^{N} h(\mathbf{X}_k) G_E(\mathbf{r}|\mathbf{r}_k), \tag{28.21}$$

where the equilibrium Green function is a solution of

$$\eta G_E - D\,\nabla^2 G_E = \delta(\mathbf{r}-\mathbf{r}'). \tag{28.22}$$

The coupled system, in the fast-relaxation limit, is now obtained by substituting (28.21) into (28.20)

$$\left.\frac{d\mathbf{X}_j}{dt}\right|_E = \mathbf{F}(\mathbf{X}_j) + K \sum_{k=1}^{N} h(\mathbf{X}_k) G_E(\mathbf{r}_j|\mathbf{r}_k). \tag{28.23}$$

Since the coupling term depends only on the current value of the dynamical variables, (28.23) is a system of coupled differential equations, much simpler to solve than the integro-differential case (28.6). If we compare both equations, we can see that (28.6) reduces to (28.23) if (i) the source function $h(.)$ does not involve time explicitly, (ii) the equilibrium Green's function is the infinite-time limit of the interaction kernel (28.11):

$$G_{Ed}(\mathbf{r}_j|\mathbf{r}_k) = \lim_{t\to\infty} \sigma_d(\mathbf{r}_j, \mathbf{r}_k; t). \tag{28.24}$$

If we take this limit on the one-dimensional interaction kernel given by Eq. (28.13) we obtain the following result

$$G_{E1}(x_j|x_k) = \frac{\gamma}{2\eta}\, e^{-\gamma(x_j - x_k)}, \tag{28.25}$$

which agrees, up to a normalization factor, with the earlier results of Kuramoto and coworkers [2, 6], in their analysis of the fast-relaxation case. In two and three dimensions the same limits applied to Eqs. (28.16)–(28.18) yield

$$G_{E2}(\mathbf{r}_j|\mathbf{r}_k) = \frac{1}{2\pi D}\, \mathcal{K}_0[\gamma|\mathbf{r}_j - \mathbf{r}_k|], \tag{28.26}$$

$$G_{E3}(\mathbf{r}_j|\mathbf{r}_k) = \frac{1}{4D\pi}\, \frac{e^{-\gamma|\mathbf{r}_j - \mathbf{r}_k|}}{|\mathbf{r}_j - \mathbf{r}_k|}, \tag{28.27}$$

where $\mathcal{K}_0$ is the modified Bessel function of order zero. These expressions coincide with those previously given by Nakao [6] in the equilibrium limit.

28.4 Green Functions in Finite Domains

If, instead of the free space, we consider that diffusion occurs only over a finite spatial domain, then we have a boundary value problem for the diffusion equation. A simplification results if we consider absorbing boundary conditions, i.e. the concentration vanishes at the boundary surface $\partial\mathcal{D}$. The solution of the inhomogeneous diffusion equation is given by (28.5).

Instead of closed-form expressions, as for the free space, the Green's functions can now be expressed as bilinear series expansions of orthogonal eigenfunctions of a self-adjoint operator [21, 22]. The expansions depend, as before, on the geometry of the boundary as well as the dimension of the underlying space. Once the corresponding Green's function is obtained, the coupled system of integro-differential equations is given by (28.6).

Let us begin by considering a one-dimensional finite domain of length L ($0 \leq x \leq L$) with absorbing boundary conditions ($A(0,t) = A(L,t) = 0$). The corresponding Dirichlet Green's function is

$$G_1(x,t|x',t') = \frac{2\Theta(t-t')}{L}\sum_{n=1}^{\infty}\sin\left(\frac{n\pi x}{L}\right)\sin\left(\frac{n\pi x'}{L}\right)\exp\left\{-\left[D\left(\frac{n\pi}{L}\right)^2+\eta\right](t-t')\right\}. \tag{28.28}$$

The second example is a rectangular domain of sides a and b with absorbing boundary conditions: $A(x=a, 0\leq y\leq b) = A(0\leq x\leq a, y=b) = 0$, for which the Green's function is

$$G_{2r}(x,y,t|x',y',t') = \frac{4\Theta(t-t')}{ab}\sum_{n=1}^{\infty}\sum_{m=1}^{\infty}\sin\left(\frac{n\pi x}{a}\right)\sin\left(\frac{n\pi x'}{a}\right)\sin\left(\frac{m\pi y}{b}\right)\sin\left(\frac{m\pi y'}{b}\right)\times$$
$$\exp\left\{-\left[D\left(\frac{n^2}{a^2}+\frac{m^2}{b^2}\right)\pi^2+\eta\right](t-t')\right\}, \tag{28.29}$$

Another example of a bounded two-dimensional domain is a circle of radius $r = a$ with an absorbing boundary ($A(r=a,\vartheta) = 0$). Using polar coordinates the Green's function is

$$G_{2c}(r,\vartheta,t|r',\vartheta',t') = \frac{\Theta(t-t')}{\pi D}\sum_{m=-\infty}^{\infty}\sum_{n=1}^{\infty}\frac{1}{[J'_m(x_{mn})]^2}J_m\left(x_{mn}\frac{r}{a}\right)J_m\left(x_{mn}\frac{r'}{a}\right)\times$$
$$\cos[m(\vartheta-\vartheta')]\exp\left\{-\left[\frac{Dx_{mn}^2}{a^2}+\eta\right](t-t')\right\}, \tag{28.30}$$

where x_{mn} is the nth positive root of the Bessel function $J_m(x)$.

28.5 Systems of Coupled Phase Oscillators

A linear coupling is given by $h(\mathbf{X}_k) = \mathbf{B}\mathbf{X}_k$, where $\mathbf{B}$ is a $M \times M$ matrix whose nonzero elements $B_{mn}^{(ij)}$ indicate that the mth variable of the jth oscillator is coupled to the nth variable of the kth oscillator. The future coupling, for which $h(\mathbf{X}_k) = \mathbf{B}\mathbf{F}(\mathbf{X}_k)$, is useful because each oscillator remains in the same range as for the isolated system, in such a way that the state variables remain normalized. Moreover, the neighboring oscillators are evolved in time before they are coupled, providing a synchronous update for the coupled lattice at any time. Finally, a general nonlinear coupling can be represented as $h(\mathbf{X}_k) = \mathbf{B}\mathbf{H}(\mathbf{X}_k)$, and $\mathbf{H}$ is an arbitrary function of its arguments.

The simplest phase oscillator is characterized by a single phase $\theta_j(t)$ which evolves with time according to a constant frequency ω_j. In this case $M = 1$ and

$$\mathbf{X}_j = \theta_j, \qquad \mathbf{F}(\mathbf{X}_j) = \omega_j, \qquad \mathbf{B} = 1, \tag{28.31}$$

where we assume that the oscillator frequencies may be different, as it is often the case in physical and biological applications.

Let us consider, in order to make contact with the classical Kuramoto model of coupled oscillators [20], the following nonlinear coupling function

$$\mathbf{H}(\mathbf{X}_j) = \frac{1}{N}\,\sin(\theta_k - \theta_j). \tag{28.32}$$

In this case the equations for chemical coupling read

$$\frac{d\theta_j}{dt} = \omega_j + \frac{K}{N}\sum_{k=1}^{N}\int_0^t dt'\,\sin(\theta_k(t') - \theta_j(t'))\,G(\mathbf{r}_j, t|\mathbf{r}_k, t'), \qquad (j = 1, 2, \ldots N), \tag{28.33}$$

whereas, in the fast-relaxation limit, the equations reduce to the form

$$\left.\frac{d\theta_j}{dt}\right|_E = \omega_j + \frac{K}{N}\sum_{k=1}^{N}\sin(\theta_k - \theta_j)\,G_E(\mathbf{r}_j|\mathbf{r}_k), \qquad (j = 1, 2, \ldots N). \tag{28.34}$$

If $G_E \equiv 1$ we obtain the classical Kuramoto model, where each oscillator is coupled with all the other ones, regardless of their relative positions [20].

In a previous paper [25] we solved the coupled integro-differential equations (28.33) using a method similar to the Born approximation used in quantum-mechanical scattering problems. More recently, an improved numerical scheme was developed to solve directly the integro-differential equations by evaluating the coupling integral in (28.33) [26].

Two or more oscillators are phase synchronized if their phases are equal, up to a given numerical tolerance. If the phase oscillators represent biological clocks, as in the example of the SCN, they are supposed to synchronize their own rhythms thanks to the coupling. In a model of SCN, this coupling is of chemical origin, corresponding to

the release and absorption of the neurotransmitter GABA. One numerical diagnostic of phase synchronization is the Kuramoto order parameter magnitude [20]

$$R(t) = \frac{1}{N}\left|\sum_{j=1}^{N} e^{i\theta_j(t)}\right|. \tag{28.35}$$

Since the time evolution of the order parameter magnitude exhibits fluctuations, we compute its time average $\overline{R}$ over a long period, discarding transients. The oscillators are completely phase synchronized if $\overline{R} \approx 1$ and completely non-synchronized if $\overline{R} \approx 0$.

We have numerically solved (28.33) for networks of $N = 100$ phase oscillators randomly distributed over distinct finite spatial domains. We have considered three examples: (i) a one-dimensional interval of length L; (ii) a rectangular domain with sides a and b; (iii) a circular domain of radius a, for which the Green's functions are given by (28.28), (28.29), and (28.30), respectively. The oscillator frequencies ω_j were randomly chosen from a given Gaussian distribution centred at $\omega = 0$ (negative frequencies are related to rotations in the opposite sense).

In these cases we obtained the time evolution of the phases for different sets of initial conditions $\theta_j(t = 0)$, $j = 1, 2, \ldots N$, and we computed the average over them. The computation is quite slow since, in order to advance a timestep in the differential equations we have to evaluate the coupling term, which involves the oscilator phases at all previous times. After a long time we computed the time-averaged order parameter magnitude $\overline{R}$, and investigated its dependence with the coupling parameters.

In Fig. 28.2a we show the variation of $\overline{R}$ with the parameters of the system, fixing the other parameters for the linear domain. We have observed synchronization transitions as K is varied through a critical value, the result can be extended for the three considered geometries, all of them with absorbing boundary conditions. The variation of $\overline{R}$ with K is similar to that observed in the Kuramoto classical model of globally coupled phase oscillators [20].

Also can be seen in Fig. 28.2b–c an opposite effect, of decreasing the synchrony when either D increases or η increases. Showing the physical effect of those parameters. When the Diffusion coefficient increases the substance diffuses faster and is absorbed by the boundaries preventing the oscillators from synchronizing. A similar result is achieved when the degradation coefficient increases, making the substance be destroyed before being sensed by the oscillators and then preventing the synchrony. Those effects occur even with the value of the $K = 10$ and can be extended to the other geometries easily [26].

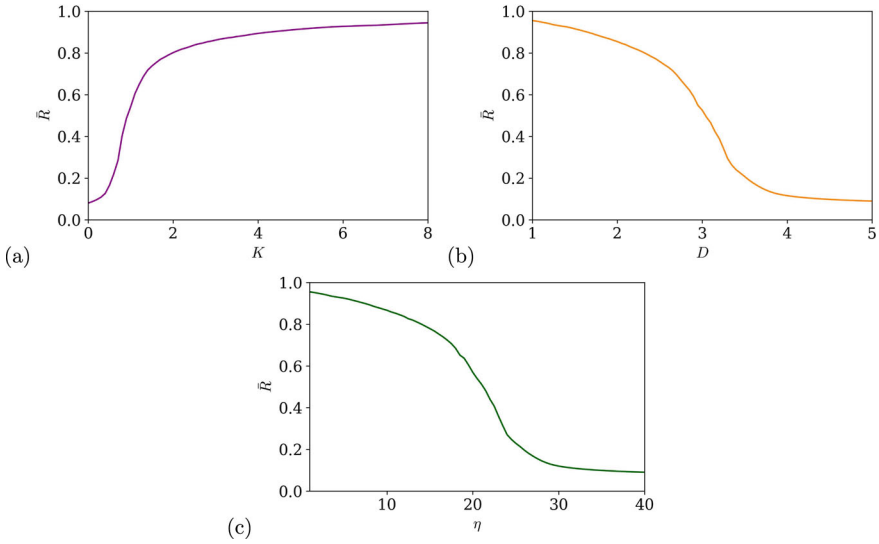


Fig. 28.2 Average order parameter magnitude as a function **a** the coupling strength, **b** diffusion coefficient and **c** chemical degradation for an assembly of $N = 100$ coupled phase oscillators in the linear domain. We kept the other parameters fixed at $K = 10$ and $\eta = D = 1.0$

28.6 Conclusions

In a variety of problems in physical chemistry and cell biology the individuals, or cells, undergo some kind of dissipative dynamics leading to a stable limit-cycle as the asymptotic state. The dynamics along this limit-cycle can describe some physico-chemical or biological rhythm, and it can be mathematically described, in a minimal model, by a phase oscillator. We consider the situation in which the oscillator cells are coupled by the diffusion of some substance through the inter-cellular medium. This diffusing chemical is secreted and absorbed according to the cell dynamics, in such a way that the coupling is effectively mediated by the substance.

We proposed a general reaction-diffusion model for this process where we do not require the diffusion to be infinitely fast, what allows the possibility of diffusion at scales comparable to the oscillator characteristic period. The model can be formulated either in the free space (in one, two, and three spatial dimensions) or within closed domains, for which absorbing boundary conditions are assumed. Such boundary conditions, besides being simpler to impose, are actually necessary to avoid saturation of the diffusing substance in the inter-cellular medium. More complicated boundary conditions can be used, though, in order to tackle specific situations.

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Chapter 29
A New Chaotic Lotka-Volterra Population Biology System, Its Dynamic Analysis, and FPGA Implementation

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Abstract In mathematical ecology, Lotka-Volterra population biology models describe dynamical systems showing the nonlinear interaction between predator and prey population species. Eilersen et al. [4] examined the Lotka-Volterra model of a population biology system consisting of one predator and two prey population

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species of which one prey is affected by a disease. Eilersen et al. [4] observed chaos in the Lotka-Volterra ecological model when the disease is contagious enough to keep going and spread over the affected prey species. A new chaotic Lotka-Volterra ecological disease model is derived in this work by adding a self-interacting nonlinear term for the infected prey species in the Eilersen chaotic disease model [4]. We show that the new chaotic Lotka-Volterra ecological disease model has two unstable rest points and a stable focus rest point. We conduct a detailed bifurcation analysis for the new Lotka-Volterra population biology model. We demonstrate that the new chaotic model exhibits multi-stability properties. Finally, we design an experimental FPGA model for the implementation of the proposed chaotic Lotka-Volterra population biology model.

Keywords Bifurcation analysis · Chaos · Chaotic systems · Circuit Design · Disease models · Dynamical systems · Ecology · FPGA Design · Lotka-Volterra Systems

29.1 Introduction

Dynamical systems with high sensitivity on changes in the initial states are known as chaotic dynamical systems [1]. Chaotic dynamical systems are applied in diverse areas such as population biology [2–4], molecular biology [5, 6], mechanical oscillators [7, 8], memristors [9, 10], neural networks [11, 12] etc.

New dynamical models of population ecology have several applications in ecological monitoring [13–15]. New disease models involving Lotka-Volterra models have many applications on epidemics [16–18]. Chaotic dynamical models have many applications in engineering areas such as encryption [19, 20], secure communication [21, 22], circuits [23, 24], etc.

Eilersen et al. [4] examined chaos in the Lotka-Volterra ecological model. Specifically, Eilersen et al. [4] considered a 4-D ecological model consisting of a susceptible prey species with healthy prey species (x_s) and infected prey species (x_i), an immune prey species (y) and a predator species (z). Eilersen et al. [4] observed chaos in the 4-D population biology model when the disease is contagious enough to keep going and spread over the affected prey species.

The main contribution of this research work is the finding of a new chaotic Lotka-Volterra population biology dynamical model by introducing a self-interacting term (px_i^2) for the infected prey species in the Eilersen ecological chaotic model [4]. We show that the new chaotic disease system proposed in this work exhibits a larger value of LE_1 (maximal Lyapunov exponent) and Kaplan dimension D_K when compared to the numerical values of LE_1 and D_K for the Eilersen ecological chaotic system [4].

We show that the new chaotic Lotka-Volterra ecological disease model has two unstable rest points and a stable focus rest point. The presence of a stable equilibrium point shows the existence of hidden attractors for the new chaotic Lotka-Volterra ecological disease model [10].