

Crossroads in Complex Systems

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BOOK OF ABSTRACTS



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Keynote talks

Parsimonious Rules in Complex Marine Ecosystems

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Complexity is inherent to biological systems and embedded at all levels of organization in marine ecosystems. In this keynote I will provide an overview of Parsimonious Rules capturing essential features of complexity across a range of Marine Ecosystems. I will summarize insights into the structure of networks in marine ecosystems, and how they can be used to examine properties and stability of meta-populations and food webs, scaling laws capturing quasi-universal patterns of organization and dynamics in marine ecosystems, and complex patterns emerging from simple rules that govern landscape formation and dynamics across marine ecosystems. This keynote summarizes two decades of cross-disciplinary collaboration between marine ecologists and scientists focussed on complex systems at IFISC, and will provide some reflections on the keys to successful collaboration toward advancing our understanding of marine ecosystems.

Quantum Brownian Motion Revisited

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Brownian motion in an inhomogeneous medium has been recently studied in the context of classical Brownian motion (CBM) and other classical diffusive systems. Precisely, explicit formulas were derived for noise-induced drifts in the small-mass (Smoluchowski-Kramers [1, 2, 3] and other limits).

In a series of papers [4, 5, 6] we analyzed the microscopic model of quantum Brownian motion, describing a Brownian particle interacting with a bosonic thermal bath, through a coupling which is linear in the creation and annihilation operators of the bath, but may be a nonlinear function of the position of the particle. Physically, this corresponds to a configuration in which damping and diffusion are inhomogeneous, namely they vary in space.

In [4] we derive systematically the quantum master equation for the Brownian particle in the Born-Markov regime, discussing the appearance of additional terms for various polynomial forms of the coupling. We pay particular attention to the cases of linear and quadratic coupling, studying, by means of a Wigner function techniques, the stationary state of a Brownian particle in a harmonic trapping potential. We predict quite generally Gaussian stationary states, and we compute the aspect ratio and the spread of the distributions. In particular, we find that these solutions may be squeezed with respect to the position of the Brownian particle, corresponding to its high spatial localization. We further describe the dynamical stability of the system, by applying a Gaussian approximation to the time-dependent Wigner function, and we calculate the decoherence rates of coherent quantum superpositions in position space. Part of the work is devoted to analyze various restrictions to the validity of our theory posed by Born and Markov approximations, leading to a breakdown of positivity of the density operator at very low-temperature and strong coupling, associated to a violation of the Heisenberg principle.

To overcome the violation of the positivity of the solution of a Born-Markov master equation in [4], we recall a Lindblad one, constructed in order to be free of such a problem. The results have been presented in [5]. We study the dynamics of the model, including the detailed properties of its stationary solution, for both linear and non-linear coupling of the Brownian particle to the bath, focusing in particular on the correlations and the squeezing of the probability distribution induced by the environment.

An immediate application of the theory of quantum Brownian motion in an inhomogeneous medium concerns the problem of an impurity in an ultracold gas, intensively studied in the context of Bose polaron. This is the purpose of the work in [6]. Here we treat the dynamics of the system by means of Heisenberg equations, in order to go beyond the approximations in [4, 5]. We solve these equations, looking to the position variance of the impurity, that may be mea-

sured in experiments for the present system. We distinguish the situation where the impurity is trapped in a harmonic potential and the case where there is no trap. In the first case, the impurity approaches an equilibrium, and its final stationary state genuine position squeezing, corresponding to high spatial localization (Fig. 1). In the situation in which there is no trap, the impurity does not approach an equilibrium. Here the position variance depends on time, and it manifests a super-diffusive behavior, precisely $\langle x^2 \rangle \sim t^2$. Such a feature represents a consequence of the presence of memory effects.

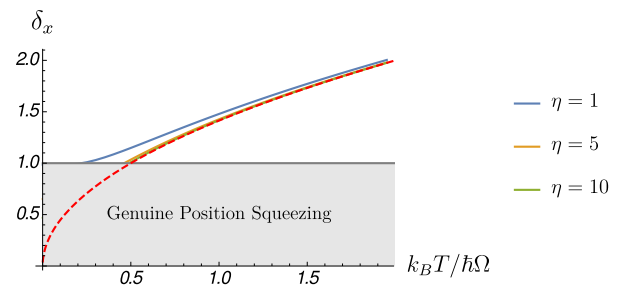


Figure 1: Temperature dependence of the position variance of an impurity of K trapped in a harmonic potential with $\Omega = 2\pi \cdot 250\text{Hz}$, in a gas made up by Rb with a density of $n_0 = 7(\mu\text{m})^{-1}$ and a coupling strength among the atoms $g_B = 2.36 \cdot 10^{-37}\text{Jm}$. The lines refer to different value of $\eta = g_{IB}/g_{BB}$, where g_{IB} is the coupling constant related to the interaction between the impurity and the atoms of the gas.

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Seeing the Light – at the end of the tunnel?

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Seeing the light is no simple task – it is accomplished with a complex system consisting of our eyes and brain, which we are only beginning to understand in a rudimentary way. This is certainly good news – there is so much interesting science left to do and so many interesting discoveries to make, experimentally and theoretically. We will look at a few examples to illustrate these points, the highly interdisciplinary nature of the problems, and tools needed to begin to unravel them. We will conclude with a description of experiments to probe the transition from randomness to determinism in a simple system, entropy production and random number generation.

Contagion Processes in Complex Systems

Alessandro Vespignani

Northeastern University, Boston, MA, USA

Recent years have witnessed the development of data driven models of contagion processes rooted in the combination of large-scale data mining techniques, computational approaches and mathematical modeling. Although these models are increasingly used to support public-health decisions they are often under debate by only considering their value as forecasting tools. Here I will discuss, by using specific modeling examples, how computational models can be used in real time to provide situational awareness, intervention planning and projections, and the identification of factors that fundamentally influence the course of contagion processes.

Levels of Reality in Weather Forecasting: the Lesson by Richardson and Von Neumann

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At first glance weather forecasting appears just a topic of practical relevance. An analysis of its main aspects shows the presence of conceptual topics which are rather interesting in complex systems:

- a) limits of extreme reductionism;
 - b) limits of naive inductivism;
 - c) relevance of old (apparently very far) classical issues;
 - d) role of models at different scales;
 - e) importance of the proper level of description.
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Solicited talks

Collective Phenomena Emerging from the Interactions Between Dynamical Processes in Multiplex Networks

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Networks are a powerful way to model and study a wide variety of complex phenomena [1]. In the recent years, the study of collective dynamical processes on complex networks has improved our understanding of many complex systems and shed light on a wide range of physical, biological and social phenomena including synchronization, disease spreading, transport and cascades. Of particular interest in these works is the interplay between the structure of the network and its dynamics [2]. In fact, the topology of a network has an effect on the dynamical processes that take place over the network, while some properties of the dynamics can reveal important information on the interaction network [3, 4]. Understanding the relations between structure and dynamics can provide a solid foundation for modeling, predicting, and controlling dynamical processes in the real world. However, save for a few notable exceptions, the majority of the studies so far have considered a single process on a single network, ignoring a very important ingredient: often the components of a complex system interact through two or more dynamics at the same time, and these dynamics usually depend on each other in highly non-trivial ways.

In this work we propose a general framework for modelling, through a multiplex network, the *coupling of dynamical processes* of the same type (e.g. the spreading of two coupled diseases) or of different types (for instance a synchronization dynamics and a diffusion process). Moreover, we demonstrate with a specific example that this coupling mechanism can give rise to the emergence of complex phenomena generated by the interactions between the different dynamical processes.

The natural way to consider M interacting dynamical processes taking place over a complex system is to use a multiplex network with M layers. Each layer contains the same number of nodes, N , and there exists a one-to-one correspondence between nodes in different layers, but the topology and the very same nature of the connections at each layer may be different. We then assign a different dynamical process to each layer. Considering for simplicity the case $M = 2$, we assume that the dynamics of the entire system is governed by the following equations:

$$\begin{cases} \dot{x}_i = F_{\omega_i}(\mathbf{x}, A^{[1]}) \\ \dot{y}_i = G_{\chi_i}(\mathbf{y}, A^{[2]}) \end{cases} \quad i = 1, 2, \dots, N \quad (1)$$

where $\mathbf{x} = \{x_1, x_2, \dots, x_N\} \in \mathcal{R}^N$ and $\mathbf{y} = \{y_1, y_2, \dots, y_N\} \in \mathcal{R}^N$ denote the states of the two dynamical processes, while the topologies of the two layers are encoded in the adjacency matrices $A^{[1]} = \{a_{ij}^{[1]}\}$ and $A^{[2]} = \{a_{ij}^{[2]}\}$ respectively, such that $a_{ij}^{[1]} = 1$ ($a_{ij}^{[2]} = 1$) if a link exists between nodes i and j in the first (second) layer, and $a_{ij}^{[1]} = 0$ ($a_{ij}^{[2]} = 0$) otherwise. The dynamical evolution of the two network processes is ruled respectively by the functions F_{ω} and G_{χ} , which depend on the sets of

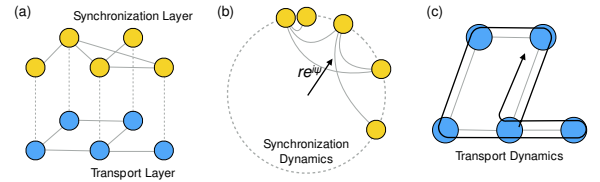


Figure 1: **Intertwined dynamical processes.** (a) An example of a two-layer multiplex of $N = 5$ nodes with neural synchronization dynamics at layer 1 (top), and transport dynamics at layer 2 (bottom). (b) The neural activity is described by the Kuramoto model, and the degree of synchronization is measured by the order parameter r . (c) The transport dynamics is modelled by biased random walkers. The two dynamical processes are bidirectionally coupled, as the natural frequencies of the oscillators at layer 1 depend on the distribution of random walkers at layer 2 and, at the same time, the random walkers are biased on the degree of synchronization of the nodes at layer 1.

parameters ω and χ , so that the state x_i (y_i) of node i at the first (second) layer is a function of the state \mathbf{x} (\mathbf{y}) and of the topology $A^{[1]}$ ($A^{[2]}$) of the first (second) layer. The key ingredient that connects the two dynamical processes is provided by the nature of the correspondence *between layers*. In fact, the parameter ω_i in function F_{ω_i} at layer 1 is itself a function of time which depends on the dynamical state y_i of node i at layer 2, while the parameter χ_i at layer 2 depends on the state x_i of node i at layer 1. Namely, we have:

$$\begin{cases} \dot{\omega}_i = f(\omega_i, y_i) \\ \dot{\chi}_i = g(\chi_i, x_i) \end{cases} \quad i = 1, 2, \dots, N \quad (2)$$

where f and g are two assigned functions.

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Epidemic Risk Evaluation From (Incomplete) Proxies of Contact Network Data

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Face-to-face contacts between individuals play an important role in social interactions and can also determine the potential transmission routes of infectious diseases, in particular of respiratory pathogens. An accurate description of these patterns is therefore of interest for the fundamental knowledge and understanding of human behaviour and social networks as well as in epidemiology, in order to identify contagion pathways, to inform models of epidemic spread, and to design and evaluate control measures such as the targeting of specific groups of individuals with appropriate prevention strategies or interventions.

An increasing number of datasets describing contacts between individuals in different contexts has become available. These datasets have been obtained using either surveys or wearable sensors that can detect contacts or simply co-presence, at varying resolution. Data are moreover often incomplete or biased, due on the one hand to population sampling and on the other hand to underreporting or bad estimation of contact durations for surveys. The low spatial resolution of co-presence data might moreover be insufficient to feed data-driven models. In this talk, I will review recent progresses in the understanding of how even incomplete, biased or low-resolution data can bias the outcome of simulations of epidemic spreading processes, and in the development of methods to compensate for such biases.

Dynamics of Opinions about One-self and Others

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We consider a model of N agents, each characterized by an opinion about itself and all the others, represented by a real number between -1 (very bad opinion) and $+1$ (very good opinion). The agents meet by randomly chosen pairs and influence each other's opinions through two processes: (i) vanity: agents increase their opinion of agents that value them highly and decrease their opinion of agents and undervalue them (ii) gossiping: agents propagate their opinions about other agents they know, in particular about themselves and about the agent they are talking with. The model includes two main additional hypotheses: (i) agents have a noisy access to the other's opinions, with a uniform symmetric noise (ii) agents adopt more easily the opinions of the agents that they highly value. We study more particularly the case where the vanity process dominates over the opinion propagation. In this case, the opinions converge to a pattern in which each agent has a small set of "friends" (agents which are valued close to $+1$) and all the others are "enemies" (agents which are valued close to -1). The network of friends tends to show the characteristics of a small world. Moreover, all the agents have a positive opinion of themselves. We unfold the interaction processes leading to this pattern, particularly the asymmetry between "friends" and "enemies". We finally discuss rapidly a different pattern showing cycles where the agents lose all their friends and their positive self-opinion and then manage to make friends again and restore their positive self-opinion.

Taming Light in Complex Aperiodic and Accelerating Photonic Lattices

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Artificially tailored photonic structures are one of the most promising concepts for the realization of functional optical systems capable to control, route and steer light accompanied with a manifold of integrated functionalities. In contrast to light propagation in prefabricated permanent structures, an increased flexibility can be achieved when light itself induces its own structure through the nonlinear response of the material. This so-called optical induction of refractive index modulations represents a highly versatile, flexible, and scalable approach to structure photosensitive materials. Photonic graphene, photonic quasicrystals and photonic random lattices are among the versatile lattices with specific band gap structures that have been successfully employed to demonstrate quantum effects. Moreover, the interplay between periodicity and nonlinearity in these structures has been shown to cause a variety of fascinating nonlinear effects, among them discrete solitons, Zener Tunneling and Bloch oscillations..

In our contribution, we present various approaches enabling the fabrication of aperiodic to random, spiral, or accelerating lattices. The resulting functional photonic systems are subsequently used to probe complex light propagation such as chiral or vortex-bearing light fields carrying orbital angular momentum. The light-matter interaction results in striking effects as oscillating solitons, Anderson localization and coherent backscattering, or controlled self-acceleration in Airy and caustic lattices.

Crossroads of Marine Megafauna Movement

Víctor M. Eguíluz

Instituto de Física Interdisciplinar y Sistemas Complejos, IFISC (CSIC-UIB),
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Technological advances offer new insights into human activity and movement, but also to animal movement thanks to the development of new sensors. We will present opportunities open in marine megafauna movement at the interface with complex systems.

Employing Complex Photonics for Neuro-inspired Information Processing

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We are currently witnessing a revolution in computing. For decades electronic computers, based on the concept of the von-Neumann machine, dominated computer hardware. The validity of Moore's law for more than five decades illustrates the enormously fast development. But the increasing demands on information processing, the physical limitations in transistor size and the power consumption of electronic computers call for alternative concepts and alternative hardware. Bringing together ideas from neuroscience, complex systems, machine learning and photonics is offering new fascinating opportunities to explore new concepts and to gain a new perspective on information processing. We deliberately choose a minimal design approach [1], allowing for the implementation of neuro-inspired computational concepts on different hardware platforms.

We present an architecture based on a nonlinear system, implemented by a nonlinear node with delayed feedback. Via time-multiplexing, we can emulate a complex nonlinear network using only a single or few nonlinear nodes [2]. By this reduction of the learning-based methods of Reservoir Computing and Extreme Learning to their bare essentials, we find that nonlinear transient responses of a simple dynamical system enable the processing of information with excellent performance. Our presented system employs a single mode telecommunication laser as nonlinear node. Delayed feedback is realized via a fiber loop mirror. Information can be injected optically by injecting the modulated intensity of a tunable laser. In recent years, we already demonstrated that with this approach we can tackle challenging tasks efficiently and at very high speed [3, 4].

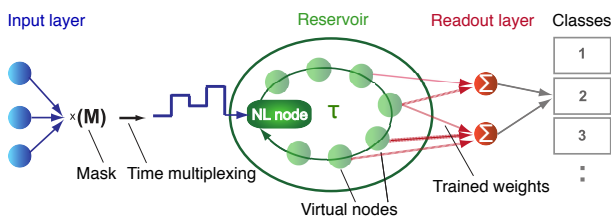


Figure 1: Reservoir computing scheme using a single nonlinear node with delayed feedback and time-multiplexing.

Building on these advances, we explore how this approach can be applied to real telecommunication tasks. To this end, we are investigating the influences of key parameters, including spectral detuning and power of the injected optical information, as well as the bias current of the information processing laser. These parameters affect two key properties, essential for the information processing: consistency and memory. Consistency is the property that the responses to multiple similar information inputs are sufficiently similar. Memory is the ability of the reservoir to keep information about previously injected inputs for a certain number of time steps. We show that both properties can be tuned via

the operating conditions in the experiment. This offers perspectives to adapt the same reservoir computing system to different information processing requirements.

First we show that the system can be tuned to show good performance in a nonlinear prediction task. Moreover, we present how photonic reservoir computing can be employed to perform all-optical information recovery after optical transmission in Ethernet or long-haul transmission systems. We demonstrate processing at input data rates up to 20 Gigasamples per second. Since our system is designed to be compatible with telecommunication hardware, it represents a promising approach to avoid the optic to electronic bottleneck and to perform all-optical information processing. After training our photonic information processing system, we show improved bit error rates (BER) of the detected signal by one order of magnitude, compared to the same benchmark that excludes the reservoir. Simulated reservoirs with shorter time delays that employ optical feedback and utilize the reservoir's memory effects show a further improved performance, while speeding up the all-optical processing.

We discuss, how in the future the time-multiplexing of virtual nodes might be complemented by the implementation of parallel nodes in reconfigurable complex laser networks [5].

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Playing Nice Together: Dynamical Sharing of Limited Resources by Cells

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Living cells are usually faced with situations in which they must share a common pool of limited resources. A standard way of solving this problem is by partitioning the resources among all players. In this talk I will discuss an alternative solution that relies on taking turns in time when utilizing the available resources. I will describe results that show, using a combination of time-lapse microscopy, microfluidics, and mathematical modeling, how bacteria use this time-sharing strategy at the levels of molecules, cells, and cellular populations.

Random Focusing in Complex Media - Can we Forecast Tsunamis?

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Wave flows propagating through weakly scattering disordered media exhibit random focusing and branching of the flow as universal phenomena. Examples are found on many scales from ballistic electron flow in semiconductor nanostructures [1, 2, 3, 4] to tsunamis traveling through the oceans. Even for very weak disorder in the medium, this effect can lead to extremely strong fluctuations in the wave intensity and to heavy-tailed distributions [4]. Besides statistically characterizing random caustics and extreme events by deriving scaling laws and relevant distribution functions we have recently studied the role of random focusing in the propagation of tsunami waves [5]. We model the system by linearized shallow water wave equations with random bathymetries to account for complex height fluctuations of the ocean floor and determine the typical propagation distance at which the strongest wave fluctuations occur as a function of the statistical properties of the bathymetry. Our results have important implications for the feasibility of accurate tsunami forecasts.

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Data Science for Energy Efficiency of Cities

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I present a complex system approach applied to large data sets. I characterize how humans interact with built environment and to plan for better usage of urban resources.

First I present a modeling framework, TimeGeo, that generates individual trajectories in high spatial-temporal resolutions, with interpretable mechanisms and parameters capturing heterogeneous individual travel choices at urban scale. Then I assign these trips to the streets. I demonstrate that the percentage of time lost in congestion is a function of the proportion of vehicular travel demand to road infrastructure capacity, and can be studied in the framework of non-equilibrium phase transitions. In the second part, I In the second part, we address strategies of retrofitting the urban building stock. We propose a novel ranking algorithm that allows the scaling of the buildings' energy consumption from records of energy bills with building footprint and physical attributes of heat losses. Implemented for 6.204 residential buildings in Cambridge, MA, we demonstrate that the proposed ranking algorithm based on the inferred heat loss rate of buildings exhibits a power-law distribution akin to Zipf's Law, which provides a means to map an optimum path for energy savings per retrofit at city scale.

Are There (*Non-Trivial*) Quantum Effects in Biology? A Discussion on Light Harvesting Processes

Susana F. Huelga (presenting group work at Uni Ulm)

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Quantum biology is an emerging field of research that concerns itself with the experimental and theoretical exploration of non-trivial quantum phenomena in biological systems (See [1, 2, 3, 4] for recent reviews on the subject). We will present an overview aimed to bring out fundamental assumptions and questions in the field, using light harvesting as a prototypical biological process. We will identify basic design principles and develop a key underlying theme – the dynamics of quantum dynamical networks in the presence of an environment and the fruitful interplay that the two may enter.

A fundamental element in the discussion is the formulation of a microscopic model able to explain the observed persisting oscillatory features in the spectral response of different pigment-protein complexes at ambient temperatures. Along delocalized electronic excitations, it is now suspected that quantum coherent interactions with near-resonant vibrations are instrumental for explaining long lived coherence and may contribute to light-harvesting performance [5, 6]. Recent experimental results on artificial systems are in agreement with this vibronic model [7, 8].

A different issue though, is providing a quantitative link between coherence and biological function, that is, *proving* the actual quantum advantage offered by such coherent vibrational interactions. A thermodynamical approach is particularly useful in this context, in the sense that it allows the introduction of measures of merit to quantify efficiency that depend explicitly on well defined coherence measures. I will discuss initial steps in this direction by showing how a basic quantum design principle, whereby coherent exchange of single energy quanta between electronic and vibrational degrees of freedom, can enhance a light-harvesting system's power above what is achievable by using thermal mechanisms alone [9].

Vibronic interactions therefore provide a framework able to encompass long lived oscillations and a consistent multidimensional response as well as allowing for a coherence-enhanced measure of efficiency, thus suggesting its wider relevance as an archetypical framework for quantum biology.

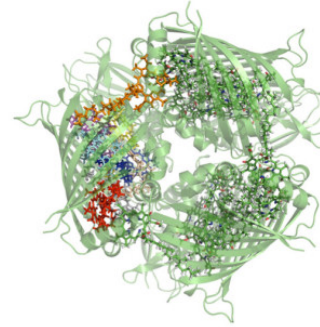


Figure 1: A model system for studying coherent effects in biological light harvesting processes: Structure of the Fenna-Matthew-Olson pigment protein complex, which is found in green sulfur bacteria. Chlorophyll pigments interact via dipole-dipole interaction and are embedded in a protein scaffold that provides a vibrational environment. The multidimensional spectral response of the complex was shown to exhibit oscillatory features on extended timescales, triggering the quest for assessing the actual relevance of quantum coherence in the primary steps of photosynthesis [3].

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Generalized Threshold Model for Social Contagion: Theory, Simulations and Data

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We generalize the Watts threshold model of social contagion by including effects of media and by introducing “frozen” nodes, which never adopt. We show analytically and by simulations that this model can account for the observed broad range of spreading speed. The crossover from slow to fast spreading is accompanied by a percolation phase transition of the induced adopting clusters. The model is calibrated and verified by data from Skype, the World largest Voice over Internet service. Similar mechanism is observed at the collapse of an online social network.

Power Grid Stability

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The human brain, power grids, arrays of coupled lasers and the Amazon rainforest are all characterized by multistability. The likelihood that these systems will remain in the most desirable of their many stable states depends on their stability against significant perturbations, particularly in a state space populated by undesirable states. Here we claim that the traditional linearization-based approach to stability is in several cases too local to adequately assess how stable a state is. Instead, we quantify it in terms of basin stability, a new measure related to the volume of the basin of attraction. Basin stability is non-local, nonlinear and easily applicable, even to high-dimensional systems. It provides a long-sought-after explanation for the surprisingly regular topologies of neural networks and power grids, which have eluded theoretical description based solely on linear stability.

Specifically, we employ a component-wise version of basin stability, a nonlinear inspection scheme, to investigate how a grid's degree of stability is influenced by certain patterns in the wiring topology. Various statistics from our ensemble simulations all support one main finding: The widespread and cheapest of all connection schemes, namely dead ends and dead trees, strongly diminish stability. For the Northern European power system we demonstrate that the inverse is also true: 'Healing' dead ends by addition of transmission lines substantially enhances stability. This indicates a crucial smart-design principle for tomorrow's sustainable power grids: add just a few more lines to avoid dead ends. Further, we analyse the particular function of certain network motifs to promote the stability of the system. Here we uncover the impact of so-called detour motifs on the appearance of nodes with a poor stability score and discuss the implications for power grid design.

Next, it will be shown that basin stability is only a first approach in studying even larger perturbations. Therefore, further techniques based on survivability and maximum thresholds are introduced and discussed.

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Synchronization of Coupled Noisy Oscillators: Coarse Graining from Continuous to Discrete Phases

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The theoretical description of synchronization phenomena often relies on coupled units of continuous time noisy Markov chains with a small number of states in each unit. It is frequently assumed, either explicitly or implicitly, that coupled discrete-state noisy Markov units can be used to model mathematically more complex coupled noisy continuous phase oscillators. Here we present conditions that justify this assumption by coarse-graining continuous phase units. In particular, we determine the minimum number of states necessary to justify this correspondence for Kuramoto-like oscillators.

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Bosonic Complex Quantum Networks: What, When and Why

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What are bosonic complex quantum networks? Do they exist in Nature? Can they be implemented experimentally? In this talk I will present some perspectives on these questions by looking at Hamiltonian models describing complex networks of quantum harmonic oscillators.

I will first show that such systems are very useful for investigating the properties of open quantum systems, namely quantum systems interacting with an environment. This framework considers one of the nodes as the open system and the other nodes of the network as part of the environment. I will show that, changing the properties of the network, it is possible to engineer ad hoc open quantum dynamics by modifying the spectral density of the environment [1]. This is particularly relevant in connection to quantum technologies where understanding and modelling environmental noise is crucial to realise robust and scalable commercial quantum devices.

With a change in perspective to the complementary view point, the node forming the open quantum system can be seen as a local probe from which one can extract certain properties of the network. Remarkably, we show that global properties can be mapped into the time evolution of the probe hence, measuring the latter one, one can extract them. I will focus in particular on the ability to measure the connectivity of the network by local probing [2].

Finally, I will briefly present the main ingredients of an experimental implementation of bosonic complex quantum networks using an optical set up [3]. I will argue that, independently of whether or not these systems exist in Nature, the ability to engineer them experimentally has great relevance to both fundamentals of quantum mechanics and applications such as quantum technologies.

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Modeling Complex Phenomena in Neuronal Circuits

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Although the brain structural architecture has been characterized and studied for over hundred years, the role of brain dynamics has been addressed much less. Models of brain activity can be categorized into a hierarchy of different levels of detail. A detailed model might include specific dependences of the voltage-gated channels to describe neurons and their interactions [1]. A less detailed, but still robust, description would include simple neurons, neural populations or even neural mass models [2]. A whole description of the brain is also possible by using, e.g., the Free Energy Principle for the brain [3].

In this presentation, we opt to use an intermediate approach. Simple models for neurons and synapses are robust enough to qualitatively describe experimental observations, while being computationally less demanding. In what follows, we show results of synchronization in coupled neuronal populations and information transmission in a chain of neuronal layers.

In the first example, we study the transition between delayed (DS) to anticipated (AS) synchronization in two unidirectionally coupled neuronal populations. Each neuron in the population is modeled using the Izhikevich equations [4]. Connectivity within the population is sparse (10%) and we assume 80% excitatory and 20% inhibitory neurons coupled via chemical AMPA and GABA_A synapses. Each neuron is subject to an independent Poisson train mimicking the input of other neurons that are not part of the population. By changing the inhibitory conductance or the oscillating frequency in the receiver population, a transition from DS to AS can occur, as shown in figure 1. This transition explains the counterintuitive results observed in experiments with monkeys performing a visual task. A positive Granger Causality (information flow) from the sender to the receiver area was observed to be accompanied by a negative delay in the activation of both areas [6].

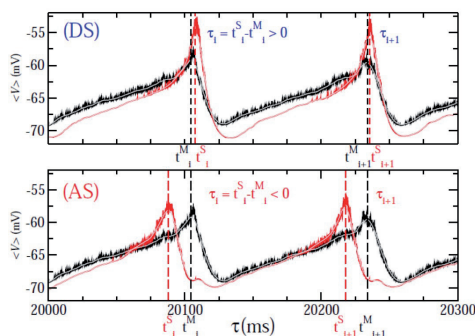


Figure 1: Time evolution of the mean value of the membrane potential of two neuronal populations coupled in a sender-receiver configuration. In the upper (lower) panel we show the case of delayed (anticipated) synchronization between the populations.

In the second example we study the transmission of signals in a chain of 11 mutually-coupled neuronal layers. We find, in the case of symmetric connections, that local perturbations on the dynamics of one layer will propagate in the network, being detected by other nodes, if the node receiving the perturbation has a higher intrinsic frequency. Moreover, we find that high frequency units determine the direction of signal propagation (see Figure 2), and consequently the effective connectivity in such a network.

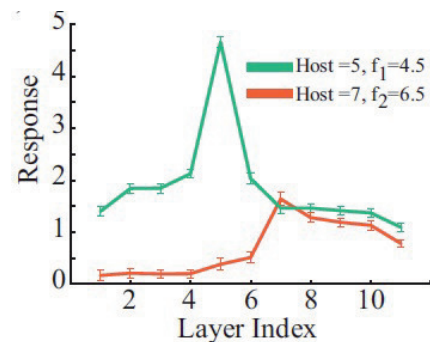


Figure 2: Propagation of signals: one signal with frequency f_1 is injected into the high-frequency layer 5 and another signal with frequency f_2 is injected into another layer with low oscillating frequency (in this case layer 7). It can be seen that the signal injected into layer 5 propagates in both directions while that injected in layer 7 only propagates in the direction opposite to the high frequency node.

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Heating without Heat

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In this talk, we will show that it is possible to increase (or decrease) simultaneously the temperature of two finite systems without any supply of energy [1]. This effect, in apparent contradiction with our basic thermodynamic intuition, can be achieved if the systems exchange particles in a narrow band of energy.

Such a selective exchange of particles does not need the action of any sort of Maxwell demon and can be carried out by passive filters without compromising the second law of thermodynamics. In fact, there are many examples of passive filters based on resonant tunneling, which are currently used in micro-refrigerators and energy transducers [2].

Here we present a detailed analysis of the thermal properties of passive filters using linear irreversible thermodynamics and kinetic theory [1]. We will prove the existence of two time scales when two systems exchange particles through an energy filter with a narrow, but finite, width. First, the global system relaxes to a pseudo-equilibrium state in a relative short time, followed by the relaxation to full equilibrium in a much longer time scale, as shown in Fig. 1. The ratio between these two time scales is given by the width of the filter.

For very narrow filters the second relaxation is very slow and the pseudo-equilibrium state is almost stationary. We will show that this pseudo-equilibrium state exhibits interesting and unexpected properties. Under certain conditions the fast relaxation to the pseudo-equilibrium state comprises the simultaneous increase of temperature of the two finite systems without any external energy supply. In other words, the possibility of “heating without heat”. The opposite, i.e., spontaneous simultaneous cooling, can also occur.

The reason behind these striking behaviors is that temperature is related to the average energy and this average depends both on the total energy and the total number of particles. As in evaporative cooling, temperature can decrease (increase) if particles with high (low) enough energy leave the system [3]. The interplay of this consideration and the selective exchange of particles induces a rich and unexpected phenomenology.

These phenomena could be exploited to design interesting setups with potential applications. For instance, one can use standard infinite thermal reservoirs to set the temperature and density of a finite system and then make them interact through an energy filter. Using this strategy, we have been able to engineer a cycle operating between two reservoirs at temperatures $T_1 < T_2$ that can be converted into an effective reservoir at temperature $T'_1 < T_1$ without the need of any mechanical work [1].

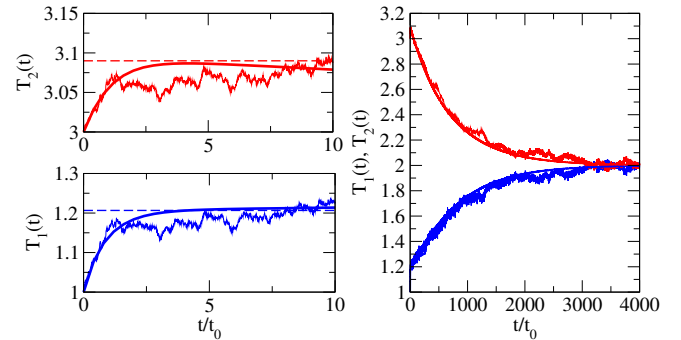


Figure 1: Numerical evolution of the temperatures of the hot $T_1(t)$ (blue) and cold $T_2(t)$ (red) gas as a function of time t , for two-dimensional gases of hard disks. *Left*: Short time evolution, where the system relaxes to the pseudo-equilibrium state (dashed lines indicate the pseudo-equilibrium temperatures). *Right*: Long time evolution, where the system relaxes to full equilibrium.

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How to Compute the Tenuous Force Networks in Amorphous Solids

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Compressed amorphous solids are held by a tenuous network of force chains. The computation of the forces between the constituents is considered an “insoluble problem” because the number of unknowns is larger than the number of constraints. I will show how to solve this problem and how to understand the implications of the solution to the statistical physics of jamming and the modes of failure of amorphous solids.

Periodic energy transport and entropy production in quantum systems

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The understanding of the energy transfer in nonequilibrium open quantum systems is a fundamental problem in physics. The separation of energy in heat and useful work and dissipation is the key for a thermodynamical description. In quantum systems under ac driving, the identification of these different components of energy is a nontrivial task which is paramount to cold atoms, nanomechanical, nanoscale optoelectronic, and mesoscopic electron systems. Typically, the central piece of these systems contains a small number of particles and are driven out of equilibrium, which renders a usual thermodynamical description unreliable. Yet, they are in contact with one or more macroscopic reservoirs with well defined thermodynamical intensive parameters.

Most of the recent literature on quantum thermodynamics focuses on static fields and the resulting stationary transport effects. However, there is a growing interest in analyzing thermodynamic properties of quantum conductors in the presence of time-dependent potentials [1]. In this case, dynamics is the main objective of the theory as fluxes and responses depend explicitly on time. In addition to the interest on fundamental aspects, it is of paramount importance for potential applications to discriminate which portion of the energy invested to operate quantum devices is amenable to be used and which one is wasted by dissipation. This distinction is at the heart of thermodynamics and is conventionally addressed in quasistationary processes where the system under study is very weakly coupled to the reservoirs. In quantum electronics, nevertheless, the generic situation is to have the driven structure strongly coupled to the rest of the circuit, which plays the role of reservoir. On the other hand, we are typically interested on the generation of currents, which implies nonequilibrium situations.

In this talk, I will discuss in detail the energy transfer in out-of-equilibrium systems coupled to external baths. The analysis is based on a phase-coherent mesoscopic sample (a confined system with discrete energy levels) attached to fermionic reservoirs held at a given temperature. In Fig. 1 we schematically show the two terminal case. The energies of the sample evolve with time due to the coupling with nearby ac gate terminals. Deep inside the reservoirs, electrons relax their excess energy and the baths can thus be considered in local thermal equilibrium. We will also consider the entropy production in the whole system and will identify the different terms arising in the redistributed energy and heat [2, 3]. Importantly, when the energies shift slowly with time the response is adiabatic and an exact Joule law can be demonstrated for the time domain. [2] In addition, we will briefly discuss the nonadiabatic regime [4] in which case the ac frequency is larger or of the order of the inverse dwell time inside the conductor. Our analysis is completely general and does not rely on the particular approach followed

to evaluate the relevant dynamical quantities, like the charge and energy fluxes and the rate of entropy production.

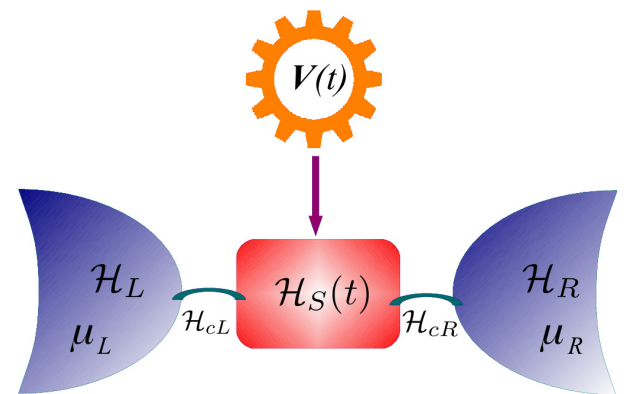


Figure 1: Sketch of the system under consideration. A quantum conductor (described by the Hamiltonian H_S), is coupled to two reservoirs (H_L and H_R) kept at the same temperature T , but with different chemical potentials μ_L and μ_R . The conductor is also driven out of the equilibrium by the application of ac local power sources, which are all collected in the vector $\mathbf{V}(t)$. The Hamiltonians representing the left and right contact regions are H_{cL} and H_{cR} , respectively.

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Quantum Networks with Optical Frequency Combs

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Photonic architectures have emerged as a viable candidate for the development of quantum information processing protocols. Photons are immune from environmental disturbances, readily manipulated with classical tools, and subject to high efficiency detection. While strong nonlinear interactions at the single photon level are difficult to achieve, it is possible to initiate an interaction among photonic channels through the act of measurement. Such measurement-induced nonlinearities are the basis of linear optical quantum computing.

Similarly, the nature of a quantum network is governed not only by the light quantum state, but also by the measurement process, and can then in particular be chosen after the light source has been generated. Multimode entanglement is not anymore an intrinsic property of the source but a complex interplay between source, measurement and eventually post processing. This new avenue paves the way for adaptive and scalable quantum information processing[1], but a lot remains to be understood in the many possibilities offered by such flexible schemes.

We present here the versatile generation of multipartite quantum networks from optical frequency combs and parametric down conversion[2]. Frequency resolved multimode detection is employed to characterize the multipartite entanglement[3]. This highly entangled source can be turned into any type of quantum network benefiting from the versatility of the measurement and the shaping of the pump of the parametric process. We demonstrate the perspectives for experimental complex quantum networks implementation.

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Brownian Duet: A Novel Tale of Thermodynamic Efficiency

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Thermodynamic machines come in many different guises: thermal and iso-thermal engines, operating periodically or in steady state, of macroscopic or microscopic scale. The efficiency and response properties of these machines have to be in agreement with the second law of thermodynamics and of its generalisation – the so-called fluctuation theorem, see, e.g., [1] – in case of a small system. We introduce a new exactly solvable model, namely a Brownian particle subjected to a duo of periodic forces, that illustrates all the connections [2]. The results are reproduced experimentally, including the experimental verification of some recent predictions concerning efficiency [3] and stochastic efficiency [4].

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**Special Session on occasion of
Prof. Maxi San Miguel 65th birthday**

MAXimum VCSEL Polarization Switching – Reflections on Intrinsic and Extrinsic Causes of Asymmetries

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Conventional wisdom, normally a useful guide bordering on intuition, often unnecessarily constrains both our imaginations and our understanding of physical phenomena. A case in point was the conventional wisdom about the causes of polarization and spatial pattern bistability and dynamics of Vertical Cavity Surface Emitting Lasers. Not surprisingly, the conventional (engineering) approach to explain and understand these phenomena presumed that breaking of cylindrical symmetry arose from physical imperfections, including structural/mechanical imperfections, intrinsic birefringence and asymmetric external reflections. While better fabrication techniques helped to reduce these causes, the multistability, switching and dynamical behavior persisted. Quite unexpectedly, a revival by MSM of the insights about polarization dynamics from atomic gas lasers (sometimes called Vector Lasers) proved to provide an elegant explanation for much of the observed VCSEL polarization switching and dynamics. I will take this occasion to compare and contrast theoretical and experimental results and their explanations as they emerged in Mallorca & Massachusetts from groups with which I had some firsthand contact.

Patterns in Liquid crystals: from driven to active realizations

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I will briefly revise my research experience in the field of liquid crystals. This history started more than thirty years ago prompted by a suggestion from Prof. M. San Miguel, and was initially motivated by the interest in looking for external noise effects on the onset of the Freedericksz transition. Much more recently, my interest in the field turned from classical and pure theoretical formulations to experimental active realizations. Active liquid crystals are a new class of soft materials that have recently raised a huge interest. In particular, reconstituted suspensions of cytoskeletal filaments and associated motor proteins have proven ideal for quantitative studies of the origin of subcellular organization. Here we refer to the system initially engineered by the group of Z. Dogic (Brandeis University), consisting of bundled microtubules powered by ATP-fueled kinesin motors. We concentrate on two-dimensional preparations showing nematic textures and streaming flows, from largely-organized to seemingly chaotic. The most striking scenario presented corresponds to interfacing the active nematic with a liquid crystal in its smectic phase. In this latter situation a totally unprecedented strategy of control of the active flows has been recently demonstrated. Other scenarios corresponding to encapsulated active nematics, both in contact with isotropic and anisotropic oils will be briefly presented.

The Role of Identities on the Formation of Social Networks: Experimental Lessons

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Identity, a person's sense of self, has been often overlooked in the study of socio-economic systems, while in fact it plays a key role in many phenomena not well explained by traditional economic approaches. Pressing societal issues ranging from discrimination through nationalism and separatism to ethnic conflicts are instances where identity is a salient feature that should be in the focus of research [1]. Identity is also relevant in the context of freedom of association, namely the right to join or leave groups of a person's own choosing, and of the group to take collective action to pursue the interests of members. In this paper, we focus on this specific aspect of identity and ask ourselves how does this freedom shape social cohesion and welfare from an experimental viewpoint.

We have carried out an experimental program with the following design: There are two groups of individuals with two possible actions. Everyone prefers to coordinate on same action; however, individuals of type A prefer one action a , individuals of type B prefer the other. Individuals choose actions, simultaneously in two settings: exogenous interaction (i.e., an externally imposed network of contacts) vs. choosing links and action (i.e., a dynamic network where individuals can offer and cut links). This setup relates to earlier experiments on both static and dynamic networks (see, e.g., [2] and references therein but brings identity into the foreplay of the interaction. On the other hand, most of those works deal with prisoner's dilemma games, except for [3, 4] that consider coordination games as we do here.

Our main finding is that the outcome of the experiment depends on the level of conflict in the society. When the experiment is started with a large majority and a small minority, both treatments lead to a situation where all players coordinate in the action of the majority. On the other hand, when conflict is high and the number of individuals of each type is similar, dynamics leads to two segregated components almost always, where everybody chooses the action they prefer and there are no links between different types even if they would positively contribute to each subject's payoff. Subsequently, we discuss a number of mechanisms that can explain this outcome, specifically players using linking as an exclusion device, or the effect of linking costs on trying to reach a coordinated system when the initial conflict is high. Interestingly, when linking is free, players link to all others but still play their preferred option instead of switching to the more profitable one. These results are extremely relevant in order to design policies that facilitate integration in the society.

This work was partially supported by the EU through FET-Proactive Project DOLFINS (contract no. 640772, AS) and FET-Open Project IBSEN (contract no. 662725,

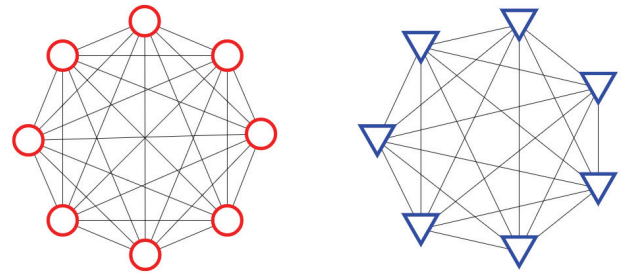


Figure 1: Typical final configuration when the experiment starts with a majority and a minority of similar size. The network segregates in two components where each player chooses what she prefers.

AS), by Fundación BBVA through project DUNDIG, by the Ministerio de Economía y Competitividad (Spain), grants FIS2015-64349-P VARIANCE and ECO2013-46550-R (MINECO/FEDER), and by Generalitat Valenciana (PROMETEOII/2014/054).

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Brownian Colloids under Non Homogeneous Temperature

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Langevin and Fokker–Planck equations have been the most used paradigm in the studies of Brownian particles motion. These equations give the correct Boltzmann equilibrium statistics and incorporate interesting nonequilibrium aspects such as the dynamical evolution to equilibrium and allows the incorporation of non equilibration elements such flows of matter and temperature gradients.

In this last situation the standard form of the Langevin equation needed some revisions due to the presence of multiplicative white noise. This problem was already studied and appropriate Fokker-Planck [1] and Langevin equations were derived [1, 2].

This study starts with the following Langevin equation for noninteracting classical Brownian particles,

$$\ddot{z} = -\hat{\gamma}_0 \dot{z} - V'(z) + g(z)\xi(\tau), \quad (1)$$

where $V(z)$ is an external potential and $\xi(\tau)$ is the thermal Gaussian white noise with zero mean and correlation $\langle \xi(\tau) \xi(\tau') \rangle = 2\delta(\tau - \tau')$. All variables and parameters have been rescaled to be dimensionless. Temperature $\hat{T}(z)$ is spatially dependent but the following local fluctuation dissipation relation is fulfilled,

$$g(z)^2 = \hat{\gamma}_0 \hat{T}(z). \quad (2)$$

Brownian motion of colloidal particles under the following spatially dependent temperature $\hat{T}(z) = 1 + 0.1z$, is studied in the spatial domain $z \in [0, 10]$.

The nonequilibrium steady densities $P_{st}(z, v)$ and $P_{st}(z)$ are evaluated and the underdamped and overdamped regimes are discussed. The existence of local equilibrium is characterized as a function of the friction parameter. Correct Langevin equations and their numerical simulations are derived.

Is important to determine if the local kinetic energy equipartition theorem

$$\langle v^2(z) \rangle_{st} = \hat{T}(z), \quad (3)$$

is fulfilled or it is friction dependent. Numerical simulations show that the underdamped and overdamped regimens are separated by de condition $\hat{\gamma}_0 = 1$. As $\hat{\gamma}_0$ is a dimensionless parameter it has to be expressed in terms of the physical parameters such as,

$$\hat{\gamma}_0 = \gamma_0 \sqrt{\frac{x_0^2}{mk_B T_0}}, \quad (4)$$

where γ_0 is the Stokes friction, m the Brownian particle mass, x_0 and T_0 are characteristic length and temperature of the specific system. When the friction is also temperature dependent the criteria have to be applied locally.

Let us take here, such as representative example, a parabolic potential fixed at the center of the system ,

$$\ddot{z} = -\hat{\gamma}_0 \dot{z} - \hat{k}(z - 5) + \sqrt{\hat{\gamma}_0 \hat{T}(z)} \eta(\tau). \quad (5)$$

Results of numerical simulations for two friction values $\hat{\gamma}_0 = 6$ and $\hat{\gamma}_0 = 0.05$ are presented in Fig. 1, where numerical results for the kinetic energy equipartition theorem are plotted. Here we see also important deviations for low friction.

Nonequilibrium state distributions for the overdamped regime were checked satisfactorily by numerical simulations. Actually it was shown that in the overdamped regime local equilibrium is also fulfilled ($\hat{\gamma}_0 = 6$ in Fig. 1). With respect the underdamped regime, numerical results show important deviations with the overdamped regime. When the space covered by a particle with a thermal velocity $v \sim \sqrt{\hat{T}}$ is of order of the system size, then particles do not feel the local temperature and the equipartition theorem is violated locally ($\hat{\gamma}_0 = 0.05$ in Fig. 1). In this regime the local kinetic energy equipartition theorem is lost, and particles feel the averaged temperature $\bar{T} = 1.5$ in any place of the system.

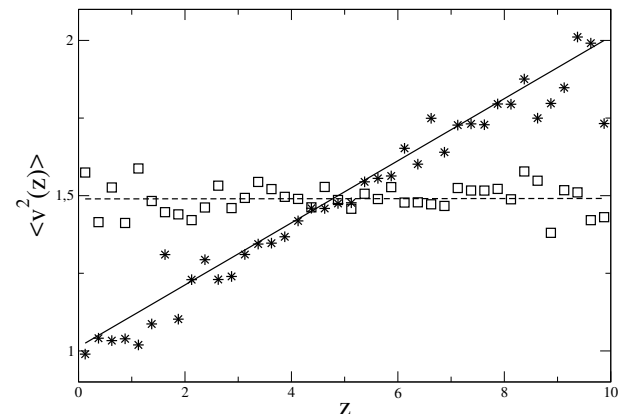


Figure 1: Local second moment for the harmonic potential: $\langle v^2(z) \rangle \sim$ kinetic energy. Continuous line corresponds to the energy equipartition theorem (3), and the dashed line is a guide of the mean temperature $\bar{T} = 1.5$. Numerical results for $\hat{\gamma}_0 = 6$ (stars) and $\hat{\gamma}_0 = 0.05$ (squares).

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Public lecture

Genes y Genealogías: Mitos y Realidades Sobre Nuestra Herencia

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¿Cómo de importante es nuestro legado genético? ¿Hasta qué punto nos condiciona? La selección natural, legado de Darwin, no se aplica solo a nuestra herencia biológica, sino también a nuestra herencia cultural. De la multitud de antepasados que han cruzado sus genes para producir los nuestros también hemos heredado el apellido que portamos o la lengua que hablamos. En esta charla revisaremos algunos datos sobre nuestras características culturales y biológicas, como individuos y como población, con el fin de comprender cómo aparecen ciertas regularidades y, a la vez, deshacer algunos mitos sobre la relevancia de la herencia.

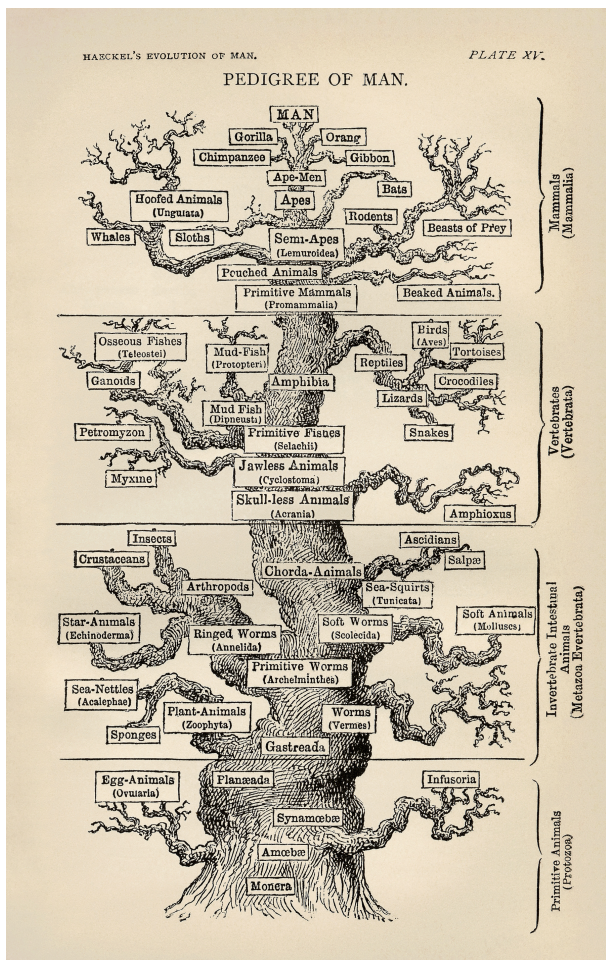


Figure 1: Tree of life by Ernst H.P.A. Haeckel. This is the English version of Ernst Haeckel's tree from the *The Evolution of Man* (Published in 1879), one of several depictions of a tree of life by Haeckel. Image taken from https://en.wikipedia.org/wiki/Ernst_Haeckel

Talks

Quantum Biomimetics

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Quantum Biomimetics is a research field devoted to the design of quantum protocols emulating processes or properties of living systems. There are two main directions to which our work is oriented, each of them associated with different biological phenomena.

In the first group, there are the rules of natural selection governing the evolution of species, rules that we have employed as an inspiration source for developing an algorithm for Quantum Artificial Life [1, 2]. Here, the living units, or individuals, are encoded in qudits of d levels, which we use as physical registers for storing the genotype and the phenotype. While the genotype contains the genetic information that is transmitted generation after generation, the phenotype allows for the expression of the genotype into the environment, and is degraded during the lifetime of the individual. In our model, both genotype and phenotype are associated with the expectation values of observables.

After defining the physical registers the task is to find the combination of quantum dynamics that these undergo from which the processes of self-replication, mutation, finite-lifetime and interactions emerge for individuals displacing along a 2D world.

The second group of works orbit around the idea of intelligence. Our goal is to engineer quantum protocols able to learn complex functions in an autonomous and efficient way.

The mechanism we have designed consists on a sequential implementation of a time delayed dynamics that in each cycle increases the probability of finding the system in the quantum state encoding the solution [3]. The problem is defined via a multitask controlled unitary operation, in which each control state performs its own gate in the target subspace. Therefore, the solution is no other than the control state implementing the desired input-output transition in the target subspace. We have tested this algorithm in the frame of quantum networks, in which the transmission of excitations along the network is controlled by the internal state of the nodes.

In parallel, we have studied the possibility of simulating quantum systems with memory [4, 5]. Our motivation was to develop a set of techniques that can contribute to the emulation of intelligent and living systems by providing the protocols with a more autonomous character.

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Detecting Migrations in Senegal through Data Analysis

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During the last few years, there has been an explosion of human behavioral studies using data generated by different kinds of Information and Communication Technologies (ICT). One of the main causes can be found in the increasing availability of data, which is stimulated by the pervasiveness of mobile phones. Although most of the works are focused on the developed world, there are also some studies on developing countries. In this work, we focus on the study of the mobility patterns of the country of Senegal by means of mobile phone data generated by the interactions of 9 million users during 2013. Our findings [1] show that agricultural activities have a key role in shaping the phenomena recorded in the data. Another important factor would be the traditional religious festivities.

Agriculture workers in Senegal represent over 70% of its labor force. We have found an increase of the number of migrants throughout the country during the harvest season. In order to do that we have built a special kind of mobility networks that we call migration networks. In a migration network the nodes are locations that, depending on the scale, can correspond to cities, districts, regions, etc.

By looking at the times and places from which a user makes her calls, we can infer the location that corresponds to her *regular residence*, as well as detect if she has changed her residence for a significant period of time; that is, if she has migrated, and where. This second location corresponds to her *temporary residence*. The links of the migration network are directed and traced from *usual residence* nodes to *temporary residence* nodes. The weights w_{ij} of the links correspond to the number of users that have migrated from node i to node j during a given time period.

In figure 1 we show the temporal evolution of the monthly migration networks for the year 2013 in Senegal. There, the nodes are the administrative regions. The color of each region is associated to the corresponding *in-strength* of its node $s_i = \sum_j w_{ji}$. It can be noticed that migration increases during the harvest season, that corresponds to the months of September, October and November (shadowed panels).

We have also identified and characterized displacement of large masses of people related to religious festivities by means of temporal evolving networks of trajectories. In these networks, nodes are locations that, depending on the scale, can correspond to cities, districts, regions, etc. A link between nodes i and j is established when a user that has made a call at time t from i makes a call at a posterior time $t + \Delta t$ from j . The result is a weighted directed network, where the weights w_{ij} are the number of displacements from location i to location j during a given time interval. We treat this as a memoryless process. If a given user makes a call from A at time t_1 , from B at time t_2 and from C at time t_3 such that $t_1 < t_2 < t_3$, we make a link from A to B

and from B to C , but not from A to C . With this methodology we have built trajectories networks corresponding to different times. In particular we have detected several relevant religious holidays, as for example the birth of prophet Muhammad, the *mawlid*, which is celebrated in the city of Tivaouane and the Grand Magal of Touba.

In summary, in this work we have extracted information from geolocalized mobile phone datasets in order to obtain insight about the mobility patterns of the people of Senegal. To this end, we have analyzed the temporal evolution of different kinds of mobility networks. This has enabled us to show the influence of the harvest season on the migration flows and study the impact of religious events on the trajectories networks.

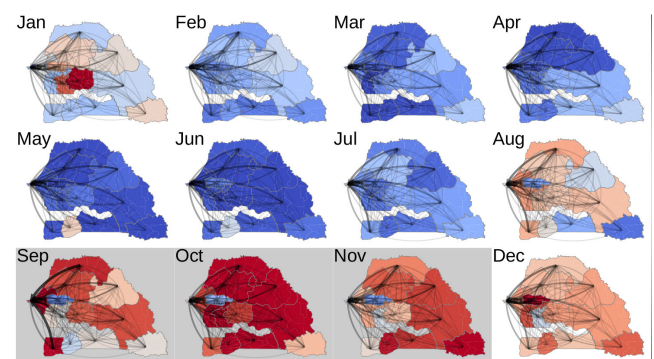


Figure 1: Temporal evolution of the monthly migration networks at the administrative region level. Link width corresponds to link weight. Arrows are traced from the *usual residence* to the *monthly residence*. The colors of each region give a notion of the number of *foreign* users within each region; that is, users whose home during a given month is not their regular home. The shadowed panels (September, October and November) correspond to the harvest season.

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Emergence of Consensus as a Modular-to-Nested Transition in Communication Dynamics

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Online social networks can be suitably represented as bipartite, user-meme networks. The features of such networks are constrained by an economy of attention (users' cognitive limits) and a rapidly changing topology. We show, using microblogging data, that competition may be minimized through consensus and that collective attention is characterized by a nested structure of the bipartite network. Our results indicate that topic consensus in social media emerges after a topological transition that minimizes modularity while maximizing the nestedness of the system (panel A in Figure 1), and that online show social networks are comparable to an ecosystem, where generalists and specialists share resources (see Figure 1, panel B). Furthermore, we exploit a set of dynamical equations from Systems Ecology, which integrate competitive/mutualistic interactions among species in time, to prove that only those systems which evolve into nested structures have larger chances of survival (in a user-meme system, "survival" means "continuity of a topic"). Our findings support the idea that nestedness is a dominant pattern in complex networked systems which has received much less attention than modularity. Finally, our results provide empirical evidence that modularity and nestedness can coexist in a single topology at its early stages, but abruptly bifurcate as the system reaches maturity. Such findings have deep implications on a system, affecting its dynamical properties in terms of diversity, stability, diffusion, and so on. This is then a valuable addition to an ongoing debate about modular and/or nested topologies coexistence, which has mainly occurred in the eco- and biological arena [1].

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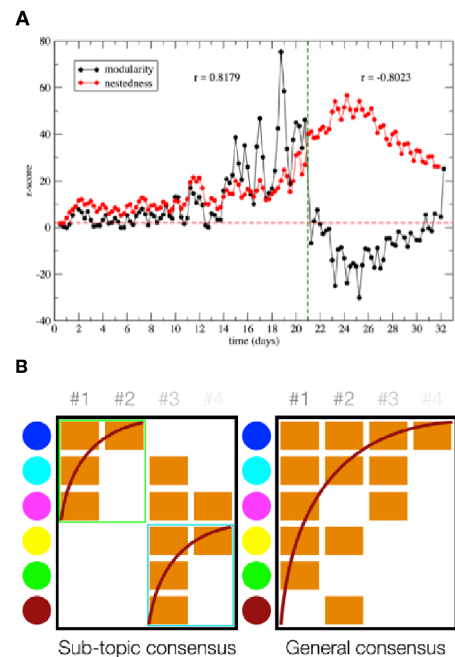


Figure 1: (A) Evolution of nestedness and modularity during the development of a topic in Twitter. Notably, modularity collapses as the topic matures, whereas nestedness keeps increasing towards a maximum. (B) Topic maturation process: from a modular-and-nested setting towards a nested-only structure.

Noise Focusing in Neuronal Tissues: Symmetry-Breaking and Localization in Metric Excitable Networks with Quenched Disorder

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We introduce a coarse-grained stochastic model for the spontaneous activity of neuronal cultures to explain the phenomenon of noise focusing [1], which entails localization of the noise activity in excitable networks with metric correlations. The system is modeled as a continuum excitable medium with a state-dependent spatial coupling that accounts for the dynamics of synaptic connections. The most salient feature is the emergence at the mesoscale of a vector quantity $\mathbf{V}(\mathbf{r})$, the avalanche field, that acts as an advective carrier of the activity noise. This entails an explicit symmetry-breaking of isotropy and homogeneity that stems from the amplification of the quenched fluctuations of the network by the activity avalanches, concomitant with the excitable dynamics. We discuss the microscopic interpretation of $\mathbf{V}(\mathbf{r})$, and propose an explicit construction of it. The coarse-grained model shows excellent agreement with simulations at the network level and with experimental data from neuronal cultures.

The purpose of this work is to transcend the qualitative picture emerging from [1] where noise focusing was first reported, by developing a theoretical framework that enables a deeper quantitative understanding of that phenomenon, and its contextualization from the perspectives of excitable systems, constructive effects of noise and transport in complex networks. The proposed model reproduces the experimental observations in cultures and at the same time provides insights on the origin of the inherent symmetry-breaking emerging from the network quenched disorder.

As in Anderson localization, the phenomenon here elucidated results from a modification of transport properties due to disorder, even though the mechanisms are completely different. As opposed to the wave interference of multiple scattering competing with diffusive transport, in our case it is the emergence of ballistic transport that competes with diffusion. Nonetheless, in both cases the localization is a collective (nonlocal) effect of disorder in extended regions, as opposed to eventual trapping in locations with special properties of the disorder.

The phenomenon of noise focusing is generic in relatively simple excitable networks, such as in neuronal cultures, but its relevance to *in vivo* neuronal tissues remains to be established. From a fundamental point of view, the direct quantitative prediction of the symmetry-breaking avalanche field for a specific network, given a set of dynamical equations, remains a nontrivial open question.

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Finite-Size Scaling Law for Word-Frequency Distributions

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The dependence on text length of the statistical properties of word occurrences has long been considered a severe limitation for the usefulness of quantitative linguistics. We propose a simple scaling law for the distribution of word frequencies that brings to light the robustness of this distribution as text grows. In this way, the shape of the distribution is always the same, and it is only a scale parameter that increases (linearly) with text length. We give evidence for the validity of such scaling law, both using analytical arguments based on the generalized central-limit theorem and careful statistical tests.

Chimeras and Clusters in Globally Coupled Chaotic Maps

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We show that chimera states, where differentiated subsets of synchronized and desynchronized dynamical elements coexist, can emerge in networks of robust chaos maps subject to global interactions. Robust chaos means the absence of periodic windows in a region of the parameter space of the map. We find that chimera states are related to the formation of dynamical clusters in the system. Both chimera and cluster states are interpreted as multistable responses of the local dynamics, which can be seen as a single map subject to a chaotic drive. By studying the dynamics of a single driven-map model as a function of parameters, the collective behavior of systems of maps subject to either external or autonomous global interactions can be predicted: complete and generalized synchronization, clusters, chimeras, and incoherence (Fig. 1). This scheme is applied to globally coupled networks of hyperbolic chaotic oscillators possessing robust chaos. Our results reveal that, under some circumstances, hyperbolicity does not impede the formation of chimera states, as it had been previously hypothesized.

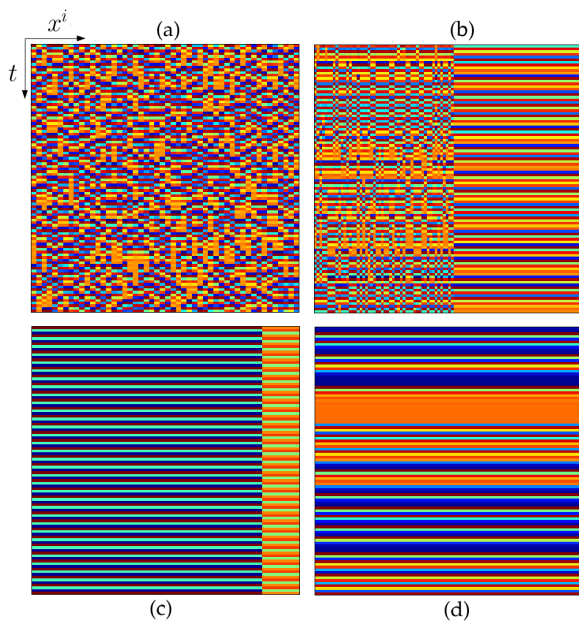


Figure 1: Asymptotic evolution of the states x^i given by a color code (horizontal axis) as a function of time (vertical axis) for the system $x_{t+1}^i = (1 - \epsilon)f(x_t^i) + \frac{\epsilon}{N} \sum_{j=1}^N f(x_t^j)$, with robust chaos local map $f(x) = \frac{1-b^{(1-x)x}}{1-\sqrt[4]{b}}$, size $N = 100$ and $b = 0.5$, for different values of the global coupling parameter ϵ . Random initial conditions are uniformly distributed in the interval $x \in [0, 1]$. After discarding 10^4 transients, 100 iterates are displayed. (a) Incoherence, $\epsilon = 0.15$. (b) Chimera state, $\epsilon = 0.198$. (c) Two-cluster state, $\epsilon = 0.39$. (d) Complete synchronization, $\epsilon = 0.62$.

Geometric Aspects of Extended Quantum Dissipative Systems

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We first [1] introduce a microscopic model to account for geometric effects when more than one dissipative unit is affected by a structured environment, showing that in some regimes there is a transition between the so-called common bath and separate baths. In the former one of the degrees of freedom of the multipartite system remains decoherence-free. This transition is shown to depend on distance as compared to a resonant wavelength for isotropic baths, while for anisotropic environments several surprising scenarios appear. The relation of this phenomenon to correlation lengths in the environment is studied, and also the appearance of a natural bath's frequency cutoff if the dissipative units have a finite size. Second [2], we investigate some models of microscopic noise in ion traps which are candidates for explaining the so-called anomalous heating, which is the fundamental hindrance for further trap miniaturization and has still an unknown origin. Probing such noise models with 2 ions and being able to discern between common bath and separate baths situations can help falsify aspects of those different models and therefore could be a fundamental tool for future experiments.

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How Does the Early Frog Embryo Coordinate Cell Division in Space and Time?

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The early *Xenopus laevis* frog embryo rapidly divides twelve times to reduce its size from a single large cell of about 1 mm to somatic cell size of about 10 micrometer. Recent experiments and modeling have shown that cell division is coordinated in space and time via traveling waves of biochemical activity sweeping through the embryo [1, 2, 3]. Such traveling waves arise from the interaction of bistability and spatial diffusive coupling within the large frog egg.

During my postdoc in the Ferrell lab at Stanford University, we used *in vitro* frog egg extracts to experimentally characterize the dynamics of such traveling waves in heterogeneous media. We found that one spatial wave tends to dominate all others on biological distance scales, which allows for well-defined regulation of mitosis within each cell. We also determined the requirements for self-organization of such spatial mitotic trigger waves using simulations. Next, we carefully characterized cell division timings in the multi-cellular early embryo and found that multiple cells also divide in a similar spatial wave pattern. By studying the response of the embryo to transient temperature perturbations, we found that all dividing cells function as uncoupled cell cycle oscillators, simply responding to their own local clock with a stable period. This lack of spatial coupling implies that the intercellular division waves are not a traveling wave phenomenon, in contrast to the cell cycle coordination within each cell. Instead, we found that the observed division waves are the result of spatially structured period differences.

Recently I started my own research lab at the University of Leuven (www.gelenslab.org), where we aim to combine theory of nonlinear dynamics and complex systems with biological experiments in order to gain new insights into the origin of these different wave patterns and their role in coordinating cell division. More generally, we are interested in understanding how the incredibly complex network of genes and proteins interacts and regulates various cell cycle processes in space and time.

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Markovian Analysis of Reaction-Diffusion Processes in Complex Metapopulations

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During the last decades we have witnessed the onset of several major global health threats such as the 2003 spread of SARS, the H1N1 influenza pandemic in 2009, the western Africa 2014 Ebola outbreaks and more recently the Zika epidemics in the Americas and Caribbean regions during 2015 and 2016. These outbreaks are increasingly characterized by the small elapsed time between initial infections in a single region to the global epidemic state affecting different cities, regions, countries and, in some cases, continents. Thus, in the recent years a great effort has been devoted to adapt classical epidemic models taking into account the multiscale nature of diseases propagation so to reproduce the fast unfold of emergent diseases and serve as theoretical frameworks to design both local and global contention strategies [1, 2].

It is clear that the spread of an emergent infectious disease is the result of human-human interactions in small geographical patches. However, in order to understand the geographical diffusion of diseases one has to combine these microscopic contagion processes with the long-range disease propagation due to human mobility across different spatial scales. To tackle this problem epidemic modeling has relied on reaction-diffusion dynamics in metapopulations [4] so that a population is distributed in a set of patches, being the size (number of individuals) of each patch in principle different. The individuals within each patch are well-mixed, *i.e.*, pathogens can be transmitted from an infected host to any of the healthy agents placed in the same patch.

The second ingredient of metapopulation frameworks concerns the mobility of agents. Each host is allowed to change its current location and occupy another patch, thus fostering the spread of pathogens at the global system level. The non-trivial mobility patterns of real populations and the recent advances of network epidemiology [5] has motivated a thorough analysis about the impact of mobility networks on the onset of global-scale contagions. In the last decade, most of theoretical works have assumed simple mobility patterns and mean-field approximations for hosts and patches behavior, to be able of predicting the onset of an outbreak. In these models random diffusion of agents between patches is often used as proxy of human mobility [6, 7, 8, 9] while, as in the case of the heterogeneous mean field approach in networks, subpopulations with identical connectivity patterns are assumed to be equally affected by the disease.

As data gathering techniques and epidemic surveillance increase their accuracy, metapopulation models face new challenges [10]. In an effort of relaxing the assumption about random diffusion of hosts and approach the realistic mobility patterns used in agent based simulations [11], recently the recurrent and spatially constrained nature of most human movements, such as daily commutes, has been addressed [12, 13], at the expense of considering either mean-field assumptions or simple mobility networks.

In this presentation we aim at going one step beyond mean field models of metapopulations in attempt to increase the realism of epidemiological models without compromising their theoretical analysis. To this aim we propose a novel theoretical framework in which the dynamical variables of each patch forming the metapopulation are treated independently. In addition this framework can accommodate any mobility network from real commuting datasets and is amenable to any particular distribution of the population across the patches. We investigate the effect of the diffusion (mobility) on the spreading of the epidemics, and obtain analytic expressions that relate mobility and incidence in all the phase diagram of the system. Interestingly, we can determine conditions where mobility detracts the spreading of epidemics. We analyze real mobility networks where epidemics is damped by the mobility patterns reported.

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Pattern Formation and Fairy Circles in *Posidonia Oceanica* Meadows

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Self-organized vegetation patterns have been studied in different ecosystems all over the world, exhibiting similar spatial distributions, which reinforces the idea of vegetation patterns as universal phenomena. While the mechanisms behind the formation of these patterns can be totally different and difficult to identify, feedbacks across space are always present in the process.

Pattern formation, well documented in terrestrial ecosystems, has more rarely been reported for seagrasses in marine environments. Of special importance is the case of *Posidonia Oceanica* meadows [1]. This clonal growth plant forms essential ecosystem for the Mediterranean sea, promoting biodiversity and offering valuable services such as CO₂ sequestration or shoreline protection. These vegetation patterns, which extend over kilometers, are abundant in the Balearic coast suggesting the prevalence of submarine patterns. However, the presence of these spatial structures evidences the fact that the growth is not completely understood. Whereas the mechanisms at the local scale are well known, non-local interactions, which are the responsible for the formation of patterns, are less clear.

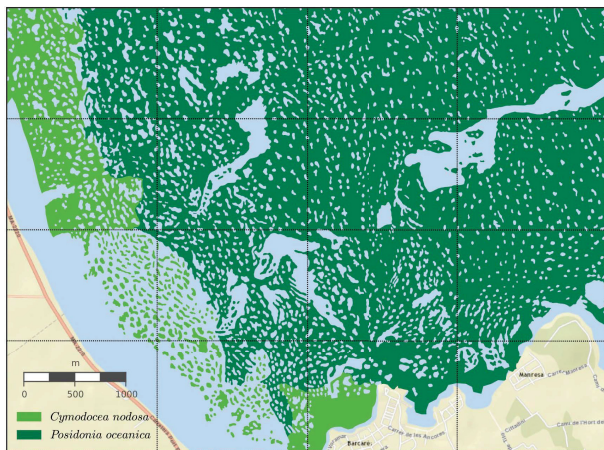


Figure 1: Side-scan map of a seagrass meadow in Pollença bay (Mallorca Island, Western Mediterranean) from LIFE Posidonia project (<http://lifeposidonia.caib.es>) showing different patterns in meadows of *Posidonia oceanica* and *Cymodocea nodosa*.

In order to shed light on this issue we have derived a general model for clonal growth plants based on basic mechanisms of growth [2]. Typically, the plant develop new shoots elongating the rhizome, which sometimes branches generating new rhizomes at a certain angle. The plant expands this way colonizing new space. As time goes on shoots can die leaving room for new ones. Such description reproduce homogeneous growth but can not explain spatial patterns like those find at the seabottom. The presence of these vegetation

patterns is then an indirect evidence of interactions across space which can be, a priori, both cooperative and competitive. From the model, we show that long-range competition is a necessary ingredient for the formation of patterns. Moreover, the scale of this spatial interaction can be determined comparing with real data, which provides useful information to look for the mechanisms behind the interaction.

The model displays all the different patterns observed in real meadow (Fig. 1). Increasing mortality, continuous meadows, isolated vegetation gaps (fairy circles), seascapes of vegetation gaps, banded vegetation, seascapes of plant patches, isolated patches and finally bare soil are observed (Fig. 2). The sequence of patterns associated to given ranges of mortalities is a feature that can be used as a diagnostic tool. Hence, given the importance of the *P. Oceanica* meadows and its vulnerability, the capacity to diagnose based on landscape configurations is a valuable tool to guide conservation strategies and prevent further losses.

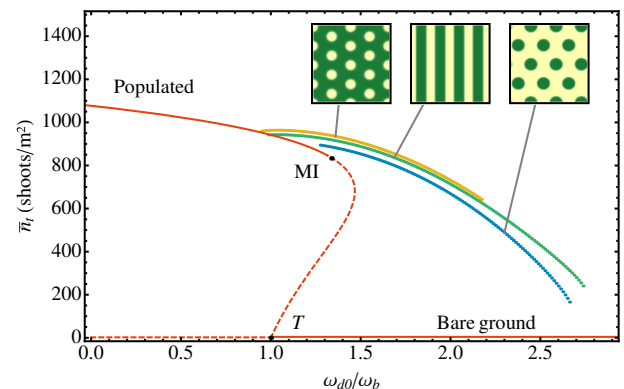


Figure 2: Mean shoot density \bar{n}_t as a function of normalized mortality ω_{d0}/ω_b for five different solutions of the model: homogeneous populated and unpopulated states (red), hexagonal arrangement of gaps (yellow), stripes (green) and hexagonal arrangement of spots (blue). Solid (dashed) lines indicate stable (unstable) solutions.

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Modeling Decision Times in Game Theory Experiments

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What makes us decide whether to cooperate or not? The answer to this fundamental question goes necessarily beyond a simple maximisation of individual utility. Recent studies contributed in this sense by using decision times to claim that intuitive choices are pro-social while deliberation yield to anti-social behavior [1]. These analysis are based on the rationale that short decisions are more intuitive than long one and summed up to keeping track of the average time taken by the subject of game theory experiment to make their decision under different conditions. Lacking any knowledge of the underlying dynamics, this simple approach might however lead to erroneous interpretations, especially on the light of our experimental evidence that the distribution of the decision times is skewed and its moments strongly correlated.

Here we use the Drift Diffusion Model (DDM) [2] to outline the cognitive basis of cooperative decision making and characterise the evolution of subject's behavior when facing strategic choices in game theory experiments. In the DDM, at each moment subjects randomly collect evidence in favour of one of two alternative choices, which are in our case cooperation and defection. This accumulation has a stochastic character as a consequence of the noisy nature of the evidence [3]. The continuous integration of evidence in time is described by the evolution of $x(t)$ as a one-dimensional brownian motion with diffusion coefficient \sqrt{D} and a drift v :

$$dx = vdt + \sqrt{D}\xi(t) \quad (1)$$

For each dt the quantity $x(t)$ is increased by vdt (drift term) plus a noise $\sqrt{D}\xi(t)$ (diffusive term), where v and $\sqrt{D} > 0$ are constant and $\xi(t)$ is a white noise. Given an initial condition $x(0) = x_0 > 0$ and two barriers at $x = 0$ and $x = a > x_0$ associated to the two alternative choices, the process is equivalent to the commonly called "gambler's ruin problem" [4], where $x_0 = z \cdot a$ represents the initial bankroll of the gambler, the absorption at $x = a$ represents the gambler leaving a possibly unfair game (if $v \neq 0$) after collecting her target winnings a , and the absorption at $x = 0$ represents the gambler's ruin. The probability distribution of the times at which the process reaches the origin $x = 0$ before reaching the exit value $x = a$ is known as Fürth formula for first passages:

$$P(t; v, a, z, D) = \frac{\pi\sqrt{D}}{a^2} \exp\left(-\frac{vza}{\sqrt{D}} - \frac{v^2t}{2\sqrt{D}}\right) \times \sum_{k=1}^{\infty} k \exp\left(-\frac{k^2\pi^2\sqrt{D}t}{2a^2}\right) \sin(k\pi z)$$

This distribution has been successfully used to model decision time in a wide range of contexts [5]. Our findings extend this use to the strategic choices of iterated Prisoner's

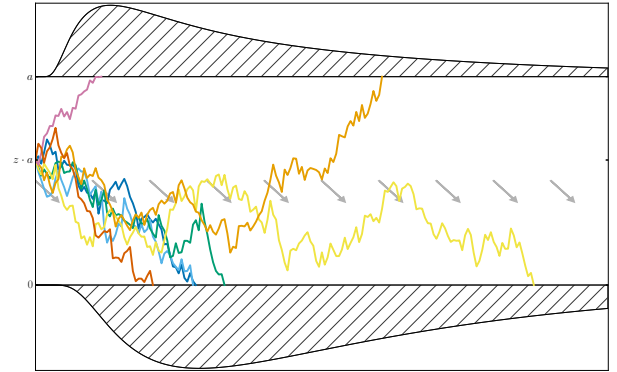


Figure 1: An illustration of the DDM: starting from an initial condition $z \cdot a$, the agents accumulate random evidence in favour of one of two alternative decisions. Once the amount of evidence reaches one of the thresholds, the associated decision is made. The arrows indicate the presence of a negative drift towards defection.

dilemma experiments. Analyzing the results of large-scale experiments [6] (169 subjects making 165 decision each) through the new lens of DDM and its characteristics free parameters (drift v , threshold a , and initial bias z) allows us to clearly discern between deliberation (described by the drift) and intuition (associated to the initial bias). Our results show that rational deliberation quickly becomes dominant over an initial intuitive bias towards cooperation, which is fostered by positive interactions as much as frustrated by a negative one. This bias appear however resilient, as after a pause it resets to its initial positive tendency.

The method we proposed here represents a novel tool for the analysis of decision times in experimental game theory from a neuro-economics [7] perspective and illustrate how an accurate modeling of decision times allows to get new detailed insight on human the decision process.

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Hierarchical Partitions of Social Networks Between Rivaling Leaders

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A model algorithm is proposed to study subsequent hierarchical partitions of complex networks describing social structures. The partitions are supposed to appear as actions of rivaling leaders [1] corresponding to nodes with large degrees. The condition of a partition is that the distance between two leaders is at least three links. This ensures that the layer of nearest neighbours of each leader remains attached to him. The process of cutting links starts from a selection of the shortest path between the leaders. If there is more than one path, we concentrate on one of them. If the length of the path is exactly three, there is only one link in the middle to be cut. If the shortest path consists of more than three links, the cutting can be performed in two ways; either we select the link with the lowest number (variant A) or the link with the highest number (variant B). As a rule, numerically calculated size distribution of fragments of scale-free Albert-Barabasi networks reveals one large fragment which contains the original leader (hub of the network), and a number of small fragments with opponents (see Fig. 1) that are described by two Weibull distributions [2].

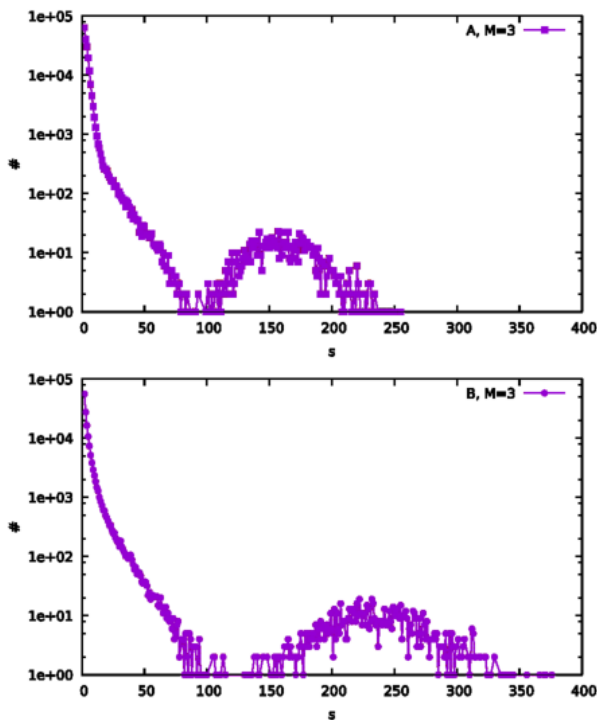


Figure 1: The histogram of the fragment size s distribution for variants A and B of hierarchical partition (top/bottom plots) of Albert-Barabasi model with a parameter $M = 3$.

Numerical simulations and mean-field theory reveal that size of the larger fragment scales as the square root of the

initial network size. The algorithm is applied to the data on political blogs in U.S. (L. Adamic and N. Glance, Proc. WWW-2005). The obtained fragments are clearly polarized; either they belong to Democrats, or to the GOP. (see Fig. 2)

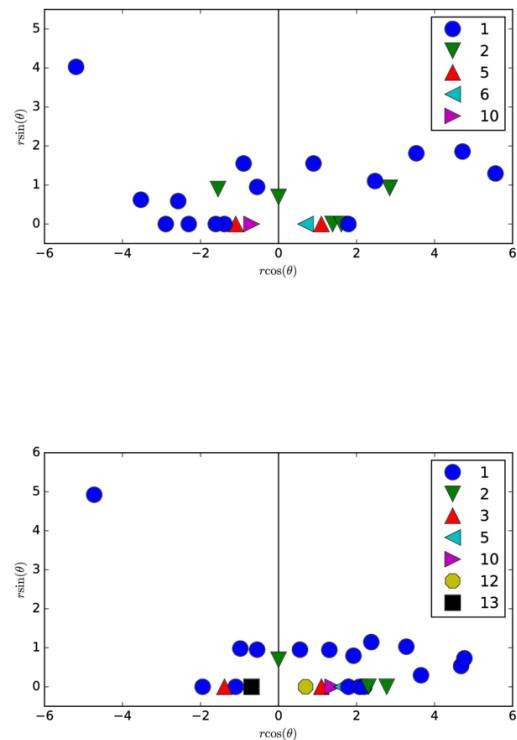


Figure 2: The fragments obtained by the partition of the network of political blogs [3]. The position of a fragment is related to its size and its content: $r = \log(N_R + N_D)$, and $\Theta = \pi N_D / (N_R + N_D)$, where N_D (N_R) is the number of blogs tagged as democratic (republican). The same data on the blogs [3] are used twice for various versions of our partition algorithm.

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Identifying the Hidden Multiplex Architecture of Complex Systems

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The architecture of many complex systems is well described by multiplex interaction networks, and their dynamics is often the result of several intertwined processes taking place at different levels. However only in a few cases can such multi-layered architecture be empirically observed, as one usually only has experimental access to such structure from an aggregated projection. A fundamental question is thus to determine whether the hidden underlying architecture of complex systems is better modelled as a single interaction layer or results from the aggregation and interplay of multiple layers. Here we show that, by only using local information provided by a random walker navigating the aggregated network, it is possible to decide in a robust way if the underlying structure is a multiplex and, in the latter case, to determine the most probable number of layers. The proposed methodology would also allow to select the optimal architecture capable of reproducing non-Markovian dynamics.

Dynamic Regime Criteria for Complex Network Reduction: Fertilization as Study Case

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The structure and dynamics of complex phenomena are often modeled by means of networks. In their study, the possibility of node reduction is commonly sought for. Here we present a strategy for such a reduction in terms of a discrete time attractor landscape analysis in conjunction with dynamical regime criteria. In doing so, we address issues such as robustness, redundancy, degeneracy, plasticity and criticality. As an exemplification, we analyze a signaling network for sea urchin flagellum calcium oscillations that control sperm swimming during fertilization [1, 2, 3, 4]. The recurrence of a critical dynamical regime after node deletions is challenging in evolutionary terms. A comparative study of the spread of initial condition perturbations as network nodes are deleted, by means of a modified version of the Derrida plot [5, 6], identifies expansive (chaotic), contractive (regular) and marginal (critical) relative dynamics. This classification provides information that complements the attractor landscape analysis. Coincidence of the reduced network with an alternative continuous time formulation [7] is encouraging. The reduction method is applicable to general logical networks.

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Disease Spreading Processes in Multilayer Networks

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Most epidemic models assume that the spreading process takes place on a single level (be it a single population, a meta-population system or a network of contacts). The latter results from our current limited knowledge about the interplay among the various scales involved in the transmission of infectious diseases at the global scale. Therefore, pressing problems rooted at the interdependency of multi-scales call for the development of a whole new set of theoretical and simulation approaches. In this talk, we show that the recently developed framework of multilayer networks allows to tackle many of the existing challenges in the study of multi-scale diseases, ranging from interacting diseases [1] to new phenomena like disease localization [2].

Specifically, we (1) characterize analytically the epidemic thresholds of two interacting diseases for different scenarios and numerically compute the temporal evolution characterizing the unfolding dynamics (Fig. 1, top panel); and (2) we present a continuous formulation of epidemic spreading on multilayer networks using a tensorial representation, showing the existence of disease localization (Fig.1, bottom panel) and the emergence of two or more transitions, which are characterized analytically and numerically through the inverse participation ratio. Our findings show the importance of considering the multilayer nature of many real systems, as this interdependency usually gives raise to new phenomenology.

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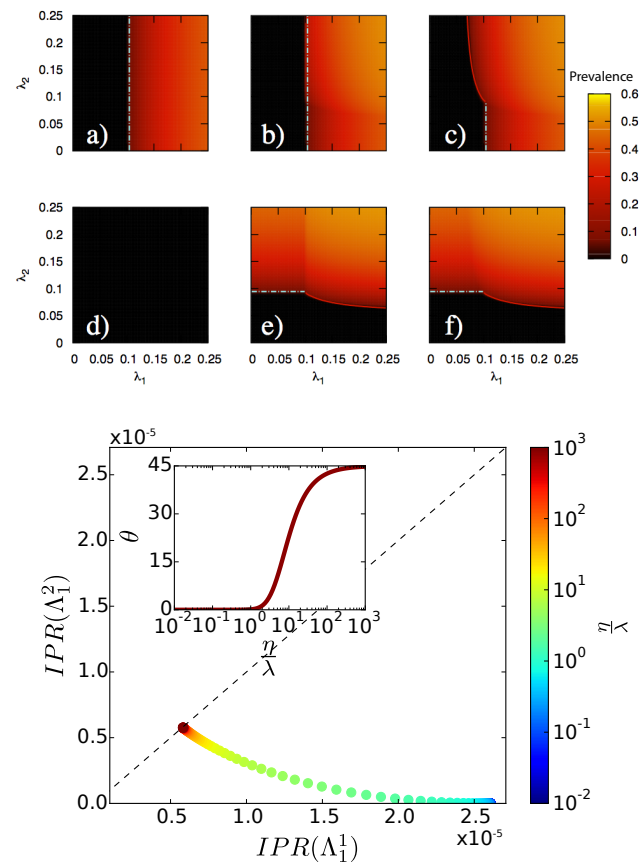


Figure 1: (Top) Phase diagram of the incidence of two interacting diseases for the case of homogeneous networks and (bottom) localization effect in the spreading of diseases in multilayer networks.

Neutral Theory of Scale-Free Neural Avalanches

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The human cortex has a special feature that is common to all mammals: it is endogenously active; i.e. cascades of electrochemical activity at multiple timescales pervade its dynamical state even in the absence of any apparent stimuli or task. Mounting evidence suggests that such an endogenous activity is essential for various information processing tasks. Spontaneous bursts of activity were reported to appear in the form of avalanches [1].

Avalanches of activity in brain networks have been empirically reported to obey scale-invariant behavior – characterized by power-law distributions up to some upper cut-off that scales with system size– both in vitro and in vivo. Elucidating whether such scaling laws stem from the underlying dynamics operating at the edge of a phase transition is a fascinating possibility. The so-called “criticality hypothesis” proposes that some aspects/parts of living systems may work in the vicinity of a critical point [2] and that they can derive functional advantages, such as exquisite sensitivity to signals, large dynamical repertoires, a large variety of attractors endowing them with large computational capabilities, etc. [3].

Here we scrutinize one of the most accepted computational models for the generation of scale-invariant avalanches of neural activity. We confirm the emergence of generic scale-free avalanches, but we also elucidate that it has nothing to do with self-organization to the critical point of a continuous phase transition. Instead, it stems from the fact that perturbations to the system exhibit a neutral drift –guided only by stochastic fluctuations– with respect to endogenous activity spontaneously present in the system. Such a neutral dynamics –similar to the one in neutral theories of population genetics of Kimura and the neutral theory of biodiversity of Hubbell– implies marginal propagation of activity, characterized by power-law distributed causal avalanches. We discuss the implications of this finding both in modeling and in experimental observations as well as its possible consequences for actual neural dynamics in real networks [4].

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Critical Dynamics on a Large Human Open Connectome Network

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Centre for Energy Research of the Hungarian Academy of Sciences

Extended numerical simulations of threshold models have been performed on a human brain network with $N = 836\,733$ connected nodes available from the Open Connectome Project [1]. While in the case of simple threshold models a sharp discontinuous phase transition without any critical dynamics arises, variable threshold models exhibit extended power-law scaling regions. This is attributed to fact that Griffiths effects, stemming from the topological or interaction heterogeneity of the network, can become relevant if the input sensitivity of nodes is equalized. Effects of link directness, as well as the consequence of inhibitory connections is studied. Nonuniversal power-law avalanche size and time distributions have been found with exponents agreeing with the values obtained in electrode experiments of the human brain [2].

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Universal Dichotomy for Dynamical Systems with Variable Delay

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Delay differential equations arise as mathematical models in various fields, such as laser physics, engineering, climate dynamics, life science, control theory, and synchronization of networks. In all these applications variations of the delay time are a common phenomenon. We show that the dynamics of systems with a time-dependent delay is fundamentally affected by the functional form of the retarded argument. Associating with the latter an iterated map, the access map, and a corresponding Koopman operator, we identify two universality classes. Members in the first are equivalent to systems with a constant delay. The new, second class is characterized by the mode-locking behavior of their access maps and by an asymptotically linear, instead of a logarithmic, scaling of the Lyapunov spectrum. The membership depends in a fractal manner only on the parameters of the delay. Details can be found in [1, 2]

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Immigrant Community Integration in World Cities

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Immigrant integration is a complex process comprehending many different factors such as employment, housing, education, health, language, legal recognition as well as the built of a new social fabric. In the last years, there have been advances in the definition of a common framework concerning immigration studies and policies, although the approach to this issue remains strongly country-based. The outcome of the process actually depends on the culture of origin, the one of integration and the policies of the hosting country government. Traditionally, spatial segregation in the residential patterns of a certain community has been taken as an indication of ghettoization or lack of integration. While this applies to immigrant communities, it can also affect to minorities within a single country. The spatial isolation reflects in the economic status of the segregated community and in social relationships of its members.

nally, Twitter has been used as a statistical database for representations of demographical characteristics of users and language identification patterns. Several attempts have been made in order to identify, characterize and group international communities in cities based on Information and Communication Technologies (ICT) data and to perform social segregation analyses.

Here we present a novel approach to quantify the spatial integration of immigrant communities in urban areas worldwide by using social media information collected through the Twitter microblogging platform; first, we characterize immigrants through their digital spatio-temporal communication patterns, defining their residence place and most probable native language; then we perform a spatial distribution analysis through a modified entropy metric, as a quantitative measure of the spatial integration of each community in cities and the corresponding relevance within countries. These results have been recently posted in a paper in arXiv [1]. Figure 1 shows, for instance, the level of spatial integration of immigrant communities in the largest world cities as detected from Twitter. The lower the spatial entropy becomes (clearer colors in the figure), the more isolated the communities are. The cities can be classified in three major groups depending on the number of immigrant communities hosted and how well they spatially assimilate them.

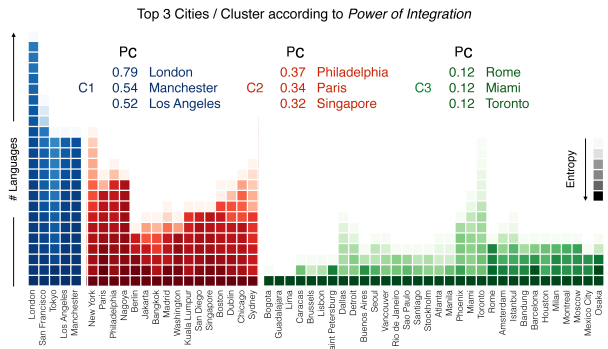


Figure 1: Clusters of cities and Power of Integration. Three groups of cities show similar behavior in the number of communities detected and in their levels of integration. The length of the vectors represent the number of languages (communities) detected in each city; the color scale is representative of the decay of the entropy metric; the Power of Integration metric lead us to evaluate the potential of each city in uniformly integrating immigrant communities within its own urban area according to entropy values.

Immigrant integration has been the focus of many research studies using traditionally national census data and similar surveys. In parallel, in the last few years we have witnessed a paradigm shift in the context of socio-technical data. Human interactions are being digitally traced, recorded and analyzed in large scale. Sources are as varied and different as mobile phone data, credit card transactions, or Twitter data. Going beyond the urban scale, Twitter data have been used to detect the diffusion of human mobility and the languages spoken. Language identification related to the spatial location of Twitter users has been investigated, towards a more complete characterization of spatial local dialects. Fi-

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Lagrangian Flow Network: Theory and Applications

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The last two decades have seen important advances in the Lagrangian description of transport and mixing in fluid flows driven by concepts from dynamical systems theory [1]. In the meantime, Network Theory approaches continue arousing scientific interests and have been successfully used, among other, for geophysical systems with climate networks. Linking the network formalism with transport and mixing phenomena in geophysical flows, we develop a new paradigm which we call Lagrangian Flow Network [2]. It consists in analyzing a directed, weighted, spatially embedded and time-dependent network which describes the material fluid flow among different locations [2, 3]. We relate theoretically dispersion and mixing characteristics, classically quantified by Lyapunov exponents, to the degree of the network nodes and then to a family of network entropies defined from the network adjacency matrix [2]. Among possible applications, this new framework allows studying the connectivity and structural complexity of marine populations by providing a systematic characterization of larval transport and dispersal [4, 5, 6]. The simulated networks are composed of an ensemble of oceanic sub-regions which are interconnected through the transport of larvae by ocean currents (Fig. 1).

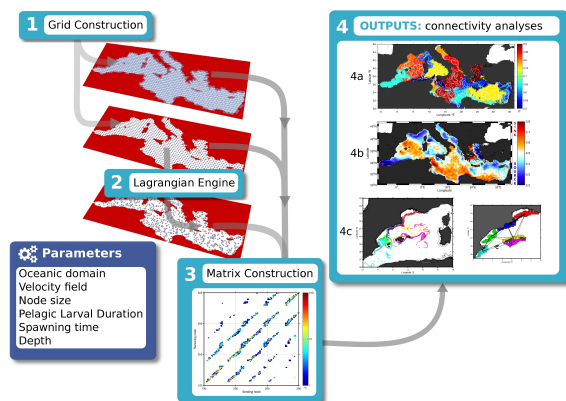


Figure 1: Simplified diagram of the Lagrangian Flow Networks set-up with 4 modules (light blue boxes). Key parameters (dark blue box) are the domain of interest, the velocity field (from any ocean model), the node size, the starting dates (e.g. release of contaminant or spawning event), the vertical layer of the model (depth of dispersion) and the tracking time (drift duration or pelagic larval duration).

The analysis of such networks allows the identification of hydrodynamical provinces (coherent oceanic regions, i.e. areas internally well mixed, but with little fluid or larvae in-

terchange between them)[4] and the computation of connectivity proxies measuring retention and exchange of larvae at multiple scales [5]. These diagnostics, whose sensitivity and robustness have been tested [6], provide useful information to design management and protection plans for marine ecosystems.

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How Far Are Two Graphs? Exploring Sets of Complex Networks Using Gromov-Wasserstein Distances

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Relations between data are often presented as graphs or networks. When a complex system is naturally described as a set of networks, as for example in studying the metabolic graphs of a set of related species or following the evolution in time of a network, one is often interested in comparing the networks of that set. Such a comparative measure can provide a way to inspect the relations that the networks themselves have between each other and provide clues about their interactions and evolution.

However, it is unclear which measure is more appropriate for comparing two or more networks. For example, it is difficult to compare two networks when the number of nodes is different or more generally, when we lack a correspondence between the nodes of one network and the nodes of the other. In the past researchers have compared global statistics of some particular attribute of the networks such as their clustering coefficient, their mean degree, or their average shortest path length. However, these approaches miss important information encoded in the graphs. Ideally one would like to compare different networks with a measure that takes into account their internal structures of distance/similarity between their respective internal nodes. In another words, one would like to come with a measure of distance between the set of distances defined inside each network.

In this work we capitalize on the recent development by F. Memoli of using optimal transportation distances for the problem of object matching (comparing 3D shapes) in computer vision [1]. In particular, Memoli derived a computationally feasible bound for the Gromov distance (a metric distance between metric spaces) named Gromov-Wasserstein distance (d_{GW}) and applied it to the problem of shape matching [1, 2]. Intuitively, the Gromov-Wasserstein distance aims to solve a certain graph isomorphism problem by finding an optimal mapping (not necessarily one-to-one) between two sets of nodes such that their respective distances are best preserved by the map. The deviation from a perfect isomorphism is related to the distance between the two objects.

In our work we show analytically that Gromov-Wasserstein distance is a well behaved metric even when the two sets of distances compared do not satisfy the metric property (i.e. they do not satisfy the restrictive condition of triangular inequality). This observation dramatically expands the application of Gromov-Wasserstein type of measures to pairs of undirected graphs in which their internal (between nodes) notions of distance/dissimilarity only need to satisfy positivity and symmetry (but not triangular inequality).

After describing a numerical method to estimate Gromov-Wasserstein distance for pairs of undirected graphs we proceed to validate the measure with toy cases (see Fig. 1 for an example on yearly networks of world trade flows) and

well-known families of complex networks. Finally, we apply Gromov-Wasserstein distances in combination with dimensionality reduction methods to visualize and explore the structure of several real-world sets of networks, including applications to biological networks.

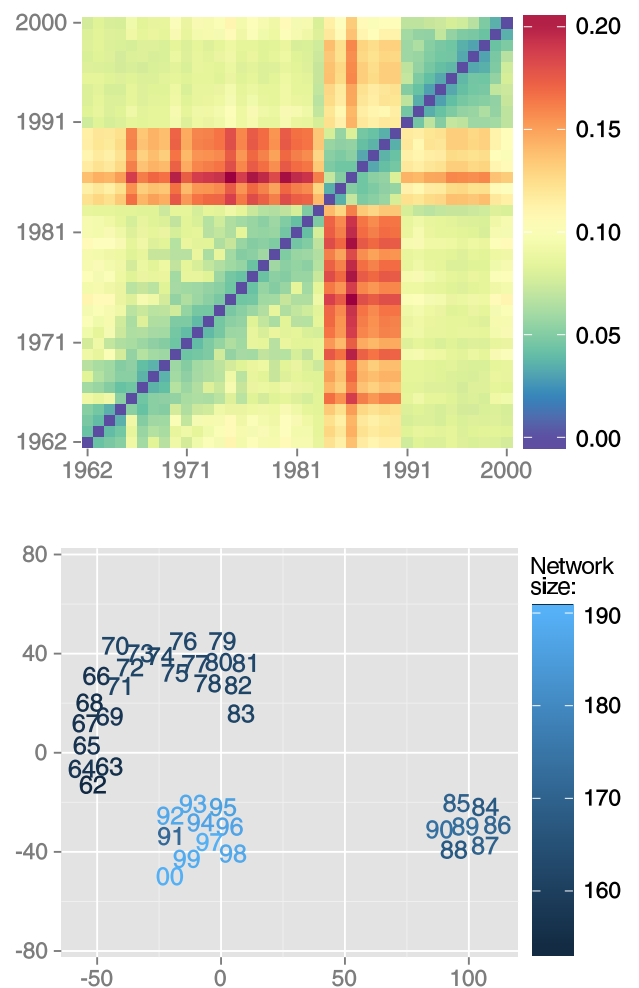


Figure 1: Matrix of Gromov-Wasserstein distances between pairs of networks (a different network is computed for every year) of world trade flows from 1962 to 2000. *Top panel*: matrix of pairwise distances (d_{GW}). *Bottom panel*: 2d embedding of the distance matrix (d_{GW}) using t-SNE. Numbers 62-99 represent years 1962-1999. Number 00 represents year 2000.

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Posters

Chaotic synchronization in circular lattices

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We investigate the relationship between the emergence of chaos synchronization in coupled dynamical systems and the properties of the spatial network where they are embedded. By employing a general model of N coupled chaotic maps in a ring lattice with $2k$ edges (each map is connected to its k nearest neighbors on either side) for such systems, we found the minimal conditions for achieving synchronization. Since we are particularly interested in chaos synchronization, we choose the logarithmic map $f(x_t^i) = b + \ln |x_t^i|$, where b is a real parameter and $x_t \in (-\infty, \infty)$. This map exhibits robust chaos with no periodic windows and no separated chaotic bands, on the interval $b \in [-1, 1]$. The synchronization in these extended systems is characterized by the asymptotic time-average $\langle \sigma \rangle$ (after discarding a number of transients) of the instantaneous standard deviations σ_t of the distribution of state variables x_t . Varying the number of elements N in the network, the edges for each node and the value of the coupling parameter ε , we found the regions where the synchronized states emerge on the space of parameters of the system. The linear stability analysis, employing the eigenvalues determined of the associated coupling matrix to the system, allows to get the stability condition for the synchronized states. Fig. 1 shows the region for synchronized states (blue), given by $\langle \sigma \rangle = 0$ and by the stability condition (green and red lines), on the space of parameters $(2k, \varepsilon)$ for a ring of $N = 500$.

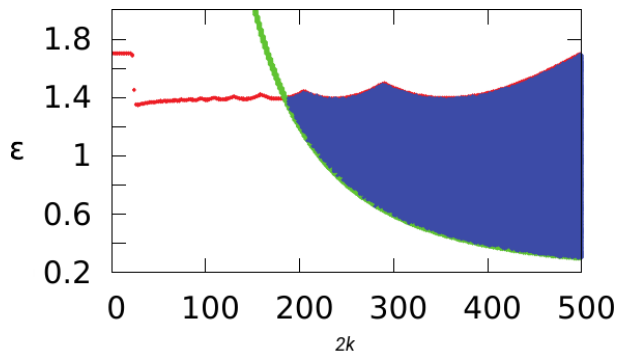


Figure 1: Boundaries $\langle \sigma \rangle = 0$ on the plane $(2k, \varepsilon)$ for synchronization (blue region). The green and red lines are obtained by the stability condition.

Coevolution of synchronization and cooperation in costly networked interactions

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Despite the large number of studies on synchronization, the hypothesis that interactions bear a cost for involved individuals has been considered seldom. The introduction of costly interactions leads, instead, to the formulation of a dichotomous scenario in which an individual may decide to cooperate and pay the cost in order to get synchronized with the rest of the population. Alternatively, the same individual can decide to free ride, without incurring in any cost, waiting that others get synchronized to her state. The emergence of synchronization may thus be seen as the byproduct of an evolutionary game in which individuals decide their behavior according to the benefit/cost ratio they accrue in the past. We study the onset of cooperation/synchronization in networked populations of Kuramoto oscillators and report how topology is essential in order for cooperation to thrive. We display also how different classes of topology foster differently synchronization both at a microscopic and macroscopic level.

Photonic reservoir computing for post-processing optical communication signals

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In the current investigation we evaluate the post-processing capability of a small-scale RC by employing a classification task in optical communication signals. Operating conditions of the RC that lead to complex dynamics, from the onset of multistability to fully developed chaos, are considered. At large distances and for signal bit rates of 10Gb/s or higher, fiber transmission impairments degrade the quality of the encoded information so that the latter is difficult to be recovered by real-time, direct-threshold, detection methods. Here we show that the nonlinear transformation of the above signals through the photonic-based RCs and the upcoming training with a ridge regression algorithm significantly improves the recovery of the bit stream.

Synchronization Transitions Induced by Topology and Dynamics

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The synchronization of coupled oscillators is a paradigmatic example of the emergence of complex behavior in a dynamical system with local interactions. It is an ubiquitous phenomena in nature, where most of the systems present a complex underlying structure. Much research has been done in the last decades to understand the interplay between dynamics and topology, obtaining successful results in the inference of the structure from the response dynamics [1, 2] and the prediction of the synchronization onset for several topologies [3, 4, 5]. However, a general theory for synchronization in complex networks is still missing and there are many theoretical and empirical challenges to face towards a complete understanding of the process [6, 7].

In this work, we study the dynamics of Kuramoto oscillators in evolving complex topologies. We construct functionally equivalent networks by constraining the distribution of coupling strengths in the nodes in order to show that the same evolution of the global order parameter in a quasi-static process can be observed due to changes either in the underlying connectivity of the network or in the dynamics of the interactions. In this framework, an explicit analogy between topological and dynamic transitions is made by using simple mean-field arguments.

We consider that the dynamics of any sparse but connected network is driven by a reduced effective coupling strength between oscillators, K_{eff} depending only on the current coupling strength of the network K and its distribution over the nodes space. For instance, for an Erdős-Rényi $G(p, N)$, the homogeneity of the network leads to the scaled coupling $K_{eff} = pK$, where p is the global fraction of existing edges, and the structural transition occurs at a critical connectivity $p_c = K_c/K, \forall K \geq K_c$ (K_c is the critical coupling for the all-to-all limit case). This result closely agrees with numerical simulations, and the mean-field approximation [4, 5] converges to it for large and highly connected systems. Beyond the prediction of the synchronization onset, we suggest that the whole evolution in the dynamic response due to structural changes is analogous to the evolution of a static structure under changes in the coupling strength among oscillators.

In order to quantify these effects, we use a model of network formation that interpolates between Erdős-Rényi and Scale-Free [8] to generate networks with increasing average connectivity constrained to the given degree distribution. For each network, we iterate the system towards the steady-state for a range of supercritical coupling strengths (for the all-to-all case), measuring the global degree of synchronization with the usual macroscopic order parameters.

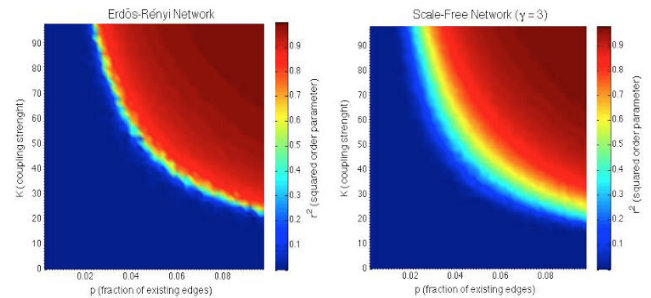


Figure 1: Steady-state of synchronization measured by the squared order parameter r^2 for both ER and SF networks in the plane (p, K) , with $N = 10^3$ nodes and a uniform distribution of natural frequencies $g(\omega) = 1/\pi$, as fixed parameters in each realization. Isochrome regions represent functionally equivalent networks that preserve the global coupling strength and the clear analogy between structural (increasing p) and dynamic (increasing K) transitions is shown for both ensembles. For the ER case, we observe the same behaviour as in the all-to-all case, where a discontinuous phase transition occurs at $K_c = 2$, and the critical connectivity $p_c(K)$ matches our theoretical prediction. For SF networks, the transition appears earlier and becomes smoother, as expected [6, 7], but the studied analogy remains present.

This work presents some analytical and numerical evidence on the close relation between topological and dynamic transitions to synchronization. We aim to shed some light on the nature of these transitions in real systems, where one can usually measure their response dynamics, but there is very little information about the underlying topology, its evolution, and the specific local interaction mechanisms.

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Dynamics on Networks: Competition of Temporal and Topological Correlations

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Networks are the skeleton that support dynamical processes in complex systems. Their connections determine which elements interact with each other, and their structural properties condition the outcome of the system dynamics. Most empirical networks are, however, not static but continuously changing in time. The node connections are themselves evolving as the dynamic process is taking place on the network. In some cases, both dynamics are coupled in which has been called co-evolution, but in many others the link activations are just a reflection of the finite capacity of the nodes to sustain interactions. As a generic empirical fact, it has been found that the inter-event times between consecutive interactions show statistical distributions with long-tailed decays. The activation patterns among elements in a network may be irregular or bursty and play an important role on the dynamics of processes. Information or disease spreading are paradigmatic examples of this situation. Besides burstiness, several correlations may appear in the process of link activation: memory effects imply temporal correlations, but also the existence of communities in the network may mediate the activation patterns of internal and external links.

In this work we study the competition of topological (community structure) and temporal (link activation) correlations and how they affect the dynamics of systems running on the network. We introduce a model such that correlations can be systematically added and their strength tuned. The procedure we propose to generate different activation patterns in the links is highly flexible. We perform the analysis with a theoretical expression for the inter-event time distribution and its conditional form. The framework is, nevertheless, general and admits any other functional forms for these distributions including those coming from empirical data. This is illustrated with an example using Twitter interaction data. We use two paradigmatic dynamical models: the SI and the voter models. We show that, when acting alone, topologically induced correlations tend to slow down the dynamics on the network, while temporal correlations speed it up. We prove that the origin of this acceleration is in the formation of what we call stable backbones, that allow for a more efficient communication of the elements of the system. In case of the SI, this brings a faster spreading in the network while in the voter model the persistence of the backbone induces the formation of ordered structures that pull the system towards consensus.

We also focus on how the presence of mixed correlations impacts model dynamics. We explore different ranges of strength of temporal and topologically induced correlations. Interestingly, when both types of correlations are present, as occur in most empirical networks, the final dynamics crucially depends on the mix. Temporal correlations can accelerate or delay the dynamics depending on how defined the

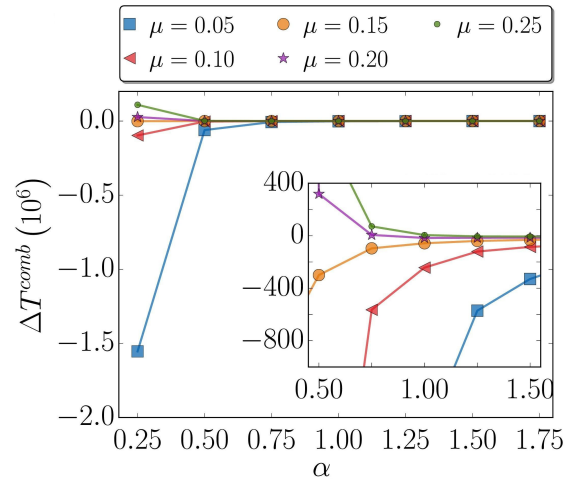


Figure 1: Bifurcation in the dynamics. In the x axis there is the temporal correlation strength and in the vertical one the time distance to reach the absorbing state between the null model and the actual correlated dynamics (positive region means acceleration and negative region means delay). We see that for different value of the topological correlation μ we can go continuously from delay (strong communities) to acceleration (weak communities).

community structure is. We observe a community mixing parameter μ (a measure of how dense a community is) for which a bifurcation on the effect correlations on the model dynamics takes place (see Figure 1). This point changes with the difference between the activation patterns of the links internal and external to the communities but its presence seems to be quite generic. The closer is the link activation between both types of links, the strongest has to be the community structure to find the bifurcation.

To summarize, we present a general framework to include realistic properties of empirical networks through temporal and topological correlations. We exhaustively study how the correlated instances of dynamical models behave when compared to null models. When correlations come alone, the outcomes are straightforwardly identified. When correlations are mixed, nevertheless, the final behavior depend on the combination of the temporal activation pace and how well connected are the communities. We believe that the results we obtain and the mechanism behind them are far from trivial and they are fundamental to have a deeper understanding on dynamics on realistic networks.

The complete article can be found in the [1].

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Clinical markers from language complexity patterns

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One of the first sources of information in psychological and psychiatric practice is language. Language can inform us about possible cognitive impairments, but also about atypical cognitive development. An example of the former is the logopenic progressive aphasia, attributed to either Alzheimer's disease or to frontotemporal lobar degeneration. An example of atypical cognitive development is the linguistic profile exhibited by people with an atypical genotype like Down syndrome or Williams syndrome. The way to approach the linguistic ability of patients with a potential linguistic impairment or atypical language development is usually based on tests (e.g., Boston test) and analyses of utterances by counting words (e.g., (in)capacity to perform a passive sentence or (in)capacity to say words that are semantically related like names of animals). However, as is well-known, sometimes the scores obtained are not fully informative, since some individuals reach scores at the edge of being classified as healthy, although the suspicion about a potential disturbing factor is evident from the speaker's spontaneous speech. There is the possibility to resort to other invasive techniques (e.g., lumbar puncture to detect abnormalities in the cerebrospinal fluid) and-or neuroimaging technologies (e.g. fMRI, DTI, EEG). We contend that there is a methodological gap between the basic tests and invasive/neuroimaging that can be filled by a data analysis technique that approaches speech data macroscopically (instead on focusing on single words/sentences).

We present a new technique for the extraction of more refined data from the language source using a combination of linguistic, morpho-syntactic analysis and network science. This methodology is able to extract complementary information about the speaker's linguistic system, that cannot be observed by the unaided eye. Complexity patterns of word combination emerge from a sample of spontaneous speech. These patterns take the form of a complex network made of words/morphemes (its nodes) and syntactic links (its edges), so that we can extract formal, objective indicators that speak about the cohesion of the speaker's linguistic system, which are the most connected words (hubs), which kind of links are crucial for the structure of her linguistic capacity. Therefore we consider that linguistic networks are good biomarkers or endophenotypes for language impairment or atypical language development.

We have applied this technique to 7 one-year-long corpora of typical children covering 6 different languages, 32 samples of Down syndrome, 20 cases of Specific language impairment and 20 cases of Hearing impairment. Moreover, we have the first data of a pilot study of Williams syndrome language network analysis. In sum, we observe that typical children develop their linguistic networks following a common developmental path, whereas the rest of atypical cases differ from that developmental path. The structure of atyp-

ical linguistic networks is different in many ways and the formal indicators support the idea that these speakers have a qualitatively different ability to combine words and information management.

The continued analysis by means of this technique provides a useful technique for tracking the (a)typical development of language or even its disintegration (in the cases of neurodegenerative diseases).

Scaling in the Recovery of Cities in Special Events

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The objective of this work is to combine the multilayer construction of multimodal transport networks with models of packets running through the network. The complex networks analysis and the multilayer approach has been used to study public transport networks but the resilience and performance of this networks under the real demand and special events still needs to be studied. Different routing protocols give more information about the structure and robustness of this networks. When modelling the use of the public transport systems the shortest path approach fails to simulate the real behaviour due to the high path degeneration, with several shortest paths with low difference in their length. We will model the normal activity of a public transport network under a shortest path routing protocol without information and with full information. While the shortest path routing protocol give rise to a few important hotspots in the city, in case with full information many smaller hotspots appear as a consequence of a higher distribution in the usage of paths.

Once we have tested how the models work, we study the recovery of public transport networks under perturbations. We introduce a huge amount of packets or individuals in the network and study the time of recovery of the network. We will use the previous model on urban mobility to simulate the normal use of the public transport system and study their recovery against perturbations, depending on the amount of agents introduced and the place in the city. First of all we divide a city in areas of 200m x 200m, where we will introduce the perturbations. In this section we will also test two routing protocols and their effect on the recovery of the network. As expected both routing protocols give rise not only to different times of recovery but also to different shapes in the evolution of individuals in the network. In the case where they follow the shortest paths (figure 1.a) we observe a linear recovery with time in a log-log plot. In fact the link with higher betweenness will dominate and the total time of recovery will depend on the load per second of that link. In the case of the adaptative routing with local information (figure 1.b) the difference on the time of recovery when we include more agents is lower specially for higher values, this is due to walking between the source and destination. Basically the different packets use all the routes until all of them collapse and the optimal time is obtained by walking. Interestingly more all the scaling exponents in a log-log plot are between 0.25 and 0.5 depending on the zone where we introduce this perturbation. This scaling exponent is related to the effective dimension of the network, in fact the exponent is equal to the inverse of the effective dimension. This dimension is modified by the appearance of different transport modalities with different speeds and capacities. We proof that the scaling exponent is 0.5 for a regular lattice and for the public transport network with only one transport modality which is equivalent to the regular lattice.

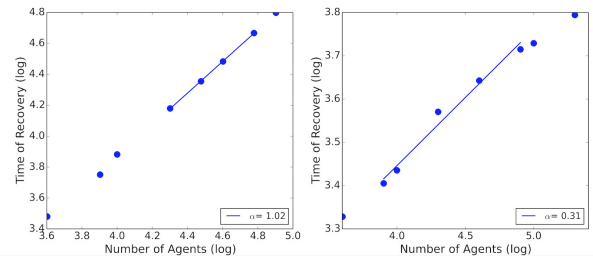


Figure 1: Time of recovery depending on the routing protocol and the number of agents introduced in the perturbation in log-log scale. a) shortest path routing protocol b) adaptive routing protocol with local information.

It is also interesting to analyze how the recovery times change when we introduce the same perturbation in different places of the city. Again we will begin studying the simplest case where all the agents follow the shortest path, this case allows us to calculate the time of recovery. The line that will dominate the recovery will be given by the rate of the betweenness and the load per second. Basically in the case where all lines have the same capacity and frequency, the congested line that should dominate is the one with higher betweenness.

The interesting case is however when the individuals use an adaptative routing protocol because the full topology of the networks comes into play. In this case we expect that the center of the city, where there is a higher density of lines, will be the place with faster recovery of the network and the recovery times will increase as we go further from the center. As each line has a load per second, beginning at the point where the perturbation is introduced, increasing the distance that an individual will walk we observe an increase of the load per second as the access to lines increases. We proof time of recovery of the different zones will be given between the point of equilibrium between walking time and total capacity in the area walked.

Clustering in a polydisperse phytoplankton population

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Phytoplankton's patchiness has profound effects on the ecology of the oceans [1]. It plays a fundamental role in microorganisms population's composition and it also modulates the encounter rate, the predation and the reproduction [2]. Clustering can occur over very different scales, from planetary to the microscale; in this work we are interested in the small scale clustering. It is due mainly to the combined effect of turbulence and phytoplankton motility [3]. Indeed it has been found that motile microorganisms are more patchy than non-motile [4].

Several species of motile phytoplankton are able to swim upward guided by a stabilizing torque arising from an unbalance distribution of the mass in the cell. The latter kind of motion is called gyrotaxis; different works have showed how this type of motility, combined with the presence of a flow (laminar, horizontal shear, turbulent), generates strongly inhomogeneous distributions [3, 5, 6, 7].

For these reasons the current study focuses on the effect of polydispersity (or variation) of the swimming parameter in a gyrotactic phytoplankton population transported by a turbulent flow.

At first we investigate the case of a bimodal distribution, composed by two different species; then we consider a more realistic case, where the swimming parameter is Gaussian-distributed within the population. By means of extensive numerical simulations, we find that the variety of the population introduces a characteristic scale R^* in its spatial distribution, that depends on the dispersion of the population. At scales smaller than R^* the swimmers are homogeneously distributed, while at larger scales an inhomogeneous distribution is observed with a fractal dimension. Our numerical results, which extend recent findings for a monodisperse population, indicate that in principle it is possible to observe small scale, fractal clustering in an experiment with gyrotactic cells.

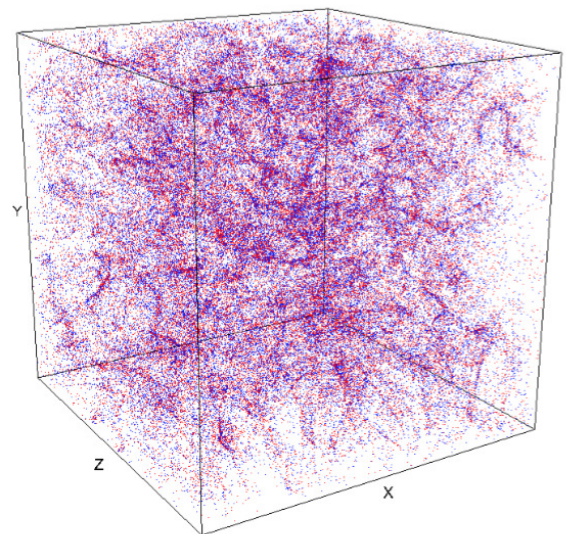


Figure 1: Distribution of the positions of two species of swimmers with two different swimming parameter (blue and red) in a turbulent flow.

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Dynamical localization in realistic kicked rotors

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We will show at the conference that dynamical localization (quantum suppression of classical diffusion) in the context of ultracold atoms in periodically shaken optical lattices subjected to time-periodic modulations having equidistant zeros depends on the impulse transmitted by the external modulation over half-period rather than on the modulation amplitude. This result provides a useful principle for optimally controlling dynamical localization in general periodic systems, which is capable of experimental realization.

Quantum effects in transport phenomena in classical systems represent an interesting fundamental issue in quantum theory that started from a remark of Einstein in his celebrated paper on torus quantization. One of such effects, widely studied in the context of time-periodic systems, is the quantum suppression of classical chaotic diffusion, or dynamical localization (DL) for short. Remarkably, this effect is a quantum manifestation of the fact that a time-periodic modulation can stabilize a system, and it is thus expected to play a key role in our understanding of the problem of quantum-classical correspondence in classically chaotic systems. While it is natural to think that, with the period fixed, this effect must depend on the temporal rate at which energy is transferred from the driving mechanism to the system, i.e., on the modulation waveform, the main target of study up to now has only been their dependence on the modulation amplitude because of the traditional use of sinusoidal modulation. Recent work has provided strong evidence for a different dependence of DL on sinusoidal and square-wave modulations. Since there are infinitely many different waveforms, a natural question arises: How can the influence of the shape of a periodic modulation on DL be quantitatively characterized. In this work, we demonstrate that for space-periodic systems subjected to a generic AC time-periodic modulation with equidistant zeros such characterization is well provided by a single quantity: the impulse transmitted by the modulation over half-period hereafter called modulation impulse. This impulse is a quantity that accounts simultaneously for the modulation's amplitude, period and waveform.

The dynamics of our model system of ultracold atoms interacting with a phase modulated light field produced using an oscillating mirror is well described by the periodic Hamiltonian

$$\tilde{H} = \tilde{p}^2/(2M) - V_0 \cos [2k\tilde{x} - \lambda F(t)], \quad (1)$$

where M is the atomic mass, \tilde{x} the position, \tilde{p} the momentum, V_0 the potential height, k the wave number, λ the dimensionless modulation depth, and $F(t)$ the AC modulation given by

$$F(t) = F(t; m, T) \equiv N(m) \operatorname{sn} [4Kt/T] \operatorname{dn} [4Kt/T], \quad (2)$$

where $\operatorname{sn}(\cdot) \equiv \operatorname{sn}(\cdot; m)$ and $\operatorname{dn}(\cdot) \equiv \operatorname{dn}(\cdot; m)$ are Jacobian elliptic functions of parameter m , and $K \equiv K(m)$ is

the complete elliptic integral of the first kind. $N(m)$ is the normalization factor given by

$$N(m) \equiv \left\{ a + \frac{b}{1 + \exp[(m-c)/d]} \right\}^{-1}, \quad (3)$$

where the values of the parameters are set equal to $a \equiv 0.43932$, $b \equiv 0.69796$, $c \equiv 0.3727$, and $d \equiv 0.26883$, in order to have the same modulation amplitude (equal to unity) and period, T , independently of the waveform, i.e. $\forall m \in [0, 1]$. Notice that F in (1) introduces a convenient (since allowing obtaining many analytical results) flexible periodic pulse which varies its form depending on the value of m . For $m = 0$, one recovers the well known harmonic excitation case since then $F(t; m = 0, T) = \sin(2\pi t/T)$. On the other hand, for $m \neq 0$ the waveform has different shapes. For example, for $m = 0.72$ a nearly square-wave pulse is obtained, whereas for the limiting value $m = 1$ the modulation vanishes.

As will be shown, the modulation impulse associated with $F(t)$, defined as

$$I \equiv I(m, T) = \int_0^{T/2} F(t; m, T) dt = \frac{TN(m)}{2K(m)}, \quad (4)$$

is a relevant quantity to characterize the effect of the modulation's waveform. As expected, it is a function of m , which has a single maximum at $m = m_{\max}^I \simeq 0.717$. Also, it tends to zero very quickly as $m \rightarrow 1$.

Our results show for AC-driven space-periodic Hamiltonians that the impulse transmitted by the timeperiodic modulation is an essential quantity to understand the phenomenon of DL, which can be optimally controlled by changing the form of the AC, i.e. the parameter m in Eq.(2). Remarkably, our results shown that the impulse principle reliably control DL irrespective of the quantity degree of the system. While this result holds for the wide class of AC modulations having equidistant consecutive zeros, one expects it to be also valid for even more general class of time-periodic modulations, at least in the adiabatic regime. This principle, which can be straightforwardly applied to other phenomena, such as field-induced barrier transparency or quasi-energy band collapse, paves the way for optimum coherent control of diverse quantum systems. Additionally, it has been shown that the classical invariant structures of phase space have a deep impact on the quantum dynamical behavior of the system, as the modulation impulse is varied.

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Photonic Information Processing at 20GS/s rates based on a Laser System with Delayed Feedback

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The demands of society on information processing rise every day. Novel information processing schemes based on machine learning approaches like reservoir computing (RC) [1] have attracted strong interest in the last years. Making use of complex dynamics, RC is capable of state-of-the-art performance at tasks traditional computers struggle with. Photonic implementations of RC are of great interest due to their high speed and easy implementation. A reservoir computer, conceptually as simple as a semiconductor laser with delayed optical feedback already proved excellent (tasks?) at 5GSamples/s rates thanks to its nonlinear responses in the GHz regime [2]. The study of the properties of the system and their impact on the RC performance is crucial to better understand the underlying physics, improve designs and tailor systems for specific tasks.

In this work we experimentally explore the potential of semiconductor lasers with optical feedback and optical injection for ultra-fast information processing. We study the fundamental properties and key parameter dependencies of this complex system, and connect them to the information processing performance. Identifying the best conditions we demonstrate excellent performance for information injection at modulation rates up to 20GS/s.

Our photonic RC setup is based on a discrete mode quantum well semiconductor laser. The laser is subject to delayed optical feedback, implementing the reservoir. The optical fiber delay loop includes components to control the conditions of the feedback light. The injection of information is realized using a single mode DFB laser emitting continuous wave and modulating its output with an amplitude modulator. We study information processing performance and properties of the photonic reservoir computer at different modulation rates up to 20GS/s. We evaluate fundamental optical and dynamical properties of the system, in particular injection locking, consistency of the responses of the system to modulated optical injection (Fig. 1a), and memory of the reservoir computer (Fig. 1b). We identify regions with different properties, and how tuning one parameter can allow access to different set of properties. Information processing performance is evaluated with a nonlinear time series prediction task (Fig. 1c), training the reservoir computer to perform three time steps prediction on a chaotic Mackey-Glass time series. Best prediction errors are obtained when memory and consistency show suitable properties. We can maintain non-degrading performance up to the highest modulation rates.

In conclusion, we show information processing with excellent performance up to modulation rates of 20GS/s. These results pave the way for novel hardware-implemented computing schemes based on complex systems properties.

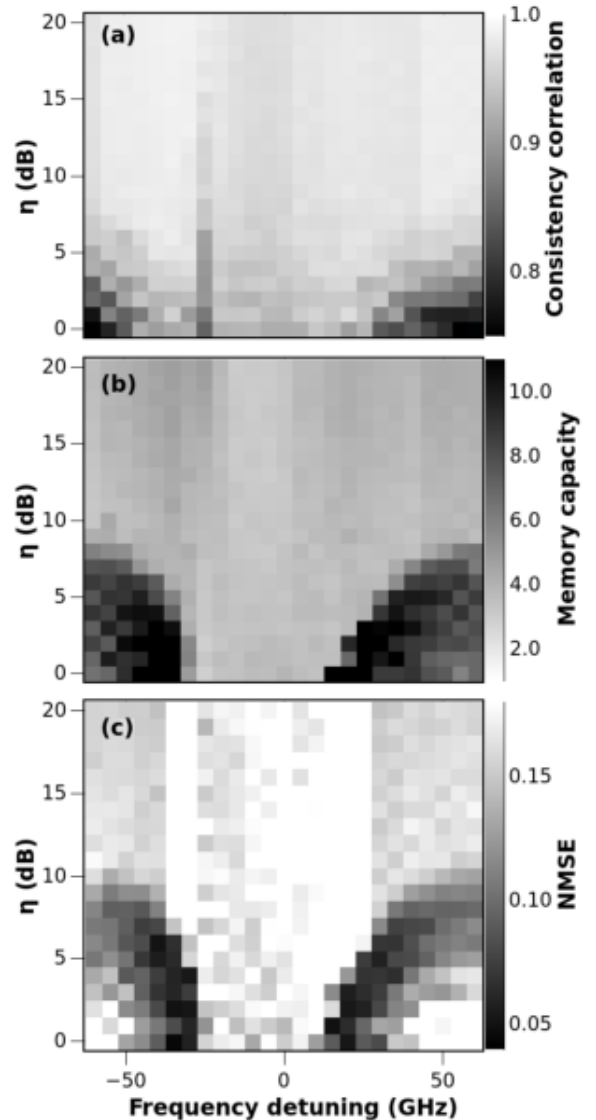


Figure 1: Results of (a) consistency, (b) memory, and (c) nonlinear time series prediction error dependence on frequency detuning and η (feedback attenuation) for a modulation injection at 10GS/s. All panels share the horizontal axis.

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Spontaneous synchronization and asymptotic entanglement in coupled optomechanical systems dissipating into a common bath

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Coupled physical systems can dissipate collectively into the same environment or common bath, a situation that is known to enable physical phenomena such as decoherence free subspaces, asymptotic entanglement or collective synchronization, amongst others. This dissipation scenario is the opposite of the usually considered separate baths scheme, in which the units of the system dissipate into different uncorrelated thermal baths. The conditions for collective dissipation have been recently established in structured environments [1] in a general theoretical framework.

In this work we consider two mechanically coupled optomechanical systems. Dissipative couplings induced by collective dissipation can arise due to the elastic radiation propagating in the surrounding crystal and have not been characterized so far. Here we analyze the effects of common dissipation onto two different physical phenomena. Firstly, we study the emergence of synchronization between the mechanical oscillators, and we compare the results with the ones of previous studies in which separate mechanical dissipation was considered. In particular we show that collective mechanical dissipation enlarges the region in which spontaneous synchronization can be found. Secondly, we study the presence of entanglement between the mechanical modes in the asymptotic state, below the threshold self-sustained oscillations. Asymptotic entanglement between the mechanical mode and the optical one is known to arise in single optomechanical systems. Here we study the novel cases of mechanically coupled devices dissipating both in common and separate mechanical baths. We report asymptotic entangled states in both cases, and we analyze the strong relation between the presence of entanglement and the degree of optomechanical cooling of the oscillators. Again we find that collective dissipation enhances the presence of asymptotic entanglement in the studied parameter region. We finally explore the presence of quantum synchronization in this regime.

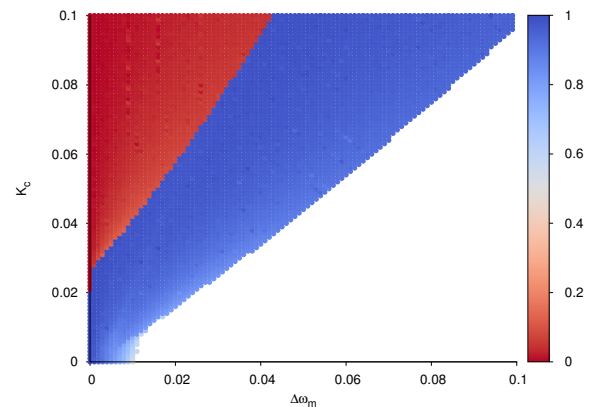


Figure 1: Synchronization diagram for two mechanically coupled optomechanical oscillators dissipating into a common bath: white region corresponds to unsynchronized oscillations, red and blue regions correspond to synchronized oscillations. The phase difference $|\delta\varphi|$ at which the mechanical oscillations lock is encoded in the color scale: dark blue regions correspond to anti-phase synchronization ($|\delta\varphi| = \pi$), dark red regions to in-phase synchronization ($|\delta\varphi| = 0$). The map is obtained varying the mechanical coupling strength K_c and the mechanical frequency detuning $\Delta\omega_m$. The other parameters are fixed to the same values as Ref. [2] in order to compare the results with the ones obtained considering separate mechanical dissipation. In particular the fixed parameter values are: $\mathcal{P}_1 = \mathcal{P}_2 = 0.36$, $\Gamma_1 = \Gamma_2 = 0.01$, $x_{01} = x_{02} = 1$, $\omega_{m1} = 1$ and $\omega_{m2} = \omega_{m1} + \Delta\omega_m$.

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Seeing the Trees for the Forest: Disentangling Delay Propagation in Airport Networks through Delay Propagation Trees

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During the last century, air transportation has grown steadily and faster than any other transportation mode, with only a minor setback in the wake of 9/11 attacks [1, 2]. The yearly cost of flight delays is measured in billions dollars/euros in the US and Europe [3, 4], and various socio-economical factors contribute to the difficulty of providing adequate infrastructural support, for example in the case of airports located in urban areas [5]. Having a thorough understanding of the processes regulating the spreading of disruption and delays in airport networks is therefore an important research goal, which is also interesting from a more theoretical point of view as these systems typically exhibit rich, complex behavior, and can be the substrate for phenomena not strictly related to air transportation, such as epidemic spreading. This type of study is made difficult not only by the domain-specific knowledge required, but also because of the scarce availability of high-quality data about flight performance outside of the US from institutional sources. In order to overcome this problem, we use data obtained from the Flightradar24 web service, which covers a period of almost two years.

In this work, we analyze daily traffic for both the US and European systems, with the goal of finding and classifying interesting, recurring patterns which characterize the days where significant perturbations took place. Of particular importance are the aircraft returning to a large hub multiple times during the day (especially in the European system, where airlines have a smaller number of operating bases), and/or depart earlier in the morning. Furthermore, the delay propagation trees can be reconstructed from the data, giving insights into the delay propagation patterns. In order to do this, we define a square lattice where each cell represents a single airport during a time window of fixed size. A directed link between two cells is established if there is at least one delayed flight departing from one cell and arriving in the other, and the weight is given by the total amount of delay. An example of this is shown in Fig. 1, where O'Hare International Airport (ORD) starts propagating delay early in the morning before receiving any significant input, from which we can infer that the delay was generated on-site. Fig. 2 shows the daily incoming and outgoing delays for the largest airports in the network during the same day. ORD is shown having both very high amounts of incoming and outgoing delay, as airports suffering from severe problems can request incoming flights to be delayed (for example to wait for better meteorological conditions). This exemplifies that the fact that delay is being transmitted from one place to another is not enough to draw conclusions about causality, making an analysis of the topology of connections necessary.

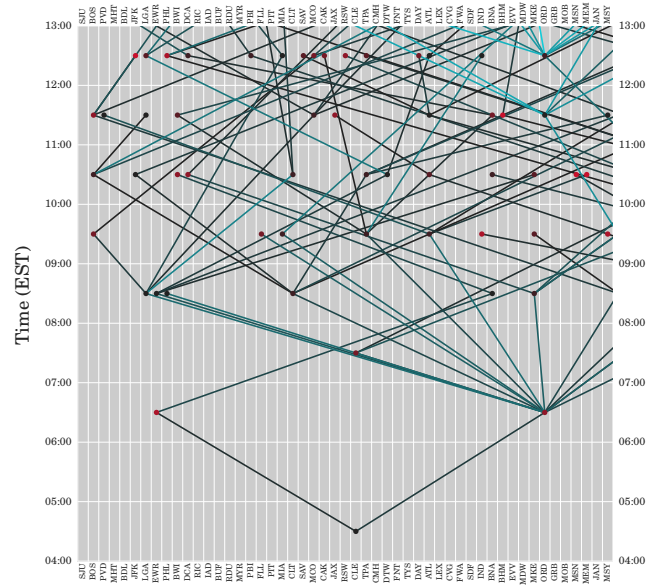


Figure 1: The beginning of a delay propagation tree from 23rd of March 2015. Brighter edges transfer higher delay, brighter nodes produce more delay than they receive.

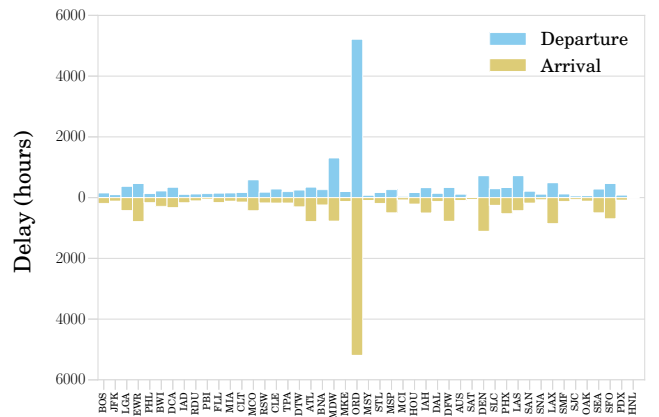


Figure 2: Daily input and output delay for the largest (in terms of movements) airports in the US in 23rd of March 2015.

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A spatial agent-based model of the UK housing market: understanding the economic roles of infrastructure

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Infrastructure systems are, in conjunction with the socio-economic environment in which they are embedded, prime examples of complex socio-technical systems. Whilst a growing number of empirical studies have addressed the relationship between infrastructure investment and economic growth, the mechanisms by which infrastructure influences economic activity are not well understood in quantitative terms. Part of the difficulty derives from the fact that infrastructure delivers services to businesses and society through networks, and thus any appraisal needs to take place at a system scale. Furthermore, infrastructure can have non-marginal economic effects, and the corresponding investments are often intended to promote structural change, innovation, and social well-being. Infrastructure systems therefore present well-known, but still unresolved, challenges from the perspective of economic appraisal.

In this contribution, we study some of the main channels and mechanisms by which infrastructure has an impact on the economy. In particular, we focus on its effect on housing markets. Housing is the largest asset class in the economy, as well as one of its main drivers: the dynamics of house prices has a direct impact on the balance sheets of banks, and thus on the availability of credit, as well as on household debt, and thus on consumption levels. At the same time, housing markets are strongly influenced by the rest of the economy. In particular, the geographical distribution of the demand for houses is, to a significant extent, driven by the availability of employment opportunities. Households are, indeed, confronted with a joint choice of employment and housing: they need to find a job corresponding to their skills and, simultaneously, search for a house that they can afford with the corresponding salary and within a feasible commuting distance from the referred employment. Transport infrastructure is essential for assessing this distance and, thus, plays a major role in determining the geographical distribution of the demand for housing. Simultaneously, it is precisely this spatial distribution of houses which determines the geographical structure of the demand for all infrastructure services, from solid waste to energy and water. Finally, as a consequence of constant improvements on the digital communications sector, different spatial distributions of houses and employments become feasible.

In order to model this complex relationship between the economy and infrastructure through the housing sector, we develop a spatial agent-based model of the housing market. In particular, we develop a district-based model, i.e., we define a discrete set of locations, each of them containing a non-spatial housing market model, and a set of couplings or commuting fluxes between those locations. The non-spatial model used in each of the districts (inspired by [1]) simulates a large pool of households with realistic life-cycles, inheritance of properties, buy-to-let investors, and it models the

rental market in detail. This approach allows us to tackle simultaneously two types of heterogeneities: on the one hand, the internal heterogeneity of each district's market, where we model the individual behaviour and interactions of first-time buyers, home owners, buy-to-let investors, and renters; and, on the other hand, the geographical heterogeneity due to different agglomeration mechanisms.

As a case study, and as a result of an ongoing collaboration with the Bank of England, we focus on data about the UK for the purposes of model calibration and validation. In particular, the model is calibrated against a large set of microdata from household surveys and housing market data sources such as the Financial Conduct Authority's (FCA) loan-level Product Sales Data (PSD) and the When-Fresh/Zoopla data on rental listings, as well as confidential data from the Bank of England. Once these microdata sources have been used to fine-tune household's individual characteristics and behaviours (e.g. the joint income and age distribution), a macro-calibration is performed to ensure consistency with different economic aggregates and housing market core indicators.

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Reconstructing networks of pulse-coupled oscillators from non-invasive observations

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We present a method for reconstructing a network of pulse-coupled oscillators from non-invasive observations of the system's output. Assuming that the pulse trains of all nodes are known and that the coupling between the elements is sufficiently weak to justify the phase dynamics description, we recover the connectivity of the network and properties of the nodes.

In our previous work, we have developed an approach to recover the connectivity of a network in the case of oscillatory processes that allow for conventional phase estimation [1]. In this work, we have tackled the problem for the case of pulse-coupled oscillators. Our basic model for the network nodes are phase oscillators which issue a spike when their phase φ reaches 2π . (We consider the phases in the $[0, 2\pi)$ interval, i.e., after the spike generation the phase of the unit is reset to zero). This spike affects all other units of the network according to the strength of the corresponding connections. Let the size of the network be N and let the connectivity be described by an $N \times N$ coupling matrix \mathcal{E} , whose elements ϵ_{km} quantify the strength of the coupling from unit m to unit k . Between the spiking events, phases of all units obey $\dot{\varphi}_k = \omega_k$, where ω_k are natural frequencies. If unit k receives a spike from oscillator m , then it reacts to the stimulus according to its phase response curve (PRC) [2], $Z_k(\varphi)$. This means that the phase of the stimulated unit is instantaneously reset, $\varphi_k \rightarrow \varphi_k + \epsilon_{km} Z_k(\varphi_k)$.

Our approach is based on making a preliminary estimation of the network connectivity by evaluating the impact an oscillator has on another oscillator's inter-spike intervals. This estimation, although crude, gives us some insight into the network, such that together with linearly approximating the phases and representing the PRC as a finite size Fourier series, we can get an approximation for the PRC. Once both approximations (connectivity and PRC) are obtained, they can be used to better approximate phases, which in turn yields better approximations of connectivity and PRC in the next iteration of the process. The more iterations one does, the better the recovery (see Fig. 1 for an example of the reconstruction).

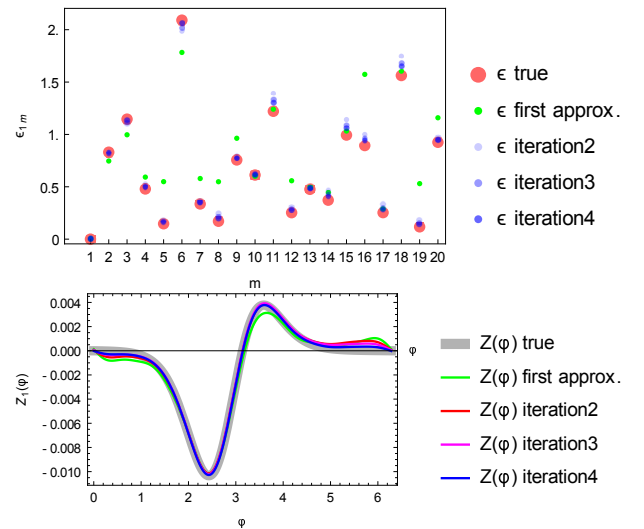


Figure 1: The reconstruction of the connectivity ϵ (top) and phase response curve $Z(\varphi)$ (bottom) of the first node in a network of 20 oscillators. Notice how the reconstruction improves with subsequent iterations (in different colors).

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Normal and anomalous diffusion of two-dimensional solitons

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The dissipative solitons that appear in nonlinear optics can suffer explosions: after remaining localized for a certain period of time without major profile changes, they can grow and become broader for a short time, returning to the original spatial profile afterwards, and repeating the cycle intermittently [1, 2, 3].

We consider the dynamics of dissipative solitons in two spatial dimensions, inspired by a model of mode-locked lasers based in the complex Ginzburg-Landau equation.

We found that there are two regimes for the spatial motion of the soliton: in the “normal” regime the soliton explodes asymmetrically most of the time; and in the “subdiffusive” regime the soliton experiences long sequences of symmetric explosions before exploding asymmetrically. We analyzed the soliton’s trajectories in both regimes using the tools of anomalous diffusion [4]. For the normal regime we found statistics similar to Brownian motion. For the subdiffusive regime we observed large trajectory-to-trajectory variations and weak ergodicity breaking that can be explained using a simple continuous-time random walk model [5].

In this presentation we analyze the distributions of generalized diffusivities [6] for the trajectories, and the distributions of relative angles [7], that explain the transition between the regimes and the “destructive” effect of additive noise.

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Immunization and targeted destruction of networks using explosive percolation

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Immunization of networks against epidemic spreading is an important topic in complex-systems. Some applications of this area include prevention of infectious diseases, computer safety strategies against malicious viruses and information spreading in social networks. Infectious spreading in a population use the network of contacts between nodes for their spread. Accordingly, immunization corresponds to an attack that fragments the network on which it can spread. We propose a new method, ‘explosive immunization’ (EI) [1], to find those nodes whose removal is most efficient in destroying connectivity. Vaccinating such nodes provides an efficient way to fragment the network and reduce the possibility of large epidemic outbreaks. While most of the works assume that important blockers are equivalent to good spreaders [2], our strategy specifically targets the first kind, improving thus the results compared to other immunization methods.

In our approach, the network consists of N nodes, out of which qN are vaccinated; the rest are left susceptible to the infection. The size of an invasion will depend on the fraction q of immunized nodes, the type of epidemic and its virulence. However, the maximum fraction of nodes infected at any time will always be bounded by the relative size $S(q)$ of the largest *cluster of susceptible* nodes. Keeping $S(q)$ as small as possible will therefore ensure that epidemic outbreaks of any type are as small as they can be for a vaccination level q . For large networks the aim of immunization is to fragment them so that $S(q) = 0$. The immunization threshold q_c is the smallest q -value at which $S(q) = 0$. Although q_c is not well defined for finite networks, it can be estimated reliably. Below this value, the existence of a giant cluster is unavoidable, thus the problem is reformulated in identifying the nodes that minimize $S(q)$.

Contrary to most of the works, we start from an inverse approach, where all the nodes are vaccinated so there is no risk of an epidemic. At each step we “unvaccinate” the node with less “blocking ability” among a finite set of randomly chosen candidates. This is directly related to the concept of *explosive percolation* proposed by Achlioptas *et al.* [3]. Explosive percolation has been discussed in a large number of papers because of its very unusual threshold behavior but, to our knowledge, our work is the first problem where it is practically used. We grade the blocking ability of a node using two different heuristic scores, depending on which side of the critical threshold q_c we are. The first score (for $q > q_c$) uses the size of the cluster that each node would join if we add it to the network, together with a parameter proportional to the node degree. When the giant cluster emerges, this method grows secondary large clusters that eventually will join the largest cluster. The cluster merging generates then an undesired explosive behavior (see red dashed line in figure 1). In order to prevent this situation, below q_c we use a

second score that specifically forces the growth of the largest cluster, but in a minimal way. This avoids the formation of secondary large clusters and minimizes $S(q)$ for $q < q_c$ (see continuous black line in figure 1).

We tested Explosive Immunization in several random models and real world networks. Our results are compared with the outcome of the Collective Influence method (CI) [2] among others. Although CI had been claimed to be the best immunization method in the literature, EI is better in detecting the critical threshold q_c (see figure 1). In general it also provides the minimal $S(q)$ below the threshold: although it is not optimal everywhere in real-world networks, a combination of the two scores always provides the bests global results. In addition, our method is also extremely fast with time complexity linear in N up to logarithms.

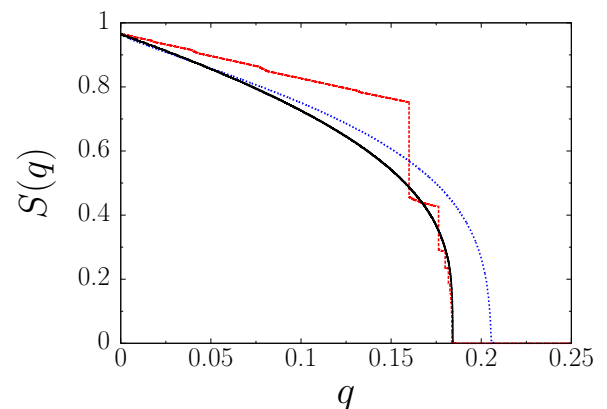


Figure 1: Relative size $S(q)$ of the largest clusters against q , for a Erdős-Rényi network with $N = 10^6$ and average degree 3.5. The red dashed curve with jumps is obtained if EI is used with the first score for all q . The continuous black curve is obtained using the second score for $q < q_c$. The blue dotted line shows the results using CI from [2]. EI estimates $q_c \simeq 0.1838$.

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Analyzing the amplification of signals in chains of unidirectionally coupled MEMS

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Over the past decade, electromagnetically transduced microelectromechanical systems (MEMS) have garnered significant interest due to their scalability, self-sensing capabilities and distinct applications ranging from mass sensing to electromechanical signal processing and computing. MEMS are systems whose dimensions are at the order of millimeter and micrometer. They are made of mechanical branches (beams, gears, plates and membranes) and microelectronic circuits for electrical branches. The main actuation and properties used in MEMS are piezo-resistivity, piezoelectricity, electrostatics, thermal, electromagnetism and optics. MEMS have a large area of applications such as automotive industry, portable devices, consumer electronic products and cell phone industries. They play a significant role on the magnetic field sensors.

MEMS can sometimes be subject to very weak signals when they are used as sensors or when they are used as actuators. In this case, one can therefore ask if such signal can propagate, be amplified or be detected in a MEMS network.

The aim of this work is to analyze the propagation and the amplification of an input signal in a chain of identical unidirectionally coupled MEMS [1]. The dynamics of the system is described by:

$$\ddot{x}_1 + \gamma_1 \dot{x}_1 + \omega_e^2 x_1 + \beta x_1^3 + \lambda_1 \dot{y}_1 = f(t) \quad (1)$$

$$\ddot{y}_1 + \gamma_1 \dot{y}_1 + \omega_m^2 y_1 + \beta y_1^3 - \lambda_2 \dot{x}_1 = 0 \quad (2)$$

$$\ddot{x}_i + \gamma_1 \dot{x}_i + \omega_e^2 x_i + \beta x_i^3 + \lambda_1 \dot{y}_i = k x_{i-1} \quad (3)$$

$$\ddot{y}_i + \gamma_1 \dot{y}_i + \omega_m^2 y_i + \beta y_i^3 - \lambda_2 \dot{x}_i = 0, \quad i = 2, \dots, n \quad (4)$$

where the variables x and y represent respectively the current in the electrical part and the displacement of the mechanical part, $f(t)$ is the external signal injected in the first MEMS, k is the coupling coefficient and we consider $\gamma_1 = 0.01$, $\gamma_2 = 0.3$, $\lambda_1 = 1.01$, $\lambda_2 = 1.06$, $\omega_e = 1$, $\omega_m = 1.1$ and $\beta = 0.9$.

Two types of external excitations are considered: sinusoidal and stochastic signals. We show that sinusoidal signals are amplified up to a saturation level which depends on the transmission rate and, despite MEMS being nonlinear the sinusoidal shape is well preserved if the number of MEMS is not too large. However, increasing the number of MEMS, there is an instability that leads to chaotic behavior and which is triggered by the amplification of the harmonics generated by the nonlinearities (see Fig. 1). We also show that for stochastic input signals, the MEMS array acts as a band-pass filter and after just a few elements the signal has a narrow power spectra (see Fig. 2).

In addition the case of non identical units is also studied and particular attention is paid to the effect of disorder in the natural frequency of electric part ω_e in the performance of the chain to amplify weak signals.

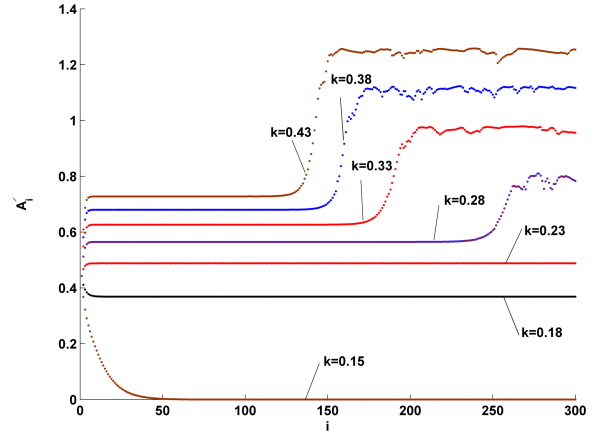


Figure 1: Variation of the response amplitude of the mechanical part versus the rank i of the MEMS in the network for seven values of the coupling strength, $f = 0.1$ and $\omega = 0.67$

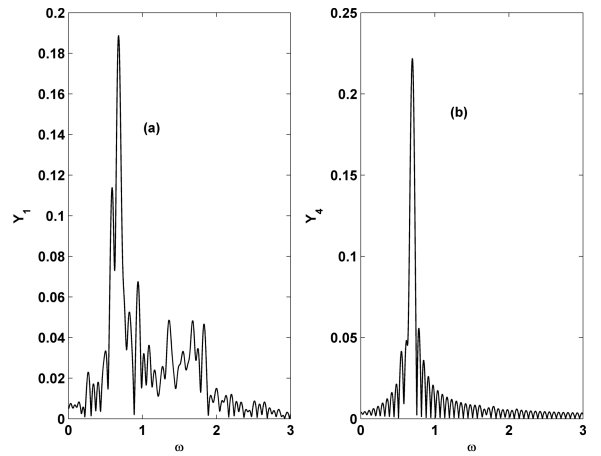


Figure 2: Power spectra of the time trace for $x_i(t)$ for $i = 1$ (a) and $i = 4$ (b).

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Competition between drift and spatial defects leads to soliton oscillatory and excitable dynamics

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Dissipative solitons (DSs) are exponentially localized structures appearing in dissipative systems far from thermodynamic equilibrium. DSs are formed due to the balance between nonlinearity and spatial coupling and then driving and dissipation.

DSs can undergo instabilities leading to a wide variety of temporal dynamics, such as periodic oscillations [1] and chaos [2, 3]. It has also been theoretically shown that in nonlinear Kerr cavities, DSs can display excitable behavior despite the fact that the local dynamics (namely the dynamics in the absence of spatial coupling) are not excitable [4]. This differs from systems where excitability is a local property, such as neural models, because excitability is now an emergent property of the DSs. However, while DS excitability may be useful in information processing [5], in two-dimensional (2D) spatial systems oscillatory and excitable DSs are elusive and for most systems only static DSs have been reported. This situation contrasts with one-dimensional (1D) systems such as fiber cavities, where periodic oscillating DSs have been demonstrated experimentally and theoretically [3].

We recently showed that the competition between spatial inhomogeneities and drift provides a way to induce oscillations and excitability of DSs [6]. This competition introduces an oscillatory instability, which can lead to a regime in which DSs are pulled one by one from the defect (referred to as a train of DSs) and to an excitable regime in which the DSs stay pinned in the defect but can be pulled out by a transient perturbation to the system.

Here we build on this work and present a detailed bifurcation analysis of the various dynamical instabilities that result from the competition between a pulling force generated by the drift and a pinning of the solitons to spatial defects [7]. For convenience we will consider the 1D Swift-Hohenberg equation (SHE) for a real field which is a prototypical system that does not exhibit any time-oscillatory dynamics. We show that oscillatory and excitable dynamics of dissipative solitons find their origin in multiple codimension-2 bifurcation points. Moreover, we demonstrate that the mechanisms leading to these dynamical regimes are generic for any system admitting dissipative solitons. Therefore we conclude that oscillatory and excitable dynamics are a general feature for any system admitting DSs in the presence of drift and defects. Such inhomogeneities or defects are unavoidable in any experimental setup, and drift is also often present in many optical, fluid, and chemical systems. In optical systems this can be caused by misalignments of the mirrors, nonlinear crystal birefringence, or parameter gradients, while in fluid and chemical systems drift is due to fluid flow.

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Population dynamics in an intermittent refuge

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Population dynamics is constrained by the environment, which needs to obey certain conditions to support population growth. We consider a standard model for the evolution of a single species population density, that includes reproduction, competition for resources and spatial spreading, while subject to an external harmful effect. The habitat is spatially heterogeneous (see Fig. 1), there existing a refuge where the population can be protected [1, 2, 3]. Temporal variability is introduced by the intermittent character of the refuge.

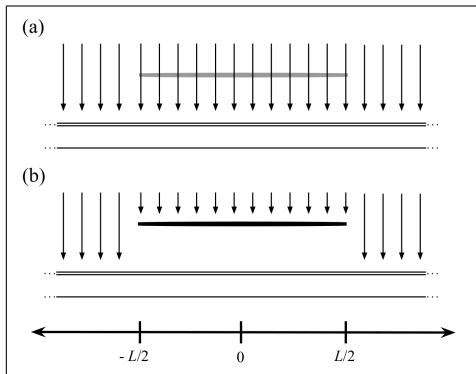


Figure 1: Pictorial representation of a one-dimensional habitat subject to an external harmful effect (downwards arrows) with a refuge (thick segment) of size L in the inactive (a) and active (b) states. In the active state, the refuge is able to block the harmful effect.

Explicitly, we assume that the temporal evolution population density distribution $u(x, t)$ is given by

$$\partial_t u(x, t) = D \partial_{xx} u(x, t) + f(u) + \psi(x, t) u(x, t), \quad (1)$$

with

$$\psi(x, t) = -A \left(1 - \Theta(L/2 - |x|) \varphi(t) \right), \quad (2)$$

with $A > a$. The parameter D is the diffusion coefficient, $f(u) = au(x, t) \left[1 - \frac{u(x, t)}{K} \right]$, with intrinsic growth rate a and carrying capacity K . The temporal behavior is given by φ which is assumed to be periodic or random. The parameter λ controls the fraction of time that the refuge is inactive and τ is the environment time scale.

Depending on the refuge size L , the population can be driven to extinction ($L < L_c$) or survival ($L > L_c$). The value of the critical size L_c depend on the problem spatiotemporal scales. We obtain approximate expressions for the critical size L_c for the slow ($\tau \ll \tau_S$) and fast environment ($\tau \gg \tau_S$), where $\tau_S \sim 1/a$ is the system time scale. Numerical simulation are also used to complement our results, investigating the conservation of the population for different refuge temporal behavior.

The results can applied to a wide range of situations, from a lab setting where bacteria can be protected by a blinking mask from ultraviolet radiation [2], to large scale ecosystems, like a marine reserve [3] where there can be seasonal fishing prohibitions.

Our results may be useful to provide insights to guide management of ecological reserves when the population is sensitive to environment temporal variability [3].

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Multiplex Brain Networks

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Neural systems consist of large numbers of interdependent components (i.e. neurons, cortical columns, etc.) that interact in qualitatively different ways across a range of different scales [1]. They are therefore naturally described using a multilayer or multiplex network approach [2, 3], in favour of the more standard single-layer network analyses [4] that have historically been widely applied to such systems. In this work we consider brain network models consisting of three layers: an anatomical layer describing the large-scale connectivity of the Macaque monkey, and a pair of functional layers that are derived by measuring pairwise correlations between time series of simulated excitatory and inhibitory neural activity. We investigate and characterize correlations between structural and functional layers, as system parameters controlling simulated neural activity are varied, by employing a range of multiplex measures [2, 3], as well as a recently forwarded structure-function clustering coefficient [5], which quantifies the emergence of functional connections that arise between structurally unconnected regions. Moreover, we demonstrate that such a simultaneous analysis of structure-function networks is better placed to capture emergent features and capabilities of neural systems than standard single-layer analyses.

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Symmetric threshold model

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Granovetter's threshold model assumes an irreversible process of adoption. Depending on the initial conditions and the threshold value there are two possible steady states of the system: an absorbing state when only adopters are present, and a frozen disordered state which matches initial conditions. We here introduce the symmetric threshold model where an adopter (a non-adopter) can become a non-adopter (an adopter) if a fraction of its adjacent non-adopters (adopters) exceeds the threshold. This work answers the question of how recovery process changes the phase diagram of the threshold dynamics. Interestingly, a new steady state arises, namely an active disordered state characterized by constant flips of the agents. In addition, there are two possible absorbing states, when only the adopters or only the non-adopters remain in the system. We observe the same qualitative behavior for several topologies, complete graph, square lattice, random network, and scale-free network. We study how a network structure modifies the shape of the transition lines on the phase diagram. Our numerical findings are also well-described by analytical calculations.

Synchronization of fluctuating delay-coupled chaotic networks

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Networks with coupling delays play an important role in various systems, such as coupled semiconductor lasers, traffic dynamics, communication networks, genetic transcription circuits or the brain [1]. Such a coupling delay typically arises due to the finite velocity of transmission of information. Here, we study the effect of a connectivity that changes over time. Such network fluctuations are essential features of some real networks, as for instance, interacting neurons, where synaptic plasticity continuously changes the topology [2].

We concentrate on the synchronization properties of chaotic maps, coupled with an interaction delay T_d . The coupling topology fluctuates between an ensemble of directed small-world networks, while keeping the mean degree constant. These network fluctuations are random, and not adaptive, i.e., the network evolution is not linked to the state in any way.

We find that the synchronization properties of the fluctuating network are strongly dependent on the two time scales T_d , the delay along the links, and T_n , the timescale of the network fluctuations. When the network fluctuations are much faster than the coupling delay ($T_n \ll T_d$) the synchronized state can be stabilized by the fluctuations: synchronization can be stable even if most or all temporary network topologies are unstable. There is a qualitative agreement with the fast switching approximation [3], however not a quantitative agreement. We complement these results with analytical findings on small fluctuating motifs.

When we increase T_n , the synchronized state destabilizes as both time scales collide ($T_n \approx T_d$). Synchronization is more probable as the network time scale increases further. However, in the slow network regime ($T_n \gg T_d$) we find that the long term dynamics is desynchronized whenever the probability of reaching a non-synchronizing configuration, it evolves sufficiently far away from the synchronized state, and the probability that subsequently sampled synchronizing networks take the system back to synchronization is negligible.

Our results are demonstrated in Fig. 1, which shows the average the synchronization level $\langle S \rangle$ (defined as the negative logarithm of the standard deviation over the nodes) in networks of Bernoulli and logistic maps, for an average of 1000 realizations. For both types of maps, and both for ensembles that are on average synchronizing and non-synchronizing, we find similar behavior. For short fluctuation times ($T_n = 1$ or 10), the average synchronization level remains close to its maximum value. As the fluctuation time increases ($T_n = 50$, $T_n = 100$), the synchronization level decreases. It increases again as the fluctuation time increases further ($T_n = 500$ and $T_n = 1000$). Eventually,

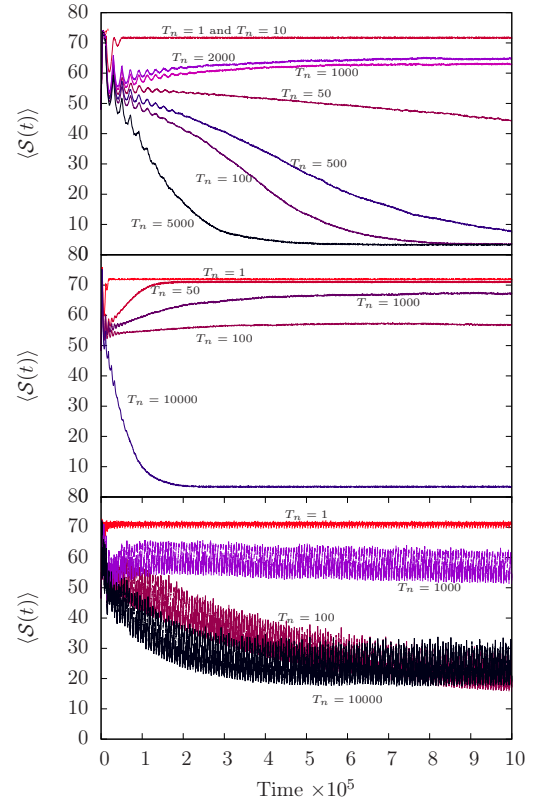


Figure 1: Realization average of the synchronization level, $\langle S(t) \rangle$, over $N_s = 1000$ samples, as a function of time for different systems. Top: Bernoulli system, $N = 40$, the mean degree is $k = 1.5$ (in average, non-synchronizing), for different values of T_n . Center: Bernoulli system with $N = 40$ sites, mean degree is $k = 1.8$ (in average, synchronizing), for different values of T_n . Bottom: logistic system, $N = 40$ and mean degree $k = 1.5$ (in average, non-synchronizing). In all cases, $T_d = 100$, and we only show time steps which are multiples of 100.

in the slow network regime ($T_n = 5000$, $T_n = 10000$) the system desynchronizes fast. The oscillatory behavior results from our choice of initial perturbation.

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Neuronal Avalanches in the Transition Between an Active and an Oscillatory Phase?

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Neuronal avalanches are bouts of spontaneous spatio-temporal activity with complex emergent properties. The probability distributions of avalanche size and duration decay as power laws $P(s) \sim s^{-3/2}$ and $P(d) \sim d^{-2}$, respectively, suggesting that the network is operating near a critical point [1].

Models from directed percolation universality class (DP) have been widely used to explain the scale invariant statistics of neuronal avalanches. However, these models do not take into account the dynamics of inhibitory neurons and besides that, as they present a phase transition between an absorbing state and an active phase, it is difficult to reconcile the model with long-range temporal correlations that are observed experimentally at different spatial scales [2, 3].

Poil et al., in an attempt to address some of these issues, proposed a computational model of excitatory and inhibitory neurons in a two-dimensional disordered network. They claim that their model shows a phase transition between an active and an oscillatory phase. At the critical line in parameter space, oscillations and neuronal avalanches emerge jointly. Moreover, detrended fluctuation analysis suggests that long-range time correlations ($1/f$ noise) also appear at the critical line [4].

In the present study we have studied this model further. We have analyzed the model's robustness against changes in system size, interaction range and the activity threshold that defines an avalanche. Besides the analysis of temporal auto-correlation, we proposed an order parameter seeking for more evidences of a phase transition.

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A general model for toxin-antitoxin dynamics in bacteria like *E. coli* can explain persister cell formation

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Inspired by my stays at IFISC (first as a postdoc now 16 years ago) on the one hand and the tradition of the “Brussels school” (mainly at ULB) on the other hand, the Applied Physics research group at VUB recently engaged in research activities in the field of systems biology. In this contribution, my aim is to give an overview of these expanding activities.

In a first research line, we model the transcription dynamics of toxin-antitoxin modules in bacteria. Toxin-antitoxin modules are small genetic elements, omnipresent in the genomes of bacteria, which code for an intracellular toxin and its neutralising antitoxin. Toxin-antitoxin modules play a significant role in the generation of persister cells. Here, we provide an overview of several methods to simulate toxin-antitoxin modules: both deterministic modelling using ordinary differential eqs, as well as stochastic modelling using stochastic differential eqs and the Gillespie method have been studied. Protein production and degradation, negative autoregulation through DNA binding, toxin-antitoxin complex formation and conditional cooperativity are gradually integrated in these models. Finally, by including growth rate modulation, we link toxin-antitoxin module expression to the generation of persister cells.

Another modelling approach addresses the human gut microbiota: a complex ecosystem wherein many microbial species interact and which is very important for human health. How the microbial interactions contribute to the collective behavior of this ecosystem remains less understood. In our approach, we focus on small communities of a few of the key bacterial species inhabiting the gut microbiota. The long term goal of this research is to be able to predict how a bacterial population reacts to perturbation such as anti-biotic administration. Two modelling approaches are chemostat (CS) equations and Lotka-Volterra (LV) equations. CS equations are based on *in vitro* experiments and incorporate resource consumption. They are therefore more realistic for the human gut and more quantitative than LV eqs. LV eqs have the advantage that they are easy to use and every term has a clear biological significance which is easier to understand intuitively. Moreover, they can easily be generalized to multiple species.

In the CS modelling approach, bacterial growth is modelled with Monod-like growth kinetics. Competition and cross-feeding are taken into account through explicit modelling of the nutrient production and consumption. Comparing our theoretical predictions with experimental results on co-cultures (in collaboration with the Raes and the De Vuyst labs in Belgium), leads to a good description of (experimentally very challenging) bi- and tri-culture dynamics. Furthermore, we observe that the time that species need to adapt to their environment influences which species eventually are dominant. In a theoretical approach, we also simplify the CS equations to a minimal model that exhibits bistability. Our

model is a relatively simple extension of LV eqs that is capable of describing a system of two species that is competitive as well as mutualist. Like LV equations the proposed model has an easy intuitive interpretation and can be generalized to multiple species, thus paving the way towards predictive multi-species modelling.

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The METER project: a study of energy demand flexibility through activity sequencing

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To achieve deep decarbonisation of our energy systems, citizens will play an increasingly important and participatory role. Demand side flexibility has the potential to reduce the need for peaking capacity, storage and grid reinforcement. The METER project is the first study of its kind, collecting time use and electricity data alongside a rich set of socio-demographic parameters at a nationally representative scale. Activities, socio-demographic data and information about routines are collected from all household members above the age of 8 using a custom app. Simultaneously, high resolution household electricity recordings are taken. The relationship between these multivariate types of information need be explored for novel insights into temporalities, causes, constraints and diversity of energy services across society.

Activities are categorised using a system of existing time-use codes, representing behavioural sequence as a finite-dimensional vector. Analysis of such highly dimensional data is naturally best carried out using standard frameworks of complex systems: (multilayer) networks, information-theoretic time-series measures, etc. Once typical dependencies (e.g. behavioural routines) are identified, there is scope of modelling representative behaviour. This would substantiate the evidence of a more targeted approach to encourage demand side flexibility than the mere provision of price signals, currently proposed by some economic and engineering disciplines.

Your electricity profile

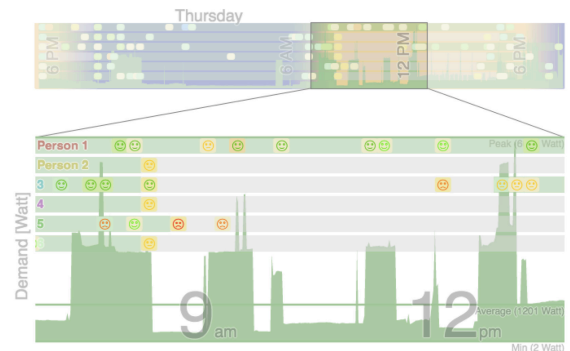


Figure 1: A snapshot of experimental data of a 6-person household, showing 28 hours of electricity reading (green), overlaid with reported activities (squares). Interactive webpages like this one are sent to users after receiving their data.

The International Mergers & Acquisitions Web: A Network Approach

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This paper analyzes the world web of mergers and acquisitions (M&As) using a complex network approach. We aggregate data of M&As to build a temporal sequence of binary and weighted-directed networks, for the 1995-2010 period and 224 countries. We study different geographical and temporal aspects of the M&As web, building sequences of filtered sub-networks which links belongs to specific intervals of distance or time. Then, we derive directed-network statistics to see how topological properties of the network change over space and time. The M&A web is a low density network characterized by a persistent giant component with many external nodes and with a few number of reciprocated links. Clustering patterns are very heterogeneous and dynamic. High-income economies are characterized by high connectivity being the main acquirers, implying that most countries might work as targets of a few acquirers. We find that distance strongly impacts the structure of the network: link-weights and node degrees are strongly non-linear. We show that the M&As web is assortative at short distances.

In the past two decades foreign direct investments (FDI) has become a major source of capital inflows for both developed and developing countries [1]. The flows of FDI may be classified in two main strategies: i) green field investments—when a parent company starts in a foreign country by constructing new operational facilities—, and ii) brown field investments—when a parent company purchases or leases a foreign existing production facilities to launch a new production activity— also known as mergers and acquisitions (M&As). Over the past 20 years, M&As have been preferred as the dominant mode of FDI, regardless of their higher volatility and sensitivity to financial conditions with respect to greenfield projects. In fact, M&As cover, on average, more than 80% of total national FDI [2].

In recent years an increasing body of literature has been studying international trade and financial flows between countries in the frame of complex-network perspective [3, 4]. Compared to traditional international-trade indicators, the topological web architecture may explain to a greater extent country growth and the development pattern. In this context, we introduce our study on Mergers and Acquisitions (M&As). With respect to the existing literature, our novelty consists in focusing on the complex system of interactions between countries in space and time.

Several empirical studies have tackled the question of M&As determinants trying to identify and evaluate the most relevant variables associated to global FDI activity. As a general conclusion, FDI are driven by quite diverse factors, ranging from differences in costs of production and trade to differences in institutional, social, cultural and financial characteristics of countries. As regards to the cost associated to geographical distance that might affect cross-border M&As, it has been stressed that information asymmetries in-

crease with distance creating a barrier to cross-border movement of capitals. From a theoretical point of view there is no clear net effect on the geographical distance to cross-border M&As. Given that it is expected that trade costs rises with distance, the simplest premise is that the decision to set up affiliates in foreign countries is positively affected by distance. In contrast to this, empirically has been found that this relation is negative. This evidence suggests that there might exists other sort of costs related to the distance that must be considered, rather than the simplest outcome of considering trade costs only.

All these sources of heterogeneity have bound the theoretical contributions in the field, leading to the opportunity of action of other sources of analytical tools, such as the network analysis. This study represents a first step towards a deeper exploration of global M&As-activity from a network perspective. We study the architecture of M&As observed in a narrow time window (a few months) in order to capture the prevailing or evolving patterns of the structure of the M&As web. And finally, we perform a statistical analysis for binary and weighted networks to provide evidence on the topological properties in different cross-sections. Then, we use the distance between countries having M&As to study how the geography determines the structure of network.

World mergers and acquisition relationships are characterized for being very concentrated in a few countries and for being strongly target oriented. We found that the M&As web is a low density network characterized by a persistent giant component with a few number of reciprocated links and with many non strongly connected external nodes. The giant component is mainly composed by developed economies which have more reciprocal investment relationships. Thus high-income economies are characterized by high connectivity and clustering, these countries mainly merge to several high and middle income economies, implying that most countries might work as targets of a few acquirers.

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Energy Landscape Analysis of Age-Related Changes in the Human Brain

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Executive cognitive functions of humans are known to decline with aging. Such functions are considered to be generated by well-coordinated activity patterns of neural signals in the brain. In the present study, we applied the so-called energy landscape analysis (ELA; schematically shown in Fig. 1) [1, 2] to resting-state fMRI signals obtained from healthy younger and older adults [3] and analyzed activity patterns in the so-called default mode network (DMN) and the cingulo-opercular network (CON), each of which was specified by a particular set of regions of interest (ROIs). ELA binarizes the signal into $\sigma = -1$ (inactive) or $\sigma = +1$ (active) at each ROI at each time point (Fig. 1). If a network contains N nodes, the activity pattern at each time point is represented by one of the 2^N possible activity patterns, denoted by $\boldsymbol{\sigma} = (\sigma_1, \dots, \sigma_N)$.

The frequency of occurrence of each activity pattern is fitted by the Boltzmann distribution given by,

$$P(\boldsymbol{\sigma}) = \frac{\exp[-E(\boldsymbol{\sigma})]}{\sum_{\boldsymbol{\sigma}} \exp[-E(\boldsymbol{\sigma})]}, \quad (1)$$

where $E(\boldsymbol{\sigma})$ represents the energy of the Ising model for a spin configuration, $\boldsymbol{\sigma}$, and is given by

$$E(\boldsymbol{\sigma}) = - \sum_{i=1}^N h_i \sigma_i - \sum_{i=1}^N \sum_{j=1}^N J_{ij} \sigma_i \sigma_j. \quad (2)$$

Using this energy value, the dynamics of the activity pattern is mapped to the motion of a “ball” constrained on an energy landscape (Fig 1).

In both networks ELA revealed that two synchronized patterns (i.e., the pattern in which all the ROIs were active, s_+ , and that in which all the ROIs were inactive, s_-) appeared most frequently, and that the duration of these activity patterns were significantly longer in the younger than older adults. To further analyze the dynamics, we defined the “attractive basin” of s_+ (s_-), denoted by b_+ (b_-), based on the energy values of the activity patterns calculated by ELA (Fig. 1). Other activity patterns were defined to be b_{others} . One of these five labels was assigned to each of the 2^N activity patterns.

We found that the transition rate between s_+ and s_- was significantly higher for the younger than older adults both in the DMN and CON. Next, we calculated the rate of peripheral transitions between b_+ and b_- that did not contribute to transitions between s_+ and s_- (i.e., the rate of transitions between b_+ and b_- subtracted by the rate of transitions between s_+ and s_-). The peripheral transitions were more frequent in the older than younger adults in the DMN (but the difference was not significant in the CON).

We defined an indicator for the ease of transitions between s_+ and s_- , called an efficiency score, by the rate of transitions between s_+ and s_- divided by the rate of peripheral transitions. The efficiency score was significantly

larger in the younger adults, in both of the two networks. We found that the behavioral performance of individuals was significantly correlated with the efficiency score at the CON in the younger adults and at the DMN in the older adults. These results support the hypothesis [4] that, differently from younger adults, older adults heavily rely on the DMN for cognitive functions rather than on the CON.

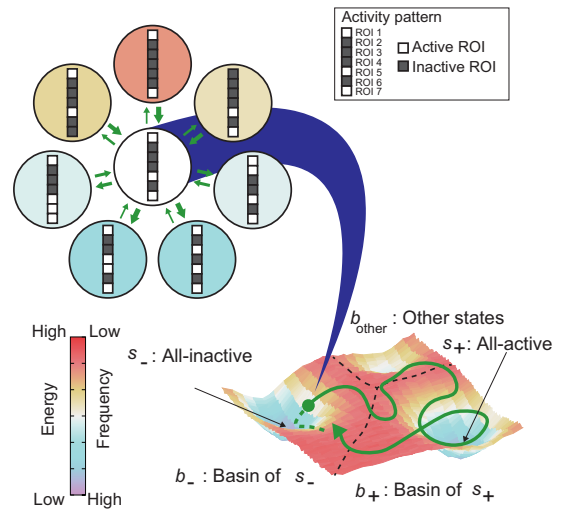


Figure 1: Schematic representation of the dynamics of the brain activity pattern constrained on an energy landscape.

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Stochastic Pair Approximation

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Binary-state models on complex networks are used to describe the effect of interactions within a population of individuals. There is a broad spectrum of models that can depict competition between two opinions, language dynamics, the spreading of diseases, neural activity, etc. Analytical and numerical methods have been proposed capable of estimating the most important macroscopic quantities that portray the global state of the system [1]. However, most of the times, they are based on deterministic assumptions, where fluctuations and finite size effects are neglected. In this work, we relax these assumptions and we generalize the previous proposed methods, taking into account the full stochastic nature of the models. Specifically, we will focus on the noisy voter (Kirman) model, which is of particular relevance on the study of price fluctuations of financial markets. The model divides the population between optimistic (state 0) and pessimistic (state 1) agents. The agents are allowed to change state randomly (idiosyncratically) with probability rate a or copying the state of a random neighbour agent in the network with probability rate h . The level of description of the method presented here includes as variables the number L of active links (connecting a node in state 0 to another in state 1) and the total number n_k of nodes that hold state 1 and have degree k (number of neighbours). When an agent with k neighbours, among which q are in state 1, changes its state, the global variables change like $n_k \rightarrow n_k \pm 1$ and $L \rightarrow L \pm (k - 2q)$. Using the pair approximation [2], we are able to obtain some effective rates for the processes mentioned above, that only depend on global variables $\{n_k\}$, L . The most problematic issue that one faces when dealing with the stochastic description of this type of models is the capability of closing the equations for the moments $\langle L \rangle$, $\langle n_k \rangle$, $\langle n_k^2 \rangle$, ... In order to overcome this issue, we propose a system size expansion (N) like

$$L = N\phi_L(\lambda) + N\delta_L + N^0\nu_L, \quad (1)$$

$$n_k = N\phi_k(\lambda) + N\delta_k + N^{1/2}\xi_k + N^0\nu_k, \quad (2)$$

with a Van Kampen like part that involves δ_k (deterministic), ξ_k and ν_k (stochastic), plus and additional non-trivial stochastic part $\phi_k(\lambda)$ that corresponds to a special deterministic trajectory which is an attractor of all the rest (where λ is a stochastic variable that corresponds to the parametrization of the trajectory). The idea behind this peculiar expansion is that the usual Van Kampen expansion fails to reproduce correctly the results in the critical region of parameters, while Eqs.(1-2) perform well in the entire region. Within this approach, we are able to obtain analytical expressions for the stationary average of the order parameter $\langle L \rangle_{st}$, the fluctuations of the total number of agents in state 1, i.e. $\sigma_{st}^2[n]$, as well as the correlation function $\langle n(t+\tau)n(t) \rangle_{st}$. The results are compared with the novel method [3], which makes use of an annealed network type of approximation, as well as,

with the pair approximation but neglecting fluctuations (deterministic), see Figure 1. The method presented here improves previous results and it is a step forward in the characterization of stochastic effects in binary-state models on complex networks.

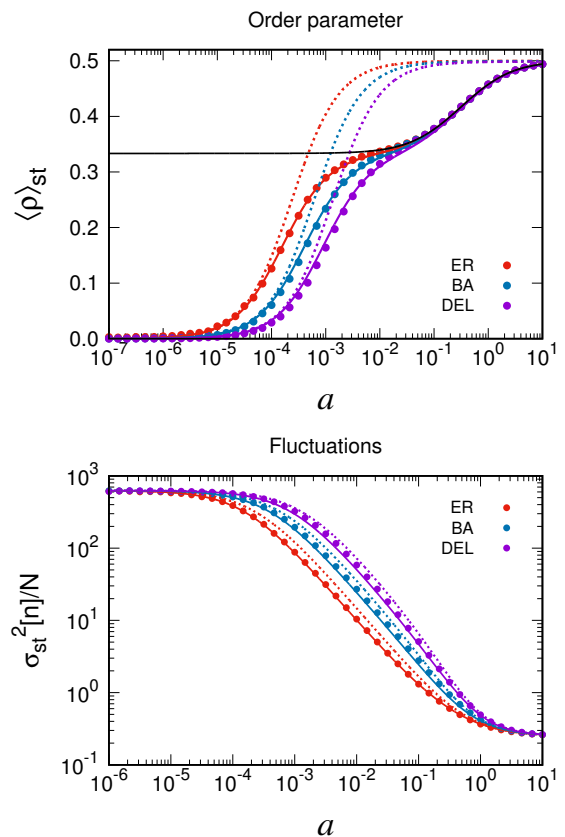


Figure 1: Stationary average density of active links $\langle \rho \rangle_{st} = 2\langle L \rangle_{st}/N\langle k \rangle$ (upper panel) and variance of the total number of agents in state 1 (lower panel). Dots correspond to numerical simulations of three different networks, Erdős-Rényi (ER), Barabási-Albert (BA) and Dichotomous (DEL), with $N = 2500$ and $\langle k \rangle = 4$. Colored solid lines are the stochastic pair approximation prediction, the black solid line is the deterministic pair approximation, while dashed colored lines are the annealed network approximation [3].

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Influence of a Patient Transfer Network of US Inpatient Facilities on the Incidence of Nosocomial Infections

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Antibiotic-resistant bacterial infections are a substantial source of morbidity and mortality and have a common reservoir in inpatient settings. Transferring patients between facilities could be a mechanism for the spread of these infections. We wanted to assess whether a network of hospitals, linked by inpatient transfers, contributes to the spread of nosocomial infections and investigate how network structure may be leveraged to design efficient surveillance systems. We construct a network defined by the transfer of Medicare patients across US inpatient facilities using a 100% sample of inpatient discharge claims from 2006-2007. We show the association between network structure and *C. difficile* incidence, with a 1% increase in a facility's *C. difficile* incidence being associated with a 0.53% increase in *C. difficile* incidence of neighboring facilities. Finally, we used network science methods to determine the facilities to monitor to maximize surveillance efficiency. An optimal surveillance strategy for selecting "sensor" hospitals, based on their network position, detects 80% of the *C. difficile* infections using only 2% of hospitals as sensors. Selecting a small fraction of facilities as "sensors" could be a cost-effective mechanism to monitor emerging nosocomial infections.

Biases and errors in the temporal sampling of random movements

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New sources of data available thanks to Information and Communication Technologies allow to track the trajectories of humans and animals at an unprecedented scale [1]. In general, the continuous spatio-temporal record of the followed individual can be described as a continuous-time random walk [2], where a *rest* time is associated to the endpoint of each *move*. Identifying these different states is an important statistical challenge [3], in particular because these new sources of information and their exploitation have new limits and biases [4] that need to be assessed.

One of these limits is introduced by the temporal sampling of the trajectory. To reconstruct the real movement patterns, one needs a time Δ between sampled points significantly smaller than the characteristic duration of rests and moves in analysis. This is often not the case. Here, we discuss the effect of sampling on the measured statistical properties of random movements. We describe trajectories as an alternating renewal process [5], a generalization of Poisson processes to arbitrary holding times and to two alternating kinds of events, moves and rests, whose durations t and τ are regarded as independent random variables. The sampling time interval Δ depends on the particular experiment and can be either constant or randomly distributed.

We first consider the case of exponential distributions for $P(t) = \bar{t}^{-1} \exp(-t/\bar{t})$ and $P(\tau) = \bar{\tau}^{-1} \exp(-\tau/\bar{\tau})$, constant sampling time interval $\bar{\Delta}$, and constant speed v . In this case we can obtain explicitly the distribution $P(\ell^*)$ of sampled displacements and its first two moments, that also allow us to quantify difference between the real $\ell = vt$ and the sampled ℓ^* displacement lengths. The observed distribution $P_{\ell^* > 0}(\ell^*)$ can have a maximum, even if the original distribution $P(\ell)$ is a monotonically decreasing function. When $\bar{\Delta} > \bar{\tau}$, the result of the sampling is manifestly different from the original exponential distribution.

We can also calculate the fraction $F_{\text{good}}(\bar{\Delta})$ of moves that are correctly sampled with a sampling time $\bar{\Delta}$. This quantity is independent of the spatial embedding and of our assumption on the speed v , and represents an excellent measure of the impact of the sampling. We note in particular that there is an optimal sampling time of the same order as \bar{t} and $\bar{\tau}$: $\hat{\Delta} \approx 2\sqrt{\bar{t}\bar{\tau}}$.

We then extend these results numerically, and show that sampling human trajectories in more realistic settings is necessarily worse than the peaked scenario we solved, which therefore allows us to define an upper bound to sampling quality. Finally, we use high-resolution (spatially and temporally) GPS trajectories [6] to verify our predictions on real data. We find that for real cases, characterized by long-tailed rest durations [7], the fraction of correctly sampled movements is dramatically reduced. Constant sampling allows to recover at best 18% of movements, while even idealized methods cannot recover more than 16% of moves

from sampling intervals extracted from human communication data [8].

These figures suggest that, in the sampling of a trajectory alternating rests and movements of animals or humans, the assumptions often made that each measure correspond to a rest and that an observed displacement correspond to a move are intrinsically flawed. Further studies and rigorous analysis of the empirical methods used in many studies are thus necessary in order to construct solid foundations for our understanding of human mobility and animal foraging.

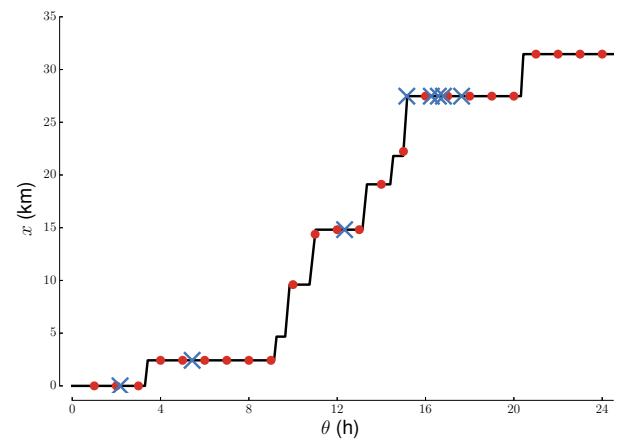


Figure 1: Examples of trajectory sampling with exponentially distributed rest and move durations, we show the case of constant sampling interval (red circles) and the case of random sampling interval (blue crosses).

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Models for Diffusion Processes in Complex Media with Applications to Biological Systems

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Transport of molecules in a cellular environment regulates many processes underlying biological functions. With the current experimental techniques, it is possible to perform single particle tracking (SPT) of long single-molecule trajectories in living cells. These experiments revealed very complex diffusion patterns, often showing anomalous subdiffusion and ergodicity breaking. We will discuss an example of such behavior, observed by recent SPT experiments in the motion of molecules in living-cell membranes [1]. These data seem to exclude conventional explanations for ergodicity breaking, based on continuous-time random walks with transient trapping. Thus the underlying microscopic mechanism for the nonergodic subdiffusion of the molecules is unclear.

In this scenario, we will discuss two stochastic models that provide a description compatible with the observation of such experiments. We will first discuss models of a particle diffusing in a disordered medium, in which particles' diffusivities vary either in time or space, reproducing the heterogeneous dynamics - characterized by frequent changes of diffusivity - revealed by the experiments [2]. Second, we will discuss a model in which a particle performs continuous Brownian motion with changes of diffusion coefficients induced by transient molecular interactions with diffusive binding partners [3].

From the biophysical point of view, the latter model reflects the scenario of a diffusing molecule which, upon interaction with another molecule, undergoes a transient change of diffusivity for the time the interaction takes place. An important feature of the model is the possibility of being experimentally tested by means of current multicolor single particle tracking techniques. As an example, in a dual color single particle tracking (DCSPT) experiment it is possible to simultaneously follow the motion of two closely spaced particles with high time and relative-distance resolution. In addition, DCSPT make it possible to experimentally verify the occurrence of interactions between diffusing species, measure the duration of such events, and check whether they affect the diffusivity of the particles involved.

Once the occurrence of the interaction mechanism in a specific system is proven, the model allows to directly calculate microscopic parameters of the system. In particular, the scaling exponent of the eMSD is a proxy for the degree of heterogeneity of the environment. But even more importantly, the timescale for the onset of subdiffusion in the eMSD curve provides an estimation of the average density of interacting particles. In Fig. 1 we show a collection of eMSD curves obtained for different densities of particles $\rho = N/L$, with L being a characteristic size of the system (length in 1D). The degree of disorder is characterized by the asymptotic value of the exponent α , and does not depend on the density (for all curves here $\alpha = 0.2$). In

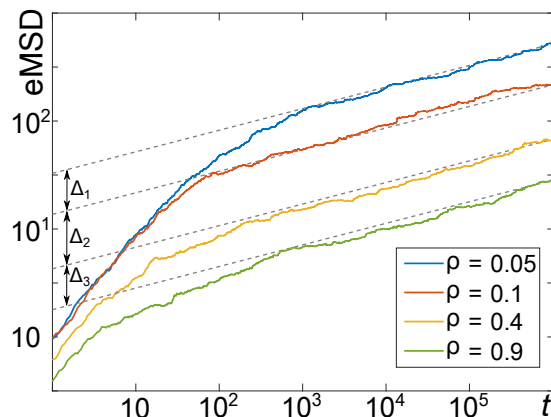


Figure 1: Evolution of the mean squared displacement (eMSD). The eMSD is obtained as an ensemble average, i.e., over many trajectories of different particles. The long-time scaling exponent of the eMSD is independent of the density ρ and corresponds to a subdiffusive motion ($\alpha = 0.2 < 1$). In the asymptotic regime, curves obtained for different densities are separated by a distance Δ , which is related to the different densities.

contrast, the onset of subdiffusion occurs at later times for more dilute systems. This corresponds to a separation Δ between two curves for different densities. This separation can be expressed in terms of the densities of the corresponding curves. For the same system size and for dilute systems, $\Delta = \log(N_j/N_i)$, $N_{j(i)}$ being the number of particles of the denser (more dilute) system.

In conclusion, both models offer a plausible and experimentally-verifiable explanation for the nonergodic subdiffusion of molecules in cellular environments. In addition, the generality of these theoretical frameworks allows them to be applied to a wider range of complex systems showing diffusion heterogeneity, such as those found in ecology, geology or soft condensed matter. As an outlook, we plan to include the coupling of the particle to a system of Ising spins, and solve with a quantum kinetic Ising Hamiltonian approach [4].

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Geometric renormalization of real complex networks

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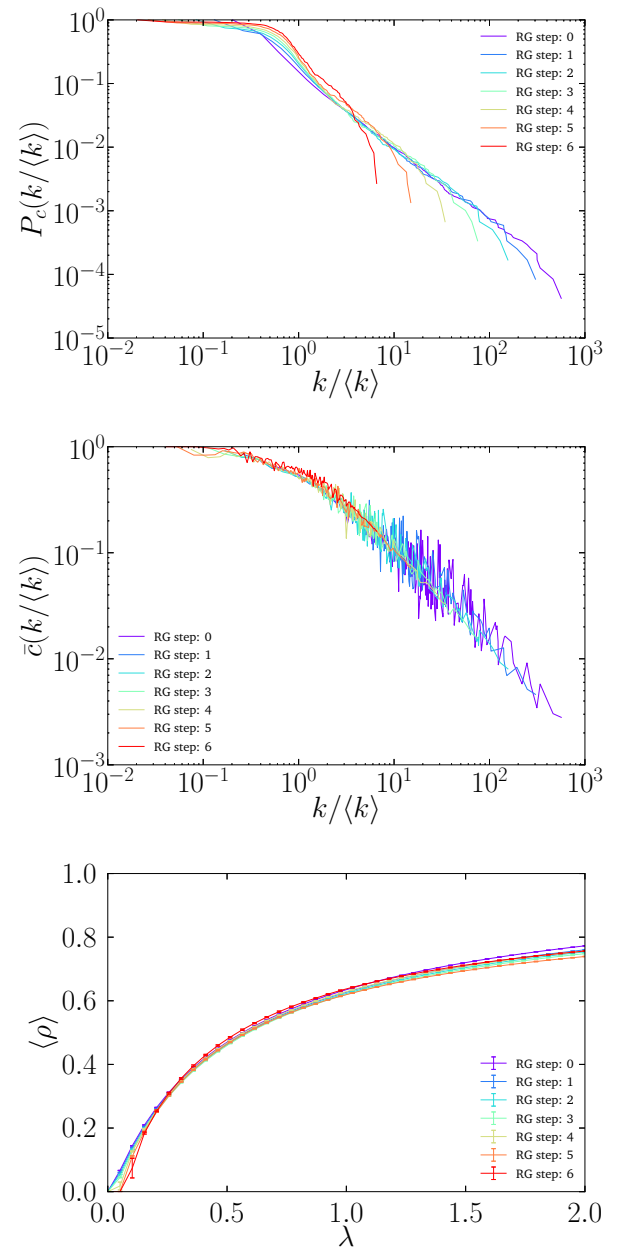
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Renormalization has proven to be a very powerful tool for a systematic investigation of systems—from condensed matter to quantum field theory—as viewed at different scales. In the field of complex networks, some topological renormalization schemes based on shortest paths between nodes have been proposed in the past [1]. However, the collection of shortest-path lengths, albeit a well-defined metric space, is a poor source of length-based scaling factors in networks due to their homogeneity and the small-world property.

We present empirical evidence that real-world complex networks are invariant under geometric length scale transformations when embedded in an underlying hidden metric space. We prove analytically [2] that the embedding model [3, 4] is also renormalizable in the same framework and take it as new evidence supporting our conjecture that hidden metric spaces underlie real networks. The congruency between real networks and the geometric model enables to define a multiscale unfolding of complex networks that allows the study of their self-similarity properties.

As applications, this geometric renormalization scheme yields a natural way of building smaller-scale replicas of real networks while simultaneously preserving their statistical properties, which can be extremely useful in the study of dynamical processes on large networks. The hidden metric space renormalization group can also be applied to design a new greedy routing protocol in hyperbolic space which exploits the multiscale unfolding of complex networks increasing the success rate of single-scale versions.



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Figure 1: **Geometric renormalization of the Internet AS network.** The plots compare the networks obtained from the geometric renormalization transformations. At every renormalization step, the number of nodes is reduced by a factor 2. **Top:** Rescaled complementary cumulative degree distributions. **Middle:** Rescaled clustering coefficient spectra. **Bottom:** Average prevalence as a function of the infection rate in the SIS dynamics on the original network and its smaller-scale replicas.

Evolutionary cooperation, an old debate, a new perspective

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Different pathogens spread often in the same host population in parallel. They can interact in different manners: for a short period cooperation between pathogens can lead to faster and larger host occupation [1, 2, 3]. Spanish Flu and HIV are examples of such cases. This cooperation, however, can lead to death of the host population and consequently also pathogens' death. Therefore on a long run, the cooperation strategy is not necessarily the best.

Here we propose and study an evolutionary game model in order to understand the co-evolutionary dynamics of two co-infecting pathogens, see Fig. 1. They have a common host and the host does not evolve on the same time scale as the pathogens. We consider two kind of disease species. In what follows, we denote the state of a pathogenic agent with X_y , where $X \in \{A, B, a, b, AB, ab, Ab, aB\}$ denotes the disease state of the pathogen, and $y \in \{C, D\}$ denotes its strategy, instead. In particular, agents (pathogens) accumulate a *payoff*, Π , based on the history of their contagion records. We assume if the host is populated by a cooperator infection from another disease is possible. If the host is populated by a defector there will be no infection at all. This gives rise to two main scenarios: The first is when the disease infects an empty host with probability p . In this scenario, the pathogen does not meet any resistance and all the host resources are available to him. For simplicity, we consider the amount of total resources available in the host equal to one. Therefore, when the pathogen enters into an empty host it receives a payoff equal to one irrespective of its type and strategy. When the host is already occupied by another disease and the probability of infecting is q things become a bit more complicated. More specifically, as shown in panel b, there are four possible combinations of pairs of strategies: (C, C) , (C, D) , (D, C) and (D, D) corresponding to different payoffs. As commented above, a cooperator pathogen does not oppose any resistance to the contagion by another disease and will share the host resources with it. A defector entering a host populated by a cooperator will seize the majority of available resources. Defining the *payoffs*, we first show under which conditions cooperation may or may not be a meaningful strategy in a mean field approximation. Then we show how underlying transmission and contact networks may promote both the spreading and the emergence of cooperation.

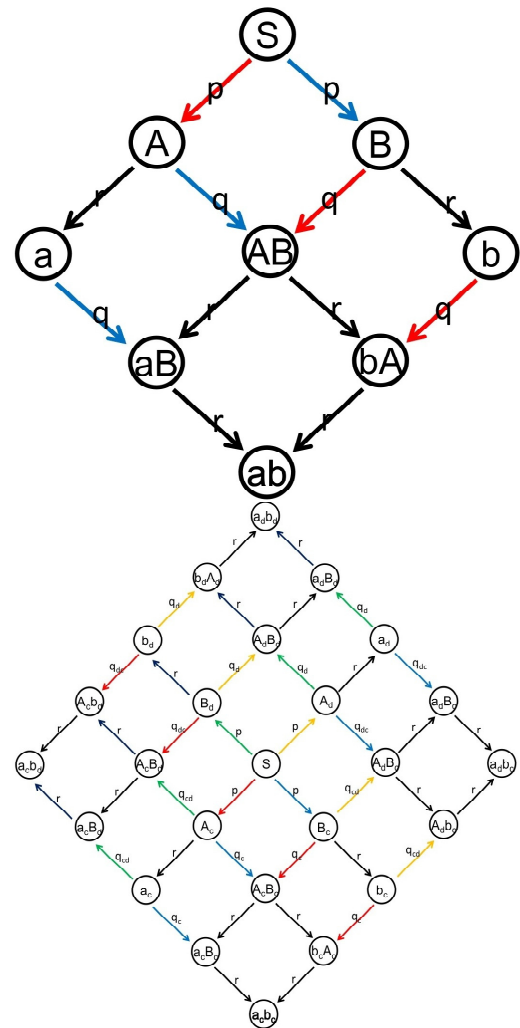


Figure 1: Schematic representation of all the possible transitions among compartments in the multi disease propagation of diseases [A] and [B] while A) only either cooperation or defection is present, B) cooperation and defection are both present. Parameters r, p, q are representing recovery, first and secondary infection rates.

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Power grid stability under proportional and derivative control

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This work investigates the resilience of an elementary electricity system (power plant - consumer) under proportional and derivative (PD) control when subject to large perturbations. Two models of power plants are used. The first one is a simple synchronous-motor model with constant power, while the second one includes primary and secondary control to modify the mechanical power to keep the frequency of the system within the statutory limits. A particular attention is paid to small power grids, representative of power grid structure in some developing countries. The considered elementary electrical system consists of a consumer (machine), a power plant (generator) and a transmission line. Runge-Kutta method is used to solve the dynamical equations. In the case where the power plant is modeled with the uncontrolled swing equation [1], it is found that the PD-control increases the resilience of the system [2]. We also show that time delays associated to the feedback loop of the controller have a negative impact on the performance [2]. These effects are also analyzed in the case with frequency control.

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Emergence of linguistic laws in human voice

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Linguistic laws constitute one of the quantitative cornerstones of modern cognitive sciences and have been routinely investigated in written corpora, or in the equivalent transcription of oral corpora. This means that inferences of statistical patterns of language in acoustics are biased by the arbitrary, language-dependent segmentation of the signal, and virtually precludes the possibility of making comparative studies between human voice and other animal communication systems. Here we bridge this gap by proposing a method that allows to measure such patterns in acoustic signals of arbitrary origin, without needs to have access to the language corpus underneath.

We have explored the equivalent of linguistic laws directly in acoustic signals, founding that human voice -which actually complies to SOC dynamics with critical exponents compatible with those found in another critical phenomena as rainfall- manifests the analog of classical linguistic laws found in written texts (Zipf’s law, Heaps’s law and the brevity law or law of abbreviation). These laws are invariant under variation of the energy threshold θ , and can be collapsed under universal functions accordingly. As θ is the only free parameter of the method, this invariance determines that the results are not afflicted by ambiguities associated to arbitrarily defining unit boundaries.

This current study focus and scans voice properties at intraphonemic timescales, where the statistical laws of language emerge directly from the physical magnitudes that govern acoustic communication. One could thus speculate that the emergence of these complex patterns is just a consequence of the presence of SOC, what in turn would support the physical origin of linguistic laws

The method has been applied to sixteen different human languages, recovering successfully some well-known laws of human communication at timescales even below the phoneme and finding yet another link between complexity and criticality in a biological system. These methods further pave the way for new comparative studies in animal communication or the analysis of signals of unknown code.

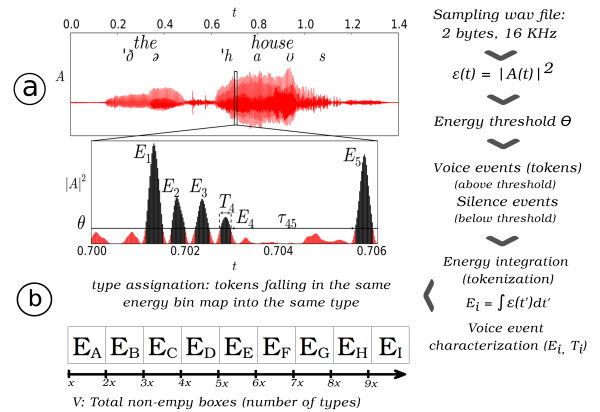


Figure 1: This figure illustrates the methodology to extract a sequence of types from an acoustic signal. Waveform series $A(t)$ are sampled at 16KHz from the system. In (a) we plot the instantaneous energy per unit time $\epsilon(t) = |A|^2$ from an excerpt of the top panel. The energy threshold θ , defined as the instantaneous energy level for which a fixed percentage of the entire data remains above-threshold, helps us to unambiguously define a token or voice event (a subsequence of time stamps for which $\epsilon(t) > 0$) from silence events of duration τ . The energy released E in a voice event is computed from the integration of the instantaneous energy over the duration of that event (dark area in the figure denotes the energy released in a given voice event). By performing a linear binning tokens are classified into several bins that we call types. The vocabulary V agglutinates those types that appear at least once

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Epidemic Spreading in Localized Environments with Recurrent Mobility Patterns

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The spreading of infectious diseases has been proved to be radically dependent on the population networked structure of interactions and on the mobility of individuals. Network scientists have made significant progress assessing the critical behavior of spreading dynamics at large geographic scales, but the prediction of the incidence of epidemics at smaller scales, localized environments, is still a challenge.

Representative examples of localized environments are university campuses, schools and work offices, to mention a few. The problem of modeling such realistic scenarios relies on finding the appropriate level of abstraction to grasp the main singularities of the epidemic spreading process for individuals using the particular environment. The analysis of these over-simplified model abstractions is of utmost importance to separate the effect of single parameters on the incidence of spreading process, yet allowing an analytical approach that could be used for prediction purposes and to test prevention actions.

In particular, we are interested in studying the spreading dynamics of influenza-like illnesses (ILI) inside university campuses. In most U.S. universities, most of the students live in the university residence halls and university dorms. The main activity of the students within campuses is dominated by a recurrent pattern of mobility that consist of attending classes and residing in dorms. This recurrent pattern of mobility between the bipartite structure of dorms and classes, is identified as a major player on the endogenous spreading of diseases between students.

We propose a metapopulation model on a bipartite network of locations, that account for the interplay between mobility and disease contagion for this particular scenario. The model is as follows: there are two types of nodes (populations): *dorms* and *classes*. Individuals correspondence to a dorm is unique, while classes are shared by individuals of any dorm. Each individual returns to its dorm after their academic activities are over. These recurrent pattern turns out to be essential to understand the impact of quarantine-like policies on the sick students, and specially on the determination of the proper time to be assigned to these isolation strategies.

The results of our analysis for a SIS dynamics on this particular scenario allows to test different strategies to contain the spreading of epidemics, identifying for example the lowest quarantine bound to be applied to sick students for the containment of the disease spreading. We find analytical expressions amenable to quantify the final incidence of the epidemics on these localized scenarios with recurrent mobility patterns.

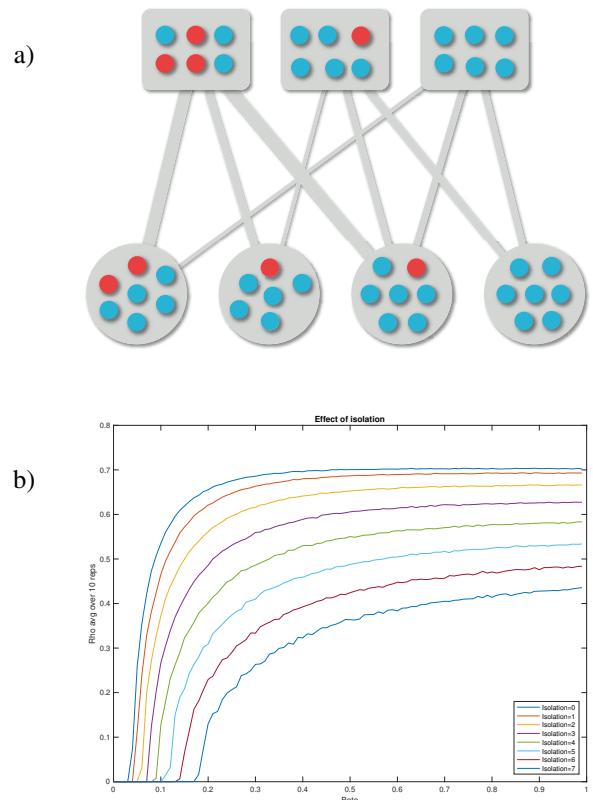


Figure 1: **(a)** Sketch of the bipartite metapopulation network accounting for the mobility of students between *dorms* and *classes*. **(b)** Number of infected students in the steady state as a function of the infectivity parameter β , for different values of the isolation policy implemented. As we can see isolation is able to shift the onset of the epidemics as well as to significantly decrease the total incidence.

Natural selection in dispersal-structured populations

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The influence of the dispersal of the individuals on the outcome of the competition has been debated for a long time. In some works it has been concluded that it is more advantageous to diffuse faster while in other ones the opposite conclusion has been drawn. The picture emerging is that the temporal fluctuations, including the stochasticity induced by demographic events, tend to give the competition advantage to species diffusing faster. Instead, the spatial heterogeneities, due to the patch formation of organisms or non-homogeneous distribution of nutrients, give the advantage to less motile species, or, in the case of the species described by different types of diffusion, to the one forming stronger clusters.

In most investigations various explicit assumptions are made, e.g., about the mutations, Allee effect, fitness, the distribution of resources, carrying capacities of different space regions, costs for faster dispersal etc. Instead, we address a simple model where the spatial distribution of organisms as well as the temporal fluctuations are generated solely by the individuals themselves, and the diffusivities leading to the competition advantage are selected by this self-created environment.

In the case of the competition between two species it is straightforward to draw the conclusions: either the species diffusing faster or slower wins, or the coexistence can occur. However, it is known that the dispersal ability can vary as much within a species as among species, indicating that the investigation of dispersal-structured populations is highly relevant. As we will demonstrate, in the dispersal-structured populations in which the organisms are characterized by a wide range of diffusivities the situation is more complex.

In accordance with other works, we observe that the general propensity is that the spatial heterogeneities tend to favor the smaller diffusivities while the increase of temporal fluctuations enhances the competition success of the individuals diffusing faster. However, beside this general trend, we observe that, instead of the utmost values, for a wide range of parameters the intermediate values of diffusion coefficient enhance the competition advantage. The optimal range of diffusion coefficients giving the competition advantage is determined by the interplay between various factors such as patch formation, temporal fluctuations, initial conditions, and carrying capacity of the system. The results of this study are particularly relevant in the problems of the motion of micro-organisms such as bacteria when the ability of an organism to move is determined by various factors such as its size, shape etc., but give useful references also for the behavior of the systems consisting of macro-organisms.

Transport in Nuclear Fusion plasmas: from Self Organized Criticality systems to Magnetohydrodynamics

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Magnetically Confined Nuclear Fusion has become the most promising candidate to control and efficiently obtain fusion energy. Particles are in a plasma state and, the magnetic fields confine and compress the plasma in a toroidal geometry to reach extreme temperatures in the core which generate the nuclear reactions. A better understanding of the radial transport is fundamental to control the confinement and losses in the plasma.

Experiments in Nuclear Fusion devices show, for example, system size scaling or superdiffusive propagation which could not be explained by the classical diffusion equations. It has been called *anomalous transport*. Those effects reduce the confinement and increase the losses in the plasma. However, at certain conditions, the plasma rotates at different speeds creating a shear in the radial direction. That shear flow creates a transport barrier which reduces the anomalous effects.

A Self-Organized Critical (SOC) system could describe qualitatively some of the anomalous effects [1]. And a simply introduction of a transport barrier could reduce those effects. A schematic of a 2D sandpile (the generalization of a SOC system) with shear flow is shown in Fig. 1.

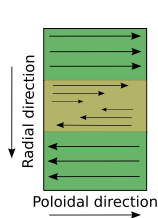


Figure 1: Schematic of a SOC system with shear flow.

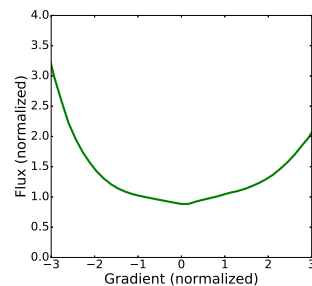


Figure 2: Normalized gradient and flux in a fixed position.

The transport in a sandpile is driven by avalanches (generated by critical gradients) inside the system. The avalanches are scale free and are only limited by the system size. Furthermore, a high Hurst exponent indicates superdiffusive behavior in SOC systems [2] as has been measured experimentally [3].

The discrete sandpile model can be extrapolated to a continuous system. The model is described by a one dimensional diffusion equation which diffusivity is controlled by a critical-gradient equation [4]. The model has the properties of a SOC system as a high Hurst exponent value [5]. Non-local effects in the transport are driven by the avalanches. The gradient-flux relation exhibits a parabola-like curve (see Fig. 2) which has been observed in fusion devices [6].

On the other hand, turbulence induced transport can be modeled by Magnetohydrodynamics (MHD) which has

been shown it has SOC properties [7]. In our resistive MHD model, the instabilities in the plasma are driven by pressure gradients. A heat perturbation is introduced in a inner region in the plasma. The left panel on Fig. 3 shows the shear flow generated in the plasma before the perturbation. The right panel illustrates the temporal evolution of the heat perturbation inside the plasma. The horizontal dashed lines indicates the location of the local maxima and minima of the shear flow. The heat perturbation propagates radially but it is slowed down by the shear flow in the system. This behaviour cannot be explained by a pure diffusive model.

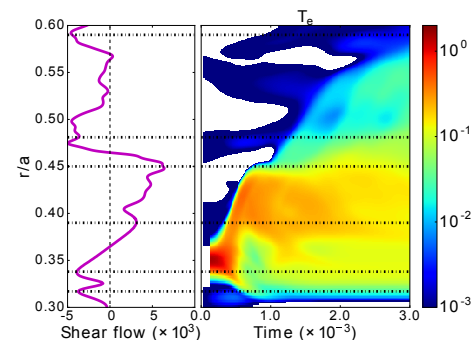


Figure 3: The left panel shows the shear flow at the initial time. Right panel illustrates the time evolution of the heat perturbation.

Similar radial propagation and slowdown has been recently observed using the Transfer Entropy method. The technique has been applied in fusion plasmas to measure the causal relation between signals.[8]

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Active cluster crystals in systems of self-propelled particles

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The collective behavior of self-propelled particles is a fascinating topic both for its numerous applications, ranging from active colloids to bacterial suspensions, and its intrinsic theoretical interest [1, 2]. Many studies focused on the formation of clusters reporting two main different cases: for “active crystals”, self-propulsion leads to a modification of the properties of a pre-existing crystal. On the other hand, for Mobility-Induced Phase Separation (MIPS), the system separates into two phases of different densities. Methodologically, both mechanisms can be studied by considering an effective density-dependent velocity replacing the two-body interacting potential.

We analyze here [3] a different case of cluster formation with active objects. It is the non-equilibrium counterpart of the so-called cluster crystals [4], which appear in equilibrium systems interacting with soft-core repulsive potentials, and are solid-like structures where the unit cell is occupied by a closely packed cluster of particles. Here, clustering

appears under a repulsive potential so that it is not a consequence of purely local effects. This is thus very different from the other cases of active crystals and it is unlikely that previous local arguments derived for active crystals or MIPS can describe it. Self-propulsion deforms the clusters by depleting particle density inside, and for large speeds it melts the crystal. Continuous field descriptions at several levels of approximation allow to identify the relevant physical mechanisms.

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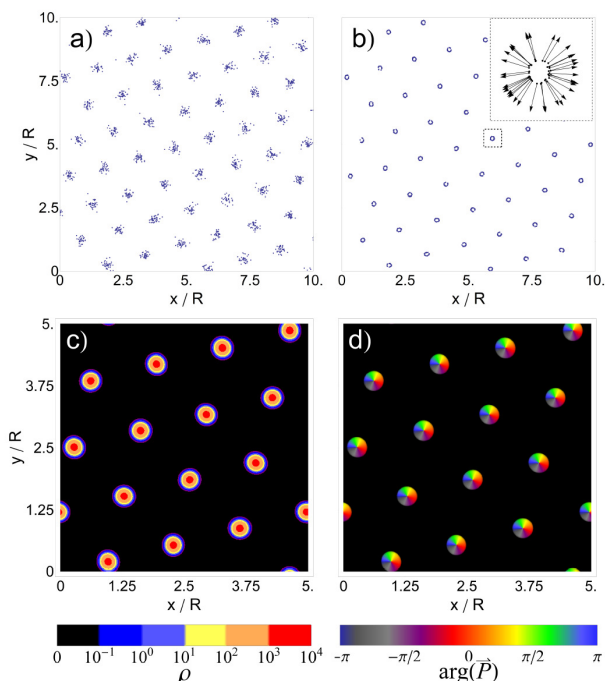


Figure 1: Panels a) and b): Particle simulations. Snapshots of particle positions at different parameter values. Top-right inset is a zoom of the boxed cluster showing the orientation of the particle’s velocity vector. Panels c) and d): Steady states obtained by numerical integration of the continuum equations for density and polarization, for the same parameters as panel a). Panel c): density field. Panel d): angle of the polarization field. Black regions denote very small polarization.

Network description of fluid transport: Lagrangian Flow Networks

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Fluid transport between different locations of a fluid domain could be conveniently represented by the concept of Lagrangian flow networks, in which a discrete representation of the transfer operator for the advection dynamics defines links between fluid regions. Fluid dispersion and mixing become naturally measured by network-theory quantities such as degree, or newly introduced network entropies. The recently developed powerful methods of community detection in graphs become useful to identify coherent regions in the fluid flow. Clustering coefficients identify the location of periodic orbits [1, 2]

Clustering coefficient and periodic orbits in flow networks, Chaos, to appear (2017).

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[4] E. Ser-Giacomi, R. Vasile, I. Recuerda, E. Hernández-García, C. López, *Dominant transport pathways in an atmospheric blocking event*, Chaos **25**, 087413 (2015)

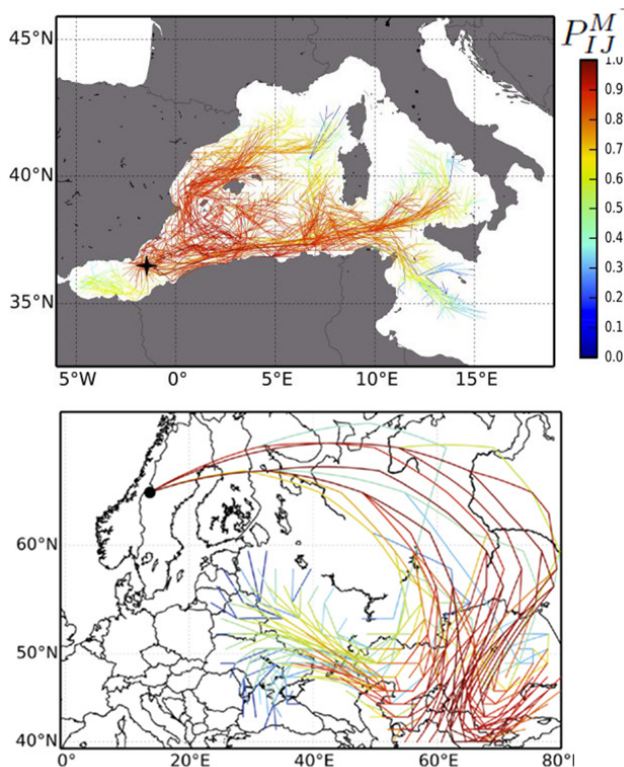


Figure 1: Examples of optimal transport paths obtained with network methods in a flow in the western Mediterranean (top) and in the atmosphere over western Europe (bottom).

In this contribution we will describe the basics of this type of network construction, with applications to realistic geophysical flows, namely the surface circulation in the Mediterranean, with ecological implications, and an atmospheric blocking event [1, 3, 4].

[1] E. Ser-Giacomi, V. Rossi, C. López, E. Hernández-García, *Flow networks: A characterization of geophysical fluid transport*, Chaos **25**, 036404 (2015).

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Convergence to attractors in the climate system

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The time evolution of the climate system is unpredictable. The inherent unpredictability originates from the irregular, chaotic nature of the solutions of the underlying dynamics. In such circumstances only probabilistic predictions can be made, and we point out that the full range of possible outcomes (called the internal variability of the climate) is described by the so-called natural distribution on a dynamical attractor. This is due to the fact that any initial probability distribution converges to the natural one with an exponential speed. We emphasize that this distribution exists, beyond what a traditional framework covers, in non-periodically time-dependent dynamical systems as well, so that this approach is applicable even if a parameter (like the greenhouse gas concentration) is shifting. In this case the natural distribution itself depends on time, and this dependence (especially shifts in expectation values) represents climate change. Numerically, the natural distribution can be represented by an ensemble of trajectories, but only after convergence has taken place. Then the statistical characteristics (like expectation values or standard deviations) are to be evaluated with respect to the ensemble.

Chimera patterns as complex systems: Examples from two-dimensional networks of coupled neurons

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Chimeras are hybrid states that emerge spontaneously, combining both coherent and incoherent parts [1]. First found in identical and symmetrically coupled phase oscillators [2], chimera states have been the focus of extensive research for over a decade now. Both theoretical and experimental works have shown that this counter-intuitive collective phenomenon may arise in numerous systems including mechanical, chemical, electro-chemical, electro-optical, electronic, and superconducting coupled oscillators. The phenomenon of chimera states has also been addressed in networks of biological neural oscillators. In this context, theoretical studies have considered Hindmarsh-Rose, leaky-integrate-and-fire, SNIPER/SNIC, and FitzHugh-Nagumo models in one-dimensional ring configurations and recently also in more complex network topologies.

arrangement of the brain. FitzHugh-Nagumo and leaky-integrate-and-fire models are chosen as widely used description for neuronal activity. Finding common synchronization patterns in the two dynamical networks could point the way toward identification of universal dynamical features present in brain activity. The oscillators are arranged on a two-dimensional lattice and couple isotropically to all other oscillators within a finite range.

The aim of the current study is to discuss the occurrence of stable chimera patterns induced by the nonlocal connectivity and to identify patterns that are common in both models. For the FitzHugh-Nagumo model a phase connectivity parameter and the coupling range are varied, while the coupling strength is kept fixed. For the leaky-integrate-and-fire model the coupling strength, coupling range, and refractory period are varied.

Our comparative study demonstrates that, although the dynamics of the single neurons in the two models are described by different equations, both systems support hybrid states composed of coherent and incoherent regions when the elements are coupled. We identify a number of common chimera patterns (cf. Fig. 1): spots, grids, rings, and stripes. Our simulations suggest that the coherent/incoherent pattern characteristics follow similar growth rules. For example, the diameter of the ring patterns grows linearly with the coupling range in both models. Other phenomena typical in nonlinear systems such as multistability and transitions between different patterns are observed as well. The common behavior of the two models supports the universal occurrence of these peculiar dynamics: Chimera patterns are persistent and independent of the specificity of the model, provided that the models retain the characteristics of spiky limit cycles.

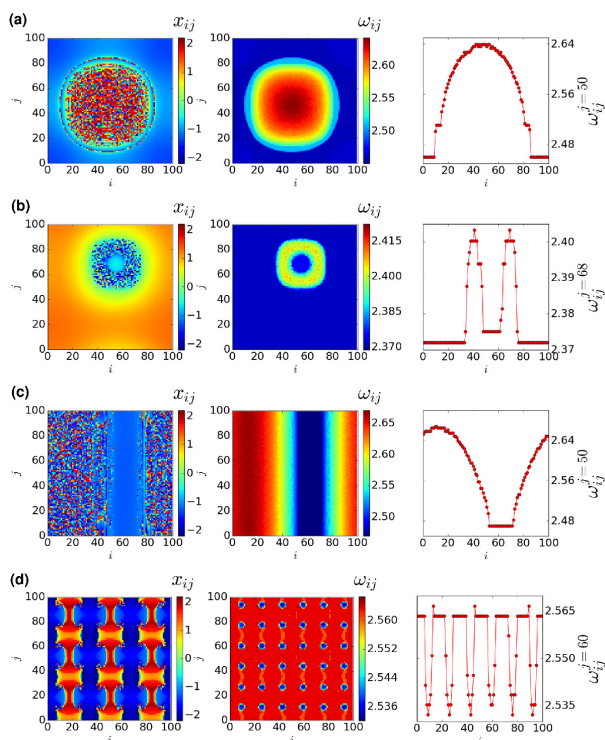


Figure 1: Examples of chimera states for the FitzHugh-Nagumo model: (a) spot, (b) ring, (c) stripe, and (d) grid. The left, center, and right panels show snapshots of the activator variable x_{ij} , the mean phase velocity ω_{ij} , and a section of ω_{ij} , respectively. The index $i, j = 1, \dots, N$ refers to the position on the two-dimensional lattice.

In our contribution, we consider a two-dimensional network configuration using two different models of neuronal oscillators with nonlocal coupling [3]. This can be seen as an intermediate step extending the intensively studied one-dimensional ring geometries towards a three-dimensional

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Complex Epidemic Spreading

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Epidemic modeling has proven to be a powerful tool for the study of spreading and contagion phenomena in biological, social and technical systems. The addition of numerous compartments and the incorporation of complex contact topologies has yielded evermore accurate models, prompting their use as real-time predictive tools. Notwithstanding, most approaches assume memoryless and independent processes, an approximation partially invalidated by empirical evidence [1]. We propose an alternative, cumulative infection mechanism, and study its effects in the susceptible-infected-susceptible model.

In our description, susceptible agents accumulate exposition time from all their infected neighbors and become infected following a given probability density. When the last infected neighbour recovers, this exposition time starts to decay with a characteristic relaxation time ζ . Infected agents recover spontaneously following a given inter-event time distribution. Here we use a Weibull distribution for infections (with shape parameter α) and exponentially distributed recoveries. We study the limit cases $\zeta = 0$ (instantaneous decay) and $\zeta = \infty$ (long-term memory) in random degree regular networks.

Performing extensive numerical simulations we obtain the bifurcation diagrams (Fig. 1) and critical properties of the absorbing phase transitions. Our results [2, 3] show a variety of phenomena, including loss of universality and, counterintuitively, an apparent memory-loss in systems equipped with long-term memory. These features arise from different combinations of infection distributions and relaxation times, evidencing a crucial role of non-Markovian effects.

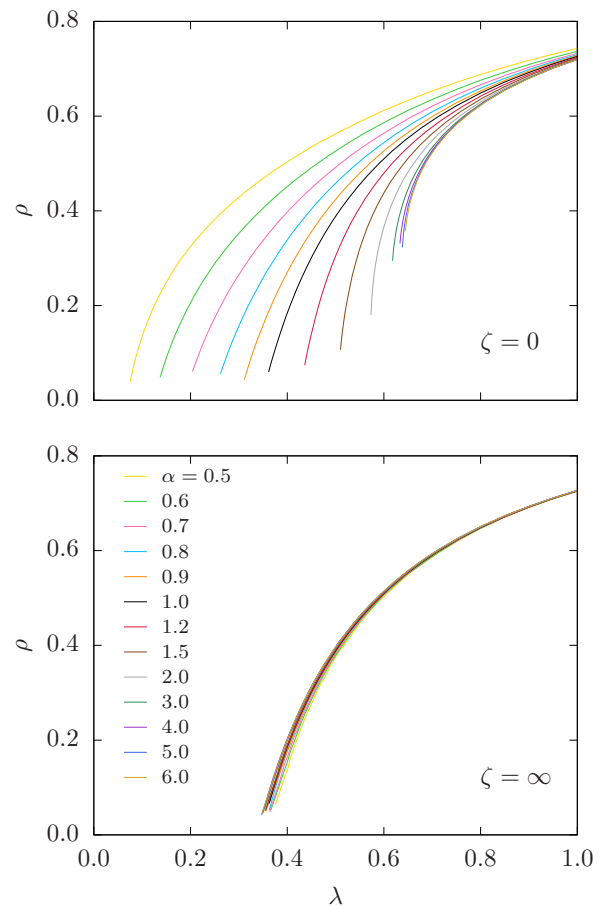


Figure 1: Fraction of infected agents, ρ , as a function of the effective spreading ratio, λ , for various infection distributions (α indicated in legend). **Top:** Instantaneous decay of exposition time (short-term memory). **Bottom:** Exposition time does not decay (long-term memory).

[1] Pastor-Satorras, R. et al. *Reviews of Modern Physics* **87** (3): 925 (2015).

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[3] In preparation.

Localized Homological Reorganization of Brain Functional Scaffolds after LSD Administration

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In this work we analyse the algebraic topological features of the functional brain networks of subjects before and after the subadministration of LSD. Recently a number of techniques rooted in algebraic topology have been proposed as novel tools for data analysis and pattern recognition [1, 2]. The fundamentally new character of these tools, collectively referred to as TDA or topological data analysis, stems from abandoning the standard measures between data points (or nodes, in the case of networks) as the fundamental building block, and focusing on extracting and understanding the shape of data at the mesoscopic scale. These techniques have been used with success in biological and neurological contexts [3, 4, 5] and play a key role in understanding complex systems in a wide range of fields by extracting useful information from big datasets.

Here we do this by summarising the persistent homology information of the functional networks in a set of surrogate networks, called persistent homology scaffolds [3]: roughly speaking, persistent homology memorizes for how long brain functional cycles are active and the scaffolds compress this information effectively yielding a topological skeleton of the original network. Scaffolds have also been shown to carry meaningful and non-trivial information about functional connectivity both in normal [6] and altered brain states [3]. In this contribution, we show how topological information is able to detect subtle differences in the fMRI homological structure with and without drug. In particular, the scaffolds in the two conditions (drug-free vs LSD) display very similar global properties, e.g. weights distributions on the scaffolds, degree centrality distribution (Figure 1 (c) and (d)). However, a careful investigation of the scaffolds shows a significant difference in the localization of the topological features leading to a significantly different modulation of the weights of the edges common to both groups: common edges suffer a strong reduction in their persistence under the effects of LSD (see Figure 1 (a) and (b)), while the distributions of weights for edges belonging to a single group do not show significant differences. This suggests the existence of an underlying topological core that is only deformed by the drug. The obtained results are robust for analysis at both the subject and group level. Finally, we compare the results for LSD with previous results on another psychedelic drug, psilocybin [3], and show that two similar drugs produce starkly different topological alteration of the brain's functional structure.

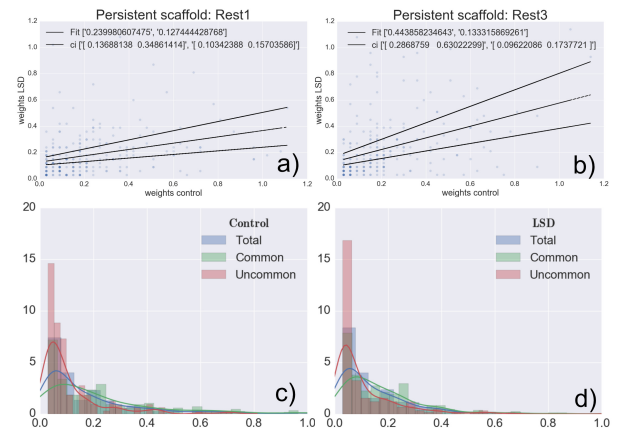


Figure 1: The comparison of common persistence scaffolds weights for control and LSD subjects shortly after the drug administration (a) and in a successive session (b) distinctly different linear slopes, highlighting a modulation in the topology (as exemplified by the fit) and a slow return to the placebo state. Notably, these patterns are not detectable by considering the edge weight distributions alone ((c) and (d), which display weight distribution from the persistence scaffolds for common and uncommon edges).

- [3] Giovanni Petri et al. *Journal of The Royal Society Interface*, 11(101):20140873, (2014).
- [4] P. Y. Lum, G. Singh et al. *Scientific reports*, 3, (2013).
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Analysis of Social Epidemic Phenomena Using Social Physics Approach

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In the present age where consumer behavior remains on record through the Internet, purchase records and action records for huge quantities of consumers are left. In this paper, we propose a method based on social physics for analyzing and forecasting social phenomena, and possibly applying it to marketing etc. by using the voices of society's people recorded by blogs and Twitter as data. Social physics is a new frontier of physics alongside economic physics, but if there is a huge amount of data, the methodology of physics that has been the subject of experimental data on natural phenomena can also be applied to social science.

We write down the equation of purchase intention at the individual level $I_i(t)$ as

$$\begin{aligned} \frac{dI_i(t)}{dt} = & \sum_{\xi} c_{\xi} A_{\xi}(t) - aI_i(t) + \sum_j d_{ij} I_j(t) \\ & + \sum_j \sum_k p_{ijk} I_j(t) I_k(t) \end{aligned} \quad (1)$$

where d_{ij} , h_{ijk} , and $f_i(t)$ are the coefficient of the direct communication, the coefficient of the indirect communication, and the random effect for person i , respectively[1]. The advertisement and publicity effects are include in $A_{\xi}(t)$ which is treated as an external force. The index ξ means sum up of the multi media exposures. Word-of-mouth (WOM) represented by posts on social network systems like blog or twitter is used as observed data which can be compared with the calculated results of the model. The unit of time is a day. Here, it is assumed that the height of interest $I(t)$ of people attenuates exponentially.

We consider the above equation for every consumers in the society. Taking the effect of direct communication, indirect communication, and the decline of audience into account, we obtain the above equation for the mathematical model for the hit phenomenon. Using the mean field approximation, we obtain the following equation as equation for averaged intention in the society. The derivation of the equation is explained in detail in ref.[1].

$$\frac{dI(t)}{dt} = \sum_{\xi} c_{\xi} A_{\xi}(t) + (D - a)I(t) + PI^2(t) \quad (2)$$

This equation is the macroscopic equation for the intention of whole society. Using this equation, our calculations for the Japanese motion picture market have agreed very well with the actual residue distribution in time [1]. Using this equation, our calculations for the Japanese motion picture market agree very well with the actual residue distribution in time. The advertisement and publicity effects are obtained from the dataset of M Data and the WOM represented by posts on social network systems are observed using the system of Hottolink.

Using the above theory, we analyze social epidemic phenomena in Japanese society, especially among female. For example, we analyze the hydrogen water. Hydrogen water became famous among Japanese women [2] in 2016 summer. We employ the equation (2) using the observed daily advertisement data on television as $A_{\xi}(t)$. In fig.1, we show the observed daily Twitter posting number and calculated theoretical prediction. As we can see in the figure, our calculation agree well with the observed Twitter posting numbers.

The parameters C , D and P in eq. (2) is adjusted for the periods, 5-8, 8-13, 18-19, 19-24, 24-26 and 26-28 of May 2016. As we can see in fig.2, the strength of the indirect communication, P is strong at the beginning of the social epidemic phenomenon. It means that the indirect communication is a key of epidemic phenomena.

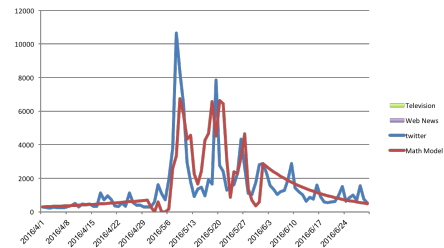


Figure 1: Observed daily number of posting on Twitter (blue) and theoretical calculation (red) for Hydrogen Water.

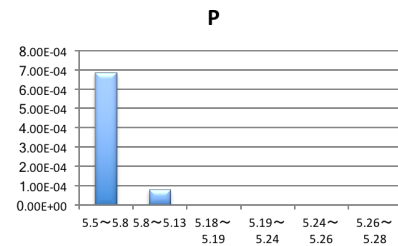


Figure 2: Strength of indirect communication of Hydrogen Water for the periods, 5-8, 8-13, 18-19, 19-24, 24-26 and 26-28 of May 2016.

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[2] ANNE BAUSO, 2016. We Tried the Miracle Water People in Japan Are Obsessed With, [online] 7 March, Available at: <http://www.allure.com/story/hfactor-hydrogen-water-review> [Accessed 31 January 2017]

Zealots in the mean field noisy voter model

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The dynamical evolution of opinions is frequently studied using the voter model [1, 2, 3], which usually considers a set of voters or agents supporting two opinions that change due to the influence to all of them (mean-field level), in such a way that a voter supporting an opinion changes it with a rate proportional to the fraction of agents holding the opposite opinion. The model exhibits a competition that ends up after a transient time to consensus (if the system is finite), the two possible absorbing states being equiprobable. This macroscopic picture may change when the model is modified in order to account for more realistic situations, such as the heterogeneity and the free will of agents.

The heterogeneity in the population of agents or units is usually reflected in two different aspects, namely, in the intrinsic properties of the agents and in the structure of the interactions. In the first case, agents may be differentiated by its intrinsic rates of change between states, an extreme case corresponding to a system of equal agents but one that does not change opinion, i.e. a zealot. In the second case, some agents are influenced only by some others in the processes of opinion changing, the system being embedded in a graph or network of interactions. Many studies incorporate both ingredients to the voter model at the same time. First studies focused on the influence of few zealots in the case of regular networks, as well as in the case of all-to-all interactions, or the so-called mean-field approximation [4, 5, 6]. In these cases, the presence of zealots changes drastically the evolution of the system. If only one zealot is present, the system approach much faster one consensus state, the one that corresponds to the zealot. When the number of zealots of different opinions are the same, the system reaches a steady state where the two opinions coexist. More recently, the effect of complex network has also been analyzed, with similar conclusions [7, 8].

The voter model has also been modified to account for the free will of the voters, leading to the so-called noisy voter model [9] or Kirman model [10]. Now, the rate at which one agent changes opinion not only depends on the fraction of opposite voters, but on an intrinsic constant, the free-will parameter. The main difference of the present model with respect to the original one is that the free will avoids the system from reaching the consensus states. Moreover, the system undergoes a finite-size transition, by increasing the free-will constant, from a bimodal behaviour, where agents spend most of the time close to the consensus states, to a unimodal one, where a non-negligible fraction of agents are at different states [11, 12]. Once again, the presence of a complex networks seems to respect the latter picture, while the critical values are modified. Few studies cover mixture of different agents in the context of the noisy voter model, see [13] as an exception, nor the influence of zealots.

In this work, we analyze the influence of zealots on the

noisy voter model, focusing on the steady-state properties. We also provide a deep relation between this problem and a system made of heterogeneous voters. More precisely, we consider three cases of interest: (a) one optimistic zealot influencing a sub-population, (b) two opposite zealots influencing a sub-population, and (c) two opposite zealots influencing different sub-populations of the system. The main results are summarized in a phase diagram ($a/h, N_1/N$) where a/h is the ratio between free-will and herding coefficients and N_1/N is the fraction of affected agents. The noisy voter model has two phases separated by an horizontal line corresponding to $a/h = 1/N$. The latter line splits into two ones in case (a) while it turns curved in cases (b) and (c).

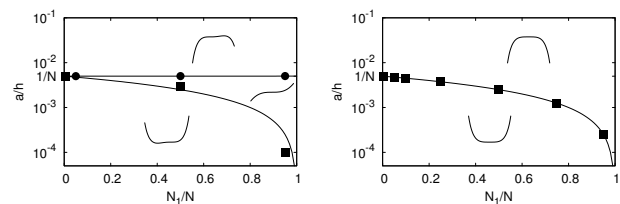


Figure 1: Phase diagram for cases (a) (left) and (b) and (c) (right).

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Model of nonlocal birth-death competition with volume exclusion

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We propose a stochastic birth-death competition model for particles with excluded volume. The particles move, reproduce, and die on a regular lattice. While the death rate is constant, the birth rate is spatially nonlocal and implements inter-particle competition by a dependence on the number of particles within a finite distance. The finite volume of particles is accounted for by fixing an upper value to the number of particles that can occupy a lattice node, compromising births and movements. In this way, we extend a previous model [1, 2] of competition between individuals of negligible size. Examples of the spatiotemporal configurations obtained with the model proposed here [3] in one spatial dimension can be seen in Figure 1.

We derive closed macroscopic equations for the density of particles and spatial correlation at two adjacent sites. Under different conditions, the description is further reduced to a single equation for the particle density that contains three terms, namely diffusion, a linear death, and a highly nonlinear and nonlocal birth term.

Steady-state homogeneous solutions, their stability which reveals spatial pattern formation, and the dynamics of time-dependent homogeneous solutions are discussed and compared, in the one-dimensional case, with numerical simulations of the particle system.

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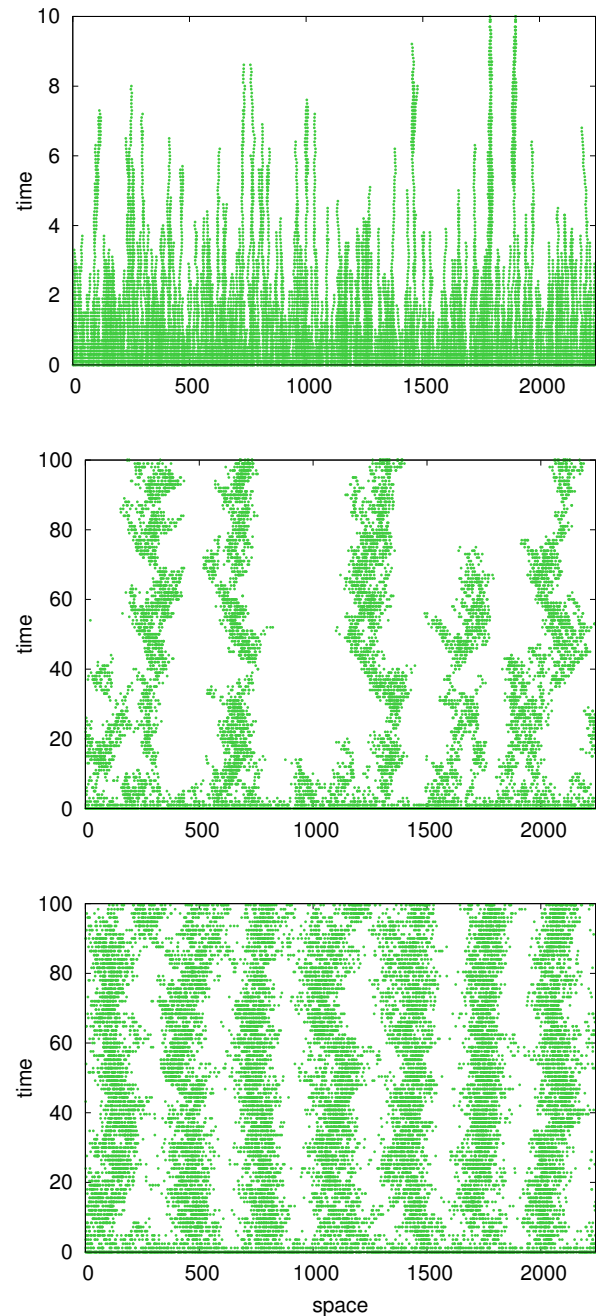


Figure 1: Three spatio-temporal configurations of the one-dimensional interacting particle system under different parameters. Green dots are the particle positions. The first panel shows extinction, the last one the emergence of a spatially periodic density state. The middle panel shows an intermediate noisy behavior.

Preferential Attachment and Edge Rewiring in Container Shipping

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In this work we approach commercial container shipping from a complex networks perspective. This is an application of network theory which remains underinvestigated when compared to other transportation and logistics systems (e.g. rail, underground or airlines), yet it presents very interesting properties such as hub-and-spoke behaviour, fat-tailed degree distributions and high correlations between node centrality and significance in the shipping network.

While previous studies focus mainly on the analysis of network measures, we propose investigating evolutionary processes to understand the network's internal workings. More specifically, we suggest modelling the global container shipping network and regional sub-networks from the viewpoint of preferential attachment and edge rewiring; we link established models in the literature to observed phenomena, such as the Bianconi-Barabási model to the growth of latecomer ports, and rewiring processes to containership re-routing, a common practice among operators. We support these observations by looking specifically at the containership network in the Mediterranean region and the port of Malta in particular.

With regards to the Bianconi-Barabási model, we propose modelling a port-node's fitness in terms of its location: how centrally it is positioned in the region where it belongs and how much it deviates from the trading lines passing through that region. We further suggest that the impact of each of these factors differs in the macro- (global) and meso- (regional) scales, with centrality being more important in the regional scale and service deviation being more important in the global scale.

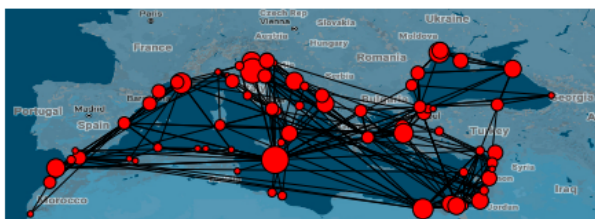


Figure 1: Regional containership network in the Mediterranean (node size represents the degree).

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Intertrade times memory and autocorrelation of price changes absolute values

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Continuous-time random walk (CTRW) is a stochastic process with continuous and fluctuating waiting (interevent) time. It was firstly introduced to physics by Montroll and Weiss [1]. Since then it has been used to model anomalous transport and diffusion, hydrogen diffusion in nanostructure compounds, electron transfer, aging of glasses, transport in porous media, diffusion of epicenters of earthquakes after-shocks, cardiological rhythms, human travel and many more [2].

CTRW is also successfully applied in econophysics [3], for example it is used to describe stock price dynamics. We can consider the stock price as the price of the last transaction, so the value of a process represents the stock price and waiting times (WT) correspond to times between transactions. If we take into consideration only the memory between price changes it may describe empirical autocorrelation function (ACF) of price changes satisfactorily (one-step memory [4], two-step and infinite-step memory [5]). However, empirical ACF of price changes absolute values decays much slower than ACF of price changes and cannot be fully explained only by dependencies between price changes.

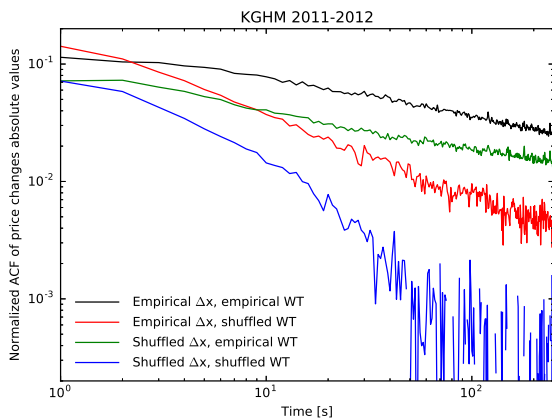


Figure 1: Normalized autocorrelation function (ACF) of price changes absolute values for KGHM (one of the most liquid polish stock) in years 2011-2012 for empirical data (black), empirical price changes and intra-daily shuffled waiting times (red), intra-daily shuffled price changes and empirical waiting times (green), and intra-daily independently shuffled price changes and waiting times (blue). Notice that considering real dependencies of waiting times reproduces ACF which decays like one for the empirical data. Considering only dependencies of price changes does not reproduce the original result.

By using empirical financial data we study the autocorrelations of the following quantities: price changes, their ab-

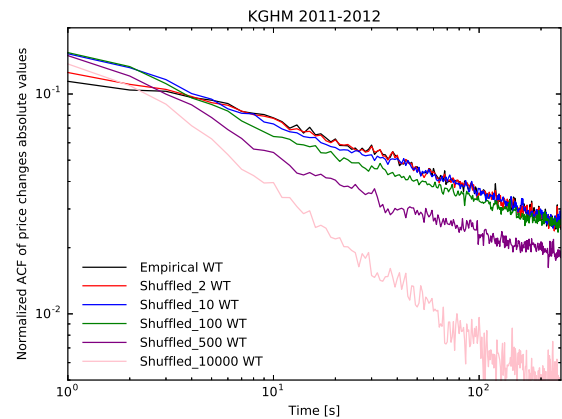


Figure 2: Normalized ACF of price changes absolute values for KGHM in years 2011-2012 for empirical data (black) and simulations. We intra-daily shuffle waiting times in non-intersecting windows of different sizes (in number of ticks): 2 (red), 10 (blue), 100 (green), 500 (purple), 10000 (pink). Notice that shuffling waiting times in windows does not significantly change pace of ACF decaying. Only taking a window bigger than the number of transactions per day (pink) accelerates decaying of ACF.

solute values and corresponding waiting times. We argue that the foundation of slowly decaying ACF of price changes absolute values are dependencies of waiting times (see Fig. 1). We show that those dependencies do not affect the ACF of price changes while they decisively influence the ACF of their absolute values. We present that considering only short-term dependencies is not enough to explain empirical ACF, we show the decisive role of long-term correlations (see Fig. 2).

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A Reaction-Diffusion System coupled to active motion in a cell

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Mitochondria are the cells' power plants. They produce ATP from an energy substrate. Energy production leads to aging and consequently to a reduced production rate. Mitochondria by themselves are produced in the cell body and in the case of neurons have to travel relatively long distances (up to the order of *mm*) to reach the location of highest need (the synapse). It is known that some Parkinsons Disease mutations lead to garbage agglomeration around the cytoskeleton – the highway for mitochondria transport, thus affecting the transport properties.

The substrate for energy production in the case of neurons is introduced into the axon via specific transporters whose functioning is essential for axon integrity.

We present a work on a reaction diffusion system spatially linking the mitochondrial motion and location to the production and consumption of diffusing species ATP and lactate.

Objectivity in non-Markovian spin-boson model

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Quantum mechanics is one of the most successful theories, correctly predicting a huge class of physical phenomena. Its validity remains confined to the microscopic regime, where such a theory provides a good explanation of the behavior of the constituents of matter. Contrariwise, there is no trace of quantum effects on macroscopic scales, fully ruled by classical physics. Accordingly, one natural question arises: how the classical features of the macroscopic world emerge from the underlying quantum domain?

In particular, from the everyday experience we are accustomed to perceive nature as *objective*: if two different observers measure the same quantity in two identical systems prepared in the same state, they surely obtain the same outcome. This point of view has been fundamentally challenged by quantum mechanics, since an act of observation generally modifies the state of a system. So it is natural to wonder how the objectivity of the classical theory emerges from not objective quantum one.

An important contribution to such a problem has been given by *quantum darwinism* attributing objectification of a quantum system to its unavoidable interaction with the environment [1]. Precisely, the environment is considered divided in several different portions, storing the same information about the central system, which can be extracted by observers.

Another important step beyond has been accomplished in [2] where the authors focused on the analysis of objectivity in terms of states: we have objectivity if and only if the post-interaction state of the central system plus the observed portion E posses the so-called *spectrum broadcast structure* (SBS):

$$\rho_{S, fE} = \sum_i p_i |x_i\rangle \langle x_i| \otimes \rho_i^{E_1} \dots \otimes \rho_i^{E_{fN}} \quad (1)$$

with $\{|x_i\rangle\}$ a pointer basis of the central system, p_i initial pointer probabilities, and some states of the observed parts of the environment $\{E_1, \dots, E_{fN}\}$ with mutually orthogonal supports.

The main purpose of our (unpublished) paper is to detect SBS for the spin-boson model, which consists of a two-level system interacting with a large reservoir of bosonic modes [3]. This model plays an important role in quantum computing, as well as in experiments on macroscopic quantum coherence, for instance in those aimed to analyse the role of quantum coherence in biological systems.

An important part of the work is devoted to explore the behavior of the model in the non-Markovian regime. By non-Markovianity we mean the presence of memory effects making the evolution of the central system strongly dependent by its past history. This situation constitutes the rule rather than the exception, especially in the low-temperature regime, or when the interaction between the central system and the surrounding degrees of freedom gets sufficiently strong. **We**

propose thus to study how non-Markovianity affects (or not) objectification processes.

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Insights into resource consumption, cross-feeding, system collapse, stability and biodiversity from an artificial ecosystem

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Community ecosystems at very different levels of biological organization often have similar properties. Coexistence of multiple species, cross-feeding, biodiversity and fluctuating population dynamics are just a few of the properties that arise in a range of ecological settings. Here we develop a bottom-up model of consumer-resource interactions, in the form of an artificial ecosystem “number soup”, that reflects basic properties of many bacterial and other community ecologies. We demonstrate four key properties of the number soup model: (1) Communities self-organise so that all available resources are fully consumed; (2) Reciprocal cross-feeding is a common evolutionary outcome, which evolves in a number of stages, and many transitional species are involved; (3) The evolved ecosystems are often “robust yet fragile”, with keystone species required to prevent the whole system from collapsing; (4) Non-equilibrium dynamics and chaotic patterns are general properties, readily generating rich biodiversity. These properties have been observed in empirical ecosystems, ranging from bacteria to rainforests. Establishing similar properties in an evolutionary model as simple as the number soup suggests that these four properties are ubiquitous features of all community ecosystems, and raises questions about how we interpret ecosystem structure in the context of natural selection.

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Entropy production and thermodynamic power of the squeezed thermal reservoir

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Thermodynamic theory was developed from the analysis of real heat engines, such as the steam engine along the 19th century [1]. Those macroscopic engines have quantum analogues, whose analysis constitute an important branch of research in quantum thermodynamics [2]. Clarifying the impact of quantumness in the operation and properties of thermal machines represents a major challenge. Quantum effects can arise in the working substance and environment, and there have been different works in the literature pointing that nonequilibrium quantum reservoirs may be used to increase both power and efficiency of the machines [2, 3]. Nevertheless, a solid understanding of these enhancements and their optimization has remained elusive, as it requires a precise formulation of the second law of thermodynamics in such nonequilibrium situations.

Using recent advances in quantum fluctuation theorems [4], we analyze the entropy production and the maximal extractable work from a squeezed thermal reservoir. The quantum nature of the reservoir induces genuine nonequilibrium features such as an entropy transfer with a coherent contribution. These nonequilibrium features allow for work extraction from a single reservoir, and are the responsible of power and efficiency enhancements for quantum heat engines operating with this kind of reservoirs. Here we consider in detail a heat engine performing a (modified) quantum Otto cycle [5], optimize it, and discuss its many striking consequences, like the appearance of multi-task regimes in which the heat engine may extract work and refrigerate a cold reservoir at the same time (see Fig. 1) [6]. Moreover, we show how our approach leads to the introduction of a *thermodynamic efficiency* based on the concept of nonequilibrium free energy, which naturally accounts for the performance of both classical and quantum thermodynamic resources. Our results hint at possible applications like squeezing-fueled batteries, multi-task thermal machines, or erasure devices operating below Landauer's limit.

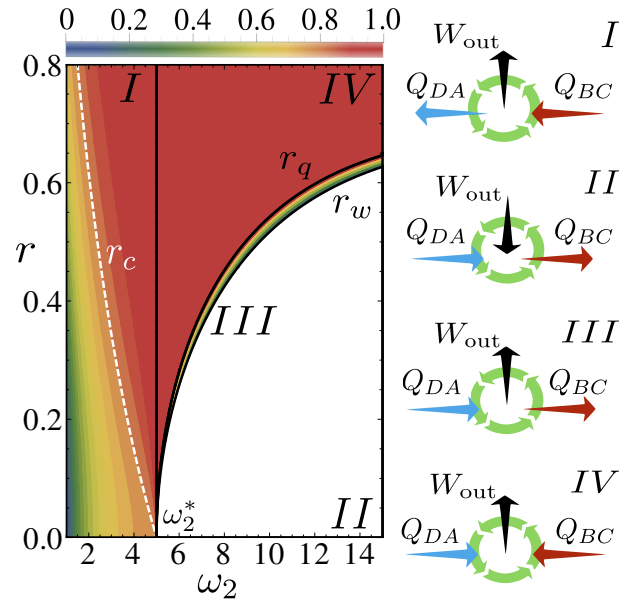


Figure 1: Phase diagram with the four regimes of operation of the cycle (I, II, III, IV) as a function of the working substance frequency modulation ω_2 and the squeezing parameter r . The color scale corresponds to the *energetic* efficiency of the cycle $\eta = W_{\text{out}}/Q_{\text{in}}$ as a heat engine, for inverse temperatures in the reservoirs $\beta_2 = 0.2\beta_1$, yielding a Carnot efficiency $\eta_c = 0.8$ (white dashed curve). In the right side the direction of the arrows represents the sign of the energy fluxes for each regime.

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Fluctuation theorems for quantum maps

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When considering small systems, quantum fluctuations, in addition to thermal ones, come into play. Furthermore, there is a wide range of phenomena without classical counterpart that cannot be neglected, such as coherence, squeezing or entanglement, in both single and many-body systems. A promising route to the understanding of thermodynamics in quantum systems are the fluctuation theorems, which establish exact statements about the fluctuations of thermodynamic quantities such as work, heat or entropy production, in systems arbitrarily far from equilibrium [1].

Work fluctuation theorems have been extensively investigated in the quantum regime under an inclusive Hamiltonian approach. Also fluctuation theorems for the exchange of heat and particles in transient and steady-state regimes has have been established within the so-called two-measurements-protocol [2, 3]. This framework has provided important results, but its rigid assumptions restrict possible extensions to more general situations, apart from being impractical in most physical situations. On the other hand, an alternative approach recently considered is the derivation of fluctuation theorems for arbitrary completely-positive and trace-preserving (CTPT) maps, as they provide a compact description of general physical processes condensing the main effects of the environmental action in a set of few relevant variables.

Here we present a novel fluctuation theorem valid for a broad class of quantum CPTP maps [4]. It is based in the concept of a *nonequilibrium potential*, an intrinsic fluctuating property of the map which allows the thermodynamic description at the single trajectory level in most situations of interest. Our theorem goes beyond previous results for specific classes such as *unital* maps —maps preserving the identity operator— [5, 6], or theorems limited by efficacy (correction) terms [7, 8].

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The interplay between environmental flow and extracellular matrix production determines lineage segregation during bacterial surface colonization.

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Contrarily to the traditional view of bacteria as single drifting organisms that inhabit liquid environments, they often form dense conglomerates attached to surfaces, termed biofilms. Within a biofilm, cells are embedded in a matrix of extracellular polymeric substances (EPS) that binds bacteria among them and to the surface, thus magnifying cell-cell interactions and the complexities of their life cycle [1, 2].

As a consequence of reinforced adhesiveness, cells become more resistant to shear forces induced by flows at the liquid-solid interface, which increases their resources exploitation rate but reduces their chances of being dispersed and colonize new environments [3]. Therefore, EPS production and the subsequent biofilm formation not only influence the spatial structure of the bacterial colony (Fig. 1), but it can also determine its survival in different environmental conditions, for example in the presence of flows.

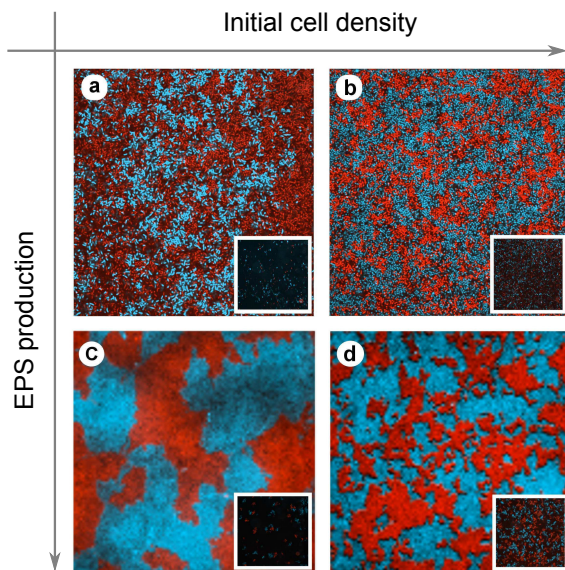


Figure 1: Experimental colonization patterns for nonadhesive EPS-nonproducers (top) and adhesive EPS-producers (bottom). Initial cell density, whose spatial distribution is shown in the insets, increases from left to right.

Surprisingly, the influence that an environmental flow may have on bacterial spatial organization has received little attention in the literature. Here, we aim to fill this gap by studying experimental and theoretically the surface colonization patterns of a population of the bacterium *Vibrio cholerae* growing in microfluidic devices from different initial densities. Our results suggest that adhesiveness plays a key role in the surface colonization pattern, with flow playing an important role even under controlled environments such as the microfluidic chamber (Fig. 2). We use spatial correlation functions to quantify the differences between the

emergent two lineage segregation patterns (each lineage is represented by a different color in the pattern, see Fig. 1), as well as to determine with numerical models the dependence of the competitive ability of the cells on both adhesiveness and strength of the flow in the chamber.

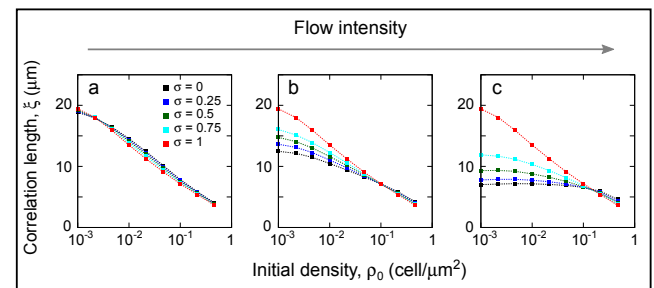


Figure 2: Effect of cell adhesiveness, σ , and flow intensity on the mean correlation distance of simulated patterns. The role of the density of founder cells is shown in the horizontal axis of each panel.

Finally, we discuss the evolutionary implications of matrix formation for the colonization strategies of founding cells, with a main focus in public good production. Our results emphasize the importance of considering both flow and adhesiveness when estimating the virulence of pathogens such as *V. cholerae*, which colonize environments that, like the human gut, are intrinsically affected by flows of different strengths. More importantly, the generality of our model and the iniquitousness of biofilms and flows like the ones described here facilitate the extrapolation of our theory to other organisms.

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Lack of ecological and life-history context can create the illusion of microbial social interactions.

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Research on social microbes often focuses on one fitness component (reproductive success within the social complex) undermining the effect of other stages of the life cycle and the role of the ecological context. This can lead to paradoxical results. The life cycle of the social amoeba *Dictyostelium discoideum* includes a multicellular stage in which not necessarily clonal amoebae aggregate upon starvation to form a possibly chimeric (genetically heterogeneous) fruiting body made of dead stalk cells and spores. Lab-measured spore contributions in these chimeras indicate a strong skew in the fraction of spores that belong to each genotype. This skew suggests a strong social antagonism that should result in low genotypic diversity, which is inconsistent with observations from nature.

Two studies have suggested that this inconsistency stems from the one-dimensional assessment of fitness (spore production) and that the solution lies in tradeoffs between multiple life-history traits [1], e.g.: number of spores versus viability; and spore-formation versus staying vegetative [2]. I will present an ecologically-grounded, socially-neutral model (i.e. no social interactions between genotypes) for the life cycle of social amoebae to theoretically explore multiple non-social life-history traits and tradeoffs [3]. Experimental results regarding apparent social interactions within chimeric mixes can be qualitatively recapitulated under this neutral hypothesis, without needing to invoke social interactions. This allows for simple potential resolutions to the previously paradoxical results, but life-history tradeoffs alone do not resolve strain coexistence. Finally, two ecological processes: spore dispersal [2] among different patches and seasonality [4] within a single patch are proposed as driving forces of diversity in *D. discoideum*

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Numerical study of the interplay of noise and a subthreshold periodic signal in the output of two coupled neurons

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We study numerically the dynamics of two mutually coupled neurons using the well-known stochastic FitzHugh-Nagumo (FHN) model. We analyze how the coupling parameters affect the detection and transmission of a periodic weak signal that is applied to only one of the neurons. In a recent work [1] it was shown that, in a single FHN neuron, the interplay of noise and periodic subthreshold modulation induced the emergence of relative temporal ordering in the timing of the spikes. Different types of relative temporal order were found, in the form of preferred and infrequent *ordinal patterns* [2] that depended on both, the strength of the noise and the period of the input signal. A resonance-like behavior was also found, as the probability of the preferred (infrequent) pattern was maximum (minimum) for certain periods of the input signal and noise strengths.

Here we analyze under which conditions the coupling to a second neuron, which is assumed to be linear and instantaneous, can further enhance the temporal ordering in the spike sequence of the first neuron, improving the encoding of the external signal. As in [1], we apply the symbolic method of ordinal analysis [2] to the output sequence of inter-spike intervals (ISIs). We find that for certain periods and amplitudes of the external signal, the coupling to the second neuron changes the preferred (and also the infrequent) ordinal patterns. A detailed study of how the ordinal probabilities vary with the coupling strength is performed. In a second step, we consider the situation in which the external signal is applied to both neurons. We discuss under which conditions mutual coupling enhances (or degrades) the encoding of the signal in the neuronal spike sequences.

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Modeling conditional waiting times: a new approach to human mobility

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Understanding how people move within a geographic area [1], e.g. a city, a country or the whole world, is fundamental in several applications, from predicting the spatio-temporal evolution of an epidemics [2, 3] to inferring migration patterns [4]. The possibility to gather information about the population through mobile phone data (recorded by mobile carriers triggered a wide variety of studies showing, for instance, that mobile phones heterogeneously penetrated both rural and urban communities, regardless of richness, age or gender, providing evidences that mobile technologies can be used to build realistic demographics and socio-economics maps of low-income countries, and also provide an excellent proxy of human mobility, showing for instance, that movements exhibit a high level of memory, i.e. the movements of the individuals are conditioned by their previous visited locations [5]).

However, the precise role of memory in widely adopted proxies of mobility, as mobile phone records, is unknown. We have used 560 millions of call detail records from Senegal [6] to show that standard Markovian approaches, including higher-order ones, fail in capturing real mobility patterns and introduce spurious movements never observed in reality. We introduce an adaptive memory-driven approach to overcome such issues. At variance with Markovian models, it is able to realistically model conditional waiting times, i.e. the probability to stay in a specific area depending on individual's historical movements.

Our results demonstrate that in standard mobility models the individuals tend to diffuse faster than what observed in reality, whereas the predictions of the adaptive memory approach significantly agree with observations. We show that, as a consequence, the incidence and the geographic spread of a disease could be inadequately estimated when standard approaches are used, with crucial implications on resources deployment and policy making during an epidemic outbreak.

The differences between the diffusion of the infective process using each mobility model are quite visible in Fig. 1. The spreading is faster for Markovian models, with some arrondissement populated by more infected individuals than adaptive memory. The incidence, i.e. the fraction of infected individuals in an arrondissement, follows different spatial patterns in the three models (Fig. 1 a – c), with a higher incidence observed in the origin of the infection that decreases as we move far from there. This effect is significantly stronger using adaptive memory because it tends to concentrate more infectious individuals close to the origin (Fig. 1d).

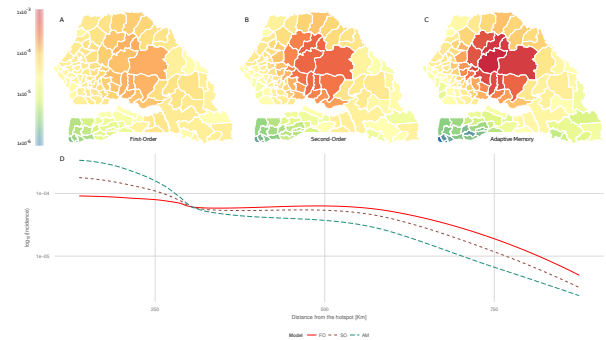


Figure 1: We show the incidence of an influenza-like virus over Senegal arrondissements a week after the infection onset, using first-order (A), second-order (B) and adaptive 2-memory (C) mobility models. The infection started in Barkedji (center of Senegal), where three individuals are initially infected. A SEIR compartmental dynamics with parameters $\beta = 0.05$, $\epsilon = 0.2$, $\gamma = 0.5$ is used to simulate the spreading of the disease within each arrondissement. We found that the number of arrondissements with infected individuals is higher using Markovian dynamics. Conversely, the adaptive memory favors a higher concentration of infected individuals in the arrondissements around the initial location of the infection. In fact, the location of the onset of the epidemic can be better identified using adaptive memory rather than Markovian models. (D) Relation between the incidence in a region and the distance from the hotspot of the infection using the three models. Adaptive memory models spread the incidence on regions closer to the hotspot and this effect is even more evident when higher memory is used.

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Front Interaction Induces Excitable Behavior

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Excitability is a concept that originally comes from biology, inspired by the behavior of neurons and heart cells. An excitable system is characterized by exhibiting a stable steady behavior, while responding to perturbations (e.g. external stimuli) in two different ways: for stimuli below a certain threshold the system decays exponentially to the steady state, while for stimuli above threshold it exhibits a non-trivial excursion in phase space before decaying back to the steady state.

In the case of spatially extended systems, one has first the case of local excitability, what leads to the propagation of travelling waves (autowaves). In addition, spatially extended systems can support local transient excitations in which just a part of the system is excited, namely if the system exhibits localized structures, that become unstable through certain global bifurcations. All these mechanisms, local excitability and excitability of localized structures, have in common an oscillatory instability in phase space, namely one in which a non-zero amplitude limit cycle is destroyed when changing a parameter. The excitable trajectory would follow the remnants of the cycle and ultimately return to the steady state.

In the context of cellular biology, transient localized excitations, also called patches, have been observed in early stages of cell migration. In [1] an explanation was suggested in terms of a spatially extended model with local FitzHugh-Nagumo dynamics in the excitable regime. However, as pointed out in [2], in cell migration, direct evidence for excitability is lacking.

Here we present an alternative mechanism [3] leading to transient patches that requires neither local excitability, nor oscillatory localized structures, not even the existence of the remnants of a limit cycle, widening the classes of extended systems that can present excitability. In particular we show that only two simple ingredients are necessary: bistability between two homogeneous stable steady states (HSSs) and spatial coupling allowing for monotonic fronts connecting these two states. We show the existence of a threshold for perturbations of the homogeneous state. Sub-threshold perturbations decay exponentially, while super-threshold perturbations induce the emergence of a long-lived structure formed by two back to back fronts joining the two homogeneous states. While in typical excitability the trajectory follows the remnants of a limit cycle, here reinjection is provided by front interaction, such that fronts slowly approach each other until eventually annihilating. This front-mediated mechanism shows that extended systems with no oscillatory regimes can display excitability.

To illustrate the new excitability mechanism we consider a prototypical model displaying bistability, namely, the Ginzburg-Landau equation for a real field $u = u(x, t)$ in one spatial dimension x

$$\partial_t u = \mu u - u^3 + \partial_{xx} u. \quad (1)$$

The system is variational and therefore does not have oscillatory solutions. For $\mu > 0$ the system has two equivalent Homogeneous Stable Steady States (HSSs) $u_{\pm} = \pm\sqrt{\mu}$ and stable fronts that connect them. The trivial solution $u = 0$ is unstable and plays the role of a separatrix for the local dynamics. There are two possible front solutions, known as kink and antikink, with opposite polarity and a monotonic tanh shape. Fronts with opposite polarity attract each other with a strength that decays exponentially with the front separation, and they ultimately annihilate in a behavior known as coarsening.

The rationale of the excitability mechanism is as follows. While the system is sitting on a HSSS, small localized perturbations decay exponentially. Instead, for perturbations exceeding $u(x) = 0$ in a wide enough spatial region, part of the system will initially evolve to the other (attracting) HSSS leading to the formation of a pair of kink-antikink fronts. In a second stage the two fronts interact, slowly approaching each other. If the resulting kink-antikink structure is relatively broad this second stage will be long-lived. Finally, in a third stage, kink and antikink annihilate each other and the system returns to the initial HSSS. These structures can be viewed as excitable excursions (see Fig. 1). Further information can be found in [3].

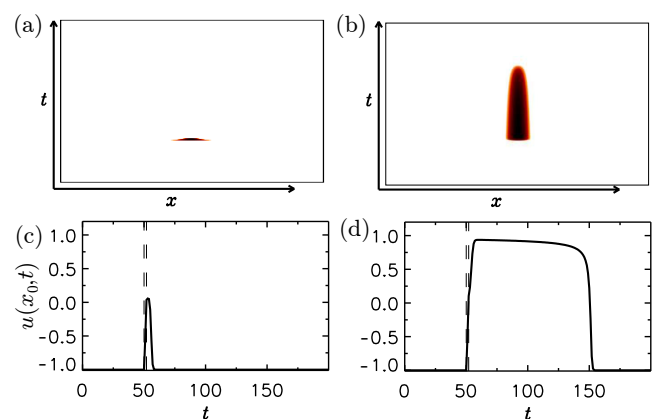


Figure 1: Evolution of $u(x, t)$ after a perturbation on u_- : (a) and (c) correspond to a sub-threshold perturbation; (b) and (d) correspond to a super-threshold perturbation.

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Information, Computation and Linguistic System

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Since the advent of molecular biology, it has been said that cell is a kind of 'machine', which stores its specification inside itself. Although the perspective of systems biology derived from this understanding well prevails, we still do not have a clue to address cellular system deductively, due to the lack of mathematical insights into the system. Here, I propose a conceptual framework where it is possible to abstract the essential features of the system and project them onto the purely mathematical problem. The framework mainly includes the following three concepts; information, computation, and linguistic system. Each concept can be understood independently with explaining specific features inherent to biological system. Nonetheless, the intersection of these concepts can provide us with the fertile results to understand their relationship and hierarchy. In this framework, 4 bases (A, T, G, C) in biology correspond to symbols in information theory and it enables us to discuss probability of occurrence of each symbols, channel capacity and entropies. The DNA-protein interaction, which is one of the most important chemical reactions within cells, corresponds to computation in automata theory, which leads to the understanding of genome as formal languages. What the molecular interactions (cascades, pathways, protein complexes and so forth) correspond in the framework is linguistic system, which I introduce as a definitely new concept in order to explain the interaction between matured components. The apparent discrepancies among those three concepts can be solved by mathematical explanation. Long-standing questions like whether viruses are to be categorized into life or not will be shed light on by viewing them as a mere set of strings which do not have a function of computation. In this paper, I aim at explaining biological system from the perspective, which is completely different from the previous ones.

Connectivity measures in the Mediterranean sea from Lagrangian Flow Networks: patterns, sensitivity and robustness

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The Lagrangian Flow Network (LFN) approach to ocean transport [1] is a modeling framework in which geographical sub-areas of the sea are represented as nodes in a network and are interconnected by links representing the transport of water, substances or propagules (eggs and larvae) by currents. In this way the tools of network theory become available to address questions of fluid transport and of ecological connectivity [2, 3].

Here [4] we compute for the surface of the whole Mediterranean basin four connectivity metrics derived from LFN that measure retention and exchange processes, thus providing a systematic characterization of propagule dispersal driven by the ocean circulation. Then we assess the sensitivity and robustness of the results with respect to the most relevant parameters: the density of released particles, the node size (spatial-scales of discretization), the Pelagic Larval Duration (PLD) and the modality of spawning. We find a threshold for the number of particles per node that guarantees reliable values for most of the metrics examined, independently of node size. For our setup, this threshold is 100 particles per node. We also find that the size of network nodes has a non-trivial influence on the spatial variability of both exchange and retention metrics. Although the spatio-temporal fluctuations of the circulation affect larval transport in a complex and unpredictable manner, our analyses evidence how specific biological parametrization impact the robustness of connectivity diagnostics. Connectivity estimates for long PLDs are more robust against biological uncertainties (PLD and spawning date) than for short PLDs. Furthermore, our model suggests that for mass-spawners that release propagules over short periods (~ 2 to 10 days), daily release must be simulated to properly consider connectivity fluctuations. In contrast, average connectivity estimates for species that spawn repeatedly over longer duration (a few weeks to a few months) remain robust even using longer periodicity (5 to 10 days). Our results give a global view of the surface connectivity of the Mediterranean Sea and have implications for the design of connectivity experiments with particle-tracking models and for evaluating the reliability of their results.

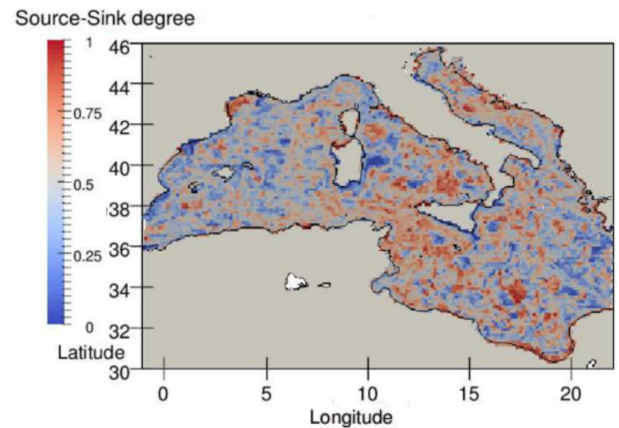


Figure 1: An example (Mediterranean surface, November 2010) of a source-sink degree map, a network measure indicating if a geographical node acts as a source of larvae (small values, blue colors) or as a sink (large values, red colors).

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Pattern Formation and Spatiotemporal Complex Dynamics in Extended Anisotropic Systems

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This research is particularly motivated by the spatiotemporal complex dynamics, especially the spatiotemporal chaos (STC), observed in the nematic electroconvection, a well-known example of a non-equilibrium driven anisotropic system. Since in anisotropic systems the minima on the neutral stability surfaces are isolated, they admit a unique reduced description through Ginzburg-Landau type amplitude equations. Phase equations can be extracted from such amplitude equations governing a pattern-forming system near onset, if solutions in the form of perfect patterns undergo long-wave instabilities. On the other hand, phase equations have also been derived as model equations for physical systems, e.g. Kuramoto-type equations for snowcup patterns and ion bombardment.

We present a comprehensive and systematic theoretical approach, through the study of Ginzburg Landau type amplitude and phase equations extracted from them, in the analysis of the specific mechanisms and features of the formation and dynamics of complex spatiotemporal patterns in anisotropic systems, such as the nematic electroconvection, and the formation of suncups. In the nematic electroconvection, as the patterns bifurcate at onset, theoretical results from normal form analysis are available in the characterization of the mechanisms generating them. Key questions we will address include what is the role of symmetry breaking of a chaotic attractor in the creation of STC, what are the routes to STC, what is the role of nonlinear interactions of wave patterns in the creation of spatiotemporal complex patterns, and which anisotropies are involved in their occurrence.

This approach therefore allows for quantitative and qualitative comparison between the solutions of the model evolution equations and the experimental results, which should significantly increase the understanding of spatiotemporal complex patterns in anisotropic systems.

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Chimeras in globally interacting populations of chaotic oscillators

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We consider a system consisting of two populations of identical chaotic oscillators, each having internal interactions, and globally coupled through their respective mean fields. We investigate the collective behavior of the system on its space of parameters, given by the strength of the global coupling (inter-population) and the strength of the internal coupling (intra-population). We find these collective states in different regions of parameters: (i) chaotic chimera states, where one population reaches a chaotic synchronized regime, while the other remains incoherent; (ii) complete synchronization, where both populations are synchronized internally and to each other; (iii) generalized synchronization, where each population is synchronized, but not to each other.; and (iv) incoherence, where both populations are desynchronized. These states are robust for different partition sizes and for different network topologies of the populations. We characterize the probability for the emergence of chimera states as a function of parameters. In addition, we find that chimera states arise even when the oscillators possess chaotic hyperbolic attractors, a relevant result since it has been recently shown that hyperbolicity prevents the occurrence of chimeras in the presence of nonlocal couplings.

Bright and dark localized structures in the Lugiato-Lefever equation

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In this work we present a detailed analysis of the bifurcation structure of localized structures (LSs) and their different dynamical regimes in the Lugiato-Lefever equation in the presence of anomalous and normal chromatic dispersion. Such analysis is expected to also provide new insights into the formation and stability of frequency combs (FCs). A FC consists in a set of equidistant spectral lines that can be used to measure light frequencies and time intervals more easily and precisely than ever before [1]. Due to the shown duality between LSs and FCs in microcavities, we can gain information about the behavior of FCs by analyzing the dynamics of LSs. In the anomalous dispersion case bright LSs are organized in what is known as a homoclinic snaking bifurcation structure [2, 3]. In contrast, in the normal dispersion regime dark LSs exist and they are organized differently, in a structure known as collapsed snaking [4, 5]. Despite the differences in bifurcation scenarios, both types of LSs present similar temporal instabilities. The similarities and differences between both scenarios correspond to two different unfoldings of the same set of codimension-two bifurcations that organize all the dynamics of the system. This work is expected to be useful to experimentalists working in the domain of FC generation as it provides a detailed map of the different dynamical regimes of LSs and FCs in microresonators. We will show how higher order effects modify the previous scenarios [6, 7].

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Structure and Dynamics of Linguistic Communities: the Cases of Basque, Mazatec, and Tseltal

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Complexity Theory represents a framework unifying natural and social sciences, in which it is possible to provide a quantitative description of social phenomena. In such a framework, in the last years many researchers have addressed problems of linguistics, such as the study of competing languages and language change, evolution, and diffusion in space and time. These topics have been subjects traditionally addressed by historical linguistics.

From the point of view of Complex Systems, languages represent self-organized systems with an interesting twofold nature.

On the one hand, one has to analyze and compare language structures (a problem considered by comparative linguistics), which can be done using various methods to characterize and visualize the usually complex network of relationships, similarities and differences between the dialects of a language or the different languages of a family [1]. One has to choose or integrate between a set of available methods providing tree-like representations or other methods, such as the wave model and its recent developments, revealing more general structures.

On the other hand, there is the problem of describing language change in time and space, i.e., how languages evolve, diffuse, and change by interacting with each other. To this aim the recently developed field of *Language Dynamics* [2] provides a wide set of models which can be used to study how languages interact and compete with each other, evolve and change, and spread across social networks and geographical landscapes. This family of models is related to other research lines such as opinion dynamics, ecological competition models, disease spreading, and genetic evolution.

These two aspects are clearly related to each other. Besides presenting an overview of the current situation, the focus of the contribution is on a possible unification of the two mentioned (structural and dynamical) sides of the problem into methods and tools which would enable us to make quantitative predictions of and comparison with the observed linguistic structures and changes. This is made by illustrating the theoretical study of some examples of linguistic communities, for which the field work of linguists has provided us with reliable and consistent linguistic databases.

The examples considered are

- the dialects of Mazatec, an endangered Otomangean language spoken in Mexico [3]
- the Basque dialects, spoken North-East Spain and North-West France [4]
- the Tseltal, a Mayan language spoken in the Mexico [5]

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Accurate and Computationally Efficient Models for Surface Reactions

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Modelling the kinetics of surface catalysed reactions is essential in many complex chemical processes. However, the majority of microkinetic models employ mean-field approximations, which lead to an approximate description of catalytic kinetics by assuming randomly distributed and spatially uncorrelated adsorbates. On the other hand, kinetic Monte Carlo (KMC) methods provide a discrete-space continuous-time stochastic formulation that enables an accurate treatment of spatial correlations in the adlayer, but at a significant computation cost. In this presentation, we show that the so-called cluster mean-field approach can be used to develop higher order approximations that systematically increase the accuracy of kinetic models for surface reactions by treating spatial correlations at a progressively higher level of detail. We focus on a reduced model for NO oxidation and construct a sequence of approximations of increasingly higher accuracy. By comparing the turnover frequencies of these models with those obtained from KMC simulation, we show that such approximations, while more computationally intense than the traditional mean-field treatment, still achieve tremendous computational savings compared to KMC simulations, thereby paving the way for employing them in multiscale modeling frameworks.

Quantum Dot Micropillar Lasers Subject to Delayed-Optical Feedback

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Semiconductor lasers are well-known to exhibit highly nonlinear behavior when subject to external optical injection and coupling [1]. Nowadays, the case of microlasers is particularly interesting given that such nonlinearities can be studied at the edge of quantum cavity electrodynamic (cQED). Due to the low mode volumes and characteristic strong photon-cavity couplings of such devices, their dynamics is highly influenced by spontaneous emission noise and single emitter effects. The exploitation of such features brings renewed interest to key applications of delay-coupled systems, like zero-lag synchronization or reservoir computing.

In the present work, we explore the phenomena of delayed optical feedback applied to quantum dot based micropillar lasers, focusing on the dynamics characterization for different key parameters. Our microlasers are based on high-quality, high- β semiconductor GaAs/AlAs micropillar cavities containing a single layer of optically pumped In-GaAs quantum dots (QD) as active medium. In those devices lasing is maintained with the gain of only few tens of quantum dots resulting in a few tens of photons in the cavity with sub- μ W output power. Therefore, we characterize their emission in a micro-photoluminescence setup by measuring their spectral and correlation signatures.

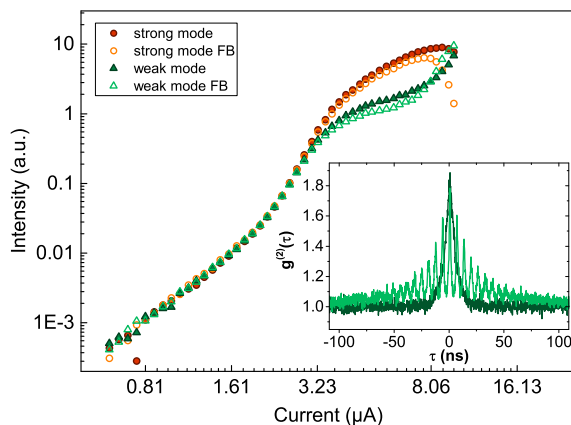


Figure 1: Output intensity of the microlaser plotted over its excitation current. The different curves correspond to the two perpendicular modes (here referred as strong and weak) without and with feedback. The inset shows the second-order autocorrelation function $g^{(2)}(\tau)$ of the weak mode at maximum current. The scenarios without and with feedback are plotted in the respective input-output curves colors.

Figure 1 shows the input-output characteristics of the microlaser. The threshold transition, occurring around $3.2 \mu\text{A}$, shows the typical shallow s-shape of high- β lasers. In vertically emitting micropillars, two orthogonally-polarized modes compete for the gain. From numerical modeling we

know that gain competition leads to mode-switching dynamics, resulting in an increase of the second-order autocorrelation function $g^{(2)}(0) > 1$ [2]. The bunching at zero delay can rise up to 1.9 (see inset in Fig. 1).

The input-output characteristics is significantly modified by self-feedback (here $\tau_d = 4.67 \text{ ns}$), i. e., the crossing point of the two competing modes shifts to lower excitation currents. Adding feedback leads to revival peaks caused by chaotic pulsing of the microlaser [3], but also increases both switching timescale and rate which is indicated by a longer decay timescale of the envelope and lower $g^{(2)}(0)$, respectively. Furthermore, switching behavior is explicitly proven by the dips in the crosscorrelation of strong and weak modes in Fig. 2.

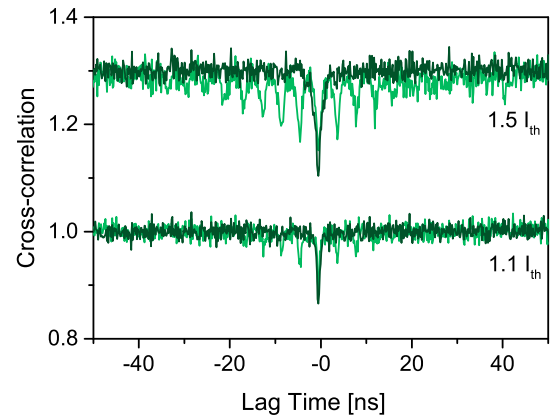


Figure 2: Crosscorrelation of strong and weak modes for two different bias currents. The curves corresponding to $1.5 I_{th}$ have been shifted upwards for clarity. The scenarios without and with feedback are plotted in the respective colors of the input-output curves (see Fig. 1).

By changing parameters in the external cavity such as cavity length and feedback strength, we can directly manipulate the switching dynamics. Here, increasing those parameters diminishes the decay of the dynamics timescales, which is in contrast to the expectations for classical lasers. Therefore, our findings pave the way for deeper understanding the particular dynamics of high- β microlasers and towards successful external quantum control of nanophotonic systems.

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The Dynamics of the Human Perception of Security

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Quantifying the perception of security from a specific region that a person has, poses a serious challenge by itself. It is affected by many factors, such as demographics, the physical condition of the place, media, social media and more and it constantly evolves according to the current condition and the past impressions of the person. However, actual crime should be the key element on how a person alters his or her own perception of security.

A variety of quantitative models exists to analyse the dynamics of opinion formation and to determine how the interactions between people lead to the emergence of a global consensus or fragmentation. However, factors that go beyond the consensus between two people are often modelled as random noise or simply ignored. However, crime cannot be modelled simply as random noise as it is far more concentrated on certain victims and regions than would be displayed by a random selection of targets. Also, crime has an extremely low frequency, which means that more people are fearful than victimised, so most of this fear must come from indirect victimisation and shared perceptions and opinions.

A model for the dynamics of the perception of security is constructed based on the specific elements of crime, that is, its low frequency and its high degree of concentration on certain victims, which also considers elements from opinion formation such as memory loss, binary interactions and consensus.

Through an agent-based model, the opinion dynamics of the fear of crime is simulated and the impact of each element of the model is quantified and so it allows to quantify the impact on the perception of security of a decrease in the crime rates or a change in the degree of concentration of crime. Also, the model allows distinguishing the multiple scenarios under which a persistent perception of insecurity emerges in a society despite a low crime rate or the polarisation between population groups who consider a certain region to be secure on the one extreme and insecure on the other extreme.

The model is then tested using data from a victimisation survey conducted in Mexico and results show, at a state level, that a model which considers how opinions of security or insecurity are exchanged provides a better understanding of the emergence of the global fear of crime.

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Identifying and Characterizing Dynamical Transitions in a Semiconductor Laser with Optical Feedback.

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Identifying transitions to complex dynamical regimes is a fundamental open problem with many practical applications. Semiconductor lasers with optical feedback are excellent testbeds for studying such transitions, as they can generate a rich variety of output signals. Here we perform an experimental investigation of the onset of two well-known dynamical regimes: low frequency fluctuations (LFFs) and coherence collapse (CC) [1, 2]. We apply three nonlinear analysis tools to quantify various aspects of the dynamical transitions that occur as the laser pump current increases. The experimental setup is described in [3].

The first diagnostic tool is based in the analysis of the standard deviation, σ , of intensity time-series recorded with different oscilloscope sampling rate. For each set of (pump current, sampling rate), 10 time series with 10^7 intensity data points each were recorded. Fig. 1a displays the 10σ values vs. the laser pump current, for three sampling rates. In this plot we can identify different behaviours as the pump current increases: at low current the wide spread in the values of σ captures the coexistence between stable noisy emission and LFF dropouts [1]; for higher currents there is an almost linear increase of σ , which captures the increase of the depth and of the frequency of the LFF dropouts; at even high pump currents (above $I/I_{th} \sim 1.08$), σ saturates or decreases depending in the sampling rate, which captures the fact that the dropouts become irregular and allows to quantitatively identify the onset of coherence collapse [2].

The second diagnostic tool is based in the analysis of the number of threshold-crossing events: first, each time series is normalized to zero mean and $\sigma = 1$, then, in each time-series we count the number of times the intensity drops below a give threshold, and plot the number of threshold-crossing events vs the pump current, for various thresholds (see [3] for details). The results are presented in Fig. 1b where we can again distinguish different regions: at low and high currents the number of events depends on the threshold, which reveals that the intensity dropouts are irregular; in contrast, for intermediate currents the number of events is the same for the different thresholds, which captures the fact that the dropouts are of similar depth.

The third diagnostic tool is based in ordinal symbolic analysis [4], by which a time series $y(t)$ is divided into non-overlapping segments of length L , and each segment is assigned a symbol, s , (known as ordinal pattern, OP) according to the ranking of the values inside the segment. For example, with $L = 3$, if $y(t) < y(t+1) < y(t+2)$, $s(t)$ is '012', if $y(t) > y(t+1) > y(t+2)$, $s(t)$ is '210', and so forth. In this way, the symbols take into account the relative temporal ordering of the values in the series. We apply the ordinal method to the sequence of time-intervals between consecutive threshold-crossing events. Specifically, we calculate the probability of consecutive intervals being increasingly

shorter. The results are presented in Fig. 1c, where again one can identify well-defined regions, with $I/I_{th} \sim 1.08$ corresponding to maximum probability of the '10', '210', etc. ordinal patterns.

Taken together, these three diagnostic tools allow delimiting the region of regular LFF dropouts, delimiting the region of coexistence LFF-stable emission, and allow identifying the onset of the CC regime. They can be used for characterizing dynamical properties of the laser output, which can be valuable for applications that exploit the complex output signals generated by semiconductor lasers with optical feedback.

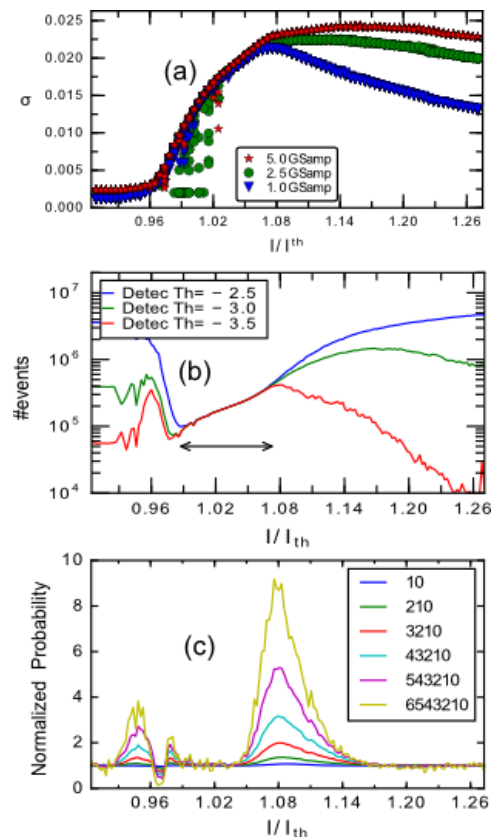


Figure 1: (a) Standard deviation, σ , of the intensity time series recorded with different oscilloscope sampling rate. (b) Number of threshold-crossing events, computed with different thresholds (in units of σ). (c) Probability of the decreasing trend ordinal pattern, normalized to the value expected if all the patterns are equally probable. In these plots different regions are observed with $I/I_{th} \sim 1.08$ indicating the onset of the CC regime.

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Optimal entrainment of the spikes emitted by a semiconductor laser with feedback

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The nonlinear dynamics of a semiconductor laser induced by optical feedback has been intensively studied in the last three decades, not only because these lasers are important practical devices, but also, because of the wide range of complex regimes that can be induced by optical feedback. The chaotic optical output generated has found various applications (secure communications, information processing, LIDAR, random number generation, etc.). In this contribution we focus on a dynamical regime known as *low frequency fluctuations* (LFFs), in which the laser emits a spiking output with dynamical properties that resemble the spike sequences of biological neurons. Operating in this dynamical regime, semiconductor lasers can be building blocks of ultra-fast information processing systems inspired in the way biological neurons process information. To use the laser as an information processing unit, it is crucial to understand how the information of a weak input signal is encoded in the output sequence of optical spikes.

In this contribution we consider the simplest situation of a weak periodic signal which is applied to the laser via direct current modulation. We present an experimental study of the role of the signal waveform and laser operation conditions in the entrainment of the output spikes to the periodic input. We propose several measures to quantify entrainment (inter-spike-interval distribution, spike success rate and ordinal spike correlations [1, 2]) and use them to analyze which waveform (at a given mean value and oscillation amplitude) produces optimal entrainment.

Figure 1 displays the ISI distributions for a semiconductor laser subject to an optical feedback and an external current modulation. Two periodic waveforms have been used. In Figure 1a we show the ISI distribution when a pulsed signal is applied while in Figure 1b illustrates the ISI distribution under a sinusoidal waveform. In both cases, four different modulation frequencies are chosen to show up the first four locking scenarios displayed by the dynamical system.

In the case of pulsed modulation, locking 1:1, 2:1, 3:1 and 4:1 (revealed by a high and narrow peak in the ISI distribution at $n \cdot T_{mod}$) are observed at modulation frequencies $f_{mod} = 7, 14, 25$ and 35 MHz respectively. On the other hand, for the sinusoidal test, a much broader ISI distributions are observed at low modulation frequencies which reveals an heterogeneous distribution of the power dropouts (i.e. poor entrainment). At higher frequencies the ISI distribution becomes narrower and the dynamical response of the system approaches to the one observed with the pulsed modulation. Therefore, our results indicate that, for entraining the power dropouts, the pulsed waveform is more efficient than the sinusoidal waveform..

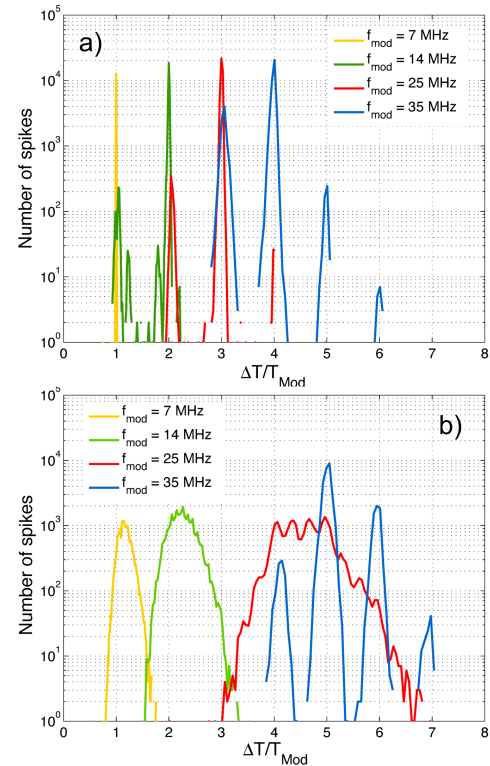


Figure 1: Experimental inter-spike-interval (ISI) distribution. The modulation amplitude is chosen to be 2.0% of I_{DC} and the modulation frequency is 7 MHz (yellow line); 14 MHz (green line); 25 MHz (red line); 35 MHz (blue line).

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Coevolving complex networks in the model of social interactions

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In the 90s Robert Axelrod have proposed the canonical model of social interactions [1] explaining one of possible important mechanisms of dissemination of culture. He have found that depending on initial conditions the system can end up in one of two states: ordered with global culture or disordered with many small subcultures. The dynamics of this model captures complexities of real interactions between people, but the square lattice which was considered is far from satisfying reflection of real-world social networks.

Others have studied Axelrod's model deeper [2], also on complex networks [3] and it turned out that the structure can have fundamental influence on the behavior of the system. Maxi San Miguel et. al. [4] made the next step by exploring the model of social interactions on coevolving random networks and finding two phase transitions with interesting properties. Unfortunately social networks are as far from randomness as from regularity.

models. All models are characterized by two phase transitions of a different nature (see Fig. 1). In case of local rewiring we obtain order-disorder discontinuous phase transition even in the thermodynamic limit, while in case of long-distance switching discontinuity disappears in the thermodynamic limit, leaving one continuous phase transition. In addition, we discover a new and universal characteristic of the second transition point - an abrupt increase of the clustering coefficient, due to formation of many small complete subgraphs inside the network.

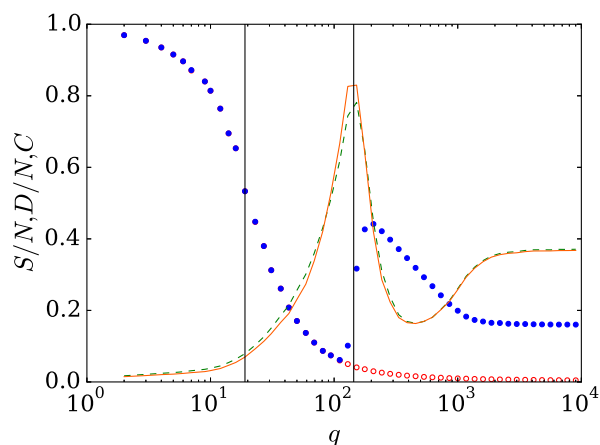


Figure 1: Average relative size of the largest network component (full blue circles) and largest domain (empty red circles), global (solid orange line) and average local (dashed green line) clustering coefficient in the stationary configuration vs parameter q , for $N = 500$, averaged over 400 realizations, for the model with preferential attachment. Vertical lines are placed at transition points, which are respectively $q_c = 19$ and $q^* = 144$.

In our work [5] we introduce four extensions with different mechanisms of edge rewiring. The models are intended to catch two kinds of interactions - preferential attachment, which can be observed in scientists or actors collaborations, and local rewiring, which can be observed in friendship formation in everyday relations. Numerical simulations show that proposed dynamics can lead to the power-law distribution of nodes' degree and high value of the clustering coefficient, while still retaining the small-world effect in three

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Influence of the memory persistence in the opinion of a mobile communit

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The propagation of a concept (an idea, a rumour, etc) among people that move in a given environment and socially interact depends, mainly, on two factors; the ability that has the cited concept to pass through an individual to another and the relevance of the concept (or the probability that people forget the idea). In the present work we study the transport rumour dynamics by means of a self-propelled agent model. Agents can move freely in a two dimensional space. Also, interactions are considered to be in pair. As a first matter of our study, we consider a dynamic determined by the agent time interaction in order to describe the oral transmission process. At a given meeting, each agent who wants to transmit the information, arises the probability to remember to the other agent. the forgotten factor is modeled by an external field that affects to all agents in the same way. By means of simulations and solving the equation system, we show a transition in the dynamics of the transport of the information. This transition divides the phase space into two regions, one where the rumour is totally forgotten and the other one where rumour persists.

Internal-external stimulus competition in a system of interacting moving particles: Persuasion versus propaganda

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We propose a general non linear analytical framework to study the effect of an external stimulus in the internal state of a population of moving particles. This novel scheme allows us to study a broad range of excitation transport phenomena. In particular, considering social systems, it gives insight of the spatial dynamics influence in the competition between propaganda (mass media) and convincement. By extending the framework presented by Terranova et al., we now allow changes in individual's opinions due to a reflection induced by mass media. The equations of the model could be solved numerically, and, for some special cases, it is possible to derive analytical solutions for the steady states. We implement computational simulations for different social and dynamical systems to check the accuracy of our scheme and to study a broaden variety of scenarios. In particular, we compare the numerical outcome with the analytical results for two possible real cases, finding a good agreement. From the results, we observe that mass media dominates the opinion state in slow dynamics communities; whereas, for higher agent active speeds, the rate of interactions increases and the opinion state is determined by a competition between propaganda and persuasion. This difference suggests that kinetics can not be neglected in the study of transport of any excitation over a particle system.

Cooperative Spreading Diseases in Temporal Networks

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The formalism of dynamical systems and network theory provides analytical tools for the research in spreading processes. In fact, simple models with three (Susceptible-Infected-Recovered, SIR) or two (Susceptible-Infected-Susceptible, SIS) possible states for the interacting nodes, allow to explore the role of topology in disease spreading.

This problem increases its complexity when considering not only interacting hosts, but also interacting diseases, accounting for whether cooperation or competition between different diseases. It has been shown that the cooperation scenario can change the global epidemic dynamics.

In this work, we implement cooperation between two diseases following SIR dynamics. This cooperation is introduced through a higher probability of getting infected with a new disease if an agent has suffered (or is suffering) from another disease; this is translated into a secondary infection probability q higher than the primary infection probability p . This simple model has been shown to exhibit first order transitions for several topologies characterized by a high abundance of long loops, in contrast with two-dimensional lattices, where this dynamics does not lead to abrupt transitions [1]. Here, we explore this dynamics in a static topology, finding some conditions for which, increasing the average degree, the transition leading to an epidemic state becomes discontinuous.

However, interactions in real world are not permanent, so more realistic models need to include temporality in the interaction pattern. Hence, we analyze the same dynamics in topologies which are similar to the previous static case, with the difference that now the network interactions are time dependent, finding that, for a slow varying network, the system experiences a continuous phase transition, while as the temporal network is modified in a faster way, a gap appears in the transition point, leading to an abrupt outbreak, and being maximum for the cases in which the networks are uncorrelated between two consecutive time steps (Fig. 1).

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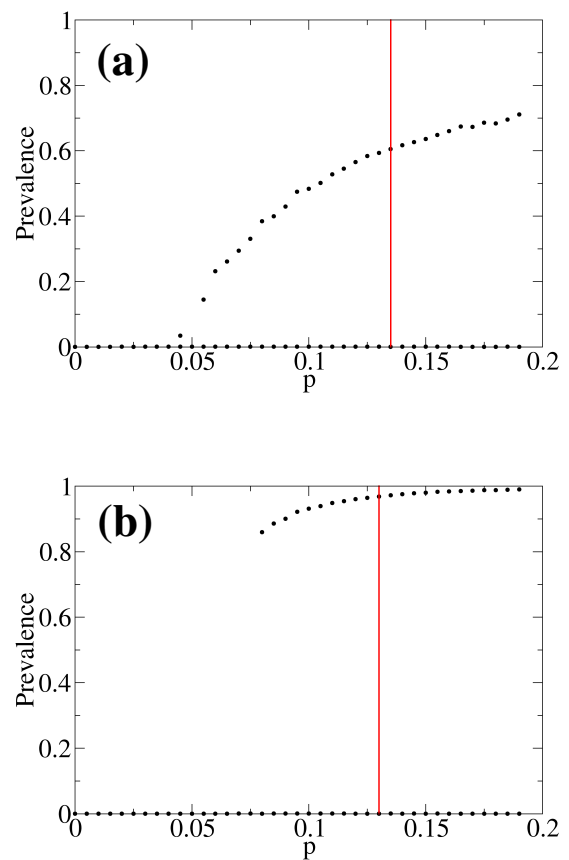


Figure 1: Prevalence of doubly recovered nodes versus the primary infection probability p for (a), network varying slowly, and (b), network varying fastly, approaching the regime in which two consecutive frames of the network are uncorrelated. We find two branches: one with low prevalence and another that grows, continuously from the low prevalence branch in (a), and after a discontinuous transition in (b). Red vertical lines indicate the critical point for continuous single disease phase transition in each topology. The secondary infection probability is $q = 0.99$.

Movement Patterns of Southern Elephant Seals from Individual to Collective Scales

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The growing number of large databases of animal tracking provides an opportunity for analyses of movement patterns at the scales of populations and even species, requiring for powerful analysis methods [1, 2]. Classical studies of human mobility developed some techniques that can be implemented for the analysis of animal movement, leading to new insights in this field.

We analyze a pooled dataset of >500,000 locations of 272 southern elephant seals individual trajectories using novel techniques (for wildlife studies), considering movements on an individual or species level without a priori assumptions about the behaviors associated with certain movements

The aggregated distribution of displacements displays power-law distribution across several temporal and spatial scales with an exponent 0.60. However, the displacements are splitted in two different groups: those originated at low occupancy locations, characterized by a higher velocity with a more directed movement, and those originated at high occupancy locations.

This pattern arises at an aggregated level despite the individual trajectories analysis shows a wide idiosyncrasy, with individuals that are very predictable, with their movement restricted in a small area, and others displaying broad and complex visitation patterns. In fact, the gyration radius, an indicator of the spatial spread of trajectories, varies considerably along trajectories (Fig. 1B).

Finally, we obtain marine provinces defined by the collective movement patterns of elephant seals, applying community detection methods to the transition probability matrix between two areas (Fig. 1C).

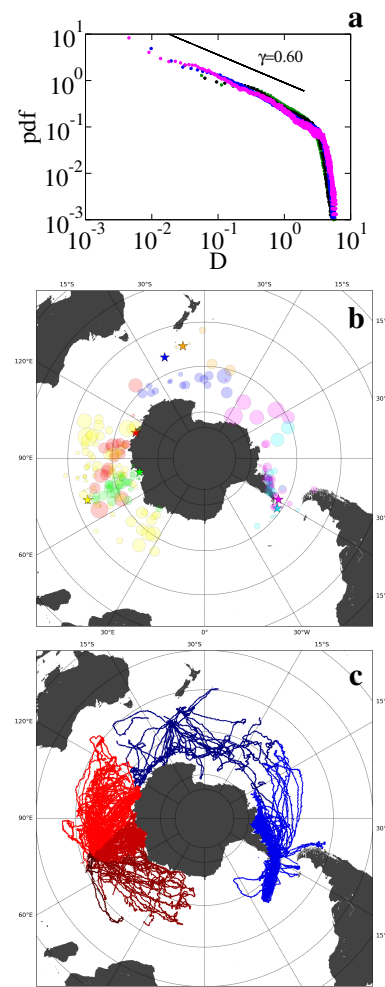


Figure 1: **a**, Probability density function (pdf) of normalized displacements D for 0.5 day (green), 1 day (black), 4 days (blue), and 10 days (magenta). The pdfs collapse into a universal function: for displacements below the average ($D < 1$), the probability decays as a power-law, while for larger displacements, the pdf decays abruptly; **b**, Map of the position of the centre of mass of each trajectory. Circle size is proportional to the gyration radius r_G ; colours indicate different deployment locations, which are represented with star symbols; **c**, Map of the marine provinces. Red and blue colours indicate the communities at level 0, while the darkness of the colours separates communities at level 1.

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Role of centrality measures in a dynamic model of competences acquisition in time-dependent networks

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How humans learn has been an open question over centuries. And still it is. The secrets of competence and knowledge acquisition remain hidden despite the efforts of experts in many fields. Qualitative studies and noisy data is not enough to predict and improve the setting which optimize ability growth. We suggest a model of performance evolution which may help us describe, quantify and better analyse this open question. We cannot neglect the apparent connection between different factors within one single individual. Our starting point is a model [1] which considers the effect of variables interacting between each other:

$$\frac{\Delta x_i}{\Delta t} = \left(r_i x_i \left(1 - \frac{x_i}{K_i} \right) + \sum_{n,n} s_j x_i x_j \right) \left(1 - \frac{x_i}{C_i} \right) \quad (1)$$

Moreover, we want to stress the effect of the interactions between different individuals, which we also ought to consider. Therefore, a graph of graphs is naturally the best representation of this type of systems, considering these two type of networks, both characterized by its topology and temporal scale and evolution.

$$\frac{\Delta x_{ij}}{\Delta t} = \left(r_{ij} x_{ij} \left(1 - \frac{x_{ij}}{K_{ij}} \right) + \sum_{k \neq j} s_{kj} x_{ij} x_{ik} + \sum_{l \neq i} w_{li} x_{ij} x_{lj} \right) \left(1 - \frac{x_{ij}}{C_i} \right) \quad (2)$$

Equation (2), besides a logistic self-growing term, considers the effect of the network of individuals and the effect of the inner network of variables for each single individual. Furthermore, we have introduced two adjacencies matrices concerning the intensities of individuals influence and the intensity of variables influence. To start with a simpler system we focus on the system described by Equation (1). We aim to prove the connection between the topology of a network and its dynamics, described by a system of coupled non-linear differential equations. The main contribution is establishing a direct correlation of certain centrality measures and the optimal performance. Katz centrality or alpha centrality can be rewritten as the solution of one of the stable solutions of the dynamic system as long as certain conditions hold.

The stability of the system depends on both the topology and the dynamics. But, how general is this result? We want to study whether the effect of time in time-dependent networks allow us to establish a similar connection between performance and centrality measures as well as allowing more freedom on parameters.

The relation of centrality measures and performance may lead us to predict the best achievements on the long run by just seeking the best configuration according to the centrality. However, when we relax some of the constrains the cor-

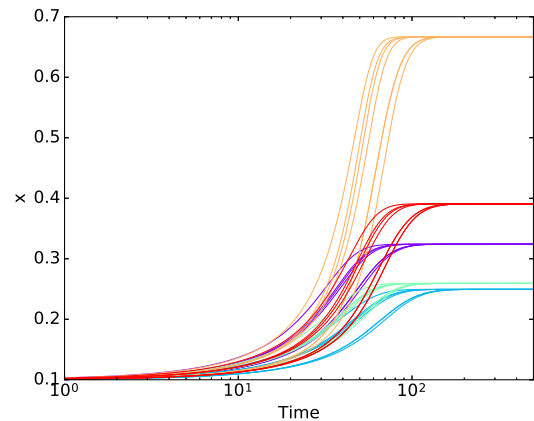


Figure 1: Temporal evolution of performance for 7 individuals and 5 inner variables

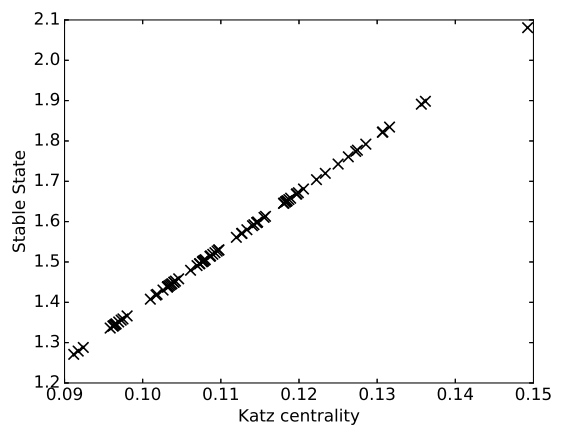


Figure 2: Stable state values as a function of the Katz centrality of the nodes, considering a random network of 80 nodes linked by 180 edges

relation with Katz centrality is no longer valid. We thus introduce a new centrality measure which takes into account not only topology but dynamics. This new centrality correlates with the new stable solutions.

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 - [2] Deanna Blansky et al. *Spread of Academic Success in High School Social Network* (2015).
 - [3] Juliette StehlÃ© et al. *High-Resolution Measurements of Face-to-Face Contact Patterns in a Primary School* (2011).

Chiral Maxwell demon in a quantum Hall system with a localized impurity

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We investigate the role of chirality on the performance of a Maxwell demon implemented in a quantum Hall bar with a localized impurity. Within a stochastic thermodynamics description we investigate the ability of such a demon to drive a current against a bias. We show that the ability of the demon to perform is directly related to its ability to extract information from the system. The key features of the proposed Maxwell demon are the topological properties of the quantum Hall system. The asymmetry of the electronic interactions felt at the localized state when the magnetic field is reversed joined to the fact that we consider energy dependent (and asymmetric) tunneling barriers that connect such state with the Hall edge modes allow the demon to properly work.

Growth Direction Distribution in Patterns of *Posidonia Oceanica*

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Vegetation patterns have been studied in the last decades mostly in semi-arid ecosystems. Feedbacks across space are always behind the formation of this intriguing structures. These spatial patterns shape the landscape and they have been argued to be an adapting strategy in scarce water environments. Beyond being limited to semi-arid ecosystems, marine environments also exhibit self-organized patterns. *Posidonia Oceanica* is a remarkable example of this phenomenon. The large extensions of submarine vegetation patterns and the importance of this seagrass for the Mediterranean are the main reasons behind its interest.

Posidonia Oceanica is a clonal growth plant characterized by a extremely slow growth. It forms large meadows under the sea which are essential for maintaining biodiversity. Furthermore, this clonal plant provides valuable services such as supporting fisheries, protecting the coast or mitigating climate change, as the meadows sequester important amounts of CO₂. *P. Oceanica* meadows are a bioindicator: the presence of this plant indicates good quality of the water due to the fact that this plant is very sensitive to external disturbances. This fact reflects the vulnerability of the ecosystem, which indeed have been assessed vulnerable and in regression because of external damages produced mainly by anthropogenic factors.

From this perspective, the characterization of the growth as well as the evolution of the spatial distribution of meadows is a valuable knowledge for the conservation of the ecosystem. In this line, there have been efforts in the characterization of their growth. First death rates, branching rates and growth of the rhizome were determined, which are the main mechanisms involved in the growth of the meadow. Second, a numerical model of the growth of clonal plants [2] was proposed. Last, a suitable model (ABD model [1]) for the description of large spatial extensions have recently been developed, which allows to understand the spatial distribution from the perspective of pattern formation theory.

In this work we test the numerical modeling of the ABD model in terms of a branching process. Apices, which is the part of the plant growing, elongate in different directions (given by the angle ϕ), and the apices density in each direction is coupled to others directions through the branching. Apices growing with a particular angle ϕ branch with a certain probability contributing to the population of apices growing in the direction $\phi \pm \phi_b$ where ϕ_b is the branching angle. *P. Oceanica* has a branching angle of $\phi_b = 45^\circ$, which determines the minimal number of growth directions needed. Thus, apices can be described with 8 fields for their density in space separated 45° . However, this opens the question if this minimal discretization is enough for an appropriate description of real meadows. A priori it is not known if an heterogeneous distribution in the population of apices with the angle can appear as a result of the dynam-

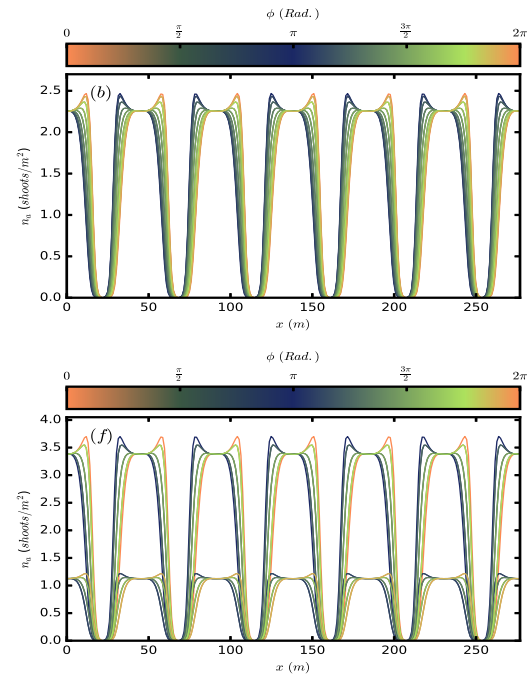


Figure 1: Stable growth direction distributions. Panel a) correspond to an initial conditions where all directions of growth have the same density of apices. Panel b) correspond to an initial condition where one set of 8 directions have $1/4$ of the total density of apices and the other set the other $3/4$ of the density.

ics. For instance in a description with 16 growth directions, there would be two sets of 8 directions which are independent from each other competing for space. Would there be a selection in the growth directions where one set prevails over the other? Or would we find an homogeneous distribution with the same amount of apices in both sets in the final state? An heterogeneous distribution can be an issue from the point of view of the numerical modeling since a greater number of directions is needed to describe heterogeneous solutions and more computational cost is necessary.

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Visitors in an exhibition room: human mobility and stopping patterns

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The study of human mobility in the context of complex systems science has gained popularity over the last years [1] and has a wide range of applications, from epidemic spreading to the inference of census data in third world countries [2]. Recently, there has been a surge in the number of data sets related to human mobility thanks to the availability of massive digital traces of human whereabouts and the development of mobile GPS technology.

We developed a public experiment of human mobility with the collaboration of a cultural center of the city. The movement of the visitors in an exhibition room of the *CCCB* in Barcelona was tracked by six infrared depth camera sensors in order to study their movement patterns. The geometry of the room is shown in Fig. 1. In its center there is a short wall section that divides the room in two main spaces. The entrance is at the right of the room and the exit at the left, both closer to the upper space than to the lower one. The six cameras were placed on shelves on the central wall section, three on each side, with a combined field of view covering a wide extent of the room's floor surface. Those cameras determine visitors' positions in the room at any given time and track their movements through it. Furthermore, the cameras are able to single out the positions of a particular individual and keep track of the movement of each of them simultaneously. The uniqueness of this data set lies on both the location studied and on the actual amount of data collected. Indeed, we were provided with camera acquired data spanning four consecutive months (almost the actual time extent of the exhibition) and we estimate that, during this period, around 15000 people visited the exhibition.

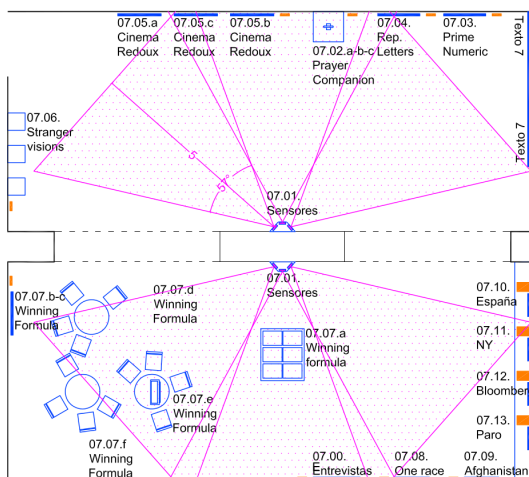


Figure 1: **Schematics of the room under study:** the field of view of each of the cameras is marked in purple and the exhibition objects are marked in blue.

We attempt to separate the data points of each visitor into two different classes. Stopped points, where the visitor is not moving, mostly correspond to the visitor watching one of the exhibition objects or points of attraction. Moving points are those where the visitor is moving from a point of attraction to another. Stopped points (see Fig. 2) are detected with a simple algorithm based on the distance between two consecutive data points [3]. The stopping statistics allow us to establish different characteristic stopping times, associated to diverse levels of attention of the visitor in front of an exhibition object, as well as the stopping patterns. From moving points, we compute the orientation of the trajectories, from which we can infer the preferred direction of exploration of the room, ie if a visitor is more likely to go left or right when they enter the room, and how many visitors leave the room without exploring a half of it.

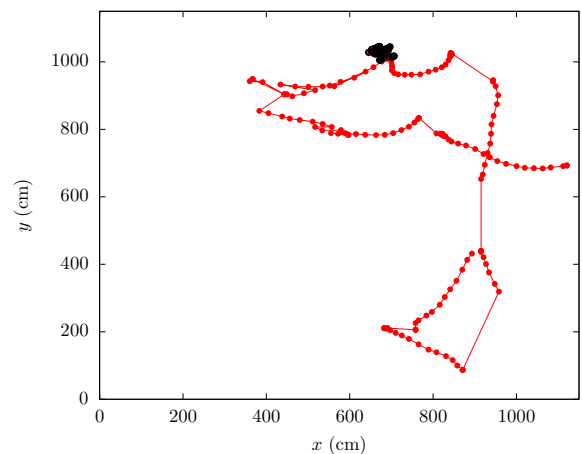


Figure 2: **Example of an individual trajectory in the exhibition room:** the origin is placed at the lower left corner of the room and stopped points are marked in black.

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Topological suppression of magnetoconductance oscillations in NS junctions

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We show that the magnetoconductance oscillations of laterally-confined 2D NS junctions are completely suppressed when the superconductor side enters a topological phase. This suppression can be attributed to the modification of the vortex structure of local currents at the junction caused by the topological transition of the superconductor. The two regimes (with and without oscillations) could be seen in a semiconductor 2D junction with a cleaved-edge geometry, one of the junction arms having proximitized superconductivity. We predict similar oscillations and suppression as a function of the Rashba coupling. The oscillation suppression is robust against differences in chemical potential and phases of lateral superconductors.

[1] Preprint, arXiv:1701.03082

Nonlinear thermoelectrics and Kondo effect in quantum dots

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The resistivity of a normal metal is a monotonically decreasing function with lowering temperature. However, when the metal contains magnetic impurities, the resistance reaches a minimum increases at lower temperatures. This anomalous behavior is called Kondo effect [1]. In this case the conductance has a logarithmic dependence on the temperature which takes place at temperatures higher than the Kondo temperature T_K . This complex phenomenon is caused by the highly correlations between the spin electron in the magnetic impurity with the spin density of the electrons in the metal. These interactions screen the magnetic moment of the impurity and creates a many-body singlet between the conducting and the localized electrons. Semiconductor quantum dots (QD) are able to mimic the magnetic impurity with the advantage of the easy tunability of the important parameters of the problem. In fact, QDs have spurred advances experimentally and theoretically. The typical setup in order to study transport consist of two reservoirs (left L and right R) connected to a quantum dot as we can observe in Fig. 1. Each reservoir is characterized by a electrochemical potential μ_α and temperature T_α ($\alpha = \{L, R\}$) and electrons travel from one reservoir to another with amplitude $\mathcal{V}_{\alpha k}$ with k the wavenumber of the electron.

Our aim in this work [2] is to study the Kondo effect in the presence of thermal gradients. In order to cover the whole range of temperature bias we consider three different approaches. First, we consider the perturbation analysis of the Kondo Hamiltonian using the procedure in Ref. [3]. This method allows us to obtain an analytical result of the relation of the Kondo temperature with the thermal bias θ ,

$$T_K(\theta) = \sqrt{\left(\frac{\theta}{2}\right)^2 + T_{K0}^2} - \frac{\theta}{2} \quad (1)$$

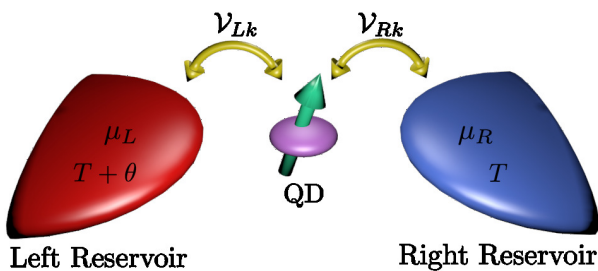


Figure 1: Sketch of the quantum dot system under the influence of a voltage ($\mu_L - \mu_R$) and temperature gradient (θ) applied between the reservoirs. The system consists of two reservoirs connected through tunnel barriers (with tunneling amplitudes $\mathcal{V}_{\alpha k}$) to an interacting quantum dot.

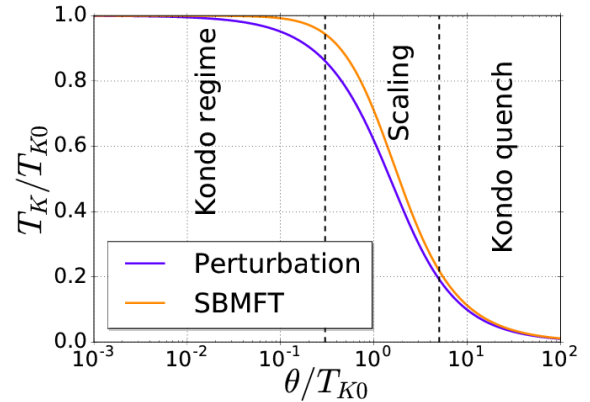


Figure 2: Normalized Kondo temperature T_K/T_{K0} as a function of the thermal gradient θ/T_{K0} applied to the quantum dot system. Blue line corresponds to the perturbative analysis result whereas orange line shows T_K derived from the SBMFT.

where $T_{K0} = T_K(\theta = 0)$. In this expression we identify three different regimes (Fig. 2): The Kondo regime where the Kondo temperature remains approximately constant, the scaling regime where it decreases quickly as the thermal bias increases and the Kondo quench where T_K slowly vanishes. In order to calculate the behavior of the Kondo temperature in the Fermi liquid case (low temperatures), we apply the slave boson mean field theory (SBMFT) to the Anderson Model at large charging energies finding the same qualitative results as in the previous model. In fact, the $T_K(\theta)$ curve shows the same shape even at temperature differences outside the regime of validity (Fig. 2).

Finally, we use the truncated equation-of-motion approach with the nonequilibrium Green's function formalism to analyze the local density of states of the system and to investigate their transport properties. In the voltage-driven case, we obtain the zero bias anomaly at $V = 0$ and different peaks around the electrochemical potentials of the leads. In the thermocurrent, we observe nonlinear transport with non trivial zeros at finite thermal bias θ . These nonlinear zeros are explained by the presence of different peaks in the density of states. Our results are relevant for the study of correlated systems driven out of equilibrium with strong thermal gradients.

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Conformational properties of a magnetic filament under flow and an external magnetic field.

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The formation of chain-like structures made of ferromagnetic colloids has been predicted more than four decades ago. Since the pioneering work of Tabata et al.[1] and due to advances in experimental techniques, it is possible to synthesise chains of magnetic colloids with different properties. The formation of these chains has important implications in the behaviour of magnetic fluids and their applications [2].

In this poster we present the results of extensive numerical simulations of a magnetic filament made of ferromagnetic particles, placed in a channel and subjected to a fluid flow and an external magnetic field perpendicular to the latter. We have considered two different flows: Poiseuille and Couette. The simulations combine a hybrid scheme in which fluid particles are coupled to the hydrodynamics via Multiple-Particle Collision dynamics and the interaction between the chain monomers is solved with standard Molecular Dynamics.

We found that, in the presence of a shear flow, the tumbling motion that is characteristic of semiflexible chains at zero field is strongly inhibited by the presence of a perpendicular magnetic field. Beyond a characteristic value, the external magnetic field is able to stabilise the filament with a rather straight conformation and a well defined degree of alignment with the flow. The latter results from the balance between hydrodynamic and magnetic torques. Under these conditions, the orientation of the net magnetic moment of the filament is imposed by the direction of the field. In addition, in the case of a Poiseuille flow, it has been found that the initial position has a long lasting influence on the behaviour of the magnetic filament when the external field is applied [3].

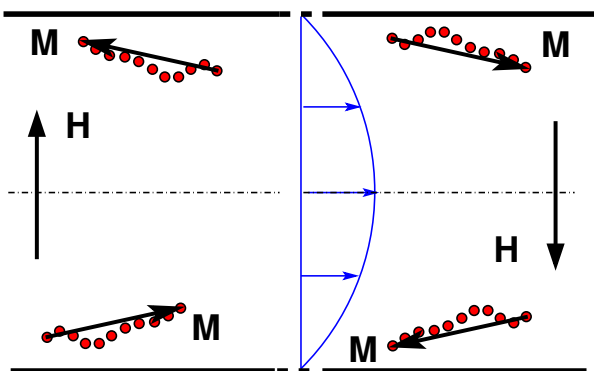


Figure 1: Possible orientations of the filament (chain magnetization M) in a Poiseuille flow and an external magnetic field H .

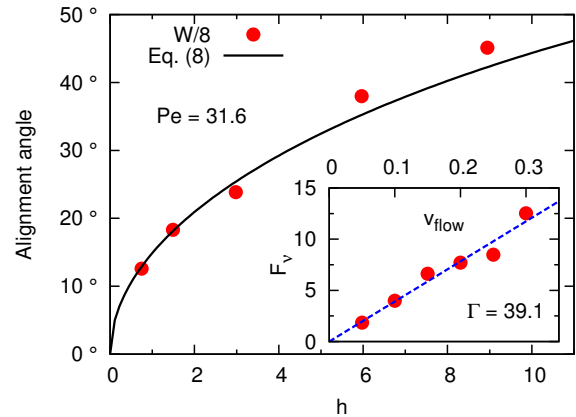


Figure 2: Alignment angle as a function of the strength of the magnetic field in a Poiseuille flow. Flow velocity: 0.3 (Pelet = 31.6). Points correspond to simulation data; black solid line to the theoretical expected behaviour in the linear rod approximation. Inset shows the fit of the friction coefficient, Γ , from simulation data.

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NestModularity Measure for the Joint Analysis of Nested and Modular Networks

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In the past years the concept of nestedness has clearly overflowed the classical ecological framework: beyond mutualistic networks, we have now evidences that nested patterns appear in diverse settings, from anthropology and sociology to economy and urban science. Parallel to the discovery of new instances of nested organizations, scholars have debated around the co-existence of two apparently incompatible mesoscale structures: nestedness and modularity. In this regard, the discussion is far from a solution mainly for two reasons. First, nestedness and modularity appear to be the result of two contradictory dynamics, a competitive and a cooperative one [1]. Second, existing methods to evaluate the presence of nestedness and modularity are flawed when it comes to the evaluation of concurrently nested and modular structures. In this work, we define the concept of NestModularity as a structural network measure that assesses to what extent the network is composed of modules where the relationship of elements within the modules exhibit a nested structure. To do so, we have developed a fitness function NQ that, given a membership variable α for rows and columns, evaluates the quality of a partition of the network into nested blocks. Function NQ incorporates the definition of nestedness (NODF [2] in particular) into a modularity-like formulation that considers the difference between the observed, O_{ij} , and the expected overlap, $\langle O_{ij}^r \rangle$. See Eq. 1.

$$NQ = \frac{2}{M+N} \left(\sum_{ij} \frac{O_{ij}^r - \langle O_{ij}^r \rangle}{k_j^r (N_{\alpha_i^r} - 1)} \delta(\alpha_i^r, \alpha_j^r) H(k_i^r - k_j^r) + \sum_{ij} \frac{O_{ij}^c - \langle O_{ij}^c \rangle}{k_j^c (M_{\alpha_i^c} - 1)} \delta(\alpha_i^c, \alpha_j^c) H(k_i^c - k_j^c) \right) \quad (1)$$

where k is the degree, δ is the Kronecker delta, H is the Heaviside function and sup-indexes r and c indicate row and column. The size of the system $M+N$ (number of rows and columns) appears for proper normalisation.

Our analysis on real networks have proven both the existence of such mesoscale structures and that our methodology is capable of detecting them. Results shown in Fig. 1 illustrates our methodology and shows that the current approach of analyzing modularity and nestedness separately can, among other intrinsic problems, easily underestimate nestedness and overestimate modularity.

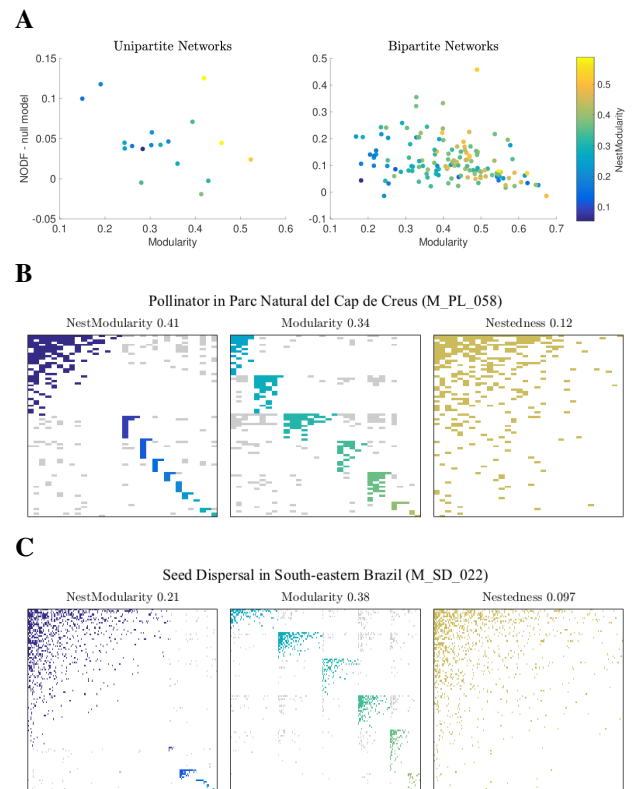


Figure 1: (A) Scatter plot confronting modularity and nestedness with the NestModularity measure (color coded). Each point represents either an ecological, urban or social network (left panel: unipartite networks; right panel: bipartite networks). (B) Example where nestedness is underestimated because of the existence of modules in the network (source: <http://www.web-of-life.es>). (C) Example where classical modularity overestimates the number of compartments in an ecological network (source: <http://www.web-of-life.es>).

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Dunbar's numbers and social structure: Models and experiments

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The analysis and modelling of social networks is a widely studied topic that has been carried out from the perspective of a variety of disciplines. Different models of social networks have been proposed across disciplines such as Statistical Physics and Computer Science [1], Economics [2, 3, 4], Statistics [5] or Sociology [6, 7]. These models have been used to study different properties like community structure, high clustering, degree correlations, small world, grannovet-erian, etc. In this work we will take all these features into account, but special attention is given to the structure of Ego networks proposed by Dunbar in the so called Social Brain Hypothesis [8]. According to this theory, human communities have a characteristic upper bound of approximately 150 individuals (*Dunbar's Number*). Furthermore, the ego networks have an structure of hierarchical inclusive layers with a scaling ratio close to three: 5, 15, 50 and 150¹. Although there is a large amount of experimental literature supporting this hypothesis [9, 10, 11, 12, 13] no model has been proposed so far that is able to explain it based on simple (and plausible) mechanisms.

In this communication we present a computational model intended to reproduce such hierarchical layering including *limited cognitive capacity* assumptions. Our model allows to identify social mechanisms that are relevant to the formation of realistic, circle-structured societies. In addition, we present results from data analysis of a large Facebook data set as well as of new experiments designed specifically to study such hierarchical structure.

This work was partially supported by the EU through FET-Proactive Project DOLFINS (contract no. 640772, AS) and FET-Open Project IBSEN (contract no. 662725, AS), by Fundación BBVA through project DUNDIG, and by the Ministerio de Economía y Competitividad (Spain), grant FIS2015-64349-P VARIANCE (MINECO/FEDER, UE).

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¹This sequence can be further extended to 500, 1500, etc. but those relationships lack a component of trust, reciprocity and obligation. See [8] for more information.

Effects of DDC on the Synchronization of the Electric Power Grid Network

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Synchronization constitutes one of the most dominant collective dynamics of complex network in social, biological and technological systems, such as communication networks, food webs, power grids and so on. The synchronization of the network deeply depends on the dynamics as well as the topology and internal properties such as the strength of the coupling of an element with the rest of the network. The electric power network is designed to operate in the synchronous state, namely the state where the units of the network behave identically with the same frequency ($50Hz$ or $60Hz$) and with constant different of phase [1]. How stable, resilient and robust is the network is determined by its aptitude to remain synchronized against perturbations such as power failures [2]. These perturbations may cause a desynchronization of the nodes which can favor the emergence of destructive power oscillations and somehow may lead to blackout or cascading blackout if the node affected is not disconnected from the network. Therefore, it is important to control the power grid in such a way that it is resilient against failures and local instabilities [3]. Thus several works have proposed methods for controlling power grid stability by stabilizing the frequency fluctuations which is the cause of desynchronization. Indeed, any generation/consumption unbalance which can be due to an input power coming from intermittent renewable energy sources or to a sudden increase in demand, lead to a variation of the frequency for a particular power source or node. Several concepts have been proposed to stabilize the frequency grid such are: the Frequency Adaptive Power energy Re-scheduler(FAPER), which is the idea of individual load control through responding to frequency. Demand response programs which are programs allowing user to consume electricity within different windows or depending on the real time price of the electricity in order to avoid peak of consumption. Dynamic Demand Control (DDC), which is a low cost technology than can be easily integrated in smart appliances (refrigerators, air conditioners, laptops, dryers, washing machines . . .), and enables them to switch on/off according to the grid frequency. It has been observed for the case of a single generator with fluctuating loads that a good stabilization of the frequency is achieved. Yet some rare events characterized by a huge frequency deviation appear due to the recovering of pending task. Including smart communication among devices can suppress these large frequency peaks [4, 5].

In this work we consider a network of power plants instead of a single generator and study how DDC improve the synchronization properties. Fig. 1 shows the network topology which has an average degree $\langle k \rangle = 2.5$. Fig. 2 shows how the frequency fluctuations as well as the phase differences are reduced.

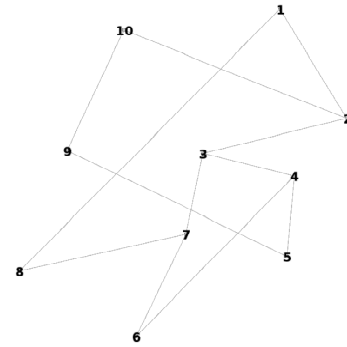


Figure 1: Network topology

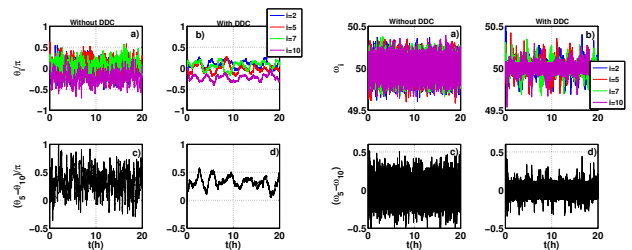


Figure 2: Time evolution of the phase, frequency fluctuations at each node, and phase and frequency differences between nodes 5 and 10 without and with DDC.

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A dynamical systems approach to multisensory integration

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Perception involves integration of inputs from individual sensory streams, e.g., visual, auditory and somatosensory. Merging information from different senses confers distinct behavioral advantages, for example, identification of objects is more rapid than with unimodal stimuli, especially when the signals are ambiguous. An experimental realization of the underlying complexity is captured by the “McGurk-effect”- incongruent auditory and visual stimuli eliciting perception of illusory speech sounds [1]. Time-delay between onset of auditory and visual signals (AV lag) [2] and perturbations in the unisensory streams are key variables that modulate perception. Here, we propose a dynamic systems model consisting of the basic ingredients of any multisensory processing, two unisensory and one multisensory sub-system (represented by nodes/oscillators) as reported by several researchers. The nodes/oscillators are connected such that biophysically inspired coupling parameters and time delays become key parameters of this network. The unimodal areas (auditory and visual) communicate via feedforward and feedback synapses with a third multimodal area (Superior Colliculus). The unimodal areas also communicate with each other via direct synaptic connections to simulate the anatomical convergences of visual inputs to primary auditory cortex. AV lag is captured by the time delayed interactions between the oscillators. The extent of multisensory integration is quantified by the degree of synchronization of the dynamical system represented by its order parameter. Despite its simplicity, our model is able to explain many basic properties of multisensory integration observed in the physiological literature such as cross-modal enhancement, inverse effectiveness and individual differences in multisensory temporal binding window. We also explore the effect of unreliable auditory and visual stimuli on multisensory integration by including noise in our model and by varying the strength of connections. Thereby, the dynamic model presents a quantitative framework for understanding multisensory information processing.

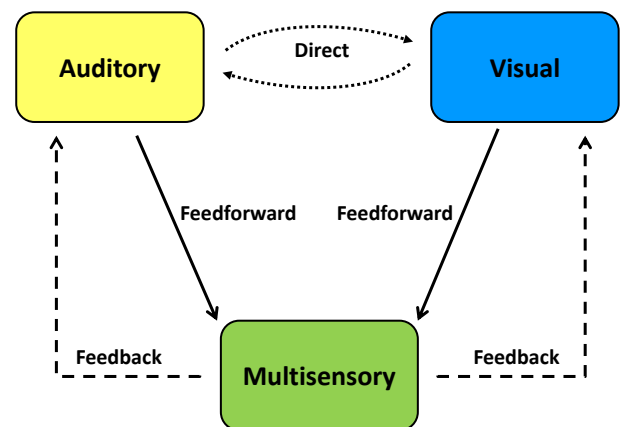


Figure 1: Dynamical model of multisensory integration.

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Are calcium signals coupled with cell nuclear movement during plant symbiosis with bacteria?

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When plant legumes encounter low nitrogen conditions, they release flavonoids as signals to soil bacteria [1]. In response, bacteria release Nod factors, marking the beginning of a symbiotic relationship. The nitrogen fixing bacteria provide the plant with ammonia, whilst the plant provides the bacteria with sugars.

Symbiosis occurs in the plants root hairs cells over the course of several hours. The root hair tip swells and curls to trap the bacteria, which then enters the cell upon the formation of an infection thread. The development of the infection thread is guided by the cell migrating nucleus [2].

In parallel with morphological changes, the generation and decoding of biochemical signals tells the plant what to do. A common hypothesis is that messages are encoded in the specific spatiotemporal patterns of calcium released by nucleus-localised ion channels.

We investigate the early stages of calcium oscillations within living root hair cells, following the addition of Nod factor, using time-lapse confocal microscopy with ratiometric fluorescent biosensors with two dyes [3]. Artefacts like bleaching, changes in focus, variations in laser intensity, etc, would affect both dyes equally. Only when calcium levels changes, are the variations in the fluorescence intensity of the two dyes anti-correlated. On the other hand, the inspection of the individual changes of the dyes intensity can provide clues into how the nucleus moves as calcium oscillates.

We present preliminary evidence that suggests that the timing of the calcium spikes is coupled with nuclear movements. However, it is not always straightforward to distinguish nucleus shape changes from movement. Additionally, nuclear movements seems to be related to other organelles movements, ranging from random kicks by floating small organelles, to the formation of vacuolar strands and cytoplasmic streaming.

Our results address the following key questions in the field. Does mechanical stretch affect the activation of the calcium-release channels? What is the role of active transport and random kicks in spatial calcium spreading? In what sense can the calcium patterns be fine-tuned to target specific decoding proteins if their timing depends on apparently randomly moving organelles? Are the observed early stages nuclear movements in anyway similar in origins to later nuclear migration at the time of the infection thread?

A complex systems framework can offer crucial insights in these problems. It may help interpret the type of synchronisation that occurs between nuclear movements and calcium oscillations, when both can be represented by typically noisy short time series. It can also provide insights into the generation of calcium spatio-temporal patterns, linking it to cytosolic streaming (which may take a variety of complex geometric flows), or to random kicks, or a combination of both.

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Modeling the dynamics of a small community of interacting human colon bacteria

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The human gut microbiota is a complex ecosystem wherein many microbial species interact. How such interactions contribute to the collective behavior of this ecosystem remains less understood despite its importance for human health. Here, we focus on a small, yet complex, community of three bacterial species inhabiting the gut microbiota. By combining an *in silico* and *in vitro* approach, we aim at predicting the dynamics of this interacting community.

Batch fermentations of mono- and co-cultures with 3 selected strains of species occurring in the human colon were performed, during which microbial growth and metabolite concentration were measured. In bi- and tri-culture, microbial interactions such as competition and cross-feeding affected the growth of a strain of a certain species.

To better understand the effect of the interactions on the observed dynamics, we developed a mathematical model consisting of ordinary differential equations. Bacterial growth was modeled with Monod-like growth kinetics. Competition and cross-feeding are taken into account through explicit modeling of the nutrient production and consumption. We used mono-culture time series to fit growth rates and yield coefficients of bacteria. Incorporating these parameters to simulate co-cultures, and comparing the prediction to the measurements, we underpredicted the growth rate of one species in co-culture, suggesting a metabolic adaptation of the bacteria when interacting with other species. We then used the data of bi-culture experiments to fit the model parameters, which led to a good description of the tri-culture dynamics. Furthermore, we observed that the time that species needed to adapt to their environment influenced which species eventually were dominant. In conclusion, the model provides a quantitative description of the measurements and highlights emergent behavior in co-cultures. Thus we are paving the way towards predictive multi-species modeling.

Hierarchical invasion of cooperation in complex networks

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The emergence and survival of cooperation is one of the hardest problems still open in science [1]. Several factors such as the existence of punishment, fluctuations in finite systems, repeated interactions and the formation of prestige may all contribute to explain the counter-intuitive prevalence of cooperation in natural and social systems. The characteristics of the interaction networks have been also signaled as an element favoring the persistence of cooperators [2]. Here we consider the invasion dynamics of cooperative behaviors in complex topologies (in particular, scale-free and random networks). The invasion of a heterogeneous network fully occupied by defectors is performed starting from nodes with a given number of connections (degree) k_0 . The system is then evolved within a Prisoner's Dilemma Game (PDG), through Unconditional Imitation (UI) or Replicator (REP) evolution rules, and the outcome is analyzed as a function of k_0 and the degree k of the nodes adopting cooperation. The payoff matrix of the PDG is

$$\hat{P} = \begin{array}{|c|c|c|} \hline & \mathbf{C} & \mathbf{D} \\ \hline \mathbf{C} & 1 & 0 \\ \hline \mathbf{D} & 1.4 & \varepsilon \\ \hline \end{array},$$

where ε is the punishment.

Carried out using both numerical and analytical approach, our results show that the invasion proceeds following preferentially a hierarchical order in the nodes from those with higher degree to those with lower degree, as shown in Fig. 1 in the case of scale-free topology (similar results hold on random networks).

However, the invasion of cooperation will succeed only when the initial cooperators are numerous enough to form a cluster from which cooperation can spread. This implies that the initial condition must be a suitable equilibrium between high degree and high numerosity, which usually takes place, when possible, at intermediate values of k_0 (see Fig. 2). These findings have many potential real-world applications, as they suggest that, in order to promote cooperative behavior on complex networks, one should infect with cooperators high-but-not-too-high degree nodes.

More details are available in Ref. [3].

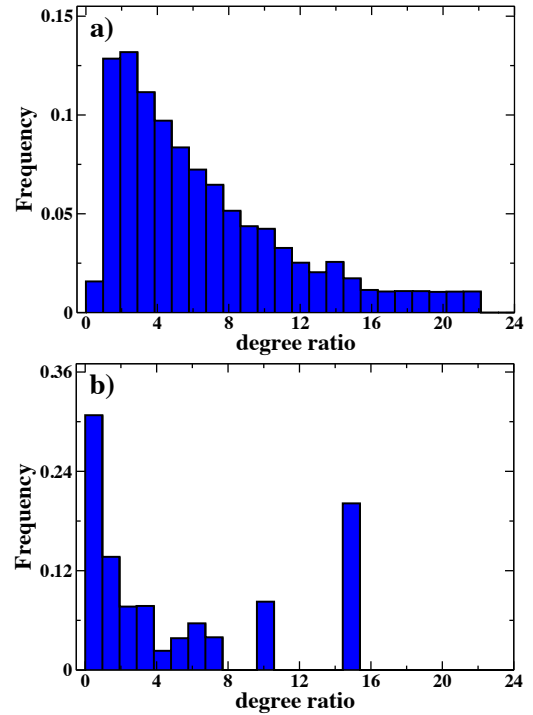


Figure 1: Histograms of the frequency of transitions from defection to cooperation as a function of the ratio k_i/k_f , being k_f the degree of the agent which flipped from defection to cooperation by imitating the agent with degree k_i , for a system on a scale free network (exponent $\beta = 1.6$ and size $N = 2000$, $\varepsilon = 0.05$ and $k_0 = 30$), in case of a) UI evolution rule, and b) REP updating. The cumulative frequency of the transitions with degree ratio larger than one (i.e. the top-down invasion acts) is $\simeq 98\%$ for UI and almost 70% for REP. From Ref. [3].

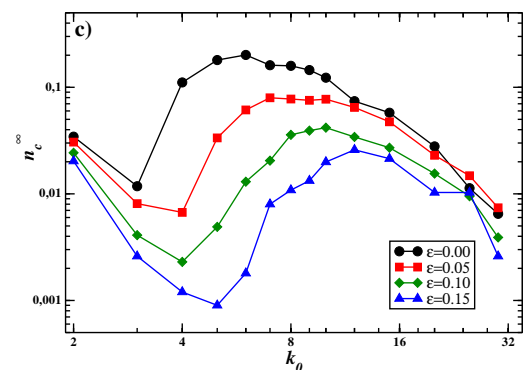


Figure 2: Final cooperator density as a function of the invasion degree k_0 for a system on a scale free network (size $N = 1000$, exponent $\beta = 1.6$).

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Struggle for existence in the world economic ecosystem

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The global trade network is a highly dynamical system, with the constant emergence of new products and technology progress.

The commercial relationships between countries depend on a variety of parameters like supply and demand, price difference, product quality and geographical location. In the global trade market there is constant competition between exporting countries. We are particularly interested in cases when this competition affects dramatically the export of the one of the countries.

We think that the economies are like predators, and they are able to displace weaker economies in many markets. A prey is defined as a pair (importer, product).

We test this theory by creating "predation network", connecting country *a* to country *b* if *a*'s appearance in a market preceded *b*'s disappearance. This is related to multilayer network [1, 2] and signed network analysis [3, 4].

To better understand how the procedure works, we present a particular example. We consider the car market (SITC code 7810) in the United States (USA as importer). We observe that in the year 1964 the roles of Japon and Italy were switched. We focus on Japan as a potential predator in this prey (the pair USA, car market), and Italy as competitor, Figure 1 depicts the share of USA car market of Japan and Italy. We will consider that Japon was predator of Italy, only if the decrease of the exports of Italy are connected with the increase of the exports of Japon.

1. *c* must have not stopped importing *p*;
2. *a* has to have ceased to export *p* to *c*
3. *b* still has to be exporting the product, this is the potential predator exporter;
4. The cessation of exports from the *a* must have been longer than a certain number of years.

We focus on longitudinal, multiplex data on commercial relations, to test the presence of predator countries in the course of time. We consider their relation to the complexity of products and national economies, predict which countries are leading the global trade network and which countries are at risk of being predated in different dimensions.

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Timelines of share of exports for Italy and Japan in the USA car market

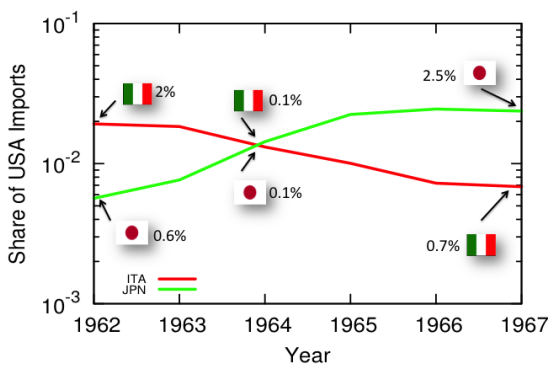


Figure 1: Timeline of Japan's and Italy's exports in the US car market in the 60s.

To establish if the countries (*a* and *b*) are actually in a predatory competition, with a pair importer *c* -product *p* as prey, there are several requirements to be satisfied:

Statistical Signatures of Photon-Subtracted Highly Multimode States

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Quantum entanglement, one of the key resources for quantum information processing, can be deterministically generated in a scalable manner in continuous variable (CV) optical systems [1]. However such CV entangled states typically display Gaussian statistics, which limits their use for quantum computing [2]. It is experimentally feasible to overcome this problem by subtracting photons from multimode Gaussian states, and thus make them non-Gaussian [3]. In the present contribution we use techniques from quantum statistical mechanics [4] to develop a new characterisation scheme for such *multimode* photon-subtracted states of light. Our aim is to characterise non-Gaussian properties of these states by ideally measuring only a small number of observables.

In the CV regime it is natural to associate a $2m$ -dimensional phase space to an m -mode system. The observables acting on this phase space are the field quadratures, $Q(f)$, which fulfil the general commutation relation $[Q(f), Q(g)] = 2i(f, Jg)$. Here f and g are arbitrary vectors in the optical phase space, and J is a matrix which represents the symplectic structure.

The states which we consider are non-displaced Gaussian states, ρ_G , from which a single photon is subtracted in a mode-selective way [3]. Such a photon-subtracted state can be described by

$$\rho = \frac{1}{\text{tr}\{a^\dagger(g)a(g)\rho_G\}} a(g)\rho_G a^\dagger(g), \quad (1)$$

where $a(g)$ is the annihilation operator for a specific mode g . The normalisation factor $\text{tr}\{a^\dagger(g)a(g)\rho_G\}$ is directly related to the success probability for heralding a photon.

To analyse these states, we study *truncated correlation functions* [4], $\langle Q(f_1) \dots Q(f_\nu) \rangle_T$. These quantities are particularly useful in the present context because for *any* Gaussian state, we find that

$$\langle Q(f_1)Q(f_2) \dots Q(f_\nu) \rangle_T = 0, \quad \text{for } \nu > 2. \quad (2)$$

In other words, for any non-Gaussian state we can find non-zero truncated correlations for orders higher than two. The centrepiece of this work is to analyse the behaviour of these truncated correlations for the photon-subtracted states as given in (1), and to investigate schemes by which they can be extracted from experiments.

The initial Gaussian state ρ_G is fully characterised by its *covariance matrix* V . However, the subtraction of a photon induces additional correlations, which is already apparent in the second-order truncated correlation functions

$$\langle Q(f_1)Q(f_2) \rangle_T = (f_1, V f_2) + i(f_1, J f_2) + A_g(f_1, f_2). \quad (3)$$

The function A_g , which describes the induced correlations between pairs of modes, depends strongly on the mode g from which the photon was subtracted.

Our key result is that this function A_g also describes all higher order truncated correlation functions. For example, one obtains that

$$\begin{aligned} \langle Q(f_1)Q(f_2)Q(f_3)Q(f_4) \rangle_T \\ = -A_g(f_1, f_2)A_g(f_3, f_4) \\ - A_g(f_1, f_3)A_g(f_2, f_4) \\ - A_g(f_1, f_4)A_g(f_2, f_3), \end{aligned} \quad (4)$$

which is in general non-zero.

We will present the *general analytical expression* for the function A_g , which can be applied to any photon-subtracted Gaussian states for which condition $\langle Q(f) \rangle_T = 0$ holds. Moreover, we elaborate on the role of these truncated correlation functions as an *experimentally feasible* tool to certify that the state cannot be represented by any mixture of Gaussian states. Finally, we analyse properties of the state's Wigner function through our understanding of the truncated correlation functions.

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Modeling Endogenous Contagion on O/N Interbank Market

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The interbank market activity in many countries has been severely impaired during the recent global financial crisis. The events of 2007 were the hard way to find out how a single shock can lead to disastrous effects on the whole international financial system. The network of complicated relations and dependencies between financial institutions across the globe was the main reason for which a single crash spread through the world like a disease [1]. From this moment on, the term *contagion* became an important topic in financial stability research. As a result, many complex networks researchers decided to follow the emerging subject of *Systemic Risk* [2].

We propose a new model of the liquidity driven banking system focusing on overnight interbank loans [3]. This significant branch of the interbank market is commonly neglected in the banking system modeling and systemic risk analysis. We construct a model where banks are allowed to use both the interbank and the securities markets to manage their liquidity demand and supply as driven by prudential requirements in a volatile environment. The network of interbank loans is dynamic and simulated every day. We show how only the intrasystem cash fluctuations, without any external shocks, may lead to systemic defaults, what may be a symptom of the self-organized criticality of the system, see Fig. 1.

terbank market impact of macroprudential tools. Finally, we confirm that central bank's asset purchase programs, limiting the declines in government bond prices, can successfully stabilize bank's liquidity demand.

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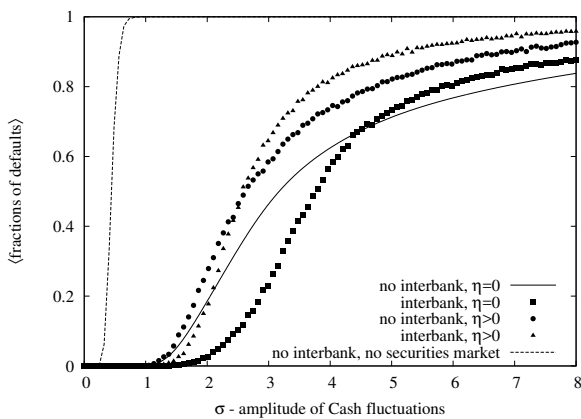


Figure 1: Relation between the size of fluctuations in the model and the fraction of defaults at the end of simulation. Parameter η defines the *depth* of the securities market ($\eta = 0$ is a perfect securities market case).

We also analyze the impact of different prudential regulations and market conditions on the interbank market resilience. Starting with leverage ratio, we also explore more complicated regulations and show which of them are actually effective and which may even amplify losses in a time of distress. Therefore, the model can be used to analyze the in-

Enhancing energy harvesting by coupling monostable oscillators

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The performance of a ring of linearly coupled, monostable nonlinear oscillators is optimized towards its goal of acting as energy harvester—through piezoelectric transduction—of mesoscopic fluctuations, which are modeled as Ornstein–Uhlenbeck noises. For a single oscillator, the maximum output voltage and overall efficiency are attained for a soft piecewise-linear potential (providing a weak attractive constant force) but they are still fairly large for a harmonic potential. When several harmonic springs are linearly and bidirectionally coupled to form a ring, it is found that counter-phase coupling can largely improve the performance while in-phase coupling worsens it. Moreover, it turns out that few (two or three) coupled units perform better than more.

Minimizing congestion in supermarkets with queuing networks

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Reducing congestion inside stores (e.g., supermarkets) is of great interest to many retailers; congestion affects customer experience, and may delay the fulfillment of online orders. We model stores as planar graphs in which nodes represent zones, and edges connect the nodes of neighboring zones. Customers traverse through the graph via the edges, and they queue to be served at each node. Once they have been served, they visit the next node. This approach allows us to apply standard results from queuing theory to find queue sizes and other quantities of interest.

Our results suggest that queuing networks can be used successfully to give insight for the design of better stores. We also investigate features of 'optimal networks' and compare these with random-graph models.

Catastrophes in optics: Analysing the dynamics and stability of caustic beams

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Catastrophe science [2] is a branch of bifurcation theory in the study of nonlinear dynamical systems; it is also a special case of more general singularity physics. Bifurcation theory studies and classifies phenomena characterized by sudden shifts in behaviour arising from small changes in circumstances, analysing how the qualitative nature of solutions depends on external control parameters. In singular optics, modelling the distribution of light according to these nonlinear potentials $P_n(\mathbf{a}, s)$ via the so-called catastrophe diffraction integral $C_n(\mathbf{a})$ leads to the formation of caustics as geometrically stable structures [1]. Emerging as natural phenomena, they are associated with the arcs close to rainbows, or may occur as ramified high-intensity networks on the floor of shallow waters. Similar to their formation behind refractive index lenses with imperfections, the occurrence of corresponding structures has been observed for numerous kinds of lenses with importance in optics, astrophysics and surface analytics.

In recent years, known catastrophic light structures that were already observed in natural phenomena in the late seventies and eighties [1] experience a renaissance since they are embedded in artificially designed caustic beams that depend on a single state parameter s and external control parameters \mathbf{a} :

$$C_n(\mathbf{a}) = \int_{\mathcal{R}} e^{iP_n(\mathbf{a}, s)} ds, \quad P_n(\mathbf{a}, s) = s^n + \sum_{j=1}^{n-2} a_j s^j. \quad (1)$$

The most prominent representative of a catastrophe that manifests as wave package is the fundamental fold catastrophe that has been realized as paraxial Airy beam $\text{Ai}(x) = C_3(x)$ in 2007 [3]. It shows a transverse-invariant and accelerated propagation on a parabolic trajectory. Benefiting from these striking properties, many linear and nonlinear applications arise in different branches of photonics like particle manipulation or signal transferring [4, 5]. In 2012, the second fundamental cusp catastrophe was transferred to optics as paraxial Pearcey beam $\text{Pe}(x, y) = C_4(x, y)$, and attracts attention due to its auto-focusing and form-invariant propagation [6].

Further, designing complex caustic light supports the field of nonlinear photonics which experiences explosive growth during the last decade and became a vital branch in modern photonics. Combining both topics opens up brand new aspects of research and enables the investigation of light guiding and localized Airy and caustic photonic structures [5].

In our contribution, we report on our recent results about embedding higher-order catastrophes, like the swallowtail and hyperbolic umbilic catastrophe [1, 2], in paraxial light. Our approach connects two control parameters with the transverse spatial coordinates, thus cross-sections through the control parameter space are mapped to the caustic light structure. We analytically derive an equation capable to cal-

culate in general the propagation of paraxial caustic beams that depend on a single state parameter, and show that the propagation of a caustic beam of order n can be expressed in terms of stationary higher-order caustic beams of order $2(n-2)$. To demonstrate this, we thoroughly study the dynamics of different swallowtail caustics analytically and experimentally, and link them with stationary higher-order butterfly catastrophes. Simultaneously, we analyze the stability of the swallowtail caustic. It decays to a cusp during propagation because its initial field was created as cross-section through the stable complete swallowtail catastrophe.

Subsequently, utilizing higher-order cusp and swallowtail catastrophes in paraxial light to inscribe photonic caustic structures in photosensitive media, we demonstrate waveguiding with a rich diversity of light guiding paths. Taking advantage of the strong auto-focusing of caustic beams in photorefractive nonlinear crystals, we realized the formation of Pearcey solitary waves.

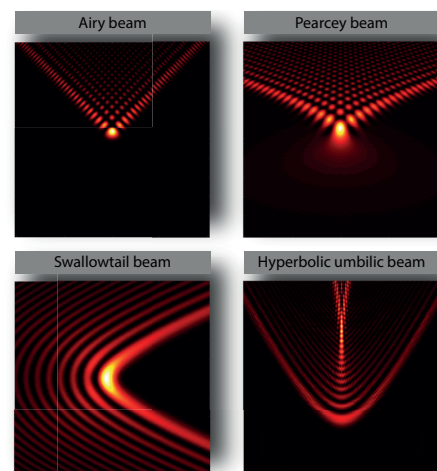


Figure 1: Caustic beams with embedded elementary catastrophes: fold, cusp, swallowtail, and hyperbolic umbilic.

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Unveiling signatures of interdecadal climate changes by Hilbert analysis

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A recent study demonstrated that, in a class of networks of oscillators, the optimal network reconstruction from dynamics is obtained when the similarity analysis is performed not on the original dynamical time series, but on transformed series obtained by Hilbert transform. [1] That motivated us to use Hilbert transform to study another kind of (in a broad sense) “oscillating” series, such as the series of temperature. Actually, we found that Hilbert analysis of SAT (Surface Air Temperature) time series uncovers meaningful information about climate and is therefore a promising tool for the study of other climatological variables. [2] In this work we analysed a large dataset of SAT series, performing Hilbert transform and further analysis with the goal of finding signs of climate change during the analysed period. We used the publicly available ERA-Interim dataset, containing reanalysis data. [3] In particular, we worked on daily SAT time series, from year 1979 to 2015, in 16380 points arranged over a regular grid on the Earth surface. From each SAT time series we calculate the anomaly series and also, by using the Hilbert transform, we calculate the instantaneous amplitude and instantaneous frequency series. Our first approach is to calculate the relative variation: the difference between the average value on the last 10 years and the average value on the first 10 years, divided by the average value over all the analysed period. We did this calculations on our transformed series: frequency and amplitude, both with average values and standard deviation values. Furthermore, to have a comparison with an already known analysis methods, we did these same calculations on the anomaly series. Finally, to gain insight in the interpretation of our results over real SAT data, we generated synthetic sinusoidal series with various levels of additive noise. By applying Hilbert analysis to the synthetic data, we uncovered a clear trend between mean amplitude and mean frequency: as the noise level grows, the amplitude increases while the frequency decreases.

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Coevolving nonlinear voter model

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We study an adaptive voter model [1, 2, 3] with cooperative interactions between agents, describing evolving opinions and topology of networks simultaneously. In particular, an agent may switch its opinion by adopting its neighbors' opinion or rewire the connections to the same opinion with the probability p [1]. In addition, the opinion of an agent relies on the opinions of its neighbors in a nonlinear way such as volatility in language dynamics [4, 5] and social pressure in social impact theory [6, 7]. We consider a nonlinear voter model which is a number α of randomly chosen neighbors influence a voter to change its opinion or connections [4, 5, 8]. We find that the model undergoes a phase transition between connected and fragmented networks (see Fig. 1), with different mechanisms depending on the degree of non-linearity α . The network splits into two ordered clusters with different opinions when $p > p_c$ regardless nonlinearity. However, when $p < p_c$, the network becomes a single connected component with either two opinions coexisting phase ($\alpha \leq 1$) or consensus phase ($\alpha > 1$).

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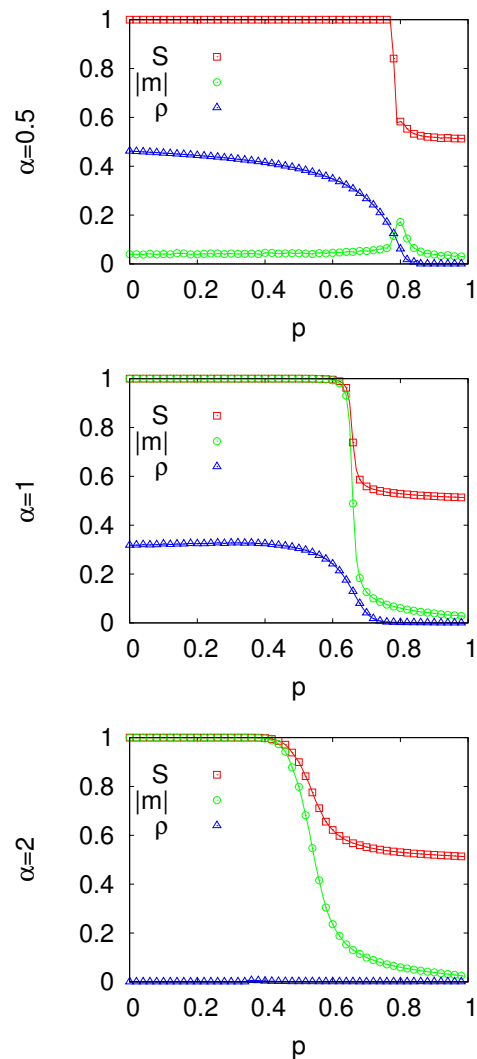


Figure 1: Size of the largest component S , link magnetization ($m = |k_{++} - k_{--}|$), and density ρ of active link as a function of p for $\alpha = 0.5, 1, 2$ on random regular networks with $k = 8$ and $N = 10^3$.

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