Network Dynamics, March 25-26; 2013, Montpellier

BOOK of ABSTRACTS

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Dynamics on and within networks: why geographers care?
Geographers have been concerned by networks for a long time. In the sixties-seventies, it became a major topic in the so called « quantitative geography » and optimisation methods (shortest-path, maximum flow, p-median problems,...) were widely used. The « GIS turn » in the eighties-nineties contributed reinforcing this tradition and networks reached the status of classic geographic « objects ». The « morphologic » anchorage of these previous works is still present today, even though geographers adapted their methods and tools (fractal geometry, complex networks,...), accompanying the underlying scientific evolutions. Therefore, handling dynamics on and within networks is quite natural in geography, even though the computation burden involved by large networks and current algorithms restrains the dissemination of this topic in the community.
I will take advantage of this workshop on "Network Dynamics" to draw a picture of these evolutions in my discipline. This general context will help understanding the position of my own researches. I will therefore focus on two recent publications [1, 2] plus several on-going projects dealing with dynamics on and within networks.
[1] BANOS Arnaud, 2012, Network effects in Schelling's model of segregation: new evidences from agent-based simulation, Environment and Planning B, Volume 39, n°2, 393 – 405
[2] BANOS Arnaud, GENRE-GRANDPIERRE Cyrille, 2012 : Towards New Metrics for Urban Road Networks. Some Preliminary Evidence from Agent-Based Simulations, in HEPPENSTALL, A.J.; CROOKS, A.T.; SEE, L.M.; BATTY, M. (Eds.), Agent-Based Models of Geographical Systems, Springer, pp. 627-642

Pierre BARBILLON
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Network impact on persistence in a finite-population dynamic exchange model.
In agriculture, farmer-to-farmer seed exchange is a crucial issue because these practices influence the distribution of crop diversity across the agricultural landscape. Because farmers are connected through social relationships, connectivity patterns among farmers are complex and heterogeneous. To better understand such dynamical process, we are studying a stochastic colonization-extinction (SCE) model that accounts for network heterogeneity constraint: seed exchanges are only possible across a fixed social network rather than extinction occurs randomly at each generation. It is possible with such a model to explore the influence of the topological properties of networks on the persistence of crop variety within the network of farmers after a given number of generations. Three main classes of social organisation are investigated to explore a large range of situations, including realistic social organisations. We take into account the finite number of farms in the model since it is responsible for a stochasticity which can lead to results different from the ones obtained with deterministic models. Furthermore, our results are obtained by exact computation when the number of farmers is small and we propose simulation otherwise. A particle filter is used to enhance the accuracy of the parameter estimation.

Marc BARTHÉLÉMY
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Evolution of spatial networks.
Many networks have a spatial component: transportation and mobility networks, Internet, power grids, social networks, neural networks are all examples where space is relevant and where topology alone does not contain all the information about these graphs. In addition, these networks evolve and grow in time and we have to face the difficulty of measuring and characterizing their evolution, and to extract useful information. I will illustrate these various problems and present some recent results on two case studies: the evolution of a road network and the evolution of the world's largest subway networks.

Hugues BERRY
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Intercellular calcium wave propagation in astrocyte networks.
Glial cells are non-neuronal cells that constitute the majority cells in the human brain. Recently, it was realized that these cells significantly modulate information processing via permanent cross-talk with the neurons. Astrocytes, the main type of glial cell in the brain, are also themselves inter-connected as networks and communicate via chemical wave propagation. In the last years, we have been developing with E. Ben Jacob (Tel Aviv University) a modeling framework of the signaling pathways that support astrocyte-neurons cross-talk and astrocyte-astrocyte communication. In this talk, I will present our recent investigation of the influence of astrocyte network topology on wave propagation. Our simulations indicate that the major classes of propagations reported experimentally can be emulated by a mere variation of the topology. In particular, propagation range improves for large mean-shortest paths and small connectivities. This unusual property sheds new light on consistent reports that astrocytes in vivo tend to restrict their connections to their nearest neighbors. Confrontation of the model with in vitro experimental data from Y. Hanein's goup (Tel Aviv University) allows validating the model and started uncovering some of the properties of calcium wave initiation and propagation.

Laurent BLANCHOIN
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Directed actin self assembly and contractility.
The organization of actin filaments into higher-ordered structures governs eukaryotic cell shape and movement. Global actin network size and architecture is maintained in a dynamic steady-state through regulated assembly and disassembly. We have developed a micro-patterning method that enables the spatial control of actin nucleation sites for in vitro assays (Reymann, Nat Mat, 2010). These actin templates were used to evaluate the response of oriented actin structures to myosin-induced contractility. We determine that myosins selectively contract and disassemble anti-parallel actin structures while parallel actin bundles remain unaffected. In addition, the local distribution of nucleation sites and the resulting orientation of actin filaments regulate the scalability of the contraction process. This "orientation selection" mechanism for selective contraction and disassembly reveals how the dynamics of the cellular actin cytoskeleton is spatially controlled by actomyosin contractility. Further application of the micro-patterning method will be presented in particular recent data on the reconstitution of a lamellipodium-type of actin organization.

Mario CHAVEZ

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Role of network symmetries on remote synchronization.
In this communication I show how network symmetries play a central role in the synchronisation of a system. I consider a Kuramoto model in which the oscillators are associated to the nodes of a network with arbitrary connectivity and the interactions include a phase frustration, thus preventing full synchronisation. The system organises into a regime of remote synchronisation where pairs of nodes with the same network symmetry are fully synchronised, despite their distance on the graph. I provide some analytical arguments to explain this result and I show how the frustration parameter affects the distribution of phases. Interestingly, an application to brain networks suggests that symmetry of anatomical connections plays a role in neural synchronisation by determining correlated functional modules across distant locations.

Emilie COUPECHOUX
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Epidemics on large clustered random graphs.
The spread of epidemics can be used to model several kinds of phenomena in real-world networks, as the spread of diseases, or the diffusion of a new technology. One wants to know if a small proportion of the population initially infected (or having the technology in question) can propagate the epidemic to a large part of the population.
We model the network on which the epidemic takes place by a random graph. Indeed several kinds of real-world networks can be represented by graphs. Since such networks are very large, their detailed topology is generally unknown, and we model them by large random graphs having the same local statistical properties as the observed networks. An example of such properties is the fact that real-world networks are often highly clustered: if two individuals have a friend in common, they are likely to also be each others friends. The random graph model we consider here has an arbitrary degree distribution and a tunable clustering coefficient, and it allows us to study the impact of clustering on the epidemic propagation.

Sarah DE NIGRIS
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Emergence of a non trivial fluctuating phase in the XY-rotors model on regular networks.
We study an XY-rotor model on regular one dimensional lattices by varying the number of neighbours. The parameter $2 \geq \gamma \geq 1$ is defined. $\gamma = 2$ corresponds to mean field and $\gamma = 1$ to nearest neighbours coupling. We find that for γ lower than 1.5 the system does not exhibit a phase transition, while for γ greater than 1.5 the mean field second order transition is recovered. For the critical value $\gamma = \gamma c = 1.5$, the systems can be in a non trivial fluctuating phase for which the magnetisation shows important fluctuations in a given temperature range, implying an infinite susceptibilty. For all values of γ the magnetisation is computed analytically in the low temperatures range and the magnetised versus non-magnetised state which depends on the value of γ is recovered, confirming the critical value $\gamma c = 1.5$.

Christophe ELOY
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Architecture of trees: growth and self-organization.
Simplifying to the extreme, trees can be viewed as the biological answer to the following engineering problem: building a mechanically stable structure that ensure maximal sunlight interception with the smallest amount of matter. To meet these requirements, trees grow, producing each year “units” of similar sizes. It can thus appear paradoxical that the structure observed after a decade or more exhibits generally a branch hierarchy. The lowest branches are indeed statistically longer and thicker than the higher ones. Yet, branches cannot grow in length from year to year, and the only possibility to realize this length hierarchy is through pruning of lateral branches and aggregation end-to-end of several branches. Hence, the architecture of trees is the result of a complex growth strategy involving the creation of new branches every year and the pruning of old ones. Although there are apparent similarities with other growth structures, such as river networks (Dodds & Rothman 1999) or dendritic structures observed in diffusion-limited aggregation (Witten & Sander 1983), the architecture of trees involves specific mechanisms. It is thus likely that the statistical self-similarity or self-affinity of tree structures exhibits also specific characteristics, although it is still an open issue today. During this communication, I will present a numerical and theoretical model of tree growth that attempts to address this issue.

Ronan HAMON (Poster)
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Transformation from dynamic graphs to non-stationary signals.
Many networks, whether physical, biological or social, can be described by graphs which become dynamic if a time evolution is added. These graphs are difficult to study because it exists only few tools to describe these objects. The aim here is to propose a new method to visualize synthetically time evolution of dynamic graphs. The originality of the proposed method is to adopt a signal theory approach by computing frequency analysis on signals representing the graphs. The transformation in a collection of signals is computed using multidimensional scaling then specific frequency patterns of these series are linked to graph properties. Performing the transformation for each time step enables us to monitor the evolution of the frequency patterns and hence of the structure of the graph.

Franck JABOT
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Ecological networks - assembly processes and dynamical consequences.
Networks are increasingly used in ecology to describe the various ways in which organisms interact. A recurrent question in ecological network studies - with evident applied implications - is whether and how perturbations may spread in ecological networks. A number of theoretical studies point that a better understanding of the ecological processes of network assembly may be critical to understand the dynamical consequences of perturbations. And a new generation of network data is emerging to refine our understanding of network assembly and the consequences of networks' architecture on their dynamics. My talk will briefly review recent advances on these topics and some current challenges for ecologists and physicists.

Pablo JENSEN
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Analyzing science dynamics through heterogeneous networks.
We use science dynamics as a "drosophila" of the understanding of social dynamics, since clean publication databases exist, and papers represent an important insight of scientists' activity. We show how "heterogeneous networks" allow to include the richness of data while allowing a simple representation of their structure. We will also present first results on the idea of graph "differential", which would allow to detect the most significant changes in the evolution of a system.

Norbert KERN
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Characterising stationary states in exclusion processes on networks.
The notion of networks arises naturally in many problems: transmission of information, road networks, cytoskeletal transport and gene regulation are timely examples. It is often useful to envisage two complementary aspects defining these systems, rules for transmission/ propagation on one hand and network topology on the other hand. We generalise a simple class of models, so-called 'exclusion processes', to networks. We outline how to solve for stationary states and provide a method to characterise these stationary states in a simple but quantifiable way. Such 'effective rate plots' will be seen to prove particularly useful for gaining intuition on the essence of these states and on the effect of the network structure.

François MASSOL
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Solving the complexity-stability paradox in ecology with spatial structure.
Robert May questioned ecologists forty years ago by showing that random Jacobian matrices, aimed at representing dynamics around an ecological equilibrium, were more prone to show instability with more complex ecosystems. Since then, this famous question has been re-asked under different forms, but the initial observation of May was right in the sense that there is an asymptotic theory for very large Jacobian matrices that constrain the stability of equilibrium. Recently, Allesina and Tang detailed May's results by looking at different types of interactions (predation, mutualism, …), thus highlighting the fact that some interaction types are more stabilizing than others. Here, I will present results obtained in the case of spatially structured ecosystems. I will show how the initial species to species problem can be transposed to a population to population one, and present some results on the effects of spatial structure for the stability of large interaction networks.

Gaëlle NICOLAS (Poster)
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The influence of specific cattle exchange practices on RVFV spread in Madagascar highlands.
G Nicolas (1,2), B Durand (2), V Chevalier (1)
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Rift Valley fever (RVF) is a mosquito-borne zoonosis which causes a potentially severe disease. In 2008-2009, a RVFV outbreak occurred in a temperate and mountainous area located on the highlands of Madagascar where vectors are absent during the cold and dry season and have a relatively low population density during the warm and wet season (1). Questions remain on the mechanisms that allow to the virus circulation. A 3 years cattle follow-up (2009-2011) was conducted in a pilot area from this highlands. The study highlights a RVFV circulation throughout the 3 years (seroprevalence rate of 28% in 2009 (2), seroconversion rate of 7% in 2009-2010 (3) and of 23% in 2010-2011 (unpublished work)). Cattle exchanges of this area were shown to be linked to the virus local spread. Through network analyses and careful description of the cattle exchange practices of the pilot area we show how cattle exchanges networks dynamics (contact vs movement) can involve different risk of exposure to RVFV transmission.
(1) Tantely LM, Rakotoniaina J-C, Andrianaivolambo L, Tata E, Razafindrasata F, Fontenille D and Elissa N, 2013 Biology of mosquitoes that are potential vectors of Rift Valley fever virus in different biotopes of the Central highlands of Madagascar. J Med Entomol In Press:
(2) Chevalier V, Rakotondrafara T, Jourdan M, Heraud JM, Andriamanivo HR, Durand B, Rollin PE and Rakotondravao R, 2011 An Unexpected Recurrent Transmission of Rift Valley Fever Virus in Cattle in a Temperate and Mountainous Area of Madagascar. PLoS Negl. Trop. Dis 5:e1423
(3) Nicolas G, Durand B, Duboz R, Rakotondravao R and Chevalier V, 2013 Description and analysis of the cattle trade network in the Madagascar highlands: potential role in the diffusion of Rift Valley fever virus. Acta Trop 126:19-27

Marta SALES-PARDO
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The role of structure in the dynamics of biological networks

Tewfik SARI
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Mathematical modeling of genetic regulatory networks using piecewise-linear models.
In order to cope with the large amounts of data that have become available in genomics, mathematical tools for the analysis of networks of interactions between genes, proteins, and other molecules are indispensable. We present modeling of genetic regulatory networks, based on a class of piecewise-linear differential equations.

Jacques-Alexandre SEPULCHRE
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A brief survey of propagation phenomena in networks, from physics to biology.
The study of propagation phenomena in spatial networks has a relatively long tradition in physics. Spatial networks typically are chains or lattices composed of material entities interacting in space, often with translational symmetries.
However, besides spatial networks, the interest of physicists has turned gradually to more general networks, where the nodes are defined in abstract interaction graphs, e.g. representing biomolecular or biological systems. In this context it is interesting to identify which physics methods are no longer relevant, which are still in use and which are awaiting development to explore propagation phenomena in networks. Without exhausting these questions, and starting with a brief survey of some results related to spatial networks, my talk will continue by presenting three examples of research results driven by the idea of studying propagation (or information transport) in non-spatial bio-networks. The first example will deal with intracellular signaling pathways, the second will concern an example of genetic network and the third one will consider a chaotic neural network. I will end by presenting a new type of exotic network where one central node can decompose a received signal on an assembly of other nodes, each of which responding only to a narrow frequency band of the incoming signal.

Ricard SOLÉ
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Hierarchies in complex networks.

Cédric SUEUR (Poster)
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Social network dynamics of alpine ibex (Capra ibex) at the Gran Paradiso National Park.

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Temporal and spatial structure of animal social groups is a fundamental topic in behavioural studies. Understanding how individuals interact can lead us to determine how genetic and cultural information spread within a population, to understand the evolution of animal sociality or to track disease transmission. In polygynous ungulates the social structure is influenced by sexual segregation and ecological factors partially influence ungulate's social group. In this work we investigated the social network of males Alpine ibex (Capra ibex) living in Valsavarenche, in the Gran Paradiso National Park (Italy). They stay in group year-round except for the rutting season when they formed mixed-sex groups. Male Alpine ibex seems to live in a "fission-fusion" society as group composition varies often during the day and the seasons. The studied population was composed of about 65 males, 70% of which were marked and individually recognizable. Data on groups' composition have been collected during 5 years (from 2008 to 2012) in the summer (from May to July), the period in which ibex showed the strongly sexual segregation. Our work explored group and individual measures with the purpose to better understand ibex social dynamics and detect if there are changes or not over a five year period in which ecological factors and anthropic disturb operated differently. Here we present the first results of social network analysis, which consist in the comparison of group-measures over the whole study period. Group size and diameter showed that groups' composition or structure was stable, even if the bigger differences were among the first and the last year. However, density and transitivity increased during the five years whilst group centrality index decreased. We also studied changes of eigenvector centrality coefficients of the twenty common individuals over 5 years and this coefficient only decreased for individuals getting from adult to old whilst it stayed stable from juveniles to adults. We need now to understand ecological or social causes of these changes in the social network.

Adrien TAUDIERE (Poster)

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Beyond Common Mycorrhizal Networks: interspecific interaction networks underlying ectomycorrhizal community ecology.

In the ectomycorrhizal (ECM) symbiosis, plant species and their fungal associates are connected by direct links toward partners of different nature (bipartite ECM network) and the fungi allow connections between different plant species (projected ECM networks). While the variation in the number and the specificity of direct plant-fungi links has been widely documented, systemic views of ECM networks are lacking. We constituted a large dataset of plant-fungi associations in Corsica and applied network analysis to describe the properties of ECM networks. We investigated the structure of both bipartite and projected networks to investigate the specialization strategies of partners, the properties of fungi-mediated links among plants and the relationships between plant ecological strategies and ECM association patterns. We found (i) a balance between the specialization of plant species and the specialization of their ECM partners (ii) a trend to saturate the projected network notwithstanding the number of ECM partners in the bipartite network and (iii) less diverse association patterns, without shift in symbiont specificity, for pioneer species comparatively to non-pioneer ones. This analysis provides insights into belowground aspects of specialization vs. generalization that may be drivers of plant coexistence and dynamics.

Aleksandra WALCZAK

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Information transmission in small gene regulatory networks.

Many of the biological networks inside cells can be thought of as transmitting information from the inputs (e.g., the concentrations of transcription factors or other signaling molecules) to their outputs (e.g., the expression levels of various genes). On the molecular level, the relatively small concentrations of the relevant molecules and the intrinsic randomness of chemical reactions provide sources of noise that set physical limits on this information transmission. Given these limits, not all networks perform equally well, and maximizing information transmission provides a optimization principle from which we might hope to derive the properties of real regulatory networks. Inspired by the precision of transmission of positional information in the early development of the fly embryo, I will discuss the properties of specific small networks that can transmit the maximum information. Concretely, I will show how the form of molecular noise drives predictions not just of the qualitative network topology but also the quantitative parameters for the input/output relations at the nodes of the network. I will also show architectures that optimally produce a delayed respond to a dynamical signal.