## Abstracts

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Stefano Allesina
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Coexistence in ecological communities
Friday, September 18, 2015. h 9.00 - 10.00

I briefly review the history of models for population dynamics, and the use of networks in ecology. Then, I review the concept of local asymptotic stability, and show the main result of Robert May’s 1972 article “Will a large complex system be stable?”. I end with a brief introduction to the field of random matrix theory.

Random matrices and stability of large ecological systems
Saturday, September 19, 2015. h 11.30 - 12.30

I show how random matrix theory can be applied to many ecological problems. I review applications to the study of stability, reactivity and persistence of large ecological communities. I show numerical results extending current methods in random matrices, and discuss their ecological implications. I conclude with a list of challenges whose solution will improve our understanding of the dynamics of large biological systems.

Antonio Celani
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Chemosensing and navigation at the microscale
Wednesday, September 16, 2015. h 14.40 - 15.40

I will discuss the general problem of how microorganisms perceive chemical cues and react accordingly, with special emphasis on bacterial chemotaxis

Olfactory communication and search
Thursday, September 17, 2015. h 9.00 - 10.00

Chemical signaling is also of paramount importance for larger organisms. I will discuss the challenges of long-range chemical communication with specific reference to insect olfactory search.
A genome increases its complexity by adding or expanding genes, which are its elementary functional modules. Genes are divided in evolutionary families, and combined and rearranged over evolutionary times, shaping the landscape of functions accessible to a species according to its environment and lifestyle. Focusing on data from thousands of sequenced genomes (mainly bacteria), these lectures will describe some notable ”laws” emerging from both the cross-species and the single genome statistics of extant gene families, and some models which may help rationalize these laws.

**Outline of main topics.**

- Protein families and protein domains / Functional annotations / Main biological interaction networks
- Partitioning of a genome into its evolutionary and functional categories
- Species-centered gene-family statistics: distribution of gene-family sizes and scaling laws for functions
- Duplication-innovation-loss models and gene-family statistics / ”Toolbox” model
- Horizontal Transfer and gene family evolution in Bacteria
- Core vs pan genome, gene frequency distribution at different phylogenetic resolutions
- Neutral and Non-neutral models for gene frequency
- Dependency networks in genome composition
- Cross-species abundance fluctuations
Amos Maritan
University of Padova, Italy. maritan@pd.infn.it

Stochastic processes in ecology
*Thursday, September 17, 2015. h 11.30 - 12.30*

TBA

Maximum Entropy in Ecology
*Friday, September 18, 2015. h 11.30 - 12.30*

TBA
Kim Sneppen
Niels Bohr Institute, Denmark. sneppen@nbi.dk

Competition and Diversity
Wednesday, September 16, 2015. h 9.00 - 10.00

The talk presents two one parameter models of competing species. In the first the focus is on sessile species growing on 1 dimensional surface. The focus is on spatial self organized spatial segregation and emergence of diversity. The second talk suggest a new view on exponential growth and population collapses in a well mixed system. The emphasis is here on non-stationary aspects of ecosystem dynamics, including a new perspective on causes of oscillations in population sizes.

References:
1) Emergence of diversity in a model ecosystem N Mitarai, J Mathiesen, K Sneppen PREE 86, 011929 (2012)

An assembly-extinction scenario for well mixed food webs
Saturday, September 19, 2015. h 9.00 - 10.00

Using the generalized Lotka-Volterra equations, we show that sustainable coexistence requiring a nonzero determinant of the interaction matrix. In cases where nonzero determinant cannot be achieved, the matrix rank can be used to quantify the lack of niches. For the species richness at each trophic level, these assembly rules specify which combination s are sustainable and provide a starting point for food web characterization. In agreement with empirical data, but in contrast to existing models, the constraints predict high species numbers at intermediate levels and thinning at the top and bottom. Considering finally a possible evolutionary path to build large ecosystems that are both stable and feasible we addition and extinction in food webs where each species are extreme specialists. This allow us to suggest a new cellular-automata like assembly and extinction model for food webs governed by Lotka-Volterra equations.

References:
Joshua Weitz
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Theoretical Principles of Virus-Microbe Dynamics
Friday, September 18, 2015. h 14.40 - 15.40

Viruses are ubiquitous in the environment and can function like microbial predators, regulating the density and diversity of microbes present in a community. However, efforts to understand the dynamics of complex virus-microbe communities remain in their infancy. In this talk, I present examples of the interplay between evolutionary and ecological dynamics arising due to virus-microbe interactions. I begin by introducing canonical models of virus-microbe population dynamics in the context of observed oscillations of E. coli and associated phage. I then present a series of examples in which novel features observed in time series data arising from phage interactions with E. coli and V. cholerae can be understood when considering both population and evolutionary dynamics together. I conclude by presenting our recent efforts to extend the results of laboratory experiments to an environmental context, with significantly higher diversity of both viruses and microbes. Despite this increase in diversity, I show how network theoretic methods can reveal common principles underlying the dynamic coexistence of complex virus and host communities.

Structure and Dynamics of Complex Virus-Microbe Communities
Saturday, September 19, 2015. h 10.00 - 11.00

Viruses are ubiquitous in natural environments and have significant direct effects on microbial communities and ecosystem functioning. In this talk, I focus on ocean viruses as a means to address how viruses can have both deleterious and stimulatory effects on target hosts and populations. The dual role of viruses can be understood given that lysis of marine microbes releases cellular debris that can then be taken up by non-targeted cells, stimulating microbial production. This redirection of cellular biomass by viruses is termed the "viral shunt". Here, I offer two perspectives on the viral shunt. First, I present an ab-initio model of the carbon and nutrient content of virus particles. In doing so, I show how the elemental stoichiometry of virus particles differs from that of microbial host cells. I explore the consequences of this difference for varying modes of exploitation of intracellular resources by viruses. Second, I present a nonlinear model of a surface marine ecosystem that extends NPZ-like models by incorporating viral-induced lysis and the viral shunt. I leverage analytical methods and numerical simulations to identify mechanisms by which viruses may stimulate increased recycling of organic matter and gross primary productivity at the ecosystem scale. In closing, I present a preview of upcoming challenges in reconciling the results of simple virus-microbe models with emerging viral datasets.
Despite a vast body of research that informs us about the general properties of spatial macroecological patterns of species-rich ecosystems, we still lack a satisfactory theory that explains their underlying interconnections. Several of such ecological measures crucially depend on the behaviour of the spatial correlation functions at all orders, and any truncation inevitably impairs the results. The calculation of spatial macroecological patterns in spatially-explicit stochastic models is challenging even in simple models, because these latter often have stationary distributions for which the detailed balance condition is not satisfied. We will present a spatially-explicit neutral model and a general method for linking several patterns, showing how we can predict one from another. Predictions are in agreement with empirical data.

* Work done in collaboration with Amos Maritan, Todd Cooke, and Andrea Rinaldo.
Paolo De Los Rios
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A physicist’s approach to protein chaperones
Thursday, September 17, 2015. h 10.00 - 10.40

Although proteins should be able to spontaneously find their native, functional state, in the complex environment of the cell, and in the presence of stress, they might have to be remodeled (unfolded/folded) and constantly supervised so that they do not aggregate or so that, if they aggregate, they can be rescued. This array of tasks is taken care of by molecular chaperones, a ubiquitous and conserved class of protein machines that, using energy from ATP hydrolysis, are able to modulate the conformational states of their protein substrates.

I will show, by a particular example, how a physicists approach can start to shed light on the fundamental principles that govern the mechanism of function of chaperones, and how this understanding can help us paint a better picture of their cellular role.

Maria Rita d’Orsogna
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Models of criminal behavior
Friday, September 18, 2015. h 17.35 - 18.15

Applying mathematical tools to criminology is a relatively new but promising and exciting avenue of research. In this talk we present several examples of mathematical models that are meant to frame and analyze basic sociological findings such as the broken windows effect and repeat victimization theories. We discuss agent based models and partial differential equations to study to burglary and the spread of opportunistic crime, game theories to investigate the role of informants within a violent society, stochastic simulations to model recidivism and rehabilitation efforts and a network model to study possible methods of dismantling a growing criminal organization. Some of our results are confirmed by data and experimental realizations conducted on actual human subjects in a behavioral laboratory.
Achille Giacometti
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Unconventional Phases in Helical Particles and Janus Fluids
Friday, September 18, 2015. h 15.55 - 16.35

This talk has two parts. In the first part I will discuss the self-assembly properties of a fluid of helical particles modelled as chains of fused hard spheres arranged in a helicoidal fashion and interacting only sterically. I will show how a rich polymorphism is found, with strong departures from the spherocylinder phase diagram. Remarkable is the presence of a special chiral nematic phase with screw-like order, where helices are well aligned along the director and their C2 symmetry axes spiral around this direction with periodicity equal to the particle pitch. Screw-like ordering was observed in colloidal helical flagella. We have fully characterized this phase and show that it is a general feature in the phase diagram of helical particles. In the second part of the talk, I will discuss another unconventional phase diagram occurring during a self-assembly process of Janus spherical colloids. The phase diagram includes a colloidal-poor (gas) colloidal-rich (liquid) phase separation, which is progressively suppressed by the insurgence of micelles. Finally, I will discuss recent developments obtained when extending the Janus paradigm to an anisotropic particle, that is a Janus “dumbbell”.

Henrik Jensen
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How interaction between co-evolving agents shape the tempo, mode and structure of the evolving ecosystems
Friday, September 18, 2015. h 10.00 - 10.40

Understanding systems level behaviour of interacting agents is very challenging for example because the interacting components can lead to hierarchical structures with different causations at different levels. In particular smooth micro dynamics may generate intermittent dynamics at the systems level. We use, what we call, the Tangled Nature approach to discuss the co-evolutionary aspects connecting the microscopic level of the individual to the macroscopic systems level. We focus in particular on evolutionary ecology and we are able to make a qualitative, sometimes even semi-quantitative, comparison in terms of e.g. species abundance distributions and tempo and mode of the fossil record. We are also able to discuss observations of the functional form of the degree distribution and the dependence of connectance on diversity in ecological networks.
River networks as ecological corridors for species, populations and pathogens of water-borne disease

Thursday, September 17, 2015. h 12.30 - 13.10

River basins are a natural laboratory for the integration of hydrological, ecological and geomorphological processes. Moving from morphological and functional analyses of dendritic geometries observed in Nature over a wide range of scales, the Lecture addresses essential processes sustaining human life and societies taking place along dendritic structures – suggesting that indeed they, and their ecosystem services, can be predicted. Population migrations and human settlements historically proceeded along river networks to follow water supply routes. Riparian systems, critically important ecosystems positioned along streams and rivers, play crucial roles in their watersheds and in the loss of biodiversity proceeding at unprecedented rates within the course of History. Human waterborne disease like cholera and schistosomiasis or proliferative kidney disease (PKD) in fish thrive in pristine or engineered watercourses, and are prone to climate-driven spread. Is there a linkage? Devastating water-borne disease, such as cholera, and invading foreign species spread through water bodies linked by river networks. Although the dynamics of such systems has been extensively studied, existing approaches were mostly within the framework of mean-field or two-dimensional landscapes that ignore directionality of dispersal implied by the network acting as environmental matrix. How does connectivity within a river network affect the emergent spreading of water-borne infections? Does the river basin act as a template for biodiversity? Are there hydrologic controls on the spreading of water-borne disease?

Here, I shall focus on the noteworthy scientific perspectives provided by ecohydrological studies centered on river networks viewed as ecological corridors for species, populations and pathogens of waterborne disease, and described mathematically as a fractal support for reactive transport. The Lecture overviews a number of topics idiosyncratically related to my own research work. To address such questions, the present Lecture addresses, through direct and indirect data collections and comparative mathematical analyses, the study of: biodiversity in the river basin (in particular, by studying comparatively observational data and dynamic models of freshwater fish in large and very large river systems, and of riparian vegetation); hydrologic controls on cholera epidemics (and possibly of other water-borne diseases); biological invasions along river networks. The Lecture aims at make a compelling case for the interest in the understanding of the functioning of river basins as a whole, including its ecosystem structure and function.

Given the great variety and yet deep symmetry of fluvial networks in Nature across scales, and notwithstanding the variety and complexity of ecosystems involved, one is tempted to conclude that there exists a unique, coherent conceptual thread of ecohydrological nature that joins seemingly disparate subjects only superficially, of course as their mathematical treatment proves very much the same. From such raw material, a general theory emerges on the role of dendritic geometries as environmental support for ecological dynamics and processes operating on fluvial networks and connected water pathways a fun and possibly even instructive novel research field.
Susanna Manrubia

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Viral war games: When evolution defeats imagination
Wednesday, September 16, 2015. h 12.30 - 13.10

Viruses count amongst the most amazing organisms on Earth regarding their evolutionary and adaptive abilities. They resort to several different forms of coding information in their genomes; together with an array of different mutational mechanisms, they have succeeded in infecting all cellular organisms and in escaping any antiviral strategy (natural or artificial). We will present two examples of viral adaptive strategies that can be formally addressed: the complex population response to combinations of antiviral drugs and the advantages of viruses with multipartite genomes. Finally, we will briefly discuss the origin of viruses and the role they may have played in the evolution of life.

Agnese Seminara

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Fungal spore discharge: physical principles to organize diversity
Wednesday, September 16, 2015. h 15.55 - 16.35

The forcibly ejected spores of ascomycete fungi must penetrate several millimeters of nearly still air surrounding the parent fungus to reach dispersive airflows, and escape is facilitated when a spore is launched with large velocity. In thousands of species spores are ejected through a small elastic ring at the tip of the cell bearing the spores. The physical constraints shaping the startling diversity of ring shapes and the adaptive benefits of specific morphologies are not understood. I will discuss an elastohydrodynamic theory of spore ejection through the ring and demonstrate that to avoid enormous energy losses during spore ejection, the four principal morphological dimensions of spore and apical ring must cluster within a nonlinear one-dimensional subspace. I will present a comparison of the prediction using morphological data for 45 fungal species from two different classes and 18 families. Although the individual dimensions of the spore and apical ring are only weakly correlated with each other, they collapse into the predicted subspace with high accuracy. The launch velocity appears to be within 2 per cent of the optimum for over 90 per cent of all forcibly ejected species: a simple principle can be used to organize the observed diversity. I will conclude with the implications of these results for the molecular mechanisms implementing forcible spore ejection.
The universe of protein folds: life emerging in a marginally critical phase

Wednesday, September 16, 2015. h 17.05 - 17.45

Protein folding is complex because of the sheer size of protein molecules, the twenty types of constituent aminoacids with distinct side chains, and the essential role played by the environment. Nevertheless, proteins fold into a limited number of evolutionarily conserved structures. Here we show that a simple model that encapsulates a few general attributes common to all polypeptide chains, such as steric constraints, hydrogen bonding, and hydrophobicity, gives rise to an emergent free-energy landscape of globular proteins. The minima in the resulting landscape correspond to putative marginally compact native state structures of proteins, which are assemblies of helices, hairpins, and planar sheets. These results are further corroborated by an atomistic level simulation in which we performed an exhaustive exploration of the conformational space of a 60 amino acid polypeptide chain described with an accurate all-atom interaction potential. This simulation confirm the existence of a fixed amount of protein conformation which plausibly represents the universe of protein folds. However, we discover that the known folds form a rather small subset, which cannot be reproduced by choosing random structures in the database. Rather, natural and possible folds differ by the contact order, on average significantly smaller in the former. This suggests the presence of an evolutionary bias, possibly related to kinetic accessibility, towards structures with shorter loops between contacting residues. Beside their conceptual relevance, the new structures open a range of practical applications such as the development of accurate structure prediction strategies, the optimization of force fields, and the identification and design of novel folds.

The complex structure of chromatin

Wednesday, September 16, 2015. h 10.00 - 10.40

Chromatin is the whole DNA chain bound to proteins and RNA in the cellular nucleus. It is believed that the biological role of chromatin is not only that of packing DNA in a small volume, but also that of controlling gene expression, resulting in an epigenetic control on the cell. Recently, a class of experimental techniques were used to obtain contact maps of chromatin on the length scale of few kilobases; these contact maps are structured in blocks, suggesting that the chromatin fibre is assembled in small globules. Making use of polymer theory and of computer simulations based on the available experimental data, we investigate the conformational properties of the chromatin chain, trying to relate them to the activity of the associated genes.
Stefano Vassanelli

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Why does the brain beat? A journey through the physiology of neuronal coding
Thursday, September 17, 2015. h 18.05 - 18.45

The nervous system of living organisms, including humans, has been shaped throughout evolution to encode real-world inputs, retain and retrieve relevant information and elaborate adequate responses in a way that remains largely unmatched by artificial systems. From simple invertebrates to humans, key features have been retained and optimized to effectively encode sensory inputs in terms of energy consumption, adaptability and tolerance to perturbations. The transduction of sensory inputs into trains of propagating excitation waves in topologically organized neuronal networks is unanimously considered as the basic common denominator. Yet, the capability of neurons and networks to generate multiple-frequency and coherent oscillations as well as to work near a critical point are hypothesized as fundamental ingredients allowing the extraordinary brain performances when mapping the sensory world. We will revisit open questions about the role of brain rhythms and criticality under the neurophysiologist lens, starting from the basics of sensory transduction and neuronal signaling in living organisms and ending with high-order coding in the mammalian brain.

Aleksandra Walczak

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Diversity in immune receptor repertoires
Thursday, September 17, 2015. h 17.25 - 18.05

Recognition of pathogens relies on the diversity of immune receptor proteins. Recent experiments that sequence the entire immune cell repertoires provide a new opportunity for quantitative insight into naturally occurring diversity and how it is generated. I will describe how we can use statistical inference to quantify the origins of diversity in these sequences and characterize selection in the somatic evolutionary process that leads to the observed receptor diversity. A well-adapted repertoire should be tuned to the pathogenic environment to reduce the cost of infections. I will finish by discussing the form of the optimal repertoire that minimizes the cost of infections contracted from a given distribution of pathogens.
Nestedness analyses are confounded by sensitivity to measurement choices and network properties

Saturday, September 19, 2015. h 12.45 - 13.00

Nestedness is a statistical property of bipartite networks that is easy to picture and hard to define. Nestedness has been applied to ecological networks representing host-parasite and plant-pollinator interactions, amongst others, and is often used to measure a hierarchical pattern whereby species in each role can be ordered such that partners for one species are a subset of partners of the next. Interest in nestedness has been stimulated by possible links to ecological stability and community assembly, but there is little agreement on how best to measure nestedness and calculate statistical significance. Many different measures and null models have been proposed, raising questions of how these methods differ, whether they agree, and if not, which choices are the most robust. Using an ensemble of synthetic networks with known nestedness we compare measurement outcomes using different combinations of measure, null model and effect size statistic. We find that measurement of nestedness is strongly sensitive to each of these choices, making robust measurement of nestedness in a single network problematic. Furthermore, nestedness depends strongly on network properties in particular, connectance making comparison of nestedness between networks difficult. Our findings have implications for empirical measurement of nestedness and the growing body of theory suggesting possible links to ecological and evolutionary processes. Looking forward, we provide an efficient software tool (FALCON) to support nestedness analysis and identify the most robust measurement choices for common situations.

Turing instability on multiplex networks

Saturday, September 19, 2015. h 12.30 - 12.45

Patterns are widespread in nature: regular forms and geometries, like spirals, trees and stripes, recur in different contexts. In a seminal paper Alan Turing set forth a theory by which patterns formation might arise from the dynamical interplay between reaction and diffusion in a system. Under specific conditions, diffusion drives an instability by perturbing an homogeneous stable fixed point, via an activator-inhibitor mechanism. As the perturbation grows, non-linear reactions balance the diffusion terms, yielding the asymptotic, spatially inhomogeneous, steady state. However, the conventional approach to network theory is not general enough to ascertain the complexity that hides behind real world applications. Self-organization may proceed across multiple, inter-linked networks. For this reason, multiplex, networks in layers whose mutual connections are between twin nodes, have been introduced as a necessary leap forward in the modelling effort. Here we aim at developing the theory of patterns formation for a reaction-diffusion system defined on this latter kind of complex networks by means of a perturbative approach. The interlayer diffusion constants act as a small parameter in the expansion and the unperturbed state coincides with the limiting setting where the multiplex layers are decoupled. The interaction between adjacent layers can seed the instability of a homogeneous fixed point, yielding self-organized patterns which are instead impeded in the limit of decoupled layers. Patterns on individual layers can also fade away due to cross-talking between layers. Analytical results are compared to direct simulations.
Claudia Cianci
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**Volume exclusion effects in detailed balance systems**  
*Thursday, September 18, 2015. h 10.40 - 10.55*

It is well known that the cell is a crowded environment and that many of the biochemical reagents exist in very low concentrations. Both of these facts increase the relevance of stochastic modelling. The accepted stochastic model of reactions on this scale is the Chemical Master Equation (CME), or Reaction Diffusion Master Equation (RDME) when spatial effects must be considered. In this paper, we show that the RDME reduces to the CME for detailed balance systems, and proceed to investigate how volume exclusion effects can alter the CME solution. We particularly focus on the crowding-induced changes that occur to the Fano factor, the coefficient of variation, and the skewness of the resulting distributions. We will consider two general classes of chemical systems, with and without chemical conservation laws. For each class of systems we will treat a specific example and we will verify our analytical results with simulation data obtained with the Stochastic Simulation Algorithm (SSA).

Otti Croze
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**Swimming algae in photobioreactors**  
*Wednesday, September 16, 2015. h 18.15 - 18.30*

Many microorganisms have evolved to swim and bias their swimming in response to useful environmental cues. Bacteria can move up gradients of chemoattractants (chemotaxis), algae can swim towards light (phototaxis), up (gravitaxis) or, in a shear flow, towards downwelling fluid (gyrotaxis). Such microscale biased swimming gives rise, at the macroscale, to new suspension dynamics and transport. I will present our work on the peculiar dispersion of swimming algae in pipe flow, describing theory and simulations. This work is relevant to photobioreactors used to grow algae industrially. We are using our own photobioreactor to test theoretical predictions and explore the biological implications of the strange biofluid dynamics of algae.
Fully automated clustering by accurate non-parametric density estimation
Wednesday, September 16, 2015. h 18.00 - 18.15

Cluster analysis aim at classifying elements into categories. We focus on the family of clustering methods based on the idea that clusters are characterized by a local density higher than their surrounding region, which automatically discern from the data the number of groups and the rule of assignment. All these clustering methods rely on different methods for local density estimation. We propose a new automatic and adaptive density estimator obtained by generalizing k-nearest neighbor method. By including an evaluation of the uncertainty on the density estimations at both cluster centers and border regions between clusters, this method can better discriminate genuine density peaks from noise. We demonstrate the power of the algorithm on complex-systems. In particular, interesting results have been obtained by analyzing rRNA sequences data from human microbiota.

Sample and population exponents of generalized Taylor’s law
Friday, September 18, 2015. h 10.40 - 10.55

Taylor’s law (TL) states that the variance $V$ of a non-negative random variable is related to its mean $M$ via a power-law $V = aM^b$. TL was confirmed broadly in ecology, physics and other natural sciences, suggesting the existence of a universal mechanism dictating its emergence. In ecology, TL typically applies to population abundances and sample exponents measured empirically are often close to $b = 2$. Population growth models, however, predict that the population exponent $b$ can assume any value, which depends on the details of the growth process. Additionally, abrupt transitions in the TL exponent associated with smooth changes in the environment were recently discovered theoretically and comparable real-world transitions could harm fish populations, forests, and public health. Here, using large deviations theory and finite-size sample arguments, we show exactly that in multiplicative growth models the sample exponent (the exponent computed via the scaling of sample mean and sample variance) is close to $b = 2$ regardless of the value of the population exponent (the exponent computed via the scaling of population mean and population variance). Therefore, the widespread observation of TL with sample exponent $b \sim 2$ may be a statistical artifact and not dependent on population dynamics under conditions that are specified exactly. Our study shows that limited sampling hinders the anticipation of abrupt transitions in the TL exponent and provides estimates for the number of samples required to reveal early-warning signals of such transitions. Finally, we show that a generalized TL applies for the scaling of the k-th vs the j-th cumulant with exponent $b_{jk}$ and that for finite samples the sample exponent $b_{jk} \sim k/j$ asymptotically in time. We verify this prediction in two empirical ecological datasets.
Jordi Hidalgo
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Bet-hedging strategies in contact-process-like dynamics
Friday, September 18, 2015. h 17.20 - 17.35

In biology and ecology, individuals or communities of individuals living in unpredictable environments often alternate between different evolutionary strategies to spread and reduce risks. Such behavior is commonly referred to as “bet-hedging”. Long-term survival probabilities and population sizes can be much enhanced by exploiting such hybrid strategies. We study a simple model based on the physics of the Contact Process in which individuals can choose between a poor but safe strategy, a better but risky alternative, or a combination of both, and we show that the benefits derived from bet-hedging strategies are much enhanced for higher environmental variabilities (large external noise) and/or for small spatial dimensions (large intrinsic noise).


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Group formation and efficiency of migratory species
Wednesday, September 16, 2015. h 18.30 - 18.45

Individual preferences and social behavior are central traits of group formation in humans and other social animals. Being in a group is often a big advantage for those individuals performing complex tasks that are usually difficult, or impossible, to be carried alone. Schooling is an example of such complex collective dynamics and it is a common feature in several fish species performing seasonal migrations from the spawning to feeding areas. Combining an evolutionary individual based models and a novel framework based on network theory we demonstrate that three factors can control school formation and migration behavior of social fish: the strength of the social group, the relative number of informed individuals and the preference each individual has on the particular feeding area. While sociality and information ability are associated to the long-term evolutionary process that have selected them, the preference is a short-term property of single individuals and is related to the experience and memory of certain places. Intensive fishing and habitat degradation can reduce the frequency of those traits in the population up to a point at which migrations to feeding and spawning grounds are suddenly stopped.
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**The Physics of Plasmid Transfer on Microbial Colonies**  
Wednesday, September 16, 2015. h 17.45 - 18.00

In addition to chromosomal DNA, many bacteria contain small pieces of DNA called plasmids. Plasmids often carry genes that provide resistance to antimicrobial drugs. Consequently, plasmid transfer (conjugation) between unrelated bacteria is an important factor contributing to the spread of antibiotic resistance. Using a computer model and simple calculations I have studied how the physics of interbacteria interactions affects the rate of plasmid transfer between adjacent cells in expanding bacterial colonies. In my talk, I will show that, although neutral (no fitness cost) plasmids may eventually spread to the whole colony, this process is hindered by spatial expansion and is thus very slow. In addition, mechanical forces acting between the cells may further decrease the rate of plasmid transfer to negligible levels.

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**Non-Markovian effects on protein sequence evolution**  
Friday, September 18, 2015. h 17.05 - 17.20

In 1968 Dayhoff et al. introduced for the first time the concept of PAM matrix. This has laid the basis for modeling amino acid replacements by a Markovian model. This seminal idea was further developed and specialized in the following years. However, in the last twenty years, some works observed that evolution seems to proceed differently at different time scales, questioning the Markovian assumption. In particular, in 2011 Kosiol and Goldman proved that, if evolution is Markovian at the codon level, it can not be Markovian at the amino acid level. We show how also the among-site variability of substitution rates introduces significant elements of non-Markovianity in protein sequence evolution. Moreover, this fact does not depend on whether one models evolution at the amino acid level or at the codon level and causes, as a first consequence, a systematic underestimation of evolutionary distances worsening for large evolutionary times. In the light of these results, protein sequence evolution can be considered Markovian at most on single sites and the transition probability matrix for this process may be deduced more efficaciously from Single Nucleotide Polymorphisms rather than from pairwise of multiple sequence alignments as it has been done so far.
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Growth, switch and memory in bacterial populations  
*Friday, September 18, 2015. h 15.40 - 15.55*

Phenotypic heterogeneity is a common feature of microbial populations, extremely interesting as it bridges genetics, the organism’s response to the environment, and evolutionary concepts such as bet-hedging. Starting from a variety of experimental data about Pseudomonas fluorescens strains evolved to perform a phenotypic switch, I will present a simple metabolic model where differential, unsteady growth rate can explain the kinetics of phenotypes’ frequencies in well-mixed populations. This will be viewed in the context of "memory" of past states at the cell level, and compared with the emergent phenomenon of sectored colonies in structured populations.

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Bet hedging among ocean plankton: Active behavioral response of phytoplankton to turbulence  
*Friday, September 18, 2015. h 18.15 - 18.30*

Phytoplankton are unicellular photosynthetic organisms that form the basis of life in the oceans and contribute a major fraction of global oxygen production. Phytoplankton are frequently exposed to turbulence, which has long been known to affect phytoplankton fitness and species succession, generally by harming motile species and thus favoring a transition to non-motile species. Here we report on a striking, unexpected behavioral response of a motile species the red-tide producing raphidophyte Heterosigma akashiwo to hydrodynamic cues mimicking those experienced in turbulence. In the absence of turbulence, H. akashiwo exhibits upwards swimming or negative gravitaxis observable as cell accumulations at the top of an experimental container. Using a new millifluidic device a computer-controlled flip chamber that allows the orientation of a small phytoplankton to be controlled arbitrarily over time we exposed H. akashiwo to periodic overturning that mimics the rotation of individual cells by Kolmogorov-scale turbulent eddies. We discovered that, after a sufficient number (30100) of flips (180 degree reorientations relative to the vertical), with a period of 530 s, an originally upward swimming H. akashiwo population robustly split in two nearly equi-abundant subpopulations, one swimming upward and one swimming downward. Control experiments with rotation of the flip chamber around a vertical axis, in which no population split was observed, revealed that the cue inducing this active response is the reversal of the gravitational acceleration. Microscopic observation at the single-cell level showed that the behavioral switch was accompanied by a rapid morphological change, and a mechanistic model of gravitaxis confirms that such a shape change can alter the cells stability and induce downward migration. The results indicate that, over timescales smaller than the cell cycle, H. akashiwo can actively switch between two alternative stable states, through phenotypic plasticity in response to mechanical cues. This active response to fluid flow, whereby nearly half of a phytoplankton population in the ocean may invert its direction of migration in response to turbulence, could be part of a bet-hedging strategy to maximize the chances of at least a fraction of the population evading high-turbulence microzones.
Particles of density different from the surrounding fluid are known to generate inhomogeneous distribution even in incompressible flows. Recent analytical and numerical works are shown that gravity conspires with turbulent accelerations to increase clustering of inertial particles; but gravity can also affect the flow itself, in presence of density fluctuations such as in the case of stratified flows. In particular the ocean dynamics is strongly affected by the presence of stable stratification, such as in the pycnocline as a consequence of temperature and salinity variations. One of the most impressive example of confinement of particles in the ocean is the formation of the thin phytoplankton layers (TPL). TPLs are aggregations of phytoplankton from several centimeters to few meters thick, extending up to kilometers horizontally. They persist for periods ranging from hours to weeks. Thin layers are observed to be formed by different species of phytoplankton, both motile and non-motile. In some case they are mostly composed by toxic species thus affecting locally the conservation of the ecosystem. Several mechanisms have been proposed for the formation of TPLs, based on different physical ingredients: from the simple deformation of a patch under shear, to accumulation due to swimming. One proposed mechanism, of possible relevance for non-swimming species (such as diatoms) is based on buoyancy force in stratified flow. Indeed, some phytoplankton layers are strongly correlated with the presence of a sharp pycnocline. By means of direct numerical simulations of Navier-Stokes equations within the Boussinesq approximation, we investigate the dynamics of light particles, affected solely by buoyancy, that we named Floaters, in a stratified turbulent flow. We derive the equation of motion for the floaters, consistently with the Boussinesq approximation and in the limit of small Stokes number. We observe particles relax on surfaces at constant density (isopycnals) where they are neutrally buoyant with the surrounding fluid. On such isopycnal surfaces they perform fractal clustering. We will show the large-scale distribution of several quantities: the height of the isopycnal surface, the vertical position of the particles and their relative distance from the surface. While the first two are gaussian distributed, the latter displays long exponential tails, since particle position is correlated to the surface geometry. On the other hand, one can consider also small-scale quantities. A good way to estimate mixing properties in the viscous scales is the correlation dimension $D_2$. We will show that it depends only on the relaxation time scale at which the particles reach the surface, and not on the stratification, that instead influences the morphology of isopycnal surface.
Individuals and populations often contend with social dilemmas in which the optimal behavior of an individual contrasts with the optimal outcome for the group. Predatory individuals face a trade-off between exploiting available resources and exploring for better conditions and often, optimize strategies for their individual foraging behavior. It is however not clear to what extent such optimization of individual strategies affect population level dynamics. Here we report on a unique predator-prey (Caenorhabditis elegans Escherichia coli) experimental system in which the foraging behavior of the predator represents a behavior optimized to achieve maximal benefit from the prey landscape. Surprisingly, this foraging behavior of the individual worm produces a growth advantage for the prey (resource), similar to that achieved via farming/ agriculture. The increased growth of the prey, in turn, benefits the predator population which increases with increasing foraging area. However, the cost associated with exploration outweighs the benefit beyond a critical foraging area, limiting the growth advantage. Further, we show that the increased production of the resource by the foraging behavior results in a common good that can be exploited by non-producers. When the wild type, producer worms are competed with a non-producing mutant phenotype, the non-producing worms are able to increase their own population by taking advantage of the foraging behavior of the wild type worms. Finally, we also exploit our experimental system to study the long range and rapid spread of evolutionary novelties in an expanding population.
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Consequences of availability of resources on scaling exponents of macroecological laws

*Thursday, September 17, 2015. h 17.10 - 17.25*

Empirical evidence of scaling relationships between ecological quantities are abundant: population abundances (Damuth law) and metabolic rates (Kleiber law) scale with body mass, the number of species in an ecosystem scales with the its area (speciesarea relationship), etc. In an ecosystem in stationary conditions abundances, body mass and total metabolic rate (summed over all individuals) are controlled by the same limiting factor: the availability of resources. In any ecosystem, in fact, the rate of resource supply is necessarily finite. Consequently, there is a limit to the total metabolic rate the ecosystem can sustain. Given the abovementioned connection between metabolism and body mass, and between body mass and abundance, the limit on total metabolic rate implies that resource availability will also impose constraints on body mass and abundance distributions. It is thus clear that species traits (body mass, metabolic rates) and ecological quantities (population abundances, number of species) must be tightly linked to each other, but how does this link reflect on scaling laws and their exponents? We present a theoretical framework, based on methods of statistical physics and finitesize scaling theory, that accounts for the limiting effect of resources and allows exploring and quantifying the interrelatedness of widespread macroecological laws. In this framework the exponents of the abovementioned scaling relationships are interconnected. In particular, the number of independent scaling exponents is smaller than the number of scaling relationships observed empirically (e.g. the speciesarea relationship, the scaling of the total biomass with area, the community size spectrum, the scale of the maximum organismic mass, the speciesmass relationship, the relative species abundance), an issue that has been often overlooked in the literature. Consequently, estimates of one exponent will give information also on the other exponents. A interesting result of this investigation is that, depending on the exponent of metabolic rate scaling vs body mass, the total biomass could scale superlinearly with the ecosystem area. This is a testable hypothesis, which may have profound implications for ecology. Most importantly, a super linear scaling of total biomass with ecosystem area may be of interest to conservation ecology. Among other consequences, in fact, superlinearity would suggest the creation of a small number of large protected areas rather than a large number of small ones.
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A spatial maximum entropy model for ecosystems structure
Poster

Until now, maximum entropy approaches have lacked the important feature of considering space in an explicit manner. We propose a spatially explicit maximum entropy model suitable to describe spatial patterns such as the species area relationship and the endemic area relationship. Starting from the minimal information extracted from presence/absence data, we compare the behavior of two models considering the occurrence or lack thereof of each species and information on spatial correlations. Our approach uses the information at shorter spatial scales to infer the spatial organization at larger ones.

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Scaling laws in the functional content of bacterial genomes
Poster

The wide availability of sequenced bacterial genomes confirms the existence of universal laws that regulate genome composition in terms of its functional content. Functional categories exhibit power-law scaling with genome size, with function-dependent scaling exponents; for instance, metabolic domains scale linearly, whereas transcription factors scale almost quadratically. While there has been debate on whether and how much these trends emerge from clade-specific family expansions, comparatively little work has been directed towards establishing how robust they are at the level of the gene families belonging to a given functional category. To address this question, we employed protein domains (from the SUPERFAMILY and PFAM database) and their functional annotations. We considered how the scaling laws change with the resolution level of families and their grouping into functional categories. Our results are the following. Grouping families by exponents, we both recover the known links to functional categories and discover new ones. However, the trends are not strict, and most functional categories contain outlier families, whose trend disagrees with the category scaling. This prompts us to introduce an novel statistics to account for the heterogeneity of family scaling, which shows that families within functional categories with higher exponents (such as transcription factors or signal transduction) tend to have more heterogeneous scaling behavior.
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Persistence of consumer-resource interactions in food-webs
Poster

Networks are regarded as static diagrams of interacting species, in which the spatiotemporal variability is not considered, despite the knowledge of the dynamics that generate. Consumer-resource interactions are strongly related to functional traits of the species, and these functional relationships can be stable in large gradients of spatial and temporal variation, therefore, we expected that consumer-resource interactions are persistent over time. We investigated the spatiotemporal consistence (sampled seasonally between winter 2004 and autumn 2007) of resource-consumer interactions in intertidal rocky-shore macrobenthic communities from four distributed over 1,000 km (from 21 to 30 south latitude) of coast in northern Chile. We used matrix consumer-resource and subsequently we add 10 matrix for each site, which correspond to each interannual seasons. Consistent resource-consumer interactions are those that repeated during the ten interannual seasons. Network structural patterns obtained from matrix consumer-resource were determined using metric commonly used to characterize network topology: degree distribution and subsequently we used rank-ordered distributions of a discrete version of a generalized beta distribution (DGBD) as a fit for the data. Despite large dissimilarities in terms of composition and environmental conditions (i.e. sea surface temperature (SST) and chlorophyll), the four sites showed virtually the same patterns of frequency of occurrence of interactions. At each site, trophic interactions seemed to be highly variable over time, as only few interactions were persistent over the sampling period and most interactions occurred only once. We observed a power-law behavior of the persistence of trophic interactions over time in each site, where degree frequency distribution fit very closely to generalized beta distribution (DGBD). This result suggests that only few consumer-resource interactions are persistent over time, reflecting the inherent dynamics of these processes in natural communities. Our results show that short-time scale studies preclude make accurate conclusions about the structure of the networks. We suggest long-time studies are more robust and useful to make predictions about networks.

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Evolutionary Models for Transcriptional Regulatory Networks
Poster

We discuss an evolutionary model of the duplication-divergence type for the human transcriptional regulatory network. We focus in particular on the organization in families of paralogous Transcription Factors (TFs). We give a mathematical description of the process and consider its steady state. The model has only one free parameter which we can fix using data taken from TRANSFAC database. Our main result is that the data are compatible with the model only if one assumes that a relevant fraction of TFs is made of singletons, i.e. genes whose duplication is selected against.
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Uptake levelling in chemotactic bacteria measured by the Gini index
Poster

Chemotactic bacteria can swim up nutrient gradients to accumulate in areas where their uptake is enhanced. Oceans and lakes being heterogeneous environments at the microbial scale, these bacteria face a landscape of attractant sources of different strengths. Among these are live micro-algae releasing organic compounds. What is the distribution of chemotactic bacteria around such sources and what are the consequences of this distribution on bacterial uptake? The way animal populations distribute according to available resources is a classical question in ecology. The most even distribution, for which each individual gets an equal share of the resources, is named the ideal free distribution, and has been observed experimentally in ducks gathering around food sources. However, in our microbial case, how much distributions deviate from the ideal free distribution is unclear: the chemotactic behaviour, although it produces an average motion of bacteria toward stronger attractant sources, is based on a biased random motion that tends to diffuse out any local accumulation of bacteria. To answer this question, we considered the simplified problem of a population of chemotactic bacteria in a 1D chamber whose left and right boundaries release an attractant at constant rates. We model the chemotactic response and the attractant distribution evolution through the Keller-Segel equations. The steady-state solutions, obtained numerically with physical parameters, show that diffusion, chemotaxis and uptake produce an unequal uptake distribution inside the bacterial population, far from the ideal free distribution result. In comparison with a non-chemotactic case, however, chemotaxis tends to level the uptake throughout the population. To quantify the extent of this effect, we adapt the Gini index, used in Economics to characterise inequalities, to our problem. We show that chemotaxis is most effective at levelling uptake when the sources are separated by a typical length scale, set by the characteristics of the attractant uptake.

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Generalized Langevin Equation for many probes in nonequilibrium environment
Poster

The generalized Langevin equations for many probe particles weakly interacting with a driven environment is derived by applying nonequilibrium linear response theory. When the driving is off, the theory correctly reproduces the equilibrium properties of the system, i.e. it fulfills the FDT and conforms to Onsagers regression principle relating the fluctuations of statistical forces to the memory kernel. Instead, in the presence of driving, we quantify in terms of both excess dynamical activity and probability currents the breaking of the fluctuationdissipation theorem and reciprocal relations. The latter results in the lack of the actionreaction principle for the environmentmediated interactions. We test our findings with numerical simulations of active and driven particles.
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Maximum Likelihood Estimation of a Point Process’s Intensity
Poster

We compare different methods aiming to correctly infer the underlying structure of a dataset. Classifying it as clustered rather than regular and, more generally, establishing the main features of its distribution, strongly depends on the “window” through which we look at it. We propose a method which, by approximating the underlying intensity function of a point process, permits us to test complete spatial randomness (CSR) hypothesis, to avoid sampling fluctuations and to give information regarding relevant characteristics of the process’s structure: homogeneity, anisotropy and radius of clumps. We test all methods on the ecological dataset of the Barro Colorado Island rainforest.