Stochastic Recurrent Dynamics of Complex Systems of Solitons

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We study networks made up of interacting solitons (solitonets), and find that their dynamics exhibits stochastic recurrent behavior, independent of the topology, where the interaction rule at the single-node level can be used to predict the dynamics of the entire network. The ideas are general, not specific to solitonets: they apply to many kinds of networks whose dynamics converges to a recurrent structure.

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Complex systems are a field that emerged simultaneously in biology, computer science, economy, sociology, and physics. It attempts to analyze systems displaying complex overall behavior, which cannot be simply explained by the properties of the system's parts. Examples range from metabolic networks and the World Wide Web to social networks [1]. The desire to explain the behavior of such systems, with the vision that similar tools can advance several fields, has led to major progress. For example, this logic has led to relating scale-free evolution, known from fractals, to complex networks [2]. In physics-related areas, complex systems research proceeds in two main avenues: topological aspects, where statistical mechanics of critical phenomena plays a crucial role (e.g., percolation [1]), and nonlinear dynamics, extending from collective dynamics of the entire system, to highly fragmented dynamics with different parts behaving in uncorrelated fashion [3].

In a recent paper, we proposed complex networks constructed from interacting fields [4]. We used solitons as "carriers of interactions," where the soliton collision sites form nodes in this network of solitons, henceforth called "solitonets." Solitons are self-localized waves which conserve many quantities under interactions [5]. Each soliton is a field, having infinite degrees of freedom, and at the same time it behaves as a particle, described by a set (in integrable systems: an infinitely large set) of conservation laws [6]. We constructed networks from vector (Manakov) solitons [7,8], where the dynamic parameter characterizing the interaction is the ratio between the field amplitudes of each soliton, while all other properties (number of solitons, power, momentum, etc.) are conserved. Solitonets display "extreme complexity": the interaction at each node has infinite degrees of freedom, while conservation laws imply that the number of different solitons in the network is uniquely defined by initial conditions [4,6]. They exhibit novel phenomena such as noise-enhanced memory and self-synchronization even for random inputs [4].

Here, we show that, when Manakov-based solitonets have large random topology, they display stochastic recurrent dynamics, whose structure is determined by the interaction rule at the single-node level, which yields a closed-form expression. We develop a Markovian approach to produce an integral discrete-time evolution equation describing the dynamics, whose solution yields the same recurrent structure found by direct simulations of the networks dynamics. Furthermore, we find that two solitonets connected by a single node exhibit autonomous dynamics despite the information flow between them. Finally, we show that these concepts are general: the recurrent structures describe the dynamics of a large class of networks, characterized by a whole variety of interaction rules, and all of those can be analyzed by the Markovian method.

We begin by describing the interaction. At each node, two vector (Manakov) solitons of the same power collide at different velocities [upper and lower solitons in Fig. 1(a)]. Thus, the node has 2 inputs/2 outputs (the input and output ratios between the complex amplitudes of the fields comprising each soliton). The Manakov system is integrable; hence, power and velocities are conserved, while the ratios between the field amplitudes of each soliton vary following the expressions in Fig. 1(a) [8]. We construct networks made of multiple identical nodes, with all solitons of the same power and two different velocities. Collisions occur at discrete time steps at all nodes simultaneously. We begin by analyzing the single-node network [Fig. 1(b)], and then construct stochastic networks with 50 000 nodes, as in Fig. 1(c) (shown 300 nodes, more appear too crowded).

Consider the simplest single-node network, where each output is fed back into the other input, resembling a butterfly [Fig. 1(b)]. The interaction rules are specified in Fig. 1(a), relating the two inputs (x and a) to two outputs (y and b), through two fixed parameters, g and h. The parameters y and b values are launched again within the butterfly network as the new a and x, respectively. The parameters g and h are identical for all nodes in the networks, and do not change during interactions [4,8–10]. Our simulations reveal that the x and a values of each of the two solitons are restricted to a circle in the complex plane. At each time step, the y values emerging from the collision reside on a single circle, likewise, the emerging b values. Moreover, we find that, when the solitons have the same power, i.e. $g = \bar{h}$, the two circles coincide [Fig. 2(a)]. Using $g = \bar{h}$, we prove analytically (see [9]) that the dynamics in the butterfly solitonet is indeed restricted to

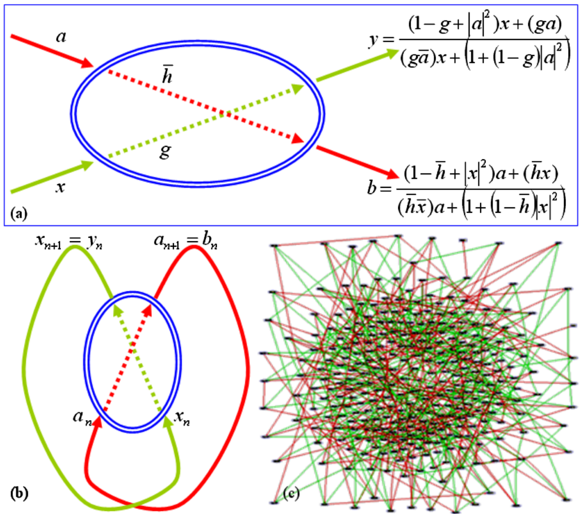

FIG. 1 (color online). (a) Interaction rule of two Manakov solitons, which follows a bilinear transformation mapping the input states onto the output states, forming a node in the network. (b) The butterfly network: a single node in which two solitons collide repeatedly. (c) Typical example of a (randomly created) large network.

a single circle. We find a close-form expression for the circle center, as a function of the initial values of a and x:

$$\text{center} = \frac{a(1 + x\bar{a}) + x(1 + a\bar{x})}{(1 + x\bar{a}) + (1 + a\bar{x})}, \qquad (1)$$
$$\{x_n, a_n, y_n, b_n\} \in \text{Circ(center, radius)}.$$

The radius can be calculated by radius $= |\text{center} - a| = |\text{center} - x|$ or by using any other values of x_n, a_n, y_n, b_n. This equation yields a single-valued function relating x_n and a_n, leaving only 1 degree of freedom, equivalent to the phase on the circle. For example, Fig. 2(a) compares the simulation results (dark and bright mark the x and a values of the solitons) to the circle calculated analytically. Note the important case of zero denominator, generating a restricting line instead of a circle. This happens for circles in the complex plane, and is referred to as a "generalized circle." Hence, the topology of the dynamics of the butterfly network resides on a generalized circle.

The results with the butterfly network raise the question on what can be said on the dynamics of a large, randomly connected, solitonet. This brings up our main result. We study numerically the relation between the internal dynamics and the topology of large solitonets, and find that the structure of their dynamics is stochastically recurrent. We find that the dynamics of the entire, very large, random network is restricted by the same (generalized) circle restricting the single-node butterfly network.

The construction of large randomly generated solitonets is as follows. We connect n collision zones (nodes) with $2n$ Manakov solitons (directed edges). We take n to be large ($\sim$20 000 in Figs. 2–4) and randomly generate n bright and n dark edges. The network is now fully connected, with no inputs or outputs relating to the outside. To characterize the network, we plot all values on the edges in the complex plane. All information related to a specific edge is omitted, keeping only statistical information (number of solitons vs complex values). Such omission makes sense since the network is homogenous (being randomly generated); hence, the positions of the nodes are unimportant. The initial conditions (complex values of the $2n$ solitons) are chosen randomly according to known probability functions. We shall later see that selecting special initial values for all solitons affects the emerging dynamics only via their distribution; hence, the dynamics of a large solitonet is invariant for permutations of the initial edges values. The statistical nature of the states through which the network evolves is found by taking a 2D histogram in the complex plane over the states [y, b of Fig. 1(a)] obtained at every time step. This yields a time-evolving density function, which converges rapidly to a stable stochastically recurrent structure. That is, the dynamics of any given network, of any physical g and h, yields a stable structure depending only on the initial conditions (and parameters g, h), while being completely independent from the networks topology.

When we produce the initial conditions from a probability distribution function, we find that different simulations recreate the same recurrent structure. This finding has profound implications: the state of the entire network can be described by the distribution functions of the initial conditions on the solitons. Given the distribution function, one can find its mean values and higher moments, and those determine the recurrent structure. There is no need to run multiple simulations to find the recurrent structure. Rather, the recurrent structure can be found from a single simulation of the network. This also implies that the recurrent structure is stable against small variations. Hence, it is possible to actually predict the recurrent dynamics of a network, given just the distribution of the initial conditions, without the network structure. To illustrate this, we simulate a network with all inputs chosen from the same dis-

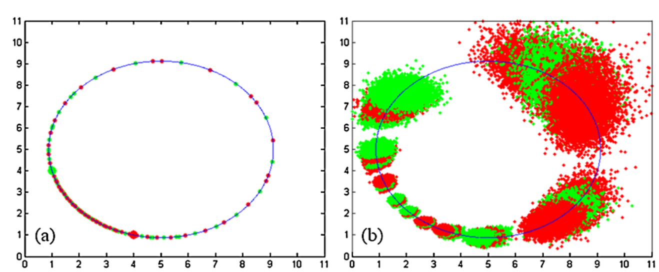

FIG. 2 (color online). (a) Dynamics of a butterfly network for 50 time steps, plotted in the complex plane; initial inputs marked by big dots ($x_1 = 1 + 4i$; $a_1 = 4 + i$). Left (right) outputs are in bright (dark). The circle is found analytically from the initial inputs. (b) Dynamics of a random network of 20 000 nodes; left (bright) and right (dark) outputs are plotted for 10 time steps; initial inputs have random distribution around $4 + i$ (left) or $1 + 4i$ (right). The outputs in b create two recurrent structures which "whirl" around the same circle restricting the dynamics in (a).

tribution, implying identical shapes for the outputs histogram, enabling to plot them together. Figure 3 shows three examples of different recurrent structures representing the dynamics in a large stochastic solitonet, for different initial conditions chosen randomly from the same distribution function but with different widths. The dynamics of the three converges to different recurrent structures: Gaussian, when the initial conditions (x, a) have narrow distribution, ring shaped, and crescent shaped, with the initial norms increasingly broader. Our findings occur for any selection of g, h; however, the actual shapes and the convergence rate depend on g, h. Adding noise to the system [e.g., in the complex states of each ''edge'' (soliton)] has negligible effects on the evolution of the system (see discussion in [9]).

The idea that the recurrent dynamics of a network can be predicted from the distribution of the initial conditions calls for an explanation. We develop a Markovian approach assuming statistical independence, and produce a set of coupled integral discrete-time equations of motion [Eqs. (2) below]. To get the equations, we treat the outputs of an interaction node as random variables, and use the Manakov interaction rule to extend their probability with the complete probability formula. We also assume statistical independence to separate the density functions. This assumption requires attention: we can assume that two colliding solitons have uncorrelated states only if they interact with a large enough number of other solitons before meeting again. More precisely, the ''environment effects'' decorrelate any statistical dependencies before consecutive collisions between any particular pair of solitons. This is where complex topology plays a critical role: only a sufficiently random topology can fulfill this requirement. This assumption fails in noncomplex networks, because such networks have an effective physical dimension restricting their topology. However, complex networks usually have an infinite effective physical dimension [11], because they have no spatial restrictions. This makes our statistical independence assumption valid in all complex networks. In [9], we provide several examples of interaction rules that are completely different than Manakov's exhibiting recurrent structures which are found by our Markovian approach. The underlying reason for the validity of the Markovian approach is that the complex topology simplifies the statistical nature of the internal dynamics in the network, that every interaction does not depend on the outcome of previous interactions with the same ''interaction carrier'' (same soliton, as for solitonets).

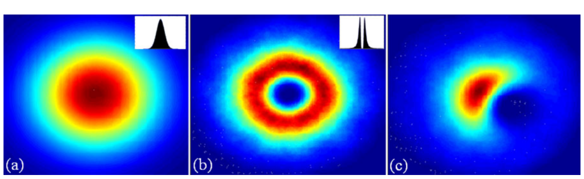

FIG. 3 (color online). Examples of the recurrent structures emerging in solitonets, and cross sections taken through the center. All pictures were created by a 2D histogram of a 20 000 nodes complex network with different initial conditions. (a) Gaussian-shaped structure. (b) Ring-shaped structure. (c) Crescent-shaped structure, which is the generalized recurrent structure, of which both the Gaussian and the ring-shaped structures are special cases.

We define P_n^{right}, P_n^{left} as the 2D probability densities for the right and left solitons, at the nth time step, evolving in (discrete) time through the interaction in each node. The equations governing the evolution are

$$P_{n+1}^{\text{left}}(y) = \int_A P_n^{\text{right}}(a) P_n^{\text{left}}\left(\frac{(1+(1-g)|a|^2)y - ga}{-g\bar{a}y + (1-g) + |a|^2}\right) \times \left|\frac{(1-g)(1+|a|^2)^2}{[g\bar{a}y - |a|^2 - (1-g)]^2}\right|^2 da$$

$$P_{n+1}^{\text{right}}(b) = \int_A P_n^{\text{left}}(x) P_n^{\text{right}}\left(\frac{(1+(1-\bar{h})|x|^2)b - \bar{h}x}{-\bar{h}\,\bar{x}\,b + (1-\bar{h}) + |x|^2}\right) \times \left|\frac{(1-\bar{h})(1+|x|^2)^2}{[\bar{h}\,\bar{x}\,b - |x|^2 - (1-\bar{h})]^2}\right|^2 dx. \qquad (2)$$

The arguments for P_n^{right}, P_n^{left} in the integrals are complex functions, derived by inverting the transformation of Fig. 1(a). Simulating Eqs. (2) reveals that they recreate the same stochastic dynamics as an entire network. Thus, solving Eqs. (2) numerically, initialized by some distribution function, can replace multiple simulations of the network, under different initial conditions chosen from the same distribution. The network structure does not matter: the dynamics is determined solely by the distribution function from which the initial conditions are chosen. For a linearized interaction rule (a and x at close proximity), we prove analytically (using tools extending from the central limit theorem) that the dynamics converges to the recurrent structures predicted by Eqs. (2). However, the Markovian approach [Eqs. (2)] is more general: we find (numerically) that the probability densities converge to the structure of the fully simulated networks even for the nonlinear case, which is extremely surprising.

An important simplification is $g = \bar{h}$ (solitons of equal powers), and initial conditions from the same probability ($P_0^{\text{Right}} = P_0^{\text{Left}}$). This makes the densities equal for all n ($P_n^{\text{Right}} = P_n^{\text{Left}}$), yields a single equation for both P_n^{Right}, P_n^{Left}. Indeed, simulating the solitonets (Fig. 3) creates the same time-invariant stochastic structures as predicted by the Markovian approach [Eq. (2)]. Importantly, Eqs. (2) are independent of the network topology. The only consequence of topology is the stability of the dynamics, which creates a recurrent shape holding complete stochastic description of the dynamics of the entire network. At the same time, the actual recurrent shape is determined by the interaction rule. To illustrate this, we simulate the dynamics with left and right inputs chosen from different distribution functions. Figure 2 shows how the dynamics of the simplest network [dots in Fig. 2(a)], coincides with the stochastic recurrent dynamics of a large network [Fig. 2(b)]. The large network is initialized by random values distrib-

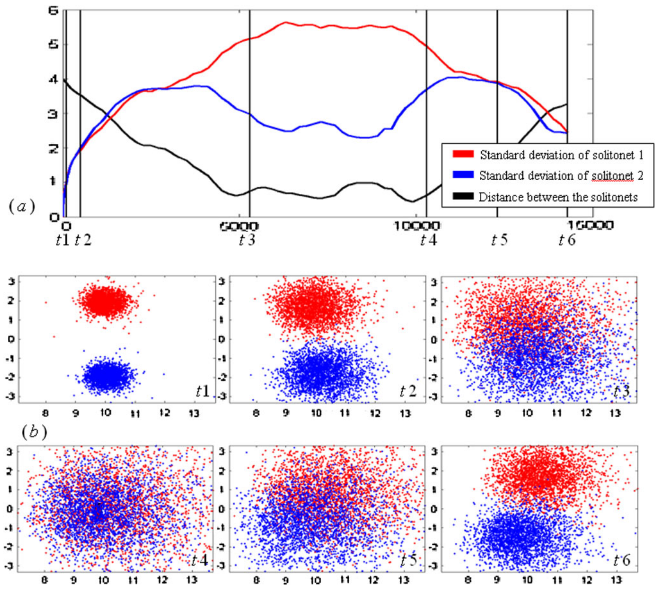

FIG. 4 (color online). Dynamics of two solitonets, each of 10 000 nodes, connected by a single-node, simulated for 15 000 time steps. (a) Standard deviation of each solitonet, and absolute distance between their mean values. Vertical lines mark the times at which each 2D plot is presented ($t1, \ldots, t6$). (b) Evolution of the solitonets at times $t1, \ldots, t6$. The images are created by placing all left and right outputs (y and b) on the complex plane. The colors emphasize that the structure of each solitonet is autonomous, without mixing.

uted around some x_1, a_1. The stochastic dynamics of a large network converges to values organized around the complex circle characterizing the single-node network, which is calculated analytically by using Eq. (1) and initial conditions x_1, a_1. The whirling dynamics goes on forever, spreading and squeezing around the analytical circle.

Finally, one can ask, where does the topology affect the dynamics? How is a solitonet different from a ''gas of solitons'' where random pairs collide at each time step? The answer has to do with constraints: when topology imposes a bottleneck, the network dynamics is constrained by the topology. For example, consider two large solitonets connected through a single node. We find that each network maintains its own stochastically stable dynamics even while they interact, while the mutual effects are dominant only during long range evolution. Figure 4 shows the simulated dynamics of two solitonets connected through a single node. As shown there, although the complex values do intersect, they always get separated afterwards. Figure 4(b) illustrate this dynamics: at times $t1$, $t2$, $t3$ both structures exhibit expansion and attract each other. At times $t3$, $t4$, $t5$ the structures ''collide'': the complex values in the outputs of the nodes are similar in both solitonets. At times $t5$, $t6$ the structures move away from one another, while each preserves its own shape. This dynamics is summarized in Fig. 4(a). At times $t1$, $t2$, $t3$ the recurrent shapes get closer while expanding, whereas at times $t4$, $t5$, $t6$ they move away from one another while shrinking. Each structure remains stable during the interaction between the networks, but the topology does affect the dynamics. The single connecting node breaks the structure symmetry, causing one formation to expand while the other shrinks. Such asymmetry is shown in Fig. 4: although the solitonets are symmetric in size and initial conditions, the expansion of the gray structure in Fig. 4(a) is significantly larger than the expansion of the black structure. This is a consequence of some parameters of the dynamics being sensitive to initial conditions. Hence, the asymmetry is governed by the random topology of both networks, creating resonant modes coupled to each other.

To summarize, we studied complex networks made of interacting Manakov solitons, and found that their internal dynamics evolves in stochastically recurrent structures, which depend on the initial conditions but not on the network topology. We find that dynamics in a large stochastic network is equivalent to the dynamics in a single-node network, both restricted to the same generalized circle. Hence, the dynamics in large stochastic networks can be predicted from the dynamics in the simplest network. We demonstrated the role of networks topology by studying cases where topology forms a bottleneck, restricting the information transfer between two large solitonets. Our findings can be realized experimentally in optical systems, where Mankov solitons and their interactions have been demonstrated [12–14]. Last but not least, the ideas demonstrated here are general, not specific to solitonets. As we show in [9], many kinds of networks display dynamics that converge to recurrent structures, and can be predicted using our Markovian approach. Are there specific conditions on the interaction rule for recurrent dynamics to emerge? Can these ideas be extended to scale-free networks containing interactions? These and related questions raise interesting ideas for further thought.

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