Editorial: Ecological complex systems

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Abstract. Main aim of this topical issue is to report recent advances in noisy nonequilibrium processes useful to describe the dynamics of ecological systems and to address the mechanisms of spatio-temporal pattern formation in ecology both from the experimental and theoretical points of view. This is in order to understand the dynamical behaviour of ecological complex systems through the interplay between nonlinearity, noise, random and periodic environmental interactions. Discovering the microscopic rules and the local interactions which lead to the emergence of specific global patterns or global dynamical behaviour and the noise's role in the nonlinear dynamics is an important, key aspect to understand and then to model ecological complex systems.

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1 Introduction

Ecological complex systems are open systems in which the interactions between the constituent parts are nonlinear and the interaction with the environment is noisy. These systems are therefore very sensitive to initial conditions, deterministic external perturbations and random fluctuations always present in nature. The study of noisy, non-equilibrium processes is fundamental for modeling the dynamics of ecological systems and for understanding the mechanisms of spatiotemporal pattern formation in ecology. Recently, considerable effort has been devoted to gain understanding of how population fluctuations arise from the interplay of noise, forcing, and nonlinear dynamics. The understanding of complexity in the framework of ecological systems may be enhanced starting from the "so called" simple systems, in order to catch the phenomena of interest, and adding details that introduce complexity at many levels. In general, the effects of small perturbations and noise, which is ubiquitous in real systems, can be quite difficult to predict and often yield counterintuitive behavior. Even low-dimensional systems exhibit a huge variety of noise-driven phenomena, ranging from a less ordered to a more ordered system dynamics [1–8].

In the past years the study of deterministic mathematical models of ecosystems has clearly revealed a large variety of phenomena, ranging from deterministic chaos to the presence of spatial organization. These models, however, do not account for the effects of noise despite the fact that it is always present in actual population dynamics. Frequently, noise effects have been assumed to be only a source of disorder. Now researchers are gaining a better understanding of population dynamics by bringing noise into nonlinear models, both for marine and for terrestrial animals [1–5,8]. A strong interaction between animals and their environment is responsible for the damsel-fish cycle and for population fluctuations of feral sheep for example. Because their survival depends on several interacting factors, the fish populations can react dramatically to what looks like small amounts of noise. Damsel-fish and feral sheep populations are only two examples of a growing list of ecological systems in which nonlinear dynamics seems to amplify the effects of noise caused by environmental forcing: Wind, waves, and the phase of the moon interact, in a multiplicative way, to produce drastic swings in fish population dynamics. The noise through its interaction with the nonlinearity of the living systems can give rise to new, counterintuitive phenomena like noise-enhanced transport, noise-sustained synchronization, noise-induced

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transitions, noise-enhanced stability, stochastic resonance, noise delayed extinction, temporal oscillations and spatial patterns. In addition, the analysis of experimental data of population dynamics frequently needs to consider spatial heterogeneity. Characterizing the resulting spatiotemporal patterns and the spatial organization is, perhaps, the major challenge for ecological time series analysis and for dynamics modeling [9].

The collection of papers of this volume gives a snapshot of the present status of this very interesting and rapidly expanding interdisciplinary research field, after the workshop on *"Ecological Complex Systems: Stochastic Dynamics and Patterns"* held in Terrasini (Palermo, Sicily) from 22 to 26 July, 2007. The workshop had its focus on the comprehension of the noise role and the formation of spatiotemporal patterns in the dynamics of ecological complex systems. The lectures of the small scale and intense workshop had a marked interdisciplinary character. The workshop gathered 40 participants, including 23 speakers, working at Universities and Research Institutions of Israel, Germany, Greece, UK, Poland, Spain, Switzerland, Russia, USA and Italy. The workshop brought together theoreticians and experimentalists, to establish a common language and exchange new ideas and recent developments in the field of ecology with the specific focus on the stochastic dynamics and spatiotemporal pattern formation in population dynamics. The discussion after each presentation made the workshop into a lively, interesting scientific event with a real stimulating and participating atmosphere. Particularly it is worthwhile to mention the round table on cancer growth dynamics, which was characterized by a passionate discussion about open problems on this interdisciplinary research subject, with an insight into cancer biology. This round table was a sort of synthesis of all previous sessions: By discussing firstly on intra and inter gene problems, then by analyzing ecosystems and finally by ending with cancer growth dynamics. The focus was on how Physics can help Biology and vice versa how Biology and Medicine can stimulate and provoke Physics with their complexity.

This topical issue contains a selection of peer-reviewed papers of the presented contributions at the Workshop, which we shortly review. Specifically the themes addressed in this issue are: self-organization and spatiotemporal patterns, bioinformatics, population dynamics, motion of proteins, motor protein and interdisciplinary physics.

2 Spatiotemporal patterns

Natural ecological structures on earth range in spatial scales from a few millimeters up to kilometers and in temporal scales from a few milliseconds to centuries. They are results of natural activity and competition between different species. On the small scale spatial pattern formation one can mention the bacterial colonies [10] and tumor growth [11], cell division and multiplication, followed in intermediate scales by insect nest and path patterns (ants, wasps, fish, etc..) [12]. At large scales these are

rainforest patterns, which cover many kilometers in space. At different temporal scales we list self-organized motion patterns in groups of animals [13,14], oscillations in epidemic spreading and in predator-prey systems [15] and stochastic resonance phenomena in protein systems. To describe complex ecosystems, therefore, it is fundamental to understand the interplay between noise, periodic and random modulations of environment parameters, the intrinsic nonlinearity of ecosystems and to comprehend spatiotemporal dynamics [5].

It is now becoming apparent that fluctuations and noise are essential ingredients of life processes. An emerging area of population dynamics where the interplay between nonlinearity and noise is essential for the outcome of the process is the virus dynamics. The interactions between viruses or other infectious agents and immune system cells together with the interaction with the noisy environment play a central role in any basic understanding of the evolution of virulence [16,17]. Modeling the dynamics of cancer growth by taking into account the noise is another emergent area of research in the field of biological complexity [18,19]. The relative rate of neoplastic cell destruction, for example, is a random process due to the action of cytokines on the immune systems and could be modeled as a random dichotomous noise in models of tumor growth. The elaboration of new models for cancer growth dynamics is a challenge for theoretical physics and at the same time may lead to new experiments in this subject area. The problem of target search of the specific binding site on a genome by a transcription factor [20] and that of the mean first passage time analysis to describe the dynamics of the complex free energy landscape of protein folding are two open problems with high research impact in ecological complex systems [21,22].

To study ecological dynamics and their spatiotemporal structures numerical approaches have been used in order to address the specific mechanisms which are responsible for the emerging patterns (spatial, temporal or both). Early numerical studies used mean field nonlinear models, with notable example the Lotka-Volterra model and its many off-springs, to address the spatial and temporal complexity of predator-prey systems. Similar birth-and-death mean field models were introduced for the study of epidemics, growth models etc... In recent studies, it was realized that mean field models only partially can represent the processes taking place on system in finite dimensions (1, 2, 3 or fractal) and that the finite size of interactions has to be seriously taken into account for a realistic representation of ecological structures. In this respect, discreet ecological models were devised which take into account the specific neighborhood environment, and factors such as noise, external conditions acting locally on the system, local diffusion rules, supports of specific geometry (including fractal supports) etc... [23]. Ideas borrowed from statistical mechanics, nonlinear dynamics, critical phenomena, non-equilibrium physics and chemistry together with detailed simulations have considerably contributed to the understanding of ecological pattern formation processes and its complex dynamics.

2.1 Self-organization

Amplifying communications are a ubiquitous characteristic of group-living animals. The self-organizing patterns associated with resource exploitation in social insects have been addressed theoretically in the paper by Nicolis and Dussutour (p. 379). Emphasis was placed on the transition from individual behaviour where only local information is available, to the collective scale where the colony as a whole becomes capable of choosing between the different options afforded by the multiplicity of the solutions of the underlying evolution laws. The basic mechanisms underlying the phenomena to be considered are: (a) competition between different sources of information, and (b) the occurrence of amplifying interactions between constituent units as reflected by the presence of feedback loops. In particular the response of the ecosystem may switch between the options available in an unexpected way, depending on the initial conditions and the ranges of parameter values considered. A mean field approach incorporating the principal sources of cooperativity was used and complemented by stochastic simulations through Monte Carlo approach. Although obtained in the context of social insect biology, the results of this paper are in many aspects paradigmatic, and they are expected to apply to a variety of other biological processes [24] or artificial systems.

There are two basic types of models designed for Lotka-Volterra systems simulation. The first one is a group of phenomenological macroscopic models based on the ODE description (for example mean-field (MF) models). The second type of models based on various stochastic cellular automata and similar numerical methods provide the direct microscopic simulation of the underlying processes. The Kinetic Monte Carlo (KMC) simulation is one of the most popular among them [25]. KMC enables one to consider all aspects of spatial and temporal dynamics of the system and therefore can serve as a more adequate tool for the analysis of ecological models. A Lattice Lotka-Volterra (LVV) model on a square lattice under external influence called "long range mixing" is presented in this issue by Shabunin and Efimov (p. 387). It consists of a random shuffling of the species across the lattice space. Such a *mixing* increases the uniformity of the units distribution on the lattice and changes the character of spatio-temporal processes on it. The LLV system on a square lattice with local random interconnections can be synchronized by external long-range mixing of sufficiently small intensity. This phenomenon has a threshold character: there is a critical value of the mixing force after which the behavior of the system is dramatically changed. On the macro-level it is observed as birth of periodic oscillations after a super-critical Hopf bifurcation. The amplitude of the induced oscillations is well defined by the mixing rate and is insensitive to the initial conditions and the lattice size variations. The observed behavior essentially differs from that predicted by the Mean-Field model which is conservative.

Complexity theory and associated methodologies are transforming ecological research, providing new perspectives on old questions as well as raising many new ones.

Patterns and processes resulting from interactions between individuals, populations, species and communities in landscapes are the core topic of ecology. Complex natural networks often share common structures such as loops, trees and clusters, which contribute to widespread processes including feedback, non-linear dynamics, criticality and self-organization. Ecologists have long noted that the distribution, abundance, and behavior of organisms are influenced by interactions with other species. The complexity and the stability of ecosystems, the study of food webs gained momentum in the late 1970s and early 1980s. Then new issues arise in ecology, such as environmental change, spatial ecology and biodiversity. Experiments on pond food webs show that the effects of species on ecosystem processes depend on the interplay between environmental factors and trophic position. In ecosystems, and in particular in food webs, the abovementioned common structures have strong implications for their stability and dynamics. Actually, a food web constitutes a special description of a biological community with focus on trophic interactions between consumers and resources [26]. Food webs are deeply interrelated with ecosystem processes and functioning since the trophic interactions represent the transfer rates of energy and matter within the ecosystem, in which the trophic webs are the result of the interaction of different subgroups or *modules*. Recently an efficient *dynamical clustering* (DC) algorithm for identification of modules in complex networks, based on the desynchronization properties of a given dynamical system associated to the network was proposed in reference [27]. Pluchino, Rapisarda, and Latora in this issue (p. 395) apply the DC algorithm to a well-known food web of marine organisms living in the Chesapeake Bay, situated on the Atlantic coast of the United States. By implementing the DC algorithm and using several dynamical systems, such as Rössler, Kuramoto, opinion changing rate model (OCR), the authors are able to discover community configurations with values of modularity higher than that calculated for the reference configuration related to the main subdivision of the Chesapeake Bay network in Benthic and Pelagic organisms. The DC algorithm is able to perform, therefore, a very reliable classification of the real communities existing in the Chesapeake Bay food web.

3 Bioinformatics

Non protein-coding RNAs (ncRNAs) are a research hotspot in bioinformatics, in fact recent discoveries have revealed new ncRNA families performing a variety of roles, from gene expression regulation to catalytic activities. In a very recent past, RNAs were considered mere intermediates between the genome and the proteins. Recent discoveries involving a variety of new ncRNA genes, biological roles and action mechanisms have shown that the diversity and importance of ncRNAs were underestimated. Non-coding RNA (ncRNA) genes produce functional RNA molecules rather than encoding proteins. Non-coding RNAs seem to be particularly abundant in roles that require highly specific nucleic acid

recognition without complex catalysis, such as in directing post-transcriptional regulation of gene expression or in guiding RNA modifications [28,29]. Nowadays, it is known that functional RNAs that do not code to proteins perform important roles. They are involved in several cellular activities such as gene silencing, replication, gene expression regulation, transcription, chromosome stability, protein stability, translocation and localization and RNA modification, processing and stability. RNA regulatory secondary structures have been detected in almost all living organisms ranging from viruses to Homo sapiens. The earliest discoveries of their regulatory role have been performed in model organisms such as the little worm C. elegans and in studies of the interaction between plants and viruses. Small noncoding RNA regulatory sequences are often characterized by the presence of hairpin structures. A comprehensive study on 1832 segments of 1212 complete genomes of viruses is presented here by Spanò, Lillo, Miccichè, and Mantegna (p. 323). The authors show that in viral genomes the hairpin structures of thermodynamically predicted RNA secondary structures are more abundant than expected under a simple random null hypothesis. The detected hairpin structures of RNA secondary structures are present both in coding and in noncoding regions for the four groups of viruses investigated in this comprehensive study. For all groups hairpin structures of RNA secondary structures are detected more frequently than expected for a random null hypothesis in noncoding rather than in coding regions. Differently from previous results obtained by the authors, they observe that the detected hairpin structures are preferentially located in the noncoding regions. However, at least in herpesviruses, the degree of evolutionary conservation of these structures is more pronounced in coding than in noncoding regions.

The idea that bacteria are simple solitary creatures stems from years of laboratory experiments in which they were grown under artificial conditions. Under the demands of the wild, these versatile life forms work in teams, in association and dynamic communications. Bacteria can self-organize into hierarchically structured colonies of 10^9 to 10^{12} bacteria, each utilizing a great variety of biochemical communication agents, such as simple molecules, polymers, peptides, complex proteins, genetic material and also viruses [10,30]. Ben-Jacob in this issue (p. 315) shortly reviews his far-reaching work on social behavior of bacteria in colonies, guided by the assumption that they might shed new light on the foundations and evolution of Biocomplexity. To face changing environmental hazards, bacteria resort to a wide range of cooperative strategies. They alter the spatial organization of the colony in the presence of antibiotics for example. Bacteria form complex patterns as needed to function efficiently. Bacteria modify their colonial organization in ways that optimize bacterial survival. Bacteria, Ben-Jacob argues, have collective memory by which they track previous encounters with antibiotics. They collectively glean information from the environment, communicate, distribute tasks, perform distributed information processing and learn from past experience. Bacteria are *smart* in their use of cooperative behaviors that enable them to collectively sense the

environment. The author proposes a striking hypothesis: bacteria use their genome computation capabilities and genomic plasticity to collectively maintain exchange of meaning-bearing chemical messages (semantic), and dialogues (pragmatic) for purposeful alteration of colony structure and even decision-making, features that are associated with intelligence. Collectively bacteria store information, perform decision make decisions (e.g. to sporulate) and even learn from past experience (e.g. exposure to antibiotics), features we begin to associate with bacterial social behavior and even rudimentary intelligence. In other words, bacteria must be able to sense the environment and perform internal information processing for thriving on latent information embedded in the complexity of their environment.

Symbolic sequences are investigated in many different fields, including information theory, biological sequence analysis, linguistics, chaotic time series, and communication theory. Many efforts have been devoted to devise methods for generating univariate or multivariate sequences with given statistical properties [31]. In the paper by Tumminello, Lillo, and Mantegna (p. 333) in this issue, a method to generate multivariate series of symbols from a finite alphabet with a given hierarchical structure of similarities based on the Hamming distance is introduced. The method presented here is based on a generating mechanism that does not make use of mutation rate, which is widely used in phylogenetic analysis. Interesting extensions of the proposed method are the possibility of generating symbolic sequences with correlations between different sites, useful to reproduce dependencies between different sites of DNA, proteins, etc.., and of assessing the role of the finite length of the series in discovering the true phylogeny.

4 Population dynamics

In the present-day context of global warming and habitat destruction, there is an enhanced general interest in the impact of environmental changes on biological populations evolution. A simple-model population, whose individuals react with a certain delay to temporal variations of their habitat, is presented in this issue by Bena Coppex, Droz, Szwabiński, and Pękalski (p. 341). In the case of a smooth variation of the environment, it was found that, in general, for populations with small mutation amplitudes it is more beneficial, in terms of the survival chance, to be slow-reacting than to answer instantaneously to the variations of the environment. However, for intermediate and large mutation amplitudes, faster reactions are preferable to slower ones. In case of a very-rapidly oscillating environment, the rapidity of reaction influences only slightly the survival chances.

The processes with some combination of randomness and periodicity occur very often in nature. Life exists in the form of cycles, but they never have exact period and amplitude. Chichigina (p. 347) proposes in this issue a new model to describe the population cycles in small rodents (lemming) of the north regions, like North America

and Siberian tundra. This model contains a noise source with memory. Multiannual lemming density fluctuations are presented as a pulse sequence, which correspond to the peaks of lemming density. The memory is presented as some delay time after each pulse. Parameter of periodicity, average period, correlation function and parameter of synchronization are calculated for different places of North America. Examples of equations modeling population dynamics of lemmings (or their predators) are considered. A model of connected oscillators gives the qualitative explanation of synchronization effects and relation between synchronization and periodicity. This model is also a very useful tool for modeling quasi-periodical nature processes.

The epidemic spread via a contact infection process in an immobile population within the Susceptible-Infected-Removed (SIR) model is analyzed in the paper by Naether, Postnikov, and Sokolov (p. 353). This model describes a population consisting of three kinds of individuals, namely the susceptible (S), the infected (I), and the recovered/removed (R) ones. The transitions between these states are governed by the infection transmission rate and the characteristic recovery time. Both deterministic macroscopic (through a partial differential equation (PDE)) and stochastic microscopic (Monte-Carlo) approaches are applied. It is shown, that the continuous description is not valid for small numbers of cells states. The results of Monte-Carlo simulations also reveal the conditions of applicability of the PDE approach.

The Verhulst model, which is a cornerstone of empirical and theoretical ecology, is one of the classic examples of self-organization in many natural and artificial systems [32]. In the theoretical paper by Dubkov and Spagnolo (p. 361), the transient dynamics of the Verhulst model perturbed by arbitrary non-Gaussian white noise is investigated. Based on the infinitely divisible distribution of the Lévy process [33], the nonlinear relaxation of the population density for three cases of white non-Gaussian noise is analyzed: (i) shot noise; (ii) noise with a probability density of increments expressed in terms of Gamma function; and (iii) Cauchy stable noise. Exact results for the nonstationary probability distribution in all cases investigated are obtained. For the Cauchy stable noise the exact analytical expression of the nonlinear relaxation time is derived. Due to the presence of a Lévy multiplicative noise, the probability distribution of the population density exhibits a transition from a trimodal to a bimodal distribution in asymptotics, and the nonlinear relaxation time as a function of the Cauchy stable noise intensity shows a nonmonotonic behavior with a maximum.

Population biologists use time-series data to infer the factors that regulate natural populations and to determine when populations may be at risk of extinction. Often, however, only a few of the systems variables can be measured, while the rest of the variables remain unobservable, or *hidden* [34]. Luchinsky, Smelyanskiy, Millonas, and McClintock (p. 369) in their paper addressed the problem of how to infer the unmeasured predator dynamics, as well as the parameters of the nonlinear stochastic dynamical models. As an example of how to solve a long-standing ecological problem, the authors inferred an unobservable preda-

tor trajectory, and parameter values, for a predator-prey model by analysis of measurements of the prey dynamics that were (as is typical) corrupted by noise.

5 Motion of proteins and motor protein

An overview over recent studies on the model of Active Brownian Motion (ABM) [35] together with applications of ABM to ratchets is given in the paper by Fiasconaro, Ebelin, and Gudowska-Nowak (p. 403). The system has been studied under the influence of smooth ratchet potentials: symmetrical (sinusoidal potential) and not symmetrical (Mateos-type potential and tilted ones). The system presents bifurcations of the asymptotic velocity as a function of the energy transfer parameter, and three dynamical regimes: 1) relaxation in a potential minimum (vanishing motion); 2) oscillating motion in a well (limit cycle), and 3) flux motion with two values of the asymptotic velocity. The motion in the flux regime is then possible in two directions, even in the presence of a tilted potential. The numerical simulations of the system under the action of white Gaussian fluctuations show the effect of noise-controlled directionality of the motion. Possible applications of the ABM system in modelling molecular motors connected to the ATP synthesis/ hydrolysis have been briefly discussed [36].

Over the past decades increasingly sophisticated techniques have been developed to follow motor protein motion and manipulate it. Processive motor proteins are tiny engines that utilize the energy released in ATP hydrolysis to literally move in a hand-over-hand fashion along a biopolymer [36,39]. Kinesin, for instance, is a dimer, consisting of two units of about 350 amino acids, that moves along microtubule. Kinesin helps maintain cell organization by pulling organelles and chemical-filled vesicles to and from different parts of the cell. In the Bier's paper (p. 415) a simple and intuitive model for chemo-mechanical energy transduction is presented, that can quantitatively account for back-stepping measured rates by experimentalists. The concept of an overdamped Brownian stepper includes few adjustable parameters, leads to a consistent accounting for the energy of ATP hydrolysis, and makes some measured data derivable as implications of other measured data.

Protein molecules represent the final result of genetic expression, and through their functions, they control key reactions in ecological processes performed by microorganisms in aquatic, terrestrial and certain artificial environments. Strategic analysis of microbial proteins to elucidate microbial diversity and ecosystem-level activities in the environment require an appreciation of complexity inherent in protein structure [37]. Based on observations that proteins can readily be detected as components of dissolved organic matter, one can use the protein analysis in ecology and environmental sciences focusing on terrestrial ecosystems [38]. Vibrational spectroscopy is a powerful tool to study the functional activity of proteins. In the experimental paper by Brandt, Chikishev, Dolgovskii, Kargovskii, and Lebedenko (p. 419), the low-frequency

vibrational motions in proteins are analyzed, by discussing the underlying physical mechanisms. The damping of these motions and the effect of solvent molecules is experimentally studied by Raman spectroscopy, by discussing their possible effect on the protein functioning.

6 Interdisciplinary physics

Although the functional role and precise physiological basis of cardio-respiratory interactions are still being revealed, it has been shown that this interaction changes between different states, such as during anæsthesia. Phase transitions like phenomena in synchronization have been shown to occur in rats as their depth of anæsthesia varies. Transitions between different orders of synchronization can potentially yield information about the couplings and their evolution with time. Kenwright, Bahraminasab, Stefanovska, and McClintock (p. 425) show in their paper in this issue, that even during a steady state, such as in repose, cardio-respiratory phase transitions exist and changes occur between close orders of synchronization ratios. Exercise not only perturbs the oscillators but also their interactions, which manifest as a temporary reduction in synchronization. The cardiac and respiratory frequencies were extracted from ECG and respiration signals by use of marked events. The analysis was based on the phase dynamics approach introduced by Kuramoto [40] and its subsequent applications to synchronization analysis. By using a phase-coupled model with low-frequency noise, the authors show that synchronization transitions are mainly due to the presence of low-frequency fluctuations resulting from the activity of lower-frequency oscillatory components.

Although cancer is a leading cause of death in the world, it is still little known about the mechanisms of its growth and destruction. A detailed theoretical study on the mechanisms of interaction between tumor tissue and immune system is necessary for planning efficient strategies of treatment. In the paper by Fiasconaro, Ochab-Marcinek, Spagnolo, and Gudowska-Nowak (p. 435) a mathematical model describing the growth of tumor in the presence of the immune response of a host organism is investigated. The model, based on a reaction scheme representative of the catalytic Michaelis-Menten scenario [19], is supplemented with periodic treatment and external fluctuations in the tumor growth rate. The resulting phenomenological equation modelling cell-mediated immune surveillance against cancer exhibits bistability. The two stationary points correspond to the state of a stable tumor and the state of its extinction. A quantitative analysis of mechanisms responsible for optimization of periodic tumor therapy in the presence of spontaneous external noise is given. Studying the behavior of the extinction time as a function of the treatment frequency, the authors found the typical resonant activation effect: For a certain frequency of the treatment, there exists a minimum extinction time.

Physical and biological systems are continuously perturbed by random fluctuations produced by noise sources always present in open systems. Noise can be responsible for several interesting and counterintuitive effects, such as resonant activation (RA) [41,42] and noise enhanced stability (NES) [43,44]. Valenti, Augello, and Spagnolo (p. 443) analyze the occurrence of these noise induced effects RA and NES in the dynamics of a FitzHugh-Nagumo (FHN) system subjected to autocorrelated noise, by finding meaningful modifications of these phenomena due to the colored noise. In particular for strongly correlated noise, the suppression of NES effect and persistence of RA phenomenon, with an efficiency enhancement of the neuronal response, is observed. The self-correlation of the colored noise causes a reduction of the effective noise intensity, which appears as a rescaling of the fluctuations affecting the FHN system.

The functionality of a complex biological system depends on the correct exchange of information between the component parts. In natural systems the environmental noise always affects the signal that carries the information. Usually high levels of noise make difficult to reveal signals, so that in everyday life the noise is generally considered harmful in detecting and transferring information. Under specific conditions, the noise can constructively interacts with the system, so that effects induced by the noise, such as stochastic resonance (SR), can improve the conditions for signal detection. The experimental paper by Spezia, Curcio, Fiasconaro, Pizzolato, Valenti, Spagnolo, Lo Bue, Peri, and Colazza (p. 453) in this issue reports on experiments conducted on the response of *Nezara viridula* (L.) (Heteroptera Pentatonide) individuals to sub-threshold signals. By investigating the role of the noise in the vibrational communications occurring during the mating behavior of *N. viridula*, the authors find evidence of stochastic resonance phenomenon [3,45]. In particular the behavioural activation of the green bugs, described by the Source-Direction Movement Ratio, has a nonmonotonic behaviour with a maximum as a function of the noise intensity. This maximum represents the optimal noise intensity which maximizes the efficiency of the sexual communication between individuals of *N. viridula*. This behavior appears as the signature of the soft threshold stochastic resonance [46]. There is a suitable noise intensity which maximizes the behavioral response of the green bugs and this effect can be described by a soft threshold model which shows the stochastic resonance phenomenon [47,48].

Almost all the processes that determine the properties of the ocean take place at the sea surface and are related to the interactions between the atmosphere and the ocean. The air-sea fluxes of momentum, water and heat are of particular importance, in relation to the patterns of currents, salinity and temperature. The importance of the physical and chemical processes of the sea on the reproductive biology of fishes (European anchovy) in the central Mediterranean is shown in the experimental paper by Grammauta, Molteni, Basilone, Guisande, Bonanno, Aronica, Giacalone, Fontana, Zora, Patti, Cuttitta, Buscaino, Sorgente, and Mazzola (p. 459) in this issue. The air-sea fluxes, the sea surface temperatures, and in less

extent the wind induced turbulence, may be considered proxies of a favorable anchovy spawning sites, where adult specimens may meet optimal environmental features for reducing the mortality of the spawning products.

7 Conclusions

The present issue aimed to gather together scientists studying different ecological structures, with different points of view and backgrounds, ranging in space and time scales from microscopic bacterial growth, to cancer growth and to fish dynamics and exhibiting temporal regular and irregular oscillations which may be due to the intrinsic dynamics or caused by external sources and modulated by noise. We hope that the readers of this issue should assess the current status of this research field, should be able to determine (a) the problems to be attacked theoretically and numerically, and (b) the best theoretical and numerical models to be used in each particular case. We expect that the experimental physicists receive new suggestions and ideas for their research by reading this special issue. From experimental and theoretical points of view recent advances in the fields of bacterial growth, RNA structure in virus genome, tumor development, social behavior in animal groups, competing species in various spatial geometries, epidemics spreading, and other ecological topics have been presented in this topical issue. Specifically the following specific topics were addressed: self-organization in ecosystems, social behavior of bacteria, cooperative phenomena, noise induced transitions, patchiness, clustering and heterogeneity, effects of initial and boundary conditions, external control of pattern formation, noise induced phenomena and stochastic dynamics of out of equilibrium systems. A broad range of new results on ecological complex systems are reported, establishing the state of the art of the field. The workshop *"Ecological Complex Systems: Stochastic Dynamics and Patterns"* has succeeded in providing a forum for the exchanges of ideas between experimentalists, theoreticians and modellers and cross-fertilization between the different ecological topics, by contributing essentially in this way to the development of the field.

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