BIFI INTERNATIONAL CONFERENCE 2018

ABSTRACTS COMPILATION

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BIFI INTERNATIONAL CONFERENCE 2018
“Complexity, Networks & Collective Behaviour”

Institute for Biocomputation
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“COMPLEXITY, NETWORKS & COLLECTIVE BEHAVIOUR”

The members of the Organizing Committee and the Institute for Biocomputation & Physics of Complex Systems (**BIFI, UNIZAR**) would like to thank all those who have sent their contributions in the different scientific areas, the Keynote Speakers, the Members of the Program Committee for their time and effort and, especially, to those who have generously disseminated this event.

This abstracts compilation is divided into different sections and the original format in which the Abstracts were sent has been preserved.

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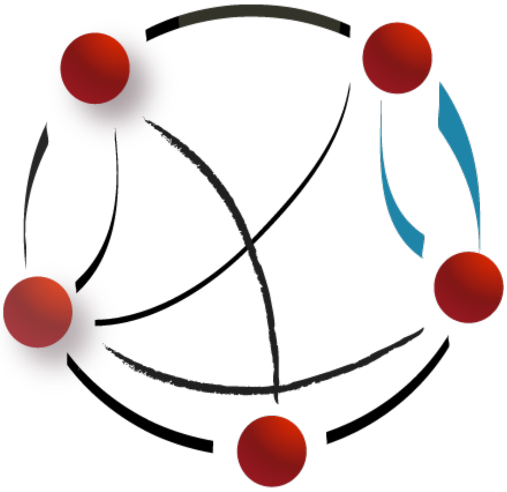
KEYNOTE TALKS

ALESSANDRO
VESPIGNANI

“Complex Systems, Networks and Epidemic Modeling”

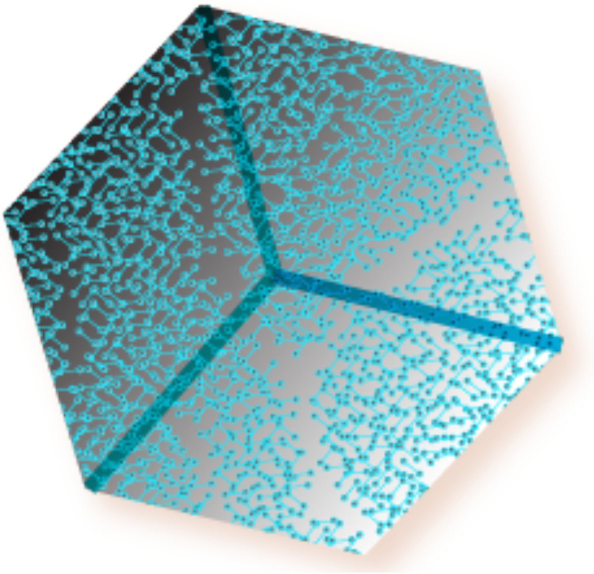
Analogous to meteorology, large-scale data-driven models of infectious diseases provide real- or near-real-time forecasts of the size of epidemics, their risk of spreading, and the dangers associated with uncontained disease outbreaks. These models are not only valuable because they predict where and how an epidemic might spread in the next few weeks, but also because they provide rationales and quantitative analysis to support public health decisions and intervention plans. Moreover, the advances in data-model integration have highlighted complex properties and heterogeneities that often elude the straightforward linear thinking we are used to, and surprise us with tipping points, emergent behaviors, and unexpected shifts in dynamical regime that characterize complex phenomena. I will present a review of recent results and challenges in the area, ranging from applied analysis for public health practice to foundational computational and theoretical challenges.



JAMES
GLEESON

“Cascade Dynamics on Networks”

Network models may be applied to describe many complex systems, and in the era of online social networks the study of dynamics on networks is an important branch of computational social science. Cascade dynamics can occur when the state of a node is affected by the states of its neighbours in the network, for example when a Twitter user is inspired to retweet a message that she received from a user she follows, with one event (the retweet) potentially causing further events (retweets by followers of followers) in a chain reaction. In this talk I will review some simple models that can help us understand how social contagion (the spread of cultural fads and the viral diffusion of information) depends upon the structure of the social network and on the dynamics of human behaviour. Although the models are simple enough to allow for mathematical analysis, I will show examples where they can also provide good matches to empirical observations of cascades on social networks.



TINA
ELIASSI-RAD

“Learning to Detect Fraud in Complex Systems”

We study companies that intentionally declare bankruptcy in order to avoid contributing their taxes -- i.e., they commit fraud. We link companies to each other through their shared resources, as some resources are the instigators of fraud. We introduce new approaches on (**1**) how to define and extract features from time-weighted networks, (**2**) how to integrate network-based and intrinsic features for fraud detection, and (**3**) how to diffuse fraud through a network, labeling the unknown and anticipating future fraud whilst simultaneously decaying the importance of past fraud. We find that domain-driven network variables have a significant impact on detecting fraud, and improve on baselines by detecting up to 55% additional fraudsters over time. This is joint work with Véronique Van Vlasselaer (SAS), Leman Akoglu (CMU), Bart Baesens (KU Leuven), and Monique Snoeck (KU Leuven).

ARNE
TRAULSEN

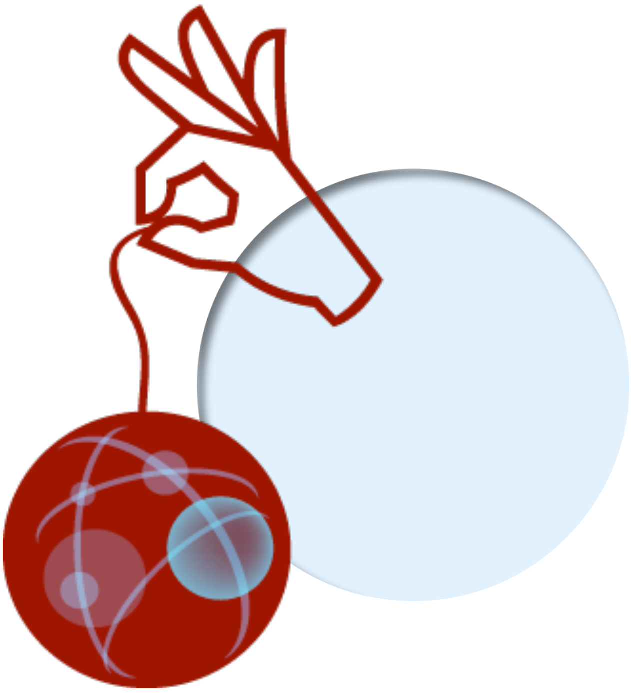
“Evolution in Network Structured Populations - from social networks to cancer”

Evolution can be strongly affected by population structure, but theoretical work shows that it is difficult to identify what exactly drives evolutionary dynamics. One possibility is to infer whether structures increase or decrease the evolutionary chances of novel mutants and even this is a challenging task. Using methods from population genetics and evolutionary demography can help to understand the underlying dynamics better, potentially paving the way for concrete applications, ranging from the evolutionary dynamics in river systems to cancer evolution.

SUSANNA
MANRUBIA

“On the Architecture of Genotype Spaces and the Dynamics of Molecular Adaptation”

Evolutionary dynamics is often viewed as a subtle process of change accumulation that causes a divergence among organisms and their genomes. However, this interpretation is an inheritance of a gradualistic view that has been challenged at the macro-evolutionary, ecological, and molecular level. Actually, the evolutionary dynamics of molecular populations shares deep qualitative and quantitative similarities with slowly driven physical systems, remarkably non-linear responses analogous to critical transitions, sudden state changes and hysteresis. Furthermore, the functional promiscuity inherent to genotypes transforms classical fitness landscapes into multiscapes where adaptation may be instantaneous in response to an environmental change. The quantitative nature of adaptive molecular processes is deeply dependent on a multilayered network-of-networks structure of genotype spaces that we begin to unveil.



SANJEEV
GOYAL

“The Rise and Fall of Empires”

In the study of war, a recurring observation is that conflict between two opponents is shaped by third parties. The actions of these parties are in turn influenced by other proximate players. These considerations lead us to propose a model with multiple inter-connected opponents. We study the influence of resources, technology, and the network of connections, on the dynamics of empires.

CIRO
CATTUTO

“High-resolution Social Networks: experiences and perspectives”

Digital technologies afford the quantification of specific human behaviors with unprecedented levels of detail and scale. Personal electronic devices and wearable sensors, in particular, can be used to map the network structure of human and animal close-range interactions in many settings relevant for complex systems research. In this talk, I will review the state of the art of sociometric measurements and discuss the experience of the *SocioPatterns* collaboration, an effort aimed at measuring and modeling high-resolution social networks using wearable proximity sensors. I will illustrate statistical regularities, network structures and heterogeneities of empirical data collected in environments that span schools, hospitals, households and low-resource rural settings. I will reflect on challenges such as generalization, sampling and data incompleteness, and illustrate modeling approaches based on ideas from machine learning. I will close with an overview of future research directions and applications.


NO L M TS
TO K OWLEDGE
COMPLEXITY, NETWORKS & COLLECTIVE BEHAVIOR
Design: COSNET Lab

REGULAR TALKS

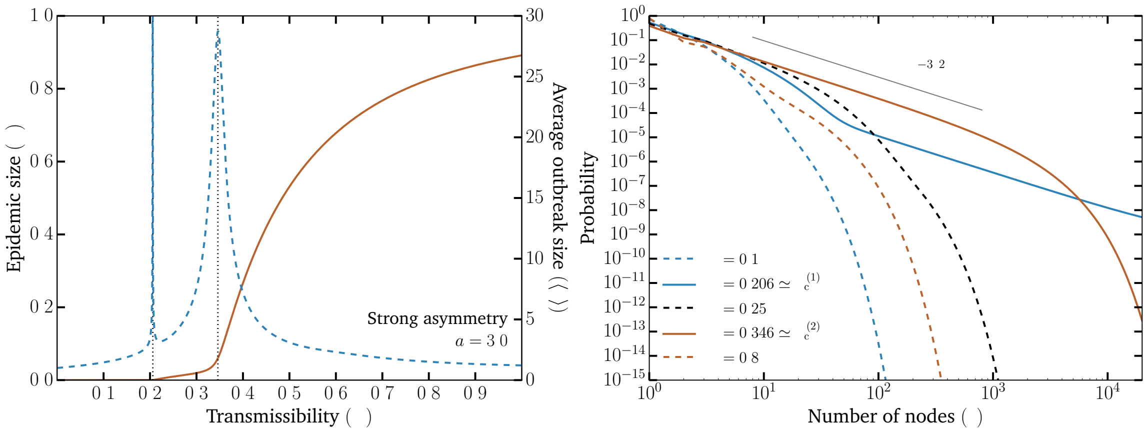
Double epidemic threshold and the potential of the Zika virus as a sustained STI

Antoine Allard[1,†], Benjamin M. Althouse[2], Laurent Hébert-Dufresne[2,3], and Samuel V. Scarpino[4]
1. Centre de Recerca Matemàtica, Bellaterra (Barcelona), Spain
2. Institute for Disease Modeling, Bellevue (Washington), United States of America
3. University of Vermont, Burlington (Vermont), United States of America
4. Northeastern University, Boston (Massasschusetts), United States of America
†Speaker, email: `aallard@crm.cat`

Zika virus (ZIKV) exhibits unique transmission dynamics in that it is concurrently spread by a mosquito vector and through sexual contact. Due to the highly asymmetric durations of infectiousness between males and females—it is estimated that males are infectious for periods up to 10 times longer than females—we show how this sexual component of ZIKV transmission behaves akin to asymmetric percolation on the network of sexual contacts. We provide an exact analytical description of this asymmetric percolation process and show that it exhibits two epidemic transitions corresponding to a core-periphery structure (see figure). This feature is not present in the underlying networks of sexual contacts, which are not distinguishable from random networks, and emerges because of the asymmetric percolation. We then discuss how ZIKV's multi-route propagation dynamic and its double epidemic threshold challenge our conventional threat assessment methodologies. We show how most approaches will significantly underestimate the risk of sustained sexual transmission, and that this blind spot can be corrected by a simple, yet a priori nontrivial, redefinition of the basic reproduction number, R_0. Most importantly, our study suggests that our current ZIKV surveillance is biased against the most at-risk group for sustained sexual transmission, implying that the most likely outcomes are the hardest to detect.

Related publications

[1] *Asymmetric percolation drives a double transition in sexual contact networks*, PNAS 114, 8969 (2017)
[2] *The risk of sustained sexual transmission of Zika is underestimated*, PLoS Pathog. 13, e1006633 (2017)



(left) Illustration of the double epidemic transition due to the asymmetric probability of sexual transmission. The core of men-who-have-sex-with-men (MSM) is first invaded at $T = T_c^{(1)} \simeq 0.206$, as indicated by the first peak in the average size of small components, $\langle s \rangle$. The infected MSM core can then lead to large, sub-critical spillover outbreaks in the heterosexual population (periphery), which can in turn sustain an extensive outbreak by its own from $T = T_c^{(2)} \simeq 0.346$, as shown by the second peak in $\langle s \rangle$. **(right)** While $T_c^{(2)}$ does not mark a phase transition in the classic sense (the order parameter S is already non-zero), the signature power-law behaviour in the distribution of the size of components is nevertheless observed over many orders of magnitude (note that the distribution goes back to the expected "homogeneous" state in-between the thresholds). These results were obtained analytically for the correlated configuration model in which nodes are split into six types (homo-/bi-/heterosexual; male/female) and where links are formed according to sexual orientations. Every nodes have a degree k distributed according to $p_k = e^{-\langle k \rangle} \langle k \rangle^k / k!$ with $\langle k \rangle = 5$. Men transmit the disease to their neighbours with probability T and women with probability T/a.

Equivalence between non-Markovian and Markovian dynamics in epidemic spreading processes

Michele Starnini[1], James P. Gleeson[2] and Marián Boguñá[1]
[1]Departament de Física de la Matèria Condensada, Universitat de Barcelona, Martí i Franquès 1, E-08028 Barcelona, Spain
[2]MACSI, Department of Mathematics and Statistics, University of Limerick, Ireland

For a long time, the Markovian assumption has been at the core of the modeling of stochastic dynamics governing many natural and technological systems, due to its mathematical tractability. Nevertheless, a new wealth of time-resolved data on different interactions, from human dynamics to natural phenomena, revealed that this modeling framework needs to be overcome. Here we introduce a general formalism to allow the steady state of non-Markovian (NM) processes on networks to be reduced to equivalent Markovian processes on the same substrates [1]. We consider the NM Susceptible-Infected-Susceptible (SIS) epidemic model [2] and show that its steady-state is equivalent to a Markovian one with an effective infection rate λ_{eff}, thus encoding all the NM effects into a single parameter. Interestingly, this result is independent of the underlying network topology.

In SIS dynamics, nodes are either susceptible or infected. An infected node decays spontaneously to the susceptible state after a random time t distributed as $\psi_R(t)$. A susceptible node, connected to a an infected one, becomes infected after a random time t has elapsed since the infection was initiated, with t distributed as $\psi_I(t)$. Distributions $\psi_R(t)$ and $\psi_I(t)$ allow us to evaluate the (time-dependent) hazard rates, defined as $\delta(t) = \psi_R(t)/\Psi_R(t)$ and $\lambda(t) = \psi_I(t)/\Psi_I(t)$, where $\Psi_R(t)$ and $\Psi_I(t)$ are the corresponding survival probabilities. In Markovian dynamics, both distributions are exponential and the corresponding hazard rates are constants.

Our mathematical formalism demonstrates the existence of an effective infection rate λ_{eff}, defined as

$$\lambda_{eff} \equiv \int_0^\infty \phi(\tau_{ji})\lambda(\tau_{ji})d\tau_{ji}, \qquad (1)$$

where $\phi(\tau_{ji}) \equiv \lim_{t\to\infty} \text{Prob}(\tau_{ji}; t|n_j = 1, n_i = 0)$ is the probability density of τ_{ji}, where τ_{ji} is the time elapsed since the start of the infection process from a node j to a node i, given that node i is susceptible and node j is infected and $\lambda(\tau_{ji})$ is averaged over all active links $i - j$ in the network. We are also able to derive an approximate analytic expression λ_{app}, in very good agreement with λ_{eff}.

We check the validity of the effective infection rates, λ_{eff} and λ_{app}, by means of extensive numerical simulations of the non-Markovian SIS dynamics. We consider a Markovian recovery process with rate δ, that is, $\psi_R(t) = \delta e^{-\delta t}$, and an infection process with a Weibull inter-event time distribution, $\psi_I(t) = \frac{\alpha_I}{b}\left(\frac{t}{b}\right)^{\alpha_I-1} e^{-(t/b)^{\alpha_I}}$ with parameter α_I controlling the infection inter-event time distribution.

Fig. 1 shows the prevalence of the disease ρ^{st} at the steady state as a function of λ_{eff} and λ_{app}, for different network substrates: a two dimensional lattice,an Erdős Rényi (ER) graph,a random degree regular (RDR) network and a scale-free (SF) network with exponent $\gamma = 2.5$. One can see that different curves of the prevalence, corresponding to different forms of the infection inter-event time distribution, collapse onto one another when plotted as a function of λ_{eff} or λ_{app}. This result is particularly noteworthy since two infection processes with the same average infection time but different forms of $\psi_I(t)$ are known to behave very differently [3] showing huge differences in the prevalence ρ^{st}.

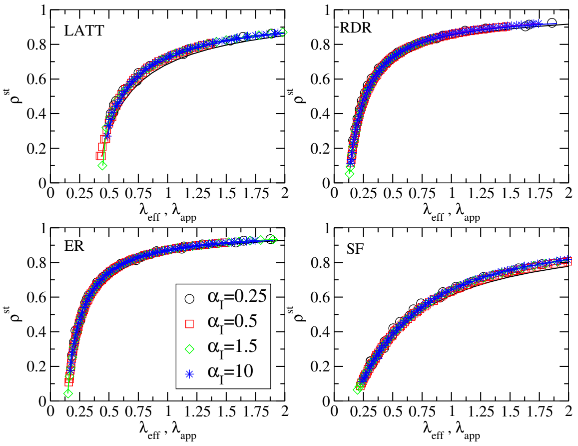


Figure 1: Steady-state prevalence ρ^{st} as a function of the effective infection rate, for different values of the exponent α_I. Symbols represent λ_{eff}, extracted by numerical simulations, continuous lines represent λ_{app}.

Interestingly, the approximate infection rate λ_{app} is expected to converge to λ_{eff} close to the epidemic threshold, and therefore the critical point and the set of critical exponents of the NM SIS dynamics, when expressed in terms of λ_{app}, are the same of those of the Markovian case. By means of a finite size scaling analysis, we obtain the epidemic threshold λ_c and the set of critical exponents for a NM SIS dynamics with $\alpha_I = 0.5$ and $\alpha_I = 2$, on top of two-dimensional lattice and RDR networks, showing that they are in very good agreement with the corresponding ones known in literature for Markovian SIS dynamics.

It is worth remarking that our formalism is not restricted to the SIS model and can be easily extended to any NM dynamics with a finite set of discrete states, allowing to determine the extent to which such dynamics can be reduced to a Markovian equivalent or whether the NM dynamics are fundamentally different. This simplification of the temporal nature of discrete-state processes promises to find application in the wide variety of areas where non-Markovian aspects are recognized as increasingly influential.

[1] M. Starnini, J. Gleeson, M. Boguñá, PRL **118**, 128301 (2017).

[2] R. Pastor-Satorras et al., Rev. Mod. Phys. **87**, 925 (2015).

[3] P. Van Mieghem et al., Phys. Rev. Lett. **110**, 108701 (2013).

Role of Structural Heterogeneity in Generalized Epidemic Process

Meesoon Ha[1], **Kihong Chung**[2], **Yongjoo Baek**[3], **Daniel Kim**[4], **and Hawoong Jeong**[2]
[1]Chosun University, South Korea; [2]KAIST, South Korea; [3]University of Cambridge, United Kingdom;
[4]Samsung SDS, South Korea

The generalized epidemic process (GEP) is a model of contagion with cooperative effects [1]. It is well known that the model exhibits tricritical points (TCPs), in the vicinity of which the system exhibits universal properties distinct from those of the ordinary bond percolation. In this study, we investigate the GEP on random scale-free networks (SFNs) characterized by power-law degree distributions, focusing on how the tricritical properties are affected by the structural heterogeneity of such networks. Applying the generating function method, we analytically obtain the locations of TCPs and the associated scaling exponents as functions of the degree exponent of SFNs. Based on them, we propose an extended finite-size scaling (FSS) theory for both dynamic and static aspects of tricritical phenomena, which is numerically confirmed with extensive Monte Carlo simulations. Our FSS results show that near TCPs the contagion is governed by two relevant length scales, whose nontrivial dependence on the degree exponent of SFNs leads to rich behaviors. Finally, it is notable that for strong heterogeneity the GEP achieves a nonzero fraction of infected nodes even in the limit of vanishing infection probability, which is in contrast to the zero fraction shown in a recent study about co-infections on SFNs [2].

[1] H.-K. Janssen, M. Müller, and O. Stenull, Phys. Rev. E **70**, 026114 (2004); P.S. Dodds and D.J. Watts, Phys. Rev. Lett. **92**, 218701 (2004); J. Theor. Biol. **232**, 587 (2005); G. Bizhani, M. Paczuski, and P. Grassberger, Phys. Rev. E **86**, 011128 (2012); K. Chung, Y. Baek, D. Kim, M. Ha, and H. Jeong, Phys. Rev. E **89**, 052811 (2014); K. Chung, Y. Baek, M. Ha, and H. Jeong, Phys. Rev. E **93**, 052304 (2016); H.-K. Janssen and O. Stenull, Europhys. Lett. **113**, 26005 (2016).

[2] P.-B. Cui, F. Colaiori, and C. Castellano, Phys. Rev. E **96**, 022301 (2017).

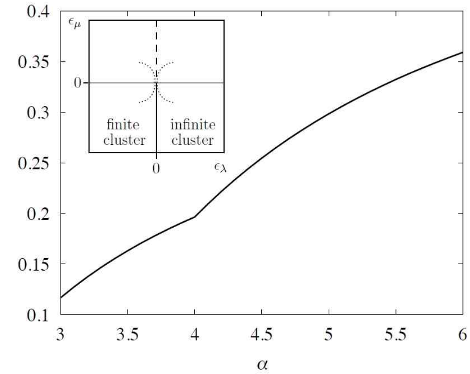


Fig. 1. The location of the TCP, μ_t, as a function of the power-law degree exponent α of random SFNs with $P(k) \sim k^{-\alpha}$. The inset shows the phase diagram in the vicinity of a TCP for $\alpha > 3$, where the solid (dashed) line indicates the continuous (discontinuous) transition line. The dotted lines represent the crossover scales given by $|\epsilon_\mu| \sim |\epsilon_\lambda|^\phi$, where ϕ is the crossover scaling exponent.

A data-driven model for the assessment of Tuberculosis transmission in evolving demographic structures.

Sergio Arregui, María José Iglesias, Sofía Samper, Dessislava Marinova, Joaquín Sanz, and Yamir Moreno

Institute for Biocomputation and Physics of Complex Systems (BIFI), University of Zaragoza, Spain

The control of Tuberculosis (TB) is one of the largest endeavors undertaken by public health authorities. Recently, the development of global strategies for diagnosis and treatment optimization have led to TB burden decay worldwide to the point that the scientific community has dreamed with its eradication by 2035. Nonetheless, such goal is yet far away, and TB still constitutes a major Public Health problem, provoking 1.8 million deaths in 2015. Among all possible novel epidemiological interventions against TB, improved preventive vaccines hold the promise of offering substantial reductions of TB burden worldwide.

In this context it would be required to develop a model for TB spreading capable of successfully describing the different age-dependent processes that affect the transmission and evolution of the disease. TB dynamics depends on age in multiple ways, some of which are traditionally simplified in the literature. That is the case of the heterogeneities in contact intensity among different age-strata that are common to all air-borne diseases, but still typically neglected in the TB case. Furthermore, whilst demographic structures of many countries are rapidly aging, demographic dynamics is pervasively ignored when modeling TB spreading. In this work, we present a TB transmission model that incorporates country-specific demographic prospects and empirical contact data around a data-driven description of TB dynamics.

Using our model, we find that the inclusion of demographic dynamics is followed by an increase in the burden levels prospected for the next decades in the areas of the world that are most hit by the disease nowadays. Similarly, we show that considering realistic patterns of contacts among individuals in different age-strata reshapes the transmission patterns reproduced by the models. Our findings provide fundamental insights if novel age-focused epidemiological interventions, such as preventive vaccines, are to be considered and established.

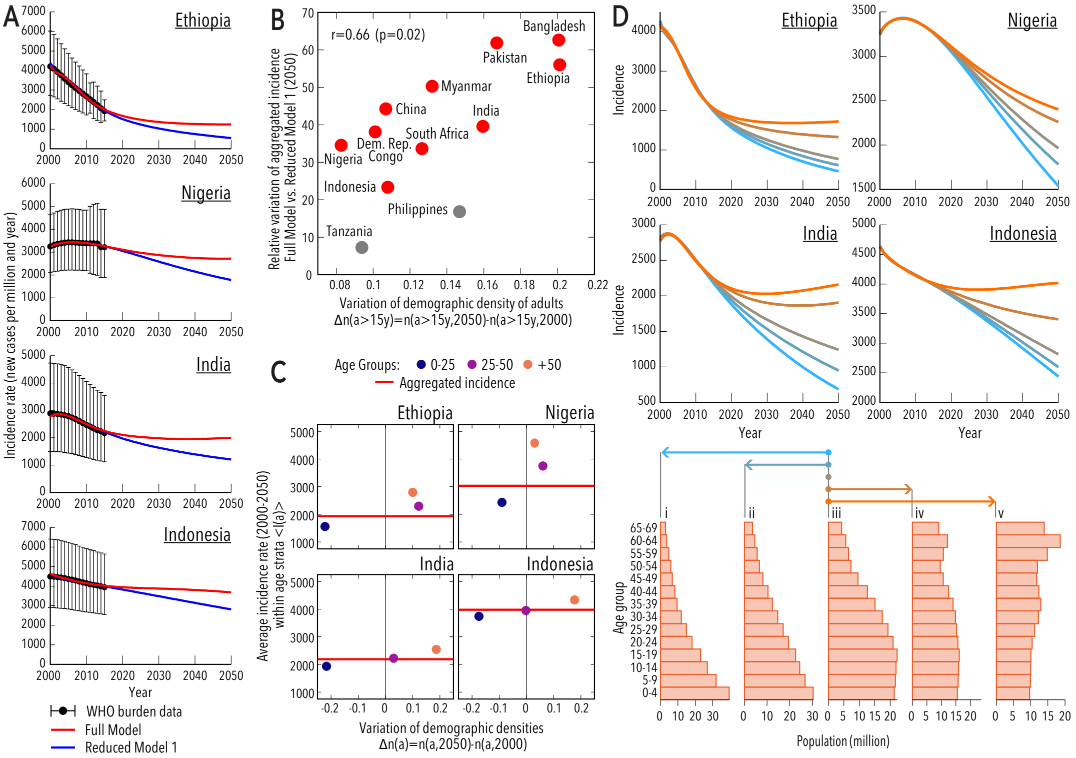


Figure 1: Effects of demographic dynamics on model forecasts. (A): Incidence rates from 2000 to 2050 obtained from the full model (red) and reduced model 1 (constant demography, blue). (B): Relative variation of aggregated incidence at 2050 for the top 12 countries with highest absolute TB burden in 2015 versus variation in the fraction of adults in the population during the period 2000-2050. In all countries but Tanzania and Philippines, in grey in the figure, the variations in incidence are significant at a nominal p=0.05. (C): Age specific average incidence rate of TB vs. variation of age-strata population density in 2000-2050. Older individuals are, at the same time, those affected by higher TB incidence rates and those whose presence in the population is increasing as a results of populations' aging. (D): Incidence projections for synthetic scenarios of demographic evolution, including transition towards younger populations (iii to i and iii to ii), static populations (iii remaining constant), and realistic transitions representing populations' aging (from iii to iv and from iii to v).

Synergistic cumulative contagion in epidemic spreading

Xavier R. Hoffmann[1,2] and Marián Boguñá[1,2]

[1]Departament de Física de la Matèria Condensada, Universitat de Barcelona, Spain
[2]Universitat de Barcelona Institute of Complex Systems (UBICS), Spain

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 [1]. Notwithstanding, most approaches assume memoryless, isolated and independent processes, an approximation partially invalidated by empirical evidence [2, 3]. We propose an alternative synergistic and cumulative infection mechanism, and study its effects in the susceptible-infected-susceptible model [4, 5].

In our description, susceptible agents accumulate pathogens from all their infected neighbors and become infected following a given probability density. When the last infected neighbour of a susceptible agent recovers, its accumulated viral load 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 $\zeta = \infty$ (perpetual accumulation) in random degree regular networks. We characterize the system's stationary and dynamical properties by means of extensive numerical simulations. In particular, we analyze the differences in approaching the steady state from above (starting from a fully infected population) and below (starting with a single infected agent).

When agents solely present short-term memory ($\zeta = 0$) the critical point of the transition between the healthy and endemic phases varies greatly depending on the shape of the infection probability density (left panel Fig. 1). Moreover, and even though the phase transition remains continuous, mean-field universality is lost. If individuals are equipped with long-term memory ($\zeta = \infty$), the system experiences a rather counterintuitive collective memory loss (right panel Fig. 1). Furthermore, for fat-tailed infection probabilities ($\alpha < 1$) an excitable phase appears before the transition to endemicity, in which the system exhibits SIR-like dynamics (left panel Fig. 2). Finally, for peaked infection probabilities ($\alpha > 1$) the transition to the endemic state is delayed when approached from below, and additionally becomes discontinuous (right panel Fig. 2).

The appearance of this wide array of features, already in unstructured substrates, evidences a crucial role of non-Markovianity in the spread of epidemic outbreaks. The inclusion of heterogeneous contact networks will shed light on the interplay between memory scales and agent heterogeneities, providing further insight on the relevance of microscopic mechanisms and topological properties in spreading processes.

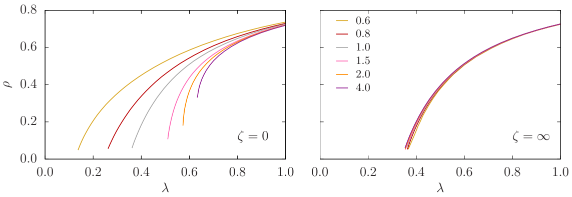


Figure 1: Fraction of infected agents, ρ, as a functon of the effective spreading ratio, λ, for various infection distributions (α indicated in legend). **Left**: Instantaneous decay of viral load (short-term memory). **Right**: Viral load does not decay (long-term memory).

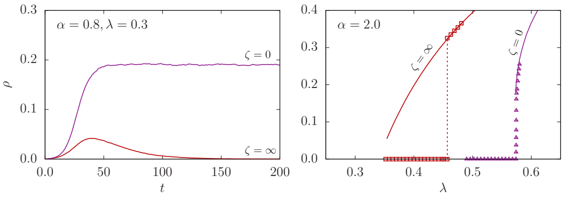


Figure 2: **Left**: Averaged prevalence evolution of single infected outbreaks for $\alpha = 0.8$ and $\lambda = 0.3$, corresponding to the endemic phase for short-term memory (purple) and the excitable phase for long-term memory (red). In the endemic phase the outbreak grows monotonically towards its stationary value. In the excitable phase the outbreak infects a large fraction of the population before being eradicated. [Conversely, in the healthy phase the outbreak is eradicated very quickly, infecting only a very small number of individuals.] **Right**: Late-time prevalence when approaching from above (curve) and below (symbols). With short-term memory (purple) both transitions are continuous and occur at the same value of λ. With long-term memory (red) the transition approaching from below is delayed and presents a discontinuous jump.

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[2] Chowell, G. et al. *BMC Medicine* **2** (1): 196 (2014).

[3] Gonzalez, M.C. et al. *Nature* **453** (7196): 779 (2008).

[4] Hoffmann, X.R. Master's thesis, Universitat de les Illes Balears (2016). http://ifisc.uib-csic.es/publications/

[5] Hoffmann, X.R. and Boguñá, M. In preparation.

Animal social networks relevant to disease transmission among free-roaming dogs in Chad

Laura Ozella,[1] Jared Wilson-Aggarwal,[2] Michele Tizzoni,[1] Ciro Cattuto,[1] Robbie McDonald.[2]

1. ISI Foundation, Turin, Italy
2. Exeter University, Exeter, UK

Animal social network analysis is increasingly used to understand many ecological and epidemiological processes. The knowledge of the contact structure of an animal population is the first step for predicting and controlling disease outbreaks, including zoonosis. Free-roaming domestic dogs (*Canis familiaris*) are hosts of a variety of zoonosis (*e.g.*, rabies) in most of Africa, and little is known about the population dynamics of these animals. Usually, modeling efforts are challenged by the limited availability of data on dogs movements and mixing patterns.

We used wearable proximity sensors to detect close-range interactions between free-roaming domestic dogs living in 4 villages in rural Chad (see Figure 1). The study included 138 dogs, 60 females and 78 males, classified by age as: pups (birth to 6 months), juveniles (6 months to 1 year), sub-adults (1-2 years), and adults (more than 2 years). Every dog belonged to one of 91 different households, with 32 households hosting more than one dog. The experimental period lasted from 2 to 12 days, depending on the village. We also used GPS trackers to estimate their home range, and to understand their movement behavior. Furthermore, we combined the proximity sensors data and the GPS data to obtain a multi-layer proximity network description based on different contact definitions.

We defined temporal contact networks and contact matrices, and determined mixing patterns by age and by gender. Contacts occurred mostly between dogs living in the same household, however, 98% of the dogs had contacts with dogs living in a different household. Contacts within households occurred mainly among pups, while inter-household contacts were between sub-adults and juveniles and sub-adults and adults. Results show that the pups are more sociable with dogs of the same litter, while dogs more than 6 months tend to interact with dogs living in different households. With respect to their gender, contacts occurred mainly between males and females both within and across households.

The temporal evolution of the number of contacts showed, in each village, some distinct temporal features, specifically daily oscillations with two activity peaks, one in the morning (6AM - 8AM) and one in the evening (6PM - 8PM), according to the typical daily activity patterns of dogs. Moreover, our results showed a positive and significant correlation between the time spent in proximity by dogs detected by the proximity sensors and by the GPS.

Our study shows the feasibility of accurate measures of contact patterns among free-roaming dogs in a rural context in Africa, providing novel insights into the structure and behavior of animal contact networks and their implication for disease transmission.

Effect of risk perception on epidemic spreading in temporal networks

Antoine Moinet,[1, 2] Romualdo Pastor-Satorras,[2] and Alain Barrat[1, 3]

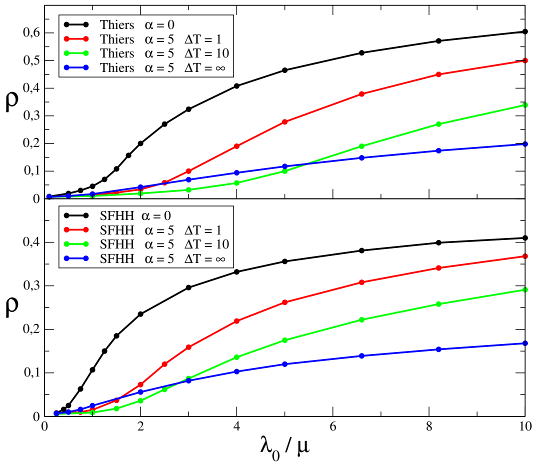
[1] *Aix Marseille Univ, Université de Toulon, CNRS, CPT, Marseille, France*
[2] *Departament de Fisica, Universitat Politecnica de Catalunya, Campus Nord B4, 08034 Barcelona, Spain*
[3] *Data Science Laboratory, ISI Foundation, Torino, Italy*

Recently, a number of epidemic spreading studies have started to go beyond the assumption of an absence of coupling between the spread of a disease and the structure of the network on which it unfolds. Models including awareness of the spread have been proposed, to mimic possible precautionary measures taken by individuals that decrease their risk of infection, but have mostly considered static networks. Here, we adapt such a framework to the more realistic case of temporal networks of interactions between individuals. To explore the effects of disease awareness we have considered the paradigmatic SIS and SIR spreading models on both synthetic temporal networks, based in the activity driven (AD) model paradigm, and empirical face-to-face contact networks collected by the SocioPatterns collaboration. In the case of network models, we consider the original AD model, and a variation, the AD model with memory (ADM), in which an memory kernel mimics some of the non-Markovian effects observed in real social networks.

We consider a discrete time modeling approach, in which the contacts between individuals are given by a temporal network encoded in a time-dependent adjacency matrix $A_{ij}(t)$ taking value 1 if individuals i and j are in contact at time t, and 0 otherwise. At each time step, the probability that a susceptible individual i becomes infectious is thus given by $p_i = 1 - \prod_j [1 - \lambda\, A_{ij}(t)\, \sigma_j]$, where λ is the infection probability, and σ_j is the state of node j ($\sigma_j = 1$ if node j is infectious and 0 otherwise). Besides, an infected has a probability μ to recover and become either immunized or susceptible again. In this context, extending previous approaches defined for static frameworks [1], we define a model in which susceptible individuals have a local perception of the overall disease prevalence measured as the ratio of the number of previous contacts with infectious individuals on a training window of width ΔT. An increased level of awareness induces a reduction in the probability λ_i that a susceptible individual contracts the disease via a contact with an infectious individual. We posit

$$\lambda_i(t) = \lambda_0 \exp\left(-\alpha\, n_I(i)_{\Delta T}\right) \qquad (1)$$

where $n_I(i)_{\Delta T}$ is the number of contacts with infectious individuals seen by the susceptible during the interval $[t-\Delta T, t[$, divided by the total number of contacts counted by the individual during the same time window, and α is a parameter gauging the strength of the awareness. We study the resulting model by analytical and numerical means on both simple models of temporal networks and empirical time-resolved contact data.



We observe in all cases a strong reduction of the prevalence of the epidemics for different values of α and ΔT, and an apparent shift of the effective epidemic threshold. However on AD and ADM networks, this shift turns out to be due to (strong) finite size effects. On the figure above, we plot the steady state fraction ρ of infected for the SIS process on both empirical networks (Thiers high-school and SFHH conference) to illustrate the prevalence reduction.

Overall, the awareness mechanism leads to a strong decrease of the prevalence and to shifts in the effective epidemic threshold even at quite large size, for both epidemic models and on both synthetic and empirical networks. However, AD and ADM networks lack numerous realistic features observed in real social systems, such as the broad distribution of contact durations. In this respect, it would be important to take into account awareness effects in larger data-driven simulations of epidemic spread, to study the relative role of the complex properties of network contacts on these effects, and we hope this will stimulate more research into this crucial topic.

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The spread of multipartite viruses

Eugenio Valdano[1], Susanna Manrubia[2], Sergio Gómez[1], Alex Arenas[1]

[1]Department of Computer Engineering and Mathematics, Universitat Rovira i Virgili,
Tarragona, Spain
[2]National Biotechnology Centre (CSIC), Madrid, Spain

e-mail: eugenio.valdano@gmail.com

Commonly studied pathogenic viruses are monopartite: Their viral particles contain the complete genome, and one particle infecting a cell is potentially enough to start replication. This is, however, not the only organization of the genetic material found in nature. Multipartite viruses have their genome divided into two or more segments, and these segments are each packaged into separate virus particles. Replication inside a host cell is possible only when the whole genome is present, thus requiring co-infection of the same host by several variants. This should represent an evolutionary disadvantage with respect to monopartite viruses, and indeed multipartite viruses infecting animals are quite rare. However, around 40% of viruses infecting plants are multipartite (Hull, Plant virology, 2014). From this observation, two questions arise. What are the evolutionary mechanisms that lead multipartite viral forms to fixation, despite their apparent disadvantage? Why are they so common among plant viruses infecting plants, and so rare among animal ones? Experimental works and modeling frameworks have so far tried to answer these questions adopting a within-host (sometimes within-cell) perspective. Knowledge of the spreading dynamics of multipartite viruses at the population level has been lacking. We analytically derive the conditions that lead to the persistence of the virus in its different forms (monopartite, multipartite), highlighting the role of the vector-driven contact topology on which it spreads. We show that multipartitism can become endemic in a host population, and it represents an evolutionary advantage as it allows the virus to adapt to a wide range of hosts and environments. Furthermore, we show that our approach can model and study other puzzling viral behaviors observed in nature, like the presence of subviral agents that need the presence of a specific virus in order to replicate, and in in return they increase the transmissibility of the virus itself.
In addition to the specific biological interest, we believe that the analytical framework developed in this work can be further generalized to study the critical behavior of pathogen interaction in other contexts.

Pareto optimality in multilayer network growth

Andrea Santoro,[1,2] Vito Latora,[1,3] Giuseppe Nicosia,[4,5] and Vincenzo Nicosia[1]
[1]*School of Mathematical Sciences, Queen Mary University of London, Mile End Road, E1 4NS, London (UK)*
[2]*Scuola Superiore di Catania, Università di Catania, Via Valdisavoia 9, 95125, Catania (Italy)*
[3]*Dipartimento di Fisica ed Astronomia, Università di Catania and INFN, I-95123 Catania, (Italy)*
[4]*Dipartimento di Matematica ed Informatica, Università di Catania, V.le A. Doria 6, 95125, Catania (Italy)*
[5]*Department of Computer Science, University of Reading, Whiteknights, RG6 6AF Reading, (UK)*

(Dated: October 10, 2017)

Multiplex networks provide a natural framework for analysing transportation systems. Within this context, nodes represent locations of interest, edges stand for connections between two locations, and each layer accounts for a different type of connections among the same set of nodes. In this work we propose a minimal, zero-parameter model of multi-layer network growth which incorporates the concurrent tendency of carriers to maximise their profit and to minimise competition with other carriers. The creation of edges is subject to the local optimisation of a multi-objective cost function, representing a trade-off between efficiency and competition. Interestingly, the proposed model is able to accurately reproduce the micro-, meso-, and macro-scale structure of the six continental airline transportation networks (Fig. 1 a-f), and provides a simple, reasonable explanation for the observed high heterogeneity in the size of airports and in the distribution of routes across the globe. The analysis of the feasible points in the resulting efficiency-competition plane reveals that the airlines whose route network is closer to the corresponding Pareto front are indeed those which attain higher per-route revenues (Fig. 1 g-h). These results shed light on the fundamental role played by multiplexity and multi-objective optimisation principles in shaping the structure of large-scale transportation systems, and provide new insights on potential strategies for individual airlines to increase their revenues by a clever selection of new routes.

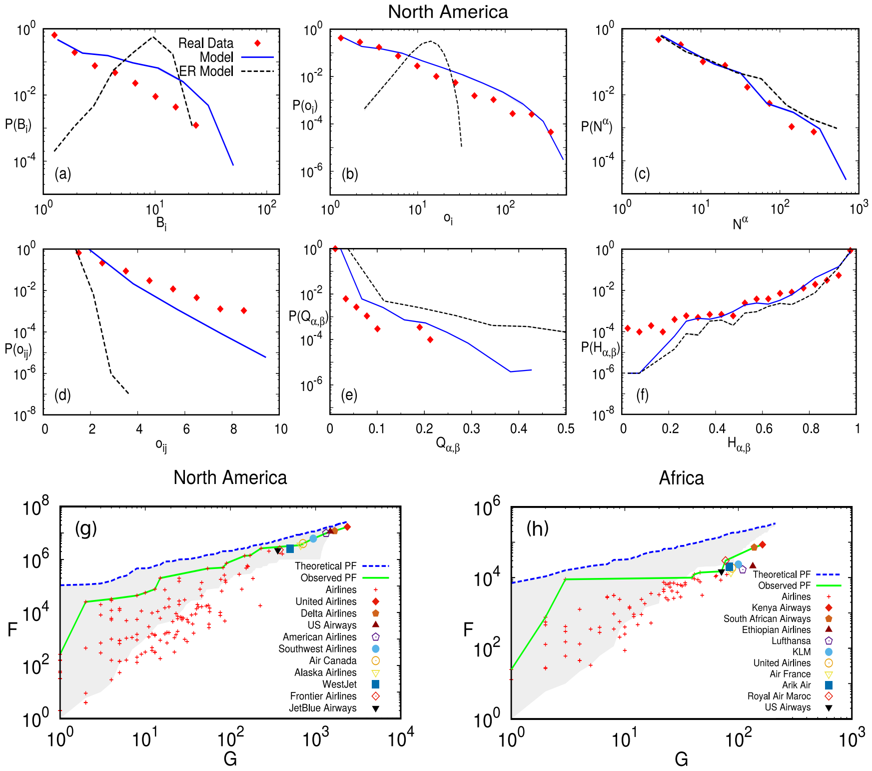

FIG. 1. Distribution of 6 different structural measures (a-f) for the real multiplex network of North America airlines (red diamonds), and for synthetic networks obtained with the proposed growth model (solid blue lines). For comparison, we also report the values obtained in multiplex networks consisting of Erdös-Rényi random graphs (dashed black lines). In addition, in (g) and (h) we respectively report the observed Pareto front (solid green line) along with the top ten Pareto airlines by F value for North America and Africa. For each continent, the Theoretical Pareto front (dashed blue line) is obtained by considering the non-dominated points of 10^5 realisations of our model (the range of variability obtained through the simulations is indicated by the shaded grey region).

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Heteregeneous degree sequences as the determinants of nestedness in mutualistic ecosystems

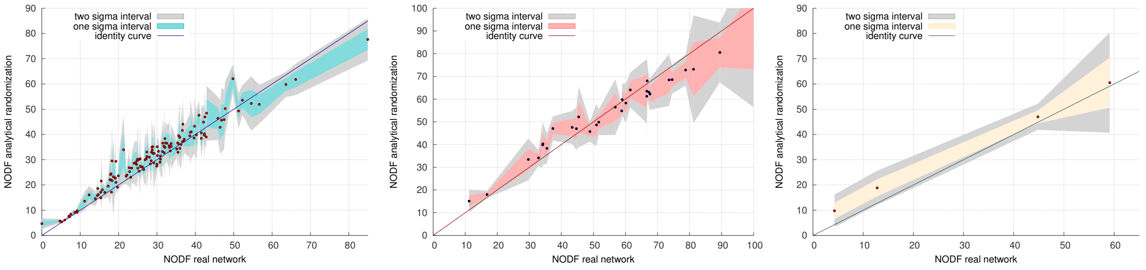
Clàudia Payrató Borràs[1,2], Laura Hernández[1], and Yamir Moreno[2]

[1] *Laboratoire de Physique Théorique et Modélisation, UMR CNRS, Université de Cergy-Pontoise, France*
[2] *Instituto de Biocomputación y Física de Sistemas Complejos (BIFI), Universidad de Zaragoza, Spain*

Mutualism is a kind of relationship that occurs when two different type of agents interact through an activity that mutually benefits them. A paradigmatic example is the pollination of a flower by a bee, which leads the plant to increase its reproductive success while the bee gets fed. Mutualistic communities can be mapped into a bipartite network representation, an object which is of special usefulness in order to model their dynamics or to unveil macroscopic patterns. In particular, ecological mutualistic communities had been shown to empirically exhibit a peculiar configuration of interactions known as *nestedness* [1]. In the network language, an ideally nested structure occurs when the counterparts of a species of degree k constitute a subset of the counterparts of all species with degree $k' > k$, this being true for both guilds. In the recent years, however, the pertinence of nestedness as a relevant characterizer has been put into question [2, 3]. Properties such as the assortativity or the heterogeneity in the number of contacts [3, 4] have been alternatively proposed as suitable indicators to bridge the gap between structure and dynamics.

In our work, we address the question of the origin of nestedness by taking into consideration its possible relation to other network features, in particular, the degree sequences. By means of exploiting a powerful randomizing scheme [5] based on the Exponential Random Graph model, we constructed an statistical ensemble under the constrain that the degree sequences are only kept in average. We analysed, both analytically and numerically, the nestedness distribution of 167 real mutualistic communities. Our results (see Fig. 1) show that empirical observations of nestedness are *not* significant when we incorporate the information provided by the degree sequences. Furthermore, we investigated how the nested pattern is related to certain traits of the degree sequences, in detail, of its heterogeneity. We found that more heterogeneity usually leads to more nestedness and discuss how this can be related to the fact that heteregeneous networks tend naturally towards disassortativity instead of assortativity [6]. This eventually could explain why nestedness, provided that real degree sequences are heterogeneous [7], emerges as the mere result of chance.

On the whole, whilst mutualistic communities are clearly non-trivially assembled, our results indicate that no selective pressures seemingly acted upon nestedness. This challenges the traditional view of nestedness as an irreducible pattern and suggests that, in the future, degree sequences should receive more attention as the informative ecological elements to target.



Plant-pollinator networks Seed-dispersal networks Plant-ant networks

Figure 1: Average of the nestedness' distribution in the statistical ensemble against the empirical measure of nestedness. Shadowed in grey and colour, the region of two and one sigma, respectively.

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Diffusion dynamics on Temporal Multiplex Networks

Emanuele Cozzo[1,2], Conrad J. Pérez-Vicente[1,2], and Albert Díaz-Guilera[1,2]

[1]Departament de Física de la Matèria Condensada, Universitat de Barcelona
[2]UBICS

In the last few years multiplex network analysis has settled as an hot topic in the field of complex network theory. Alongside, and with a quite older history, temporal network analysis also represents a point of interest. Both these lines of research try to capture more accurately the complexity in the organization of many real-world systems. In particular, the focus is on how these topological factors (multiplexity or temporal variation) affect the dynamical behavior of a system.

In this work, we make step in the line of combining together temporal variation and topology, studying the effect on diffusion dynamics.

In particular, we generalize the theory of Masuda et al. [1] to temporal multiplex networks. Thus, we investigate the supra-Laplacian spectrum of temporal multiplex networks and compare it with that of different corresponding aggregate networks.

In the case of single-layer temporal networks [1], under given conditions, a closed analytical relation exists between the eigenvalues of the temporal aggregate network and the original one. In the case of multiplex networks, we show that, under proper conditions, this relation can be recovered given a proper rescaling of the coupling parameter of the supra-Laplacian.

The speed-up or the slowing down of the diffusion dynamics depends on the relation between tree temporal scale:

- that of the inter-layer interaction
- that of the intra-layer interaction
- abd that of the topological variation.

Since the proper rescaling of the coupling parameter is non-linear, the relation between these temporal scales and its effect on the diffusion dynamic are non-trivial.

Statistical Physics of Balance Theory

Andres M. Belaza[1,2], Kevin Hoefman[2], Jan Ryckebusch[1], Aaron Bramson[2,3,4], Milan van den Heuvel[1,2], and Koen Schoors[2,5]

[1]Department of Physics and Astronomy, Ghent University, Ghent, Belgium
[2]Department of General Economics, Ghent University, Ghent, Belgium
[3]Laboratory for Symbolic Cognitive Development, RIKEN Brain Science Institute, Wakoshi, Saitama, Japan
[4]Department of Software and Information Systems, University of North Carolina Charlotte, Charlotte, North Carolina, USA
[5]Higher School of Economics, National Research University, Moscow, Russia

Abstract

Triadic relationships are accepted to play a key role in the dynamics of social and political networks. Building on insights gleaned from balance theory in social network studies and from Boltzmann-Gibbs statistical physics, we propose a model to quantitatively capture the dynamics of the different types of triadic relationships in a network. Central to our model are the triads' incidence rates and the idea that those can be modeled by assigning a specific triadic energy to each type of triadic relation. We emphasize the role of the degeneracy of the different triads and how it impacts the degree of frustration in the political network. In order to account for a persistent form of disorder in the formation of the triadic relationships, we introduce the systemic variable temperature. In order to learn about the dynamics and motives, we propose a generic Hamiltonian with three terms to model the triadic energies. One term is connected with a three-body interaction that captures balance theory. The other terms take into account the impact of heterogeneity and of negative edges in the triads. The validity of our model is tested on four datasets including the time series of triadic relationships for the standings between two classes of alliances in a massively multiplayer online game (MMOG). We also analyze real-world data for the relations between countries during the Cold War era. We find emerging properties in the triadic relationships in a political network, for example reflecting itself in a persistent hierarchy between the four triadic energies, and in the consistency of the extracted parameters from comparing the model Hamiltonian to the data. A natural extension of classical Social Balance Theory is the introduction of "neutral interactions" between the agents. This extension could, for example, be used to accommodate the changes in the inter-country relationships from "neutral" to "hostile" or "friendly"

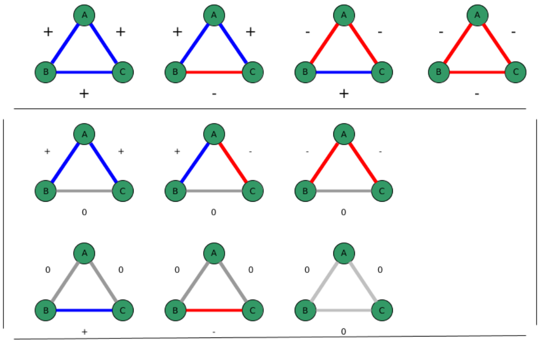

Figure 1: (Above) Different kinds of possible triads in classical SBT (Positive and negative links). (Below) the natural extension with neutral links.

Construction of and efficient sampling from the simplicial configuration model

Jean-Gabriel Young,[1] Giovanni Petri,[2] Francesco Vaccarino,[2, 3] and Alice Patania[4]

[1] *Département de Physique, de Génie Physique, et d'Optique, Université Laval, Québec (Québec), Canada*
[2] *ISI Foundation, Torino, Italy*[*]
[3] *Dipartimento di Scienze Matematiche, Politecnico di Torino, Torino, Italy*
[4] *IU Network Institute, Indiana University, Bloomington, Indiana*

(Dated: October 11, 2017)

Network Science's approach to complexity rests onto the tacit hypothesis that the structure of complex systems is reducible to the pairwise interaction of their constituents. It is often a valid premise and, as a result, Network Science has been extremely successful in, e.g., both predicting [1] and controlling [2] the behavior of complex systems, inferring their function from their structure [3, 4], and so on. Networks, however, might not be as ubiquitous as previously thought. It has been shown recently that the structure of a number of complex systems, such as the brain [5, 6], protein interactions [7] and social systems [8, 9], cannot always be reduced to the sum of pairwise interactions. For these systems, it is now known that network representations can give an incomplete picture: when many-body interactions are broken down into multiple pairwise interactions (cliques), high order information simply disappears [10].

Simplicial complexes generalize graphs by encoding many body interactions explicitly; they have hence been proposed as a complementary description of the structure of complex systems [11–13]. This new application of simplicial complexes has led to promising discoveries: we now better understand, for instance, how to detect large viral recombination events [14], how brain networks reorganize under drugs [15], and how the atomic structure of amorphous solids is hierarchically organized [16]. It has become crucial to establish the statistical significance of these findings, a task for which random null models will be needed. There is already a rich and growing literature on random simplicial complexes and topology, ranging from simplicial generalization of Erdös-Rényi models, amendable to analytical treatment [17, 18], to equilibrium formulations of simplicial complex ensembles [10, 19], and growth models that reproduce various emergent patterns observed in real systems [20, 21]. However, null models—in the sense of network science—are still wanting [22, 23].

We address this issue by refining a recently proposed generalization [19] of the (simple) configuration model of network science [22, 24, 25], which we dub the simplicial configuration model (SCM). Our contribution is threefold. One, we define the model and argue why this particular line of generalization should be chosen. Two, we propose and analyze an efficient and rigorous sampling algorithm. Three, we use the SCM as a null model for a number of real datasets and show—using sound statistical arguments—that the local structure of these systems does not always explain their mesoscale structure.

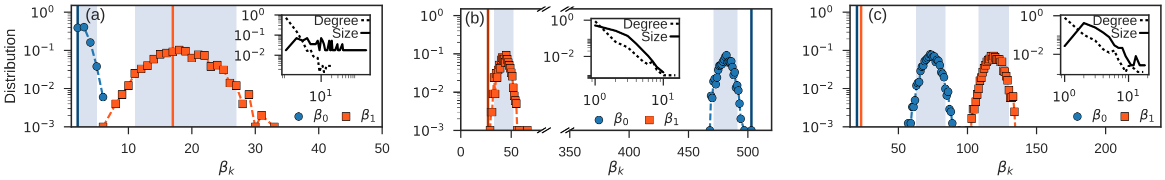

FIG. 1. **Significance of the Betti numbers of real systems**. The datasets are bipartite networks, which we convert to simplicial complexes. They map the relation between: (a) flower-visiting insects (nodes, $n = 679$) and plants (facets $f = 57$) in Kyoto [26], (b) human disease (nodes $n = 1100$) and genes (facets $f = 752$) linked by known disorder–gene associations [27], (c) crimes (nodes, $n = 829$) and suspects / victims / witnesses (facets, $f = 378$) in St.-Louis [28]. The Betti numbers of these real systems appear as solid vertical lines, and are equal to (a) $\beta_0 = 2$, $\beta_1 = 17$ (b) $\beta_0 = 503$, $\beta_1 = 27$, (c) $\beta_0 = 20$, $\beta_1 = 23$. We show the distributions of Betti numbers for the equivalent SCM with solid symbols (computed from 1000 instances of the model). The shaded regions contain 95% of the samples. We observe that for the second and third datasets the expected Betti numbers are very different from the real ones, implying that the corresponding networks display a non-random homological structure, as opposed to the first dataset, which instead lacks it.

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[*] giovanni.petri@isi.it

Lagrangian Flow Networks: a new paradigm to characterize geophysical transport

Enrico Ser-Giacomi (speaker), Emilio Hernández-García, Cristóbal López, Vincent Rossi, Ruggero Vasile, Alberto Baudena, Francesco D'Ovidio.

Transport in geophysical flows plays a fundamental role in many different contexts (e.g. marine biology, pollutants spreading, moisture advection) and over a wide range of scales (from global climate to sub-mesoscale ocean and atmospheric dynamics). The last two decades have seen indeed important advances in the Lagrangian description of transport and mixing in fluid flows driven by concepts from dynamical systems theory. 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 Networks (LFNs)[1]. It consists in analysing directed, weighted, spatially embedded and time-dependent networks which describe the material fluid flow among different locations of the ocean or the atmosphere.

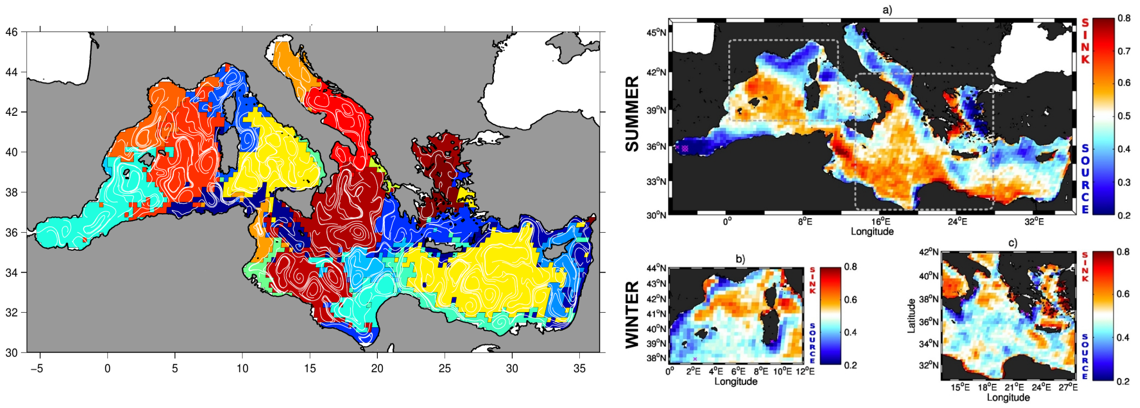

Figure: Network communities from Infomap algorithm (left) and source-Sink ecological metric derived from degrees (right) for the surface circulation in the Mediterranean Sea.

The theoretical foundations behind this paradigm allows to link network measures with dynamical properties of the flow, promoting connections among Dynamical Systems and Network Theory. Local network measures such as degrees and clustering coefficient are related to Lyapunov exponents fields and periodic orbits[2]. Communities in LFNs (Figure, left panel) are instead identified as hydrodynamical provinces (coherent oceanic regions, i.e. areas internally well mixed, but with little fluid interchange between them)[3]. Most probable paths in temporal LFNs, and its associated betweenness centrality, are finally able to unveil the main avenues and hidden bottlenecks of fluid transport[4].

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. In such way we define new sets of ecological diagnostics (Figure, right panel) that provide useful information to design management and protection plans for marine ecosystems[5].

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Maxmin-ω: Deterministic Asynchrony on Networks

We introduce the maxmin-ω system, an intuitive model of asynchronous dynamics on a network. Each node in this system updates its state upon receiving a proportion ω of inputs from neighbourhood nodes. Crucially, the update of nodal states depends on local exchanges; the maxmin-ω system is therefore deterministic, and a departure from traditional asynchronous schemes (e.g., [1,2]).

The maxmin-ω rule is applied to three synthetic networks: a 'regular' network, whose nodes are arranged in a ring, and the neighbourhood $\mathcal{N}_i$ of each node i is symmetric, of size n; a 'random' network, where each node takes fixed neighbourhood size n, but the nodes $\mathcal{N}_i$ are selected at random, quantified by a randomization depth $\gamma \in [1, n]$; a network whose nodes take variable neighbourhood size. The edge weights in these networks represent transmission times between nodes. Thus, we demonstrate the sequence of update times of each node to be periodic. Figure 1(a) shows the periods of these sequences as a function of ω. These results show period peaking when ω is approximately 0.5.

Implementing a cellular automaton (CA) under this scheme demonstrates the impact of maxmin-ω on the network state. Here, nodes play the role of cells, having states 0 or 1, depending on a local CA rule. Figure 1(b) shows the space-time output of a CA as ω varies. There is some correspondence in complexity between timing and CA; specifically, the pattern is most complex when $\omega \approx 0.5$, and is periodic when ω is close to 0 or 1.

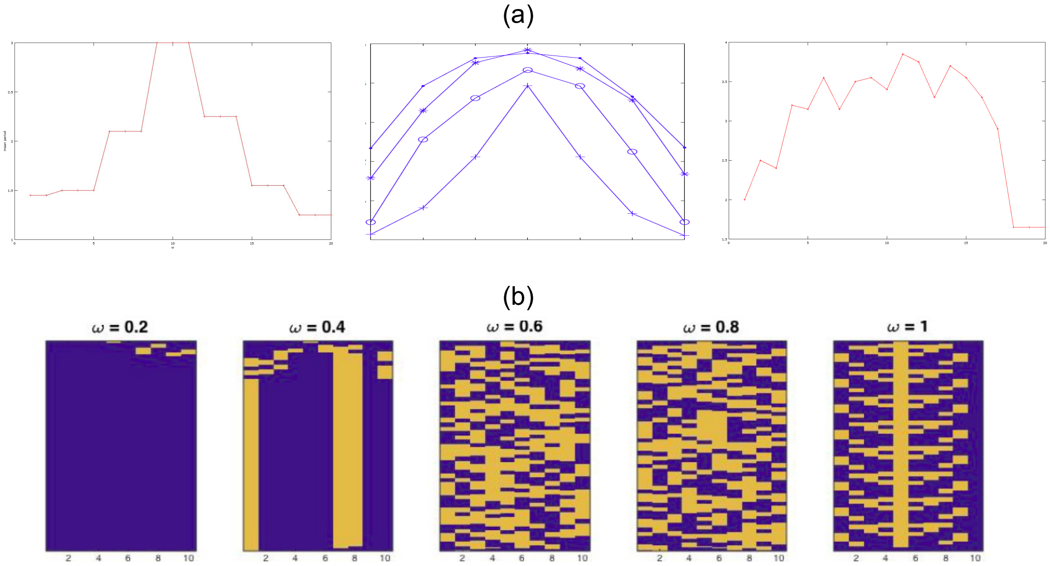

Figure 1: (a) The maxmin-ω model applied to a network of size 20. The horizontal axis represents ω, the vertical axis represents mean period ρ. Transmission times on all networks are randomly chosen integers up to 5; ρ is taken from 20 such randomisations. From left to right: (left) a regular network with $n = 7$, (middle) a random network with $n = 7$; there are four overlaid plots, representing randomization depths $\gamma = 1, 3, 5$, and 7. A larger γ gives a higher ρ. (right) a network where neighbourhood size is variable with each node. (b) CA space-time patterns as a function of ω. The underlying lattice is a regular network of 10 nodes with $n = 3$. State 1 is coloured light and state 0 is dark. Node index is indicated on the horizontal axis, time travels vertically down.

Results suggest complexity at $\omega \approx 0.5$, regardless of network type. This leads us to investigate the existence of this 'middle system complexity' in applications such as neural networks and epidemic outbreaks, which rely on threshold parameters like ω for local interactions. Since it is also much simpler than traditional asynchrony models, maxmin-ω thus provides a new and accessible way of looking at dynamics on networks of the real world.

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Iacopo Iacopini (i.iacopini@qmul.ac.uk) •• **BIFI International Conference 2018**

Network dynamics of innovation processes

Iacopo Iacopini[12], Staša Milojević[3], Vito Latora[14]

[1]School of Mathematical Sciences, Queen Mary University of London, London E1 4NS, UK
[2]The Alan Turing Institute, The British Library, London NW1 2DB, UK
[3]Center for Complex Networks and Systems Research, School of Informatics and Computing, Indiana University, Bloomington IN 47408, US
[4]Dipartimento di Fisica ed Astronomia, Università di Catania and INFN, I-95123 Catania, IT

October 7, 2017

Abstract

We introduce a model for the emergence of innovations, in which cognitive processes are described as random walks on the network of links among ideas or concepts, and an innovation corresponds to the first visit of a node. The transition matrix of the random walk depends on the network weights, while on turn the weight of an edge is reinforced by the passage of a walker. The presence of the network naturally accounts for the mechanism of the "adjacent possible", and the model reproduces both the rate at which novelties emerge and the correlations among them observed empirically. We show this by using synthetic networks and by studying real data sets on the growth of knowledge in different scientific disciplines. Edge-reinforced random walks on complex topologies offer a new modeling framework for the dynamics of correlated novelties and another example of co-evolution of processes and networks.

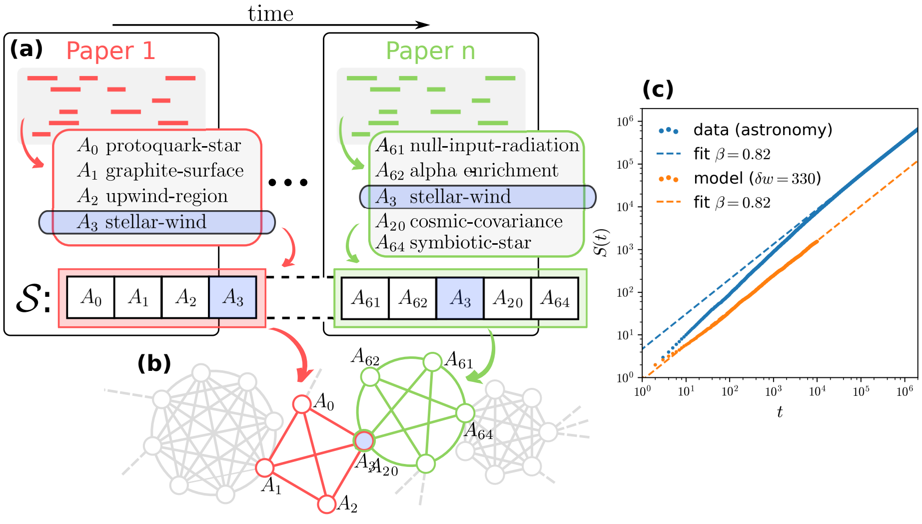

Figure 1: Growth of knowledge in science. **(a)** An empirical sequence of scientific concepts $\mathcal{S}$ is extracted from a temporally ordered sequence of papers by concatenating, for each scientific field, the relevant concepts present in the abstracts. **(b)** The network of relations among concepts is constructed by linking all the concepts appearing in the same abstract. The network is then used as an underlying structure for running our edge-reinforced random walk model. **(c)** The model is then tuned to the empirical data by selecting the amount of reinforcement δw that reproduces the Heaps' exponent β obtained by fitting the Heaps' curve extracted from $\mathcal{S}$ as a power law.

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Variational approximations for stochastic dynamics on graphs

A Pelizzola[1,2] **and M Pretti**[3,4]

[1] Dipartimento di Scienza Applicata e Tecnologia (DISAT), Politecnico di Torino, Corso Duca degli Abruzzi 24, I-10129 Torino, Italy
[2] INFN, Sezione di Torino, Via Pietro Giuria 1, I-10125 Torino, Italy
[3] Consiglio Nazionale delle Ricerche—Istituto dei Sistemi Complessi (CNR-ISC), Via dei Taurini 19, I-00185 Roma, Italy
E-mail: marco.pretti@isc.cnr.it

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Abstract. We investigate different mean-field-like approximations for stochastic dynamics on graphs, within the framework of a cluster-variational approach. In analogy with its equilibrium counterpart, this approach allows one to give a unified view of various (previously known) approximation schemes, and suggests quite a systematic way to improve the level of accuracy. We compare the different approximations with Monte Carlo simulations on a reversible (susceptible-infected-susceptible) discrete-time epidemic-spreading model on random graphs.

Keywords: dynamical processes, stochastic processes, stationary states, random graphs, networks

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[4] Hosted at DISAT, Politecnico di Torino, Corso Duca degli Abruzzi 24, I-10129 Torino, Italy

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Characterization of the adopters of the Bitcoin

Francesco Parino [1], Mariano Beiro [2,1] and Laetitia Gauvin [1]

1. ISI Foundation, Turin, Italy
2.INTECIN (UBA-CONICET), Facultad de Ingeniera, UBA, Ciudad de Buenos Aires, Argentina

Bitcoin is a cryptocurrency which became very popular during the recent years. The bitcoin transactions are recorded in a public ledger, the bitcoin blockchain, and can be collected since its creation. The bitcoin blockhain works without a central authority but is based on a peer-to-peer system. The transactions take place between users directly and not necessarily with a transaction fee. More exactly the bitcoins exchanged during a transaction are sent from an address to another, each address belonging to a user. One of the challenge to study such a system and understand the behaviour of users in this new transaction system is the possibility for any user to generate multiple addresses.

Here we propose a preliminary analysis to get a sense of the users of the bitcoin despite the high degree of anonymity inherent to the system. We do not attempt to identify single users but to charaterize the spatial distribution of users at the country level. Even though it is not possible to link an IP address to the authors of a transaction, one can obtain the IP of the first user which relays the transaction. The current literature on the bitcoin blockchain would tend to support that this IP has some chance to be the IP of the source of the transactions. As a first attempt we thus assume that these IP addresses allow to estimate where the users come from. In order to test this assumption, we compare the countries of provenance of the IP addresses to the geolocalization of the user downloading wallets which are softwares to access the bitcoin technology. We observed a good agreement between the two. This confirms that the IP address that relay transactions can be used to some extent as a good proxy to identify the provenance of the users. However due in particular to the increasing broadcasting of transactions by services instead of single users, the IP addresses are only accessible for a given time interval. For this reason, in order to characterize the evolution of the adoption in different countries we use Google Trends data to quantify the collective attention for the bitcoin, this appears as good proxy when compared to the unique IP addresses. Looking at the evolution of the bitcoin search through Google trends for different countries we can have an hint on the early and new adopters. To complete the study we also build the network of users where a link is given by a transaction and look at the bilateral exchanges among countries using the IP addresses mentioned earlier as well as some heuristic developed in the literature to assign a country to each transaction. We finally compare this to a null model to extract what are the preferred relationships between countries for transactions. To summarize, we propose a way to measure the collective interest for the bitcoin at the level of the country and to understand how the transactions are distributed among the countries.

Data-driven discovery of circadian rhythms of urban people - are we like fruit flies?

Daniel Monsivais[1], Kunal Bhattacharya[1], Asim Ghosh[1], Robin Dunbar[2,1], Kimmo Kaski[1,2,3]

[1] Department of Computer Science, Aalto University School of Science, P.O. Box 15400,
FI-00076 AALTO, Espoo, Finland

[2] Department of Experimental Psychology, University of Oxford, South Parks Rd,
Oxford, OX1 3UD, United Kingdom

[3] Complexity Science Hub Vienna,
Josefstädter Strasse 39, A-1080 Vienna, Austria

All living organisms, including humans, have internal biological or circadian clock that helps them anticipate and adapt to the regular rhythm of the day. The timings of human activities are marked by circadian clocks which in turn are entrained to different environmental signals. In an urban environment, the presence of artificial lighting and various social cues tend to disrupt the natural entrainment with the sunlight. However, it is not completely understood to what extent this is the case. Here we exploit the large-scale data analysis techniques to study the mobile phone calling activity of people in large cities to infer the dynamics of urban daily rhythms. From the calling patterns of about 1,000,000 users spread over different cities but lying inside the same time-zone, we show that the onset and termination of the calling activity synchronizes with the east-west progression of the sun. We also find that the onset and termination of the calling activity of users follows yearly dynamics, varying across seasons, and that its timings are entrained to solar midnight. Furthermore, we show that the average mid-sleep time of people living in urban areas depends on the age and gender of each cohort, most likely as a result of biological and social factors.

Multiscalar sociospatial dynamics in the city

Julien Randon-Furling[a], Madalina Olteanu[a,b]
[a] SAMM (EA4543), Université Paris 1 Panthéon Sorbonne
[b] MaIAGE, INRA, Université Paris Saclay

Cities may be regarded as an epitome of complex systems: individual and institutional agents interact on multiple levels of numerous networks (both physical and virtual), leading to nontrivial collective behaviour and nontrivial dynamics at many scales. Among a number of intricate questions that have emerged in the study of urban systems, that of sociospatial dissimilarities stands out as one that has aroused interest for decades, dating back at least to Schelling's and Sakoda's pioneering works [1, 2].

In this paper we develop a novel approach to capture segregation on multiple levels. Segregation is indeed often simply perceived as spatial separation of two or more groups, and therefore measured in terms of the relative proportions of each group in the different neighbourhoods of the city. This forms the basis of segregation indices, such as Reardon's H index and other information-theoretic or entropy indices [3].

We argue that segregation is best apprehended as a multiscalar phenomenon and we introduce a mathematical framework that allows to capture and measure it as such. Think for example of a statistical variable that may be measured at different scales, *eg* social housing rate, income distribution or ethnic group proportions. Then, to any local neighbourhood there corresponds a sequence of values for the variable, as one zooms out around the starting neigbourhood, scaling all the way up to the whole city. Such sequences encode in a precise manner spatial dissimilarities (see examples pertaining to the social housing rate on Figures 1 and 2). Thus, analyzing these sequences (using for instance stochastic clustering algorithms, or speed of convergence to the city's average) provides much finer descriptions of segregation phenomena. We also show how this leads to novel modeling opportunities, beyond the traditional agent-based models.

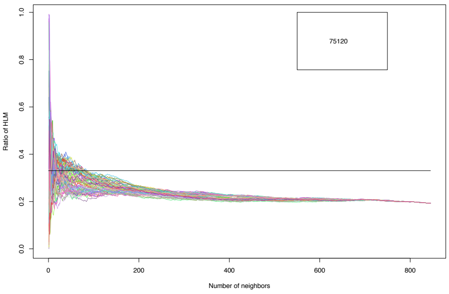

Figure 1 Trajectories for the social housing ("HLM") rate, starting from each statistical census block in Paris's 20th district. The solid flat line gives the district's average social housing rate. Each colour corresponds to the trajectory one obtains with the successive values of the social-housing rate as one scales out from each census block to the whole city. All trajectories obviously converge to the city's value of just about 0.2.

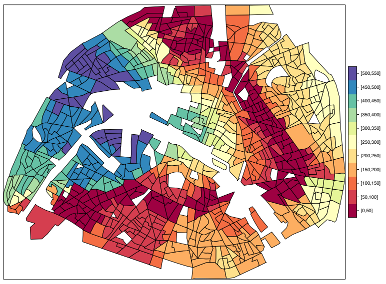

Figure 2 A map of Paris with census blocks coloured according to their scale of convergence to the city's average social housing rate. The scale of convergence is the number of blocks that need to be aggregated around the initial one in order to be (and remain) within ±0.05 of the city's average of 0.2. (White areas correspond to parks, riverbanks and blocks where data is not available.)

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Statistical features of the passage of a pedestrian crowd through a bottleneck

Alexandre NICOLAS[1] (speaker)
LPTMS, CNRS, Univ. Paris Sud, Univ. Paris-Saclay, F-91405 Orsay, France.

Sebastián BOUZAT and Marcelo KUPERMAN
Centro Atómico Bariloche, CONICET, Bariloche, Argentina.

Requested format : Oral presentation

The motion of a pedestrian often looks erratic when it is examined individually. Investigations conducted in the last fifteen years have however revealed that the dynamics of pedestrian crowds exhibits interesting statistical features. This is especially true for flows through a bottleneck, a problem that is central for the optimisation of flows and the design of facilities that can be evacuated quickly. Controlled evacuations through a narrow door conducted by Zuriguel et al. (*Scientific Reports* **4**, 2014) have shown that the microscopic escape dynamics can be robustly characterised, with statistical laws strongly reminiscent of granular flows through an orifice. In the wake of this work, we experimentally studied the influence of the individual behaviours on the dynamics of evacuation, by prescribing either a selfish behaviour or a polite one to participants (Nicolas et al., *Transp. Research B* **99**, 2017) . An original setup allowed us to conduct the analysis is in a macroscopically quasi-stationary regime.

Macroscopically, in the regime of limited crowd pressure, we observe that several flow properties are insensitive to the behavioural details, but rather depend on the local pedestrian density at the door, at least for limited crowd pressure. In particular, the global flow rate grows monotonically with the pedestrian density, under these conditions. Microscopically, the following statistical laws are inferred : (i) In competitive settings, the distribution of time gaps between successive escapes displays a heavy (power-law-like) tail, hinting at long-lived clogging events ; (ii) surprisingly, these time gaps are anticorrelated in time, pointing to an alternation between shorter time intervals and longer ones ; (iii) bursts of almost uninterrupted escapes (i.e., separated by small time gaps) are exponentially distributed. We develop and exploit simple quantitative models to shed light on the mechanisms at the origin of these statistical features, whose generality is thus underlined.

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[1] alexandre.nicolas@polytechnique.edu

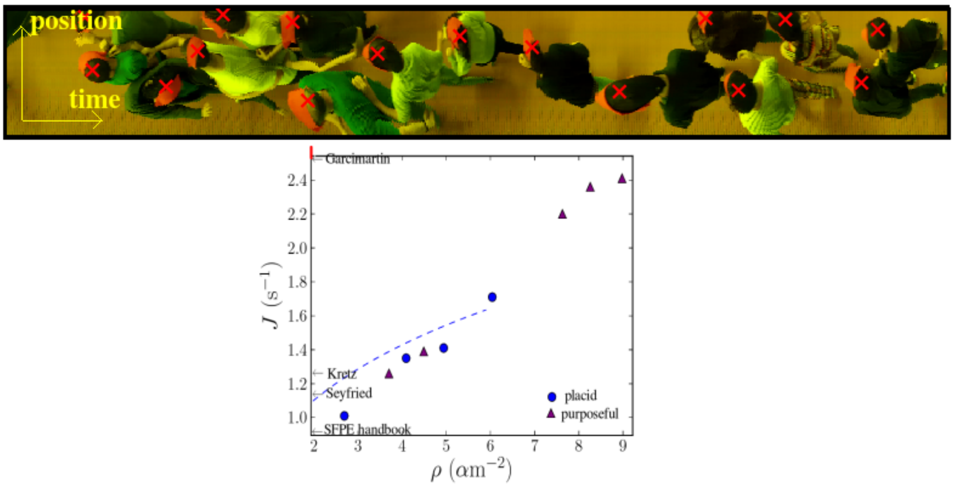

FIGURE 1. (Top) Time line of successive escapes through a narrow door in a controlled evacuation experiment in which the participants wearing red head scarves are asked to behave selfishly, while the others remain polite. (Bottom) Variations of the global pestrian flow rate J on the local density at the door, for diverse behavioural prescriptions.

The Effects of Alternative Wage Regimes in a Monetary Union: a Multi-Country Agent Based-Stock Flow Consistent Model

Alessandro Caiani, Ermanno Catullo, and Mauro Gallegati

October 9, 2017

Abstract

The paper presents an Agent Based-Stock Flow Consistent (AB-SFC) Multi-Country model to analyze the impact of different wage growth regimes on the long term economic dynamics of a monetary union broadly comparable to the European Economic and Monetary Union (EMU).

The computational framework proposed is at once simple in its behavioral assumptions and sophisticated in the structure and types of interactions considered. Simple, in that agents' behavior is based on relatively simple adaptive heuristics. In addition, there is no investment in tangible assets so that labor is the only productive factor and only final goods are produced. Only credit to firms is modeled.Finally, public expenditure takes the form of a lump-sum monetary transfer to households. Still, the model is sophisticated in the following aspects: first, its dynamics endogenously emerges from the decisions undertaken by many heterogeneous agents interacting in a decentralized way on several types of markets (i.e. labor, tradable and nontradable consumption goods, credit, deposit, and bond markets). Furthermore, the model encompasses international flows of both real and financial assets, which arise from trade and credit flows between member countries. Consumers' preferences and firms' products are differentiated using Salop's (1979) circular specification of Hotelling's (1929) locational model. Technological change and sectoral technological spillovers, affecting the evolution of labor productivity across firms and countries, are modeled as an endogenous process related to firms' investment in R&D.

In addition to this, the model also shows several important innovations with respect to the AB macro-modeling literature to which we aim at contributing: to our knowledge, this is one of the first, if not the very first, fully-fledged multi-country AB macroeconomic model presented in the literature. Indeed most models developed till now either displayed a closed-economy or, at most, a two-country economy. Our model instead can run with a variable number of countries: for the present work experiments were performed under the 2, 6, and 10-countries cases. Secondly, the accounting consistency of the model is ensured by the adoption of an SFC framework (Godley, 1997; Godley and Lavoie, 2007) along the line traced by Caiani et al. (2016, 2017); Deissenberg et al. (2008).Third, instead of assuming that the number of firms is fixed as in most of the macro AB literature where defaulted firms and banks are automatically replaced by an equal number of new entrants, we endogenized equity investment by households and the entry-exit process of firms and banks. The creation of new firms (and banks) is modeled as the outcome of households' savings portfolio allocation between equity participations in new firms and deposit accounts, based on their relative rates of return and their perceived riskiness. Finally, we propose a simple procedure to initialize the model in an SFC manner without having to set initial values of stocks and flows in an arbitrary way, inspired by the logic employed in the "SIM model" presented in Godley and Lavoie (2007).

For the sake of analyzing the impact on our artificial Union of different wage and labor market regimes, we first identified a parameter configuration yielding realistic and relatively stable systemic dynamics. Then, we introduce a wage regime switch occurring at period 500, modeled as a variation of the parameter governing the likelihood of upward wage revisions by workers and downward wage revisions by firms. To analyze the impact of these policies, we first analyze the results of a wage compression (i.e. increase of the parameter) for a single country.

Preliminary results show that the dynamics of main economic aggregates improves for the country following the wage-compression strategy, thanks to an improvement of its international competitiveness, while slightly worsen for the countries sticking to the original wage regime. However, the greater the number of countries following the wage-compression/'beg-your-neighbor' strategy, the more the strategy looses its efficacy and generates negative feed-backs between countries which deteriorate the systemic dynamics of the Monetary Union, as well as that of all member countries (see figure 1).

Understanding the patterns of success in online petitioning

Taha Yasseri
Oxford Internet Institute, University of Oxford, Oxford, UK
Alan Turing Institute, London, UK
taha.yasseri@oii.ox.ac.uk

Petition platforms, where citizens may create and sign petitions to the government or legislature, have been adopted in many liberal democracies, including the US, the UK and Germany. These platforms can be mined to generate 'big data' on petition signing which provides new insight into the ecology of this form of political participation, data of a kind rarely seen in political science.

This paper visualizes and models such data for all petitions created on the UK government petition platform over a three-year period (including a comparison with similar data for the US); We have collected the counts of the number of signatures to more than 20,000 petitions with hourly resolution and by analysing these data try to reveal the patterns and mechanisms of success in such platforms. The first observation is that the success is quite rare and only few petitions can gain considerable numbers of signatures. More surprising is that the success/failure of petitions is determined within few days after the creation indicating the very high pace dynamics of the online platform.

We model the dynamic of the system using a multiplicative growth model and by that are able to quantify this high pace.

We further discuss the role of the social media in the success of online petitions by collecting and analysing social media mentions of petitions as well as the web traffic data that we are provided by the UK government. Here, we find that the social media activity is the main driving force behind the success of petitions. We also investigate the role of social information and peer influence by performing a natural experiment in which a design change on the petitioning platform is involved. We show that the promotion of the trending petitions indeed has a significant effect on increasing the success rate even further.

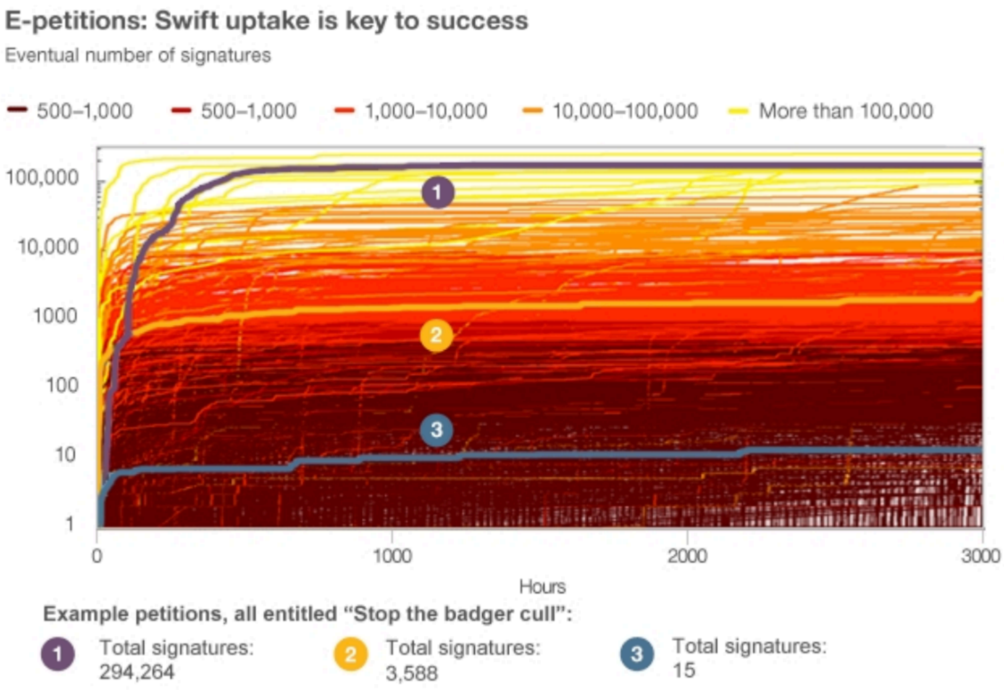

Figure: Time evolution of the number of signatures for 20,000 petitions. The colour codes the eventual number of the signatures by the end of the data collection period. The three high ligated petitions are about the same topic but with different success scenarios, indicating the complex behaviour of the system.

Publications:
Yasseri, T., Hale, S. A., & Margetts, H. Z. (2017). Rapid rise and decay in petition signing. *EPJ Data Science*, *6*(1), 20.
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From network of families to network of kins: aspects of migration, fertility and cultural homophily

Kunal Bhattacharya[1], Venla Berg[2], Daniel Monsivais[1], Asim Ghosh[1], Janos Kertesz[3], Anna Rotkirch[2], Kimmo Kaski[1,4]

[1] Department of Computer Science, Aalto University School of Science, P.O. Box 15400, FI-00076 AALTO, Espoo, Finland

[2] Finnish Family Federation, Helsinki, Finland

[3] Center for Network Science, Central European University, Budapest, Hungary

[4] Complexity Science Hub Vienna,
Josefstädter Strasse 39, A-1080 Vienna, Austria

Using a large dataset with individual-level demographic information of almost 60,000 families in contemporary Finland, we study the effects of fertility, migration and cultural homophily on the structure of a network between extended families. Families are considered as vertices and unions between males and females who have a common child are considered as edges in such a network. We characterize the network in terms of the basic structural properties and then explore the network transitivity and assortativity with regards to regions of origin and linguistic identity. Transitivity is seen to result from linguistic homophily in the network. Additionally, we study the structure of the kinship network derived from the dual graph of network of families. Overall, we distinguish between two linkage patterns, the 'metropolitan' and the 'cultural' pattern.

References: arXiv:1708.02432; arXiv:1708.06186

Revealing In-Block Nestedness in social and ecological networks

A. Solé-Ribalta[1], M. Mariani[2], C. Tessone[3], and J. Borge-Holthoefer[1]

[1] *Internet Interdisciplinary Institute (IN3), Universitat Oberta de Catalunya*

[2] *University of Fribourg, Switzerland*

[3] *University of Zürich, Switzerland*

The identification of macroscale connectivity patterns in complex networks has been central to the development of the field. Besides an interest in the methodological challenges, these patterns matter to the community inasmuch they result from a complex structure-dynamics interactions. It is in this context –network architecture as emergent phenomena– that nestedness and modularity arise as prominent macrostructural signatures to study. Nestedness was originally developed in ecology, to characterise the spatial distribution of biotas in continental and isolated landscapes, and to describe species-to-species relations. In structural terms, a nested pattern is observed when specialists (nodes with low connectivity) interact with proper nested subsets of those species interacting with generalists (nodes with high connectivity); see Fig. 1A (left). A modular network structure (Fig. 1A (middle)) implies the existence of well-connected subgroups, which can be identified given the right heuristics to do so.

In the last years we have become increasingly aware that nestedness is not exclusive to plant-animal interaction assemblages. Rather, it appears often in systems where positive interactions play a certain role. Perhaps this fact, and the remarkable evidence that modularity is observed in many systems, has spurred research on the (possible) co-existence of both features. Here we will focus on particular socio-technical settings in which modularity and nestedness are observed together, and discuss some possible explanations and methodological problems.

We first prove that detecting communities (modularity Q optimization) and measuring nestedness (NODF) is not a feasible pipeline to confirm (or discard) the existence of networks with in-block nestedness (IBN), neither sequentially or in parallel. This is not because of any inherent flaw of Q or NODF, but rather because they are not meant to tackle IBN (see Fig. 1B). We close this methodological gap by introducing a compact, new framework that quantifies to what extent a network displays IBN, according to the expression:

$$\mathcal{I} = \frac{2}{N_r + N_c} \left\{ \sum_{s,t}^{N_r} \frac{O_{s,t} - \langle O_{s,t} \rangle}{k_t (C_s - 1)} \Theta(k_s - k_t) \delta(\alpha_s, \alpha_t) + \sum_{\sigma,\tau}^{N_c} \frac{O_{\sigma,\tau} - \langle O_{\sigma,\tau} \rangle}{k_\tau (C_\sigma - 1)} \Theta(k_\sigma - k_\tau) \delta(\alpha_\sigma, \alpha_\tau) \right\}$$

which, along the lines of Q, has to be maximized. We then exploit our framework on hundreds of real networks originated on the most variegated fields of research to assess the existence of in-block nested structures, unveiling that this hybrid pattern is surprisingly widespread.

Using such proper formulation of the problem, we first exploit synthetic networks as a testbed for our approach. Once validated, we proceed to analyse hundreds of real networks to evidence by example that this type of structures exist in both uni- and bi-partite networks (Fig. 1C,D), and discuss possible directions from here.

Projections of bipartite networks and dynamical aftereffects

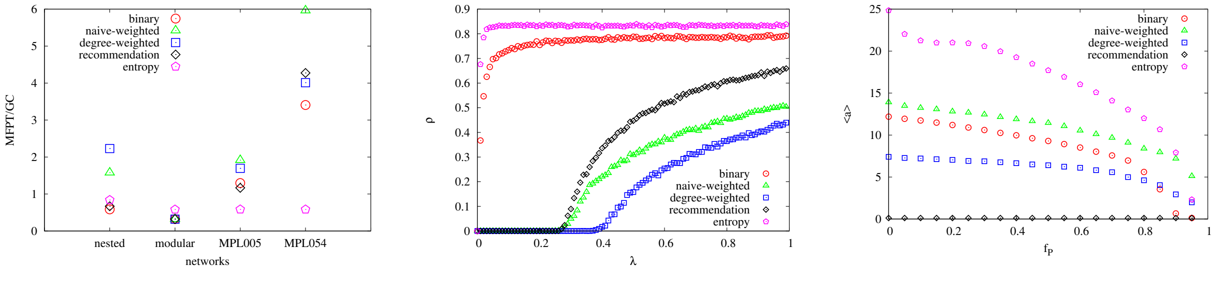
A. Czaplicka, S. Meloni and Y. Moreno

Institute for Biocomputation and Physics of Complex Systems (BIFI), University of Zaragoza, Spain

Bipartite networks are natural representations of many real systems. They provide a description of connections between two different types of nodes. Examples of such networks range from financial networks, through user-movie data bases, author-article collaborations up to ecological networks of species interactions. Although these networks provide valuable information about inter-species dependencies, at the same time they lack intra-species links. To address this problem, several ways of projecting bipartite networks into two unipartite systems have been developed. Unfortunately, the choice of projection method for the particular topology seems to be a neglected problem. Other appealing questions are dynamical aftereffects of those projections. In this study we compare five different and commonly used projection methods from the literature. We apply them on a large set of real ecological networks and artificial networks with nested, modular and nested-modular structures. In order to check their effects on the dynamical properties of the networks we employ three types of dynamics: diffusion (modelled as Random Walk), disease spreading (SIS model) and a population dynamic model taking into account mutualistic interactions among species. Results show that the choice of the projection can significantly change the behavior of the system.

The Mean First Passage Time (MFPT) for a random walker for a particular network changes depending on the projection and also changes for the particular projection depending on the network (see Fig. 1(a)). For disease spreading, we observe a dramatic change in the dynamical properties of the system depending on the projections applied. As it is shown in Fig. 1(b), the epidemic threshold varies from $\lambda \approx 0$ up to intermediate values of the infection rate (e.g. $\lambda = 0.4$ in Fig. 1(b)). Qualitative conclusions are very similar for all considered bipartite networks, which means that projection determines disease spreading on unipartite network. In the case of mutualistic interactions we observe that not only the average abundance of the species depends on the projection but also it affects the stability of the system (Fig. 1(c)).

Finally, in our study we have shown that the method of projecting a bipartite into an unipartite network can dramatically change the dynamical properties of the system and therefore the choice for the projection should be done with care and justifies.



(a) RW (b) SIS (c) Population dynamics

Figure 1: (a) The mean first passage time normalized by the size of the giant component $MFPT/GC$ for two artificial networks (nested and modular) and two real networks (M-PL-005 and M-PL-054) projected into five different ways (binary projection, naive-weighted projection, degree-weighted projection, personal recommendation based projection and entropy based projection). (b) Fraction of the infected nodes ρ in the stationary state as a function of λ for Plant-Pollinator M-PL-054 network. (c) Average abundance $\langle a \rangle$ as a function of the fraction of deleted nodes for Plant-Pollinator M-PL-054 network.

Upscaling species richness and abundances in tropical forests

Samir Suweis*, Anna Tovo*, Marco Formentin, Igor, Volkov, Marco Favretti, Jayanth
R. Banavar, Sandro Azaele, Amos Maritan

The quantification of tropical tree biodiversity worldwide remains an open and challenging problem. In fact, more than two-fifths of the global tree population can be found either in tropical or sub-tropical forests, but species identities are known only for ≈ 0.000067% of the individuals in all tropical forests. For practical reasons, biodiversity is typically measured or monitored at fine spatial scales. However, important drivers of ecological change tend to act at large scales. Conservation issues, for example, apply to diversity at global, national or regional scales. Extrapolating species richness from the local to the global scale is not straightforward. Indeed, a vast number of different biodiversity estimators have been developed under different statistical sampling frameworks, but most of them have been designed for local/regional-scale extrapolations, and they tend to be sensitive to the spatial distribution of trees, sample coverage and sampling methods. Here, we introduce an analytical framework (see Figure below) based on stochastic modeling of ecosystems dynamics and scaling theory that provides robust and accurate estimates of species richness and abundances in biodiversity-rich ecosystems, as confirmed by tests performed on various in silico-generated forests and on empirical data. The new framework also quantifies the minimum percentage cover that should be sampled to achieve a given average confidence in the upscaled estimate of biodiversity. Our analysis shows that previous methods have systematically overestimated the total number of species and leads to new estimates of hyper-rarity at the global scale, known as Fisher's paradox. We show that hyper-rarity is a signature of critical-like behavior in tropical forests, and it provides a buffer against mass extinctions. When biotic factors or environmental conditions change, some of these rare species are more able than others to maintain the ecosystem's functions, thus underscoring the importance of rare species.

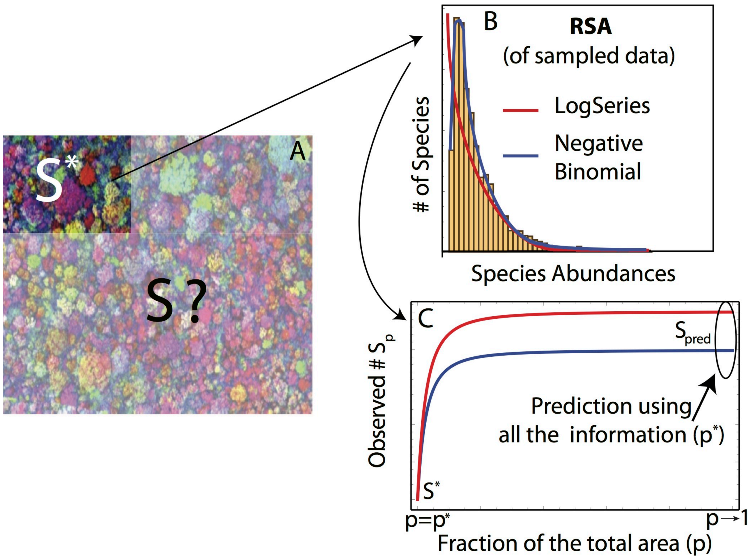


Figure
. Schematic presentation of our theoretical upscaling framework. It consists of three steps. (A) We know the abundances of S* species within a given region covering a fraction p* of the whole forest. (B) We perform the best fit maximum likelihood) of the RSA (relative species abundance) given by our stochastic model. (C) Using the best-fit parameters obtained in (B) and using our upscaling framework, we predict the biodiversity Spred of the whole forest.

. Full pre-print at https://www.biorxiv.org/content/early/2016/12/15/088534

* Contributed equally to the work

Mechanisms driving the evolution of species-rich interaction networks

Cecilia S. Andreazzi[1], Julia Astegiano[2] and Paulo R. Guimarães Jr.[3]

[1]Campus Mata Atlântica, Fundação Oswaldo Cruz (FIOCRUZ), Rio de Janeiro, Brazil, candreazzi@fiocruz.br; [2]Instituto Multidisciplinario de Biología Vegetal, Universidade Nacional de Córdoba, (UNC-CONICET), Argentina; [3]Departamento de Ecologia, Universidade de São Paulo (USP), Brazil

Complex networks are powerful analytical tools used to represent ecological interactions among species. The structural patterns that are widely observed in ecological networks are nestedness and modularity. Nestedness measures the degree to which specialists interact with subsets of the species with whom generalists interact. Modularity measures the degree of species grouping into semi-independent units. The changes on phenotypic traits driven by reciprocal selection between species (i.e., coevolution) is considered to play a key role in assembling and maintaining species interactions (Thompson 2013). Yet the underlying processes shaping the observed network structure and their consequences for species evolution remain poorly understood. Here, we explore how coevolution driven by different functional mechanisms shapes the structure and dynamics of ecological networks.

We use an adaptive network framework (Andreazzi et al. 2017) to study how trait matching (probability of interaction increases with trait similarity) and exploitation barriers (probability of interaction increases with trait dissimilarity) functional mechanisms drive coevolution and shape network organization. In these networks nodes represent species and each species have an attributed trait value. There are two sets of species: resources and consumers. Interactions are either antagonistic, in which consumers are benefited while resources are exploited or mutualistic, in which both consumers and resources are benefited. Phenotypic traits, such as body size, modulate the likelihood of interactions according to the functional mechanism. This approach combines the evolution of species traits due to antagonistic or mutualistic selection and feedbacks of coevolution on network dynamics.

We parameterize the models with data from 122 antagonistic and 122 mutualistic empirical networks comparing scenarios with weak and strong coevolutionary selection. In Fig. 1 we show that the models tend to underestimate nestedness and overestimate modularity of both antagonistic and mutualistic networks. We also show that trait matching reproduce better the structure of antagonistic networks while explotation barriers are more related to mutualistic interactions. Weak coevolutionary selection driven by trait matching reproduce better the structure of antagonistic networks, predicting 70% of the empirical networks (Fig. 1a, 1c). Contrary to the traditional claim, we show that coevolution poorly reproduce the structure of mutualistic networks. Indeed, weak coevolutionary selection driven by exploitation barriers predict only 20% of the empirical mutualistic networks (Fig. 1b, 1d).

Coevolution prevents networks from achieving a stable state and interaction rewiring varies from 0-50% of the interactions. This rewiring is drastically reduced when the functional mechanism have a strong effect on the probabilities of interactions. Strong coevolution by trait matching reduces interaction rewiring in antagonistic networks, while strong coevolution by exploitation barriers reduces interaction rewiring in mutualistic interactions. The different mechanisms also favor different trait dynamics. Exploitation barriers favor coevolutionary arm races in consumer and resource functional traits, while trait matching favors fluctuating selection dynamics in both types of networks. In summary, coevolution better predict the structure of antagonistic than mutualistic networks. Neutral processes and additional mechanisms, such as differences in abundance, dispersal, drift and speciation, may be more relevant predictors of the structure of mutualistic networks. Our results highlight the relevance of combining eco-evolutionary models with network analysis to understand the dynamics of interactions in species-rich communities and its consequences on the organization of biodiversity.

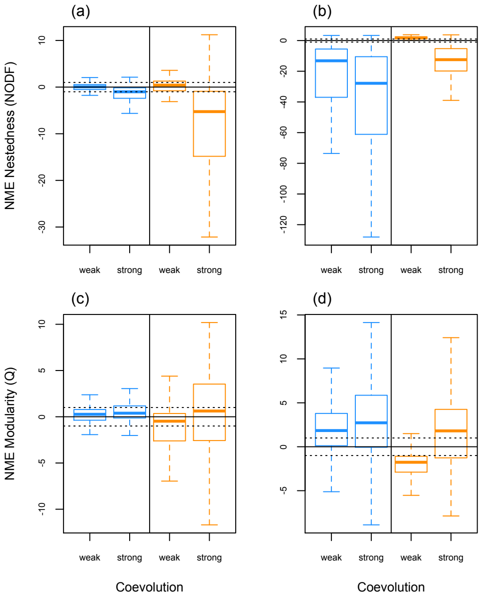


Fig. 1: Normalized model error (NME) for nestedness (a, b) and modularity (c, d) metrics predicted by trait matching (blue) and exploitation barriers (orange) models for the antagonistic (a, c) and mutualistic (b, d) networks in weak and strong coevolutionary scenarios. Thick lines within boxes represent median values for 122 networks. Upper and lower limits of boxes represent 1st and 3rd quartiles, respectively. The black lines highlight the NME values between -1 and 1, which are considered not significantly different from the empirical network structures.

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Collective memory in primate conflict implied by temporal scaling collapse

Edward D Lee,[1*] Bryan C Daniels,[2] David C Krakauer,[2,3] Jessica C Flack[2,3]

[1*]Department of Physics, Cornell University, 142 Sciences Drive, Ithaca, NY 14853

[2]ASU–SFI Center for Biosocial Complex Systems, Arizona State University, Tempe, AZ 85287

[3]Santa Fe Institute, 1399 Hyde Park Rd, Santa Fe, NM 87501

In biological systems prolonged conflict is costly whereas contained conflict permits strategic innovation and refinement. Causes of variation in conflict size and duration are not well understood. We use a well-studied primate society model system to study how conflicts grow. We find conflict duration is a “first to fight” growth process that scales superlinearly with the number of possible pairwise interactions. This is in contrast to a “first to fail” process that characterizes peaceful durations. Rescaling conflict distributions reveals a universal curve, showing that the typical timescale of correlated interactions exceeds nearly all individual fights. This temporal correlation implies collective memory across pairwise interactions beyond those assumed in standard models of contagion growth or iterated evolutionary games. By accounting for memory, we make quantitative predictions for interventions that mitigate or enhance the spread of conflict. Managing conflict involves balancing the efficient use of limited resources with an intervention strategy that allows for conflict but keeps it contained and controlled.

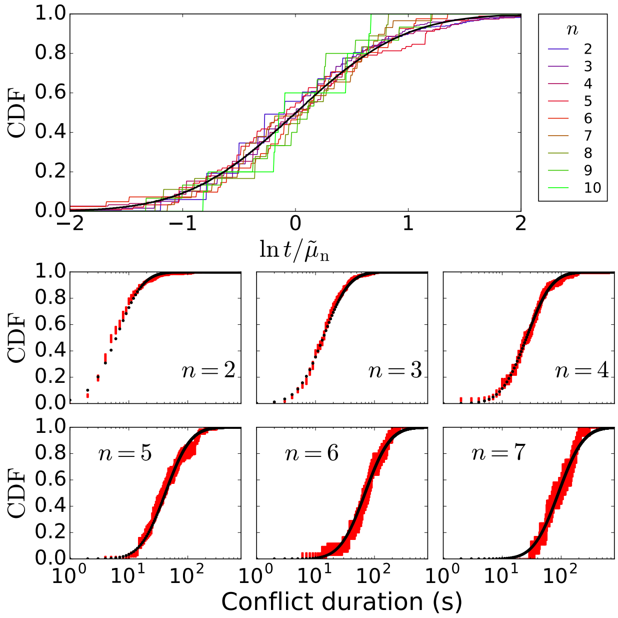
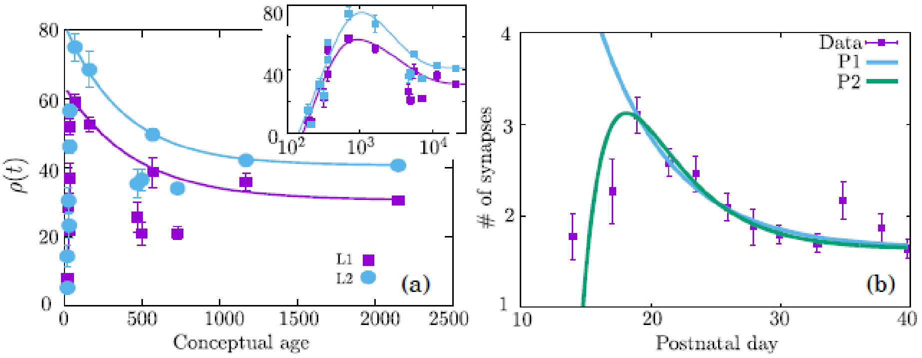


Figure 1: Scaling collapse of conflict duration. (top) Scaling collapse for conflict duration of fights of sizes 2–10, accounting for 97% of the data. Universal lognormal curve fit to the shown data overlaid in black. All shown duration distributions except for fights with $n = 2$ participants are statistically indistinguishable from the discretized lognormal. (bottom) We show for example more detailed comparisons for a few conflict sizes (red with 90% confidence intervals) with the universal lognormal curve discretized by seconds (black).

Mind, Complexity and Phase Transitions

Joaquin Marro, Emeritus Professor, University of Granada

Many intricate aspects of nature are now well understood from the mathematical perspective of the theory of phase transitions and critical phenomena. It does not therefore came as a surprise that recent studies try to deep on the structure and high-level functions of the brain —where, incidentally, *complexity* and kind of *avalanches* have been observed— by using analogies which involve the concept of non-equilibrium phase transition. This talk will illustrate and ground this situation based on the papers "Brain performance versus phase transitions", *Sci. Rep.* 5, 12216 (2015), by J.J. Torres and J. Marro, and "*The concurrence of structure and function in developing networks: An explanation for synaptic pruning*" and "*Growth strategy determines networks performance*", both to be soon published by Ana P. Millán, J. J. Torres, S. Johnson and J. Marro, and the book "*La Mente es Crítica — Descubriendo la Admirable Complejidad del Cerebro*", J. Marro & D. R. Chialvo, *Editorial Universidad de Granada* 2017.



Synaptic pruning in an auto-associative neural net with an evolving mechanism for the birth and death of synapses. The model also explains other evolving nets such as those of protein interaction. The figure shows experimental data-sets on connectivity during infancy (points) and corresponding model fits (solid lines).

(a), left: Connectivity data points [P. R. Huttenlocher and A. S. Dabholkar, *J. of Comparative Neurology* 387, 167 (1997)] in the human infant brain, obtained in autopsies by directly counting synapses in tissues from different layers of the auditory cortex (here shown layers 1 (L1, purple) and 2 (L2, blue). Inset shows the fit of the maximum on a log-log scale, labels as in the main plot.

(b), right: Synaptic density data [S. Navlakha, A. L. Barth and Z. Bar-Joseph, *PLoS Comput. Biol.*, 11:e1004347 (2015)] is here measured via large-scale brain imaging experiments that quantify the number of connections in the developing somatosensory cortex of the mouse. P1 (blue) is a fit from the linear model; P2 (green) is a model fit including the growth factor.

Topology and curvature of brain functional networks under psychedelic drugs

Esther Ibáñez-Marcelo,[1,*] Alice Patania,[2] Angkoon Phyniomark,[3] and Giovanni Petri[1]
[1]*ISI Foundation, Torino, Italy*
[2]*Indiana University Network Institute, Indiana University, Bloomington, Indiana, USA*
[3]*Institute of Biomedical Engineering, University of New Brunswick, Fredericton, NB, Canada*

keywords: persistent homology, curvature, brain functional networks

Network geometry has been very successful recently in highlighting how real or latent spaces that underlie real networks can provide insights on their organizing principles and on their effects on dynamical processes [1]. While well-behaved latent spaces are usually required for modeling [2], recent work on growing simplicial complexes [3] has shown that there is a rich interdependence between the geometrical and the (potentially non-trivial) topological structure of networks.

In this contribution we leverage TDA and a recent geometric curvature measure, the Foreman-Ricci curvature [6], to investigate how and to what extent the topological and network geometrical structure of brain functional networks are related to each other. In particular, we analyse the homological structure of functional connectivity of the human brain under the effect of two different psychedelic drugs, psilocybin [7] and LSD [8] via persistent homology, which captures network topology without requiring any embedding. Roughly speaking, persistent homology highlights the heterogeneity and disconnections in the fabric of a network thus encoding brain *functional cycles*, which can then be represented again in network form as homological scaffolds [9]. We find that in the LSD and psilocybin cases the overall topological properties are very similar to the respective placebo controls. However, we capture differences between placebo and drug subjects using a similarity measure through a kernel on persistence diagrams (output from persistent homology) and results show that the two drugs seem to perform differently in their effects on the brain. We investigate how topological changes are related to geometrical ones in the structure of the brain networks. We find that the difference captured by both quantities are similar between the two drugs. However, we show that the curvature, carrying local information about the network geometry, and the homology, carrying mesoscale topological information, are uncorrelated. Also, topological information (obtained from scaffolds [9]) captures an adaptive behaviour across different times after drug administration while geometrical information is not able to capture it. That is, generally the edges common across drug and placebo suffer a strong reduction in their persistence with respect to placebo and after a while this reduction starts to vanish. In conclusion, our results highlight in this case a preheminent change in topology that is then followed by a change in the differential structure, strengthening previous observations that brain altered states originate in large-scale reorganization of the brain functional connectivity. Finally, we show that the LSD produces small but very heterogeneous functional topology changes (from the placebo state) across the subjects, whereas those induced by psilocybin are larger but consistent across subjects (see Figure), suggesting a more coherent and reliable alteration of functional connectivity and opening the door to potential therapeutic applications.

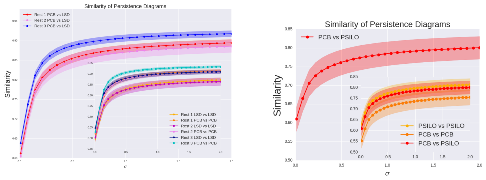


FIG. 1. Similarity measure on persistent diagrams: on LSD data (left), on psilocybin data (right). We calculate all the pairwise similarities among subjects in the same condition and group (e.g. placebo Rest1) and comparing these with the pairwise similarities among subjects in the corresponding drug condition (e.g. LSD Rest1). The values together provide a measure of how uniform or heterogenous are the changes in the functional topology induced by the drug. It is showed that LSD induces heterogenous topological changes across subjects, making them topologically more different among themselves than they are under placebo.

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[*] esther.ibanez@isi.it

Biological conservation law as an emerging functionality in dynamical neuronal networks

Marko Jusup[1] with Boris Podobnik[a,b,c], Zoran Tiganj[d],
Wen-Xu Wang[e], Javier M. Buldú[f,g], and H. Eugene Stanley[a]

[1]Center of Mathematics for Social Creativity, Research Institute for Electronic Science, Hokkaido University, Sapporo 060-0808, Japan; **presenter**
[a]Center for Polymer Studies, Boston University, Boston, MA 02215
[b]Faculty of Civil Engineering, University of Rijeka, 51000 Rijeka, Croatia, European Union
[c]Zagreb School of Economics and Management, 10000 Zagreb, Croatia, European Union
[d]Department of Psychological and Brain Sciences, Boston University, Boston, MA 02215
[e]School of Systems Science, Beijing Normal University, 100875 Beijing, China
[f]Laboratory of Biological Networks, Center for Biomedical Technology, Universidad Politécnica de Madrid, 28223 Pozuelo de Alarcon, Madrid, Spain
[g]Complex Systems Group, Universidad Rey Juan Carlos, 28933 Móstoles, Madrid, Spain

Scientists strive to understand how functionalities, such as conservation laws, emerge in complex systems. Living complex systems in particular create high-ordered functionalities by pairing up low-ordered complementary processes, e.g., one process to build and the other to correct. We propose a network mechanism that demonstrates how collective statistical laws can emerge at a macro (i.e., whole-network) level even when they do not exist at a unit (i.e., network-node) level. Drawing inspiration from neuroscience, we model a highly stylized dynamical neuronal network in which neurons fire either randomly or in response to the firing of neighboring neurons (Fig.1). A synapse connecting two neighboring neurons strengthens when both of these neurons are excited and weakens otherwise. We demonstrate that during this interplay between the synaptic and neuronal dynamics, when the network is near a critical point, both recurrent spontaneous and stimulated phase transitions enable the phase-dependent processes to replace each other and spontaneously generate a statistical conservation law—the conservation of synaptic strength. This conservation law is an emerging functionality selected by evolution and is thus a form of biological self-organized criticality in which the key dynamical modes are collective.

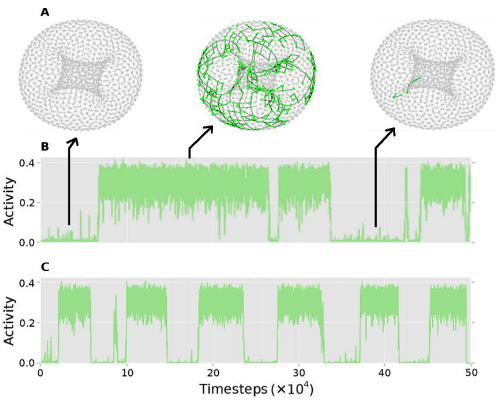

Fig. 1: Activity of a phase-flipping neuronal network. ***A,B****, A graphical representation of the simulated network with phase flipping between a mainly excited and a mainly resting phase, which emerges if the network is set appropriately inside a bistable region of the phase space.* ***C****, In addition to completely spontaneous phase flipping, regulated stimuli may exert substantial control over the timing of transitions between the two phases. Here, the time series of activity is progressively more periodic as the value of the control parameter increases. Generally, if the control parameter equals zero, the network exhibits only spontaneous phase flipping. As this parameter approaches unity, stimuli start to dominate over the spontaneous flipping mechanism.*

Network dissimilarity measure and application to brain network differentiation

Tiago A. Schieber[1], Laura Carpi[2], Albert Dıaz-Guilera[3], Panos M. Pardalos[4], Cristina Masoller[5] and Martın G. Ravetti[1]

1 Universidade Federal de Minas Gerais, Belo Horizonte, Brazil.

2 Centro Federal de Educacao Tecnologica de Minas Gerais, Brazil.

3 Universitat de Barcelona, Spain.

4 University of Florida, USA.

5 Universitat Politecnica de Catalunya, Spain.

– Name of the speaker: Cristina Masoller, cristina.masoller@upc.edu

Abstract:

We propose a discriminative and computationally efficient metric to distinguish and quantify graph dissimilarities, which is based on the comparison of the set of probability distribution functions, $\{p_i(j)\}$, that represent the node's connectivity distances ($p_i(j)$ being the fraction of nodes that are connected to node i at distance j) [1]. The distance metric is applied to brain networks constructed through electroencephalography exams (EEG). Time-series recorded from control and alcoholic subjects are mapped to graphs via the horizontal visibility graph algorithm [2]. We are able to detect two regions of the brain called 'nd' and 'y', where the weight of the connections between these regions is higher in control than in alcoholic networks, as shown in Fig. 1, left. In contrast, when considering the Hamming distance, it is not possible to distinguish between the two groups (Fig. 1, right).

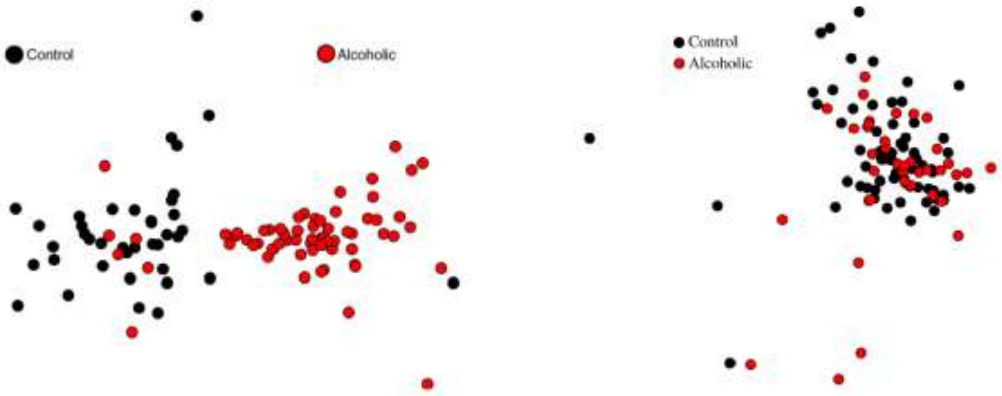

Fig. 1. Left: alcoholic and control groups differentiated by using the dissimilarity measure proposed in [1]; right: results considering the Hamming distance instead.

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Cognitive resource allocation determines the structure of personal networks

Ignacio Tamarit[1,2], José A. Cuesta[1,2,3,4], Robin I.M. Dunbar[5,6] & Angel Sánchez[1,2,3,4].

[1] Grupo Interdisciplinar de Sistemas Complejos, Departamento de Matemáticas, Universidad Carlos III de Madrid, 28911, Leganés, Madrid, Spain.
[2] Unidad Mixta Interdisciplinar de Comportamiento y Unidad Social (UMICSS) UC3M-UV-UZ, Universidad Carlos III de Madrid, 28911 Leganés, Spain.
[3] Institute for Biocomputation and Physics of Complex Systems (BIFI), University of Zaragoza, 50018, Zaragoza, Spain.
[4] Institute UC3M-BS of Financial Big Data, Universidad Carlos III de Madrid, 28903, Getafe, Spain
[5] Department of Experimental Psychology, University of Oxford, UK.
[6] Department of Computer Science, Aalto University, Finland.

Abstract

The typical human personal social network contains about 150 relationships including kin, friends and acquaintances, organised into a set of hierarchically inclusive layers of increasing size but decreasing emotional intensity. Data from a number of different sources reveal that these inclusive layers exhibit a constant scaling ratio of ~ 3. While the overall size of the networks has been connected to our cognitive capacity, no mechanism explaining why the networks present a layered structure with a consistent scaling has been proposed. Here we show that the existence of a cost to relationships (in terms of time or cognitive investment) and heterogeneity in the relationships (in terms of their benefits) naturally yield, without further assumptions, the existence of layers and the scaling between them. We develop a one-parameter Bayesian model that fits empirical data remarkably well. In addition, the model predicts the existence of a new, unexpected regime in the case of small communities, such that layers have an inverted structure (increasing size with increasing emotional intensity). We test the model with five communities and provide clear evidence of the existence of

Strategies in the repeated prisoner's dilemma when the cooperation is established

Jelena Grujić[1,2], Tom Lenaerts[1,2]

[1] *AI Lab, Vrije Universiteit Brussel, Brussels, Belgium, jgrujic@vub.ac.be*
[2] *MLG, Université libre de Bruxelles, Brussels, Belgium*

Although there is a large body of research dedicated to Iterated Prisoner's Dilemma (IPD) experiments, there is still no clear answer to the question of what strategies human players actually use when they participate in that game. Most of the earlier experiments too short to produce sufficient data to infer strategies. Apart from the experiments, there have been intensive theoretical studies wherein the aim was to identify the most successful strategies like Tit-For-Tat, Win-Stay-Lose-Shift, etc. were determined as being successful in generating cooperation in IPD. Yet it remains unclear whether human participants actually use those strategies.

Two recent experiments [1, 2], deal with this problem by making the participants play multiple repeated games in which, after they finish *n* rounds of one repeated game, the participants are assigned a new partner with whom they play another game. Afterwards they perform a maximum likelihood analysis with the aim to fit a number of strategies to the experimental data. However this method is very sensitive to the group of strategies they choose to fit and consequently their experiments arrive at very different conclusions. Furthermore, each repeated game is rather short and in a previous experiment it was observed that although in the first 10 rounds the level of cooperation is decreasing, the trend can be changed drastically when the game continues [3].

Here, we report on the results of long IPD (around 100 rounds), with the aim to see if participants arrive at higher levels of cooperation. At the same time we use the behavioral data to identify the strategies of the participants in order to determine how humans really behave in IPD experiments. We apply methods from machine learning and complex networks to identify the groups of behaviors that can be found in the data. We connected each player into a fully connected network where the nodes are the players and the links are similarities of their strategies. We then performed a modularity analysis to see whether behavioral clusters could be identified. As can be seen in the Figure 1, five distinct communities were identified in this way and their significants was confirmed by bootstrapping.

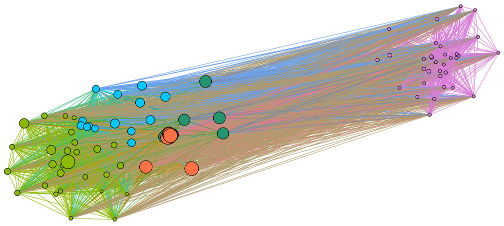

Figure 1: **The network of strategies.** Each node on the network is one player (the size of the node corresponds to cooperativeness of the player) and the links are the similarity between their strategies. Orange and green nodes are Cooperators (Pure Cooperators and Mostly Cooperator, respectively), purple nodes are Defectors and blue and green are adapting their actions to what the opponent is playing. Blue nodes roughly correspond to Generous Tit-For-Tat strategy and green nodes to what we call Generous Grim Trigger.

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Endogenous Repeated Cooperation and Surplus Distribution - An Experimental Analysis

Sibilla Di Guida[1], The Anh Han[2], Georg Kirchsteiger[3], Tom Lenaerts[3], Ioannis Zisis[3]
[1] University of Southern Denmark
[2] Teesside University
[3] Universite Libre de Bruxelles

This work investigates how endogenous group formation combined with the possibility of repeated interaction impacts cooperation levels and surplus distribution. We developed and tested experimentally a Surplus Allocation Game where the cooperation of four agents is needed to produce a surplus, but only two agents have the power to allocate it among the members of the group. Different matching procedures were used to test the impact of exogenous vs. endogenous group formation. Contrary to commonly hold beliefs, the possibility of repeated interaction with the same partners per se did not lead to higher average cooperation levels and more equal (on average) allocations of the surplus, but to a self-selection of agents into groups with different life-spans, correlated with the behavior of both distributors and receivers. We developed a behavioral model based on a few straightforward assumptions which captures the dynamics observed in the experimental data, sheds light into the rationales that drive the agents' individual behavior, and allows us to understand how group duration is linked to different agents´ characteristics. Our model suggests that the most generous distributors are those acting for fear of rejection, rather than for true generosity. Moreover, the groups lasting the longest (and the most efficient ones) are those composed by this type of distributors and "undemanding" receivers.

Onymity promotes cooperation in social dilemma experiments

Zhen Wang[1] with Marko Jusup[a], Rui-Wu Wang[b], Lei Shi[c],
Yoh Iwasa[d], Yamir Moreno[e,f,g], Jürgen Kurths[h,i,j]

[1]Center for OPTical IMagery Analysis and Learning (OPTIMAL),
Northwestern Polytechnical University, Xi'an 710072, China; **presenter**
[a]Center of Mathematics for Social Creativity, Research Institute for Electronic Science,
Hokkaido University, Sapporo 060-0808, Japan
[b]Center for Ecology and Environmental Sciences,
Northwestern Polytechnical University, Xi'an 710072, China
[c]Statistics and Mathematics College,
Yunnan University of Finance and Economics, Kunming 650221, China
[d]Faculty of Science, Kyushu University, Fukuoka 819-0395, Japan
[e]Institute for Biocomputation and Physics of Complex Systems (BIFI),
University of Zaragoza, 50009 Zaragoza, Spain
[f]Department of Theoretical Physics, University of Zaragoza, 50009 Zaragoza, Spain
[g]Institute for Scientific Interchange (ISI), ISI Foundation, 10126 Turin, Italy
[h]Potsdam Institute for Climate Impact Research (PIK), 14473 Potsdam, Germany
[i]Department of Physics, Humboldt University, 12489 Berlin, Germany
[j]Institute for Complex Systems and Mathematical Biology,
University of Aberdeen, Aberdeen AB24 3UE, U.K.

One of the most elusive scientific challenges for over 150 years has been to explain why cooperation survives despite being a seemingly inferior strategy from an evolutionary point of view. Over the years, various theoretical scenarios aimed at solving the evolutionary puzzle of cooperation have been proposed, eventually identifying several cooperation-promoting mechanisms: kin selection, direct reciprocity, indirect reciprocity, network reciprocity, and group selection. We report the results of repeated Prisoner's Dilemma experiments with anonymous and onymous pairwise interactions among individuals. We find that onymity significantly increases the frequency of cooperation and the median payoff per round relative to anonymity (Fig. 1). Furthermore, we also show that the correlation between players' ranks and the usage of strategies (cooperation, defection, or punishment) underwent a fundamental shift, whereby more prosocial actions are rewarded with a better ranking under onymity. Our findings prove that reducing anonymity is a valid promoter of cooperation, leading to higher payoffs for cooperators and thus suppressing an incentive—anonymity—that would ultimately favor defection.

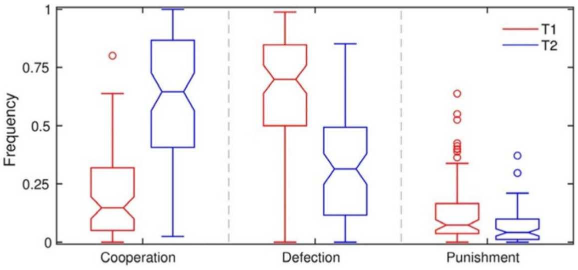

Fig. 1. Onymity brings out the best in people. Cooperation takes over defection as the dominant action if the anonymous treatment (T1) is replaced with the onymous one (T2). Pairwise comparisons indicate that the increase in the frequency of cooperation and the decrease in the frequency of defection between the two treatments are significant at the 5% level. The frequency of punishment decreases, but the difference between the medians is insignificant. Box-and-whisker plots with notches reveal the empirical distribution of the frequency of each action. Box height indicates the interquartile range with the median in between. Notches indicate the 95% confidence intervals for the median, thus permitting a visual pairwise comparison. Whisker height is such that 99.3% of the normally distributed data would be covered. The points drawn as outliers fall outside of the whisker coverage.

Modelling decision times in game theory experiments

Riccardo Gallotti[1], Jelena Grujić[2,3]

[1]Instituto de Física Interdisciplinar y Sistemas Complejos (IFISC), CSIC-UIB, Campus UIB, ES-07122 Palma de Mallorca, Spain
[2]I-lab, Computer Science Department, Vrije Universiteit Brussel, Pleinlaan 2, 1050 Brussels, Belgium.
[3]MLG, Département d'Informatique, Université Libre de Bruxelles, Boulevard du Triomphe, CP 212, 1050 Brussels, Belgium.

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 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 a one-dimensional brownian motion

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

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:

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

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 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.

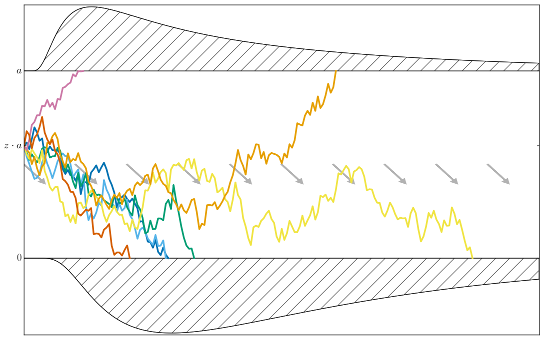

Figure 1: An illustration of the DDM: starting from an initial condition $z\cdot a$, the agents accumulate random evidence in favour of one of two alternative decisions. Once the amount of evidence reaches one of the thresholds, the associated decision is made. The arrows indicate the presence of a negative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

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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Evolution of signalling and memory for consensus decisions in public good games

Luis A. Martinez-Vaquero,[1,*] Francisco C. Santos,[2] and Vito Trianni[1]

[1] *Institute of Cognitive Sciences and Technologies, National Research Council of Italy (ISTC-CNR), via San Martino della Battaglia 44, 00185 Rome, Italy*

[2] *Instituto Superior Técnico (IST), University of Lisbon, Av. Prof. Dr. Cavaco Silva, 2744-016 Porto Salvo, Portugal*

Self-organising social systems such as insect colonies and animal or human groups need specific mechanisms to achieve coordination and avoid free-riding, especially when cooperation comes with a cost. Signalling is one such mechanism, but it may entail costs associated with the signal expression. Memory of social experience can also be exploited, but requires that coordination result from an iterated process. In this work, we study from the perspective of evolutionary game theory under what circumstances signalling and memory may emerge.

We model the evolution of consensus decisions in a iterated public good game. We consider a finite population of Z individuals, which form random groups of N individuals at the beginning of each generation. Within each group, their members play a N-player iterated game, with a probability ω that another round takes place. We assume that groups can face either of two different exogenous circumstances: a public good game state (PGG) with probability λ and a non public good game one (nPGG) with probability $1-\lambda$. This duality can be interpreted as starvation and abundance states [1], respectively, or as a consensus decision between a potentially profitable or a invaluable option [2]. In the PGG state, each member of the group obtains a benefit $b = rcN_C/N$, hence proportional to the cooperation cost c and to the number of cooperators N_C, with a multiplicative constant $r > 1$. Such benefit is obtained only if the number of individuals that cooperate is higher than a threshold M. In any other case, nobody obtains anything. The behaviour of individuals is characterised by strategies that represent the two decisions that they are facing within each round of the game: signalling or not, as a function of the exogenous circumstances that they can recognise, and cooperating or not, as a function of whether the group is signalling and whether the group reached the threshold M in the previous round. It is considered that the group is signalling when more than Q members do so, assuming that signalling has an associated cost c_S. In this way, the decision of cooperating is influenced by the signal perceived and/or memory. We compute the fixation probabilities among all the possible pairs of strategies. Then, we obtain the stationary distribution of strategies from which to obtain information on their relative importance.

Our results show that there exist two sets of strategies that emerge in the system. The first set is formed by strategies that discriminate signals, and specifically (i) strategy SC, which signals only under the PGG state and cooperates only when the group signals, and (ii) strategy SD, which signals only under nPGG and cooperates only when the group is not signalling and (iii) strategy SF, which does not signal at all and cooperates only when the group is not signalling. Analysing the graphs of invasions, we have seen that one cluster is formed around SC and another one around SD and SF , revealing the coordination problem behind the absence of a predetermined meaning of signals: some strategies exploit signals as a way to communicate when they should cooperate and others in the other way around. The other important set of strategies (MB) that emerge in our model are those that do not signal under any circumstance and defect if not enough individuals cooperated in the previous round. These strategies are using memory and completely neglect signalling. In this way, these strategies can avoid exploitation since the only rule they implement is to refrain from cooperating if the group is not doing it. Figure 1 shows the difference between the aggregated probabilities of the signalling strategies (SC+SD) and the aggregated probabilities of the four that use memory (MB). We see that, in general, SC and SD can be important only for intermediate or high values of λ ($\lambda > 0.4$) and when c_S is not too high.

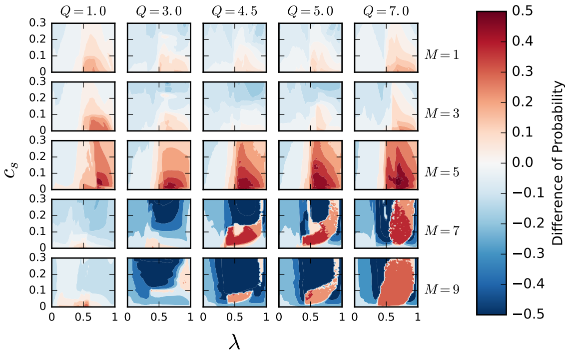

FIG. 1. Difference of the probabilities in the stationary distribution of SC+SD and MB strategies in the $c_S - \lambda$ parameter space and for different values of thresholds M and Q. We assumed $\omega = 1$, $r = 20$, $c = 1$, $N = 9$, and $Z = 100$.

We have also seen that the longer the game is repeated (high values of ω), the more successful signalling becomes, *i.e.* signalling is beneficial when groups have enough time to self-organise. In this condition, another strategy—linked to SD—emerges and becomes important when c_S is high: this strategy does not signal at all, but cooperates only when the group is not signalling, hence it free rides on the signalling costs. This is especially important in the case of SF strategy, which becomes successful also when c_S is higher. On the other hand, our results also shows that when λ presents extreme values close to 0 and 1, signalling becomes a mechanism to identify rare states or the nature despite its costs. Finally, we have observed that increasing the group size leads to the disappearance of signalling strategies and the prevalence of those that use memory to avoid exploitation.

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[*] Corresponding author: l.martinez.vaquero@gmail.com

Optimal prediction of decisions and model selection in social dilemmas using block models with metadata

S. Cobo-López[1], A. Godoy-Lorite[1], J. Duch[3], R. Guimerà[1,4], and M. Sales-Pardo[1]
[1]*Departament dEnginyeria Química, Universitat Rovira i Virgili,*
43007 Tarragona, Catalonia, Spain
[3]*Departament de Matemàtiques i Enginyeria Informàtica,*
Universitat Rovira i Virgili,
43007 Tarragona, Catalonia, Spain
[4]*ICREA, 08010 Barcelona, Catalonia, Spain*

(Dated: October 10, 2017)

Strategic decision making has been studied in the political and social sciences, and in behavioral economics. Experimental approaches, in which individuals play simplified games that pose specific social dilemmas, have been particularly insightful and have demonstrated that individuals often do not act "rationally" to maximize their profits. This makes their behaviors more unpredictable than one may have anticipated. However, approaches to analyze data from these experiments have focused mostly on characterizing behaviors qualitatively or on measuring deviations from rationality, rather than assessing the power of existing theories to predict accurately the actions of each individual.

The lack of such analyses is significant because quantifying predictability in strategic decision-making would lead to important insights and improve our understanding of human behavior [1]. Here, we aim at narrowing this gap by proposing models for strategic decision making, by developing rigorous model inference approaches, and by showing that individual strategic decisions are, to a large extent, predictable.

Specifically, we focus on a recent large-scale study of individuals playing a variety of 121 dyadic games (Fig. 1 b) in a controlled setting [2]. We propose two models: a single-strategy model in which each player has a unique decision-making strategy [3], and a mixed-strategy model in which players are not limited to following a unique strategy [4]. We also develop the corresponding inference approaches, that are more predictive than those built upon expectations of individuals' rationality (Fig. 1). Our models are based on the assumption that there are groups of individuals that use similar decision-making strategies (have similar behavioral phenotypes [2]), and groups of games that are perceived similarly by individuals. Importantly, our approach gives predictive models that are interpretable, which enables us to conclude that: (i) the perception of games by individuals is at odds with what should be expected from game theory; (ii) individuals tend not to follow single strategies, but rather mixtures of multiple strategies.

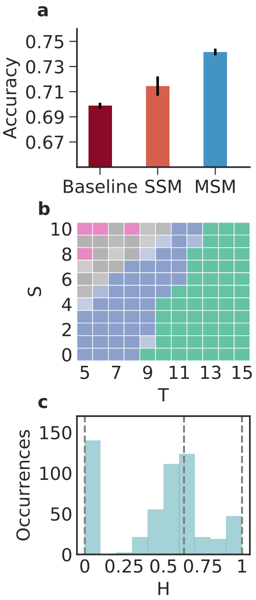

FIG. 1. **(a)** Predictive accuracy of the baseline model (red), the Single Strategy Model (orange) and the Mixed Strategy Model (blue). Each bin represents the average of a 5-fold cross-validation; error bars indicate the standard error of the mean. **(b)** Top group memberships for each game in the $S - T$ plane of the dyadic games. Each color indicates a different group of games. The saturation of the color indicates how distributed a game is among groups, so that games with multiple memberships are paler. S and T indicate values of the so-called Sucker and Temptation payoffs that correspond to each game. **(c)** Distribution of Shannon Entropies of the player membership . Gray dashed lines represent limit values of entropies corresponding to single-strategy, double and triple-strategy players.

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Cooperation-driven hierarchy is interpreted as good reputation

Alberto Antonioni,[1,2,3] María Pereda,[2] Katherine A. Cronin,[4] Angel Sánchez,[2,3] and Marco Tomassini[5]

[1] Department of Economics, University College London, UK
[2] Grupo Interdisciplinar de Sistemas Complejos (GISC),
Departamento de Matemáticas, Universidad Carlos III de Madrid, Léganes, Spain
[3] Instituto de Biocomputación y Física de Sistemas Complejos, Universidad de Zaragoza, Spain
[4] Lester E. Fisher Center for the Study and Conservation of Apes,
Lincoln Park Zoo, Chicago, IL,United States of America
[5] Faculty of Business and Economics, University of Lausanne, Switzerland

The interplay of social structure and cooperative behavior is under much scrutiny lately since human behavior in social contexts becomes increasingly relevant for everyday life. Earlier experimental work showed that the existence of a social hierarchy, earned through competition, is detrimental for cooperation. We here study the case in which individuals in a group are ranked according to their performance in a collective effort, by having them play a public goods game in separate groups and subsequently ordering groups according to their total earnings. Our experiments using this setup show that, when faced with a cooperation dilemma in such a ranked group, there are no detrimental effects of the hierarchy, while when ranking is assigned individually we observe a decrease in cooperativeness. Our results show that the different response to the two types of rank assignment protocols arises from the fact that rankings are interpreted as reputation, indicating which subjects were cooperators in the previous phase. Our results point to the power to monopolize or assign resources as a key ingredient without which a hierarchy does not have effects.

We set out to study the case in which hierarchies are not linear but instead there is more than one individual at each ranking level. We also contribute to the knowledge of cooperation on hierarchical structure by considering the case in which one's ranking can arise competitively or with some contribution of cooperativeness. We study these issues by means of a novel experimental design which allow us to shed light on unexplored facets of cooperative behavior.

The experimental setup consists of three treatments: Selfish (or individual) Hierarchy (SH), Collaborative (or group) Hierarchy (CH) and Random Hierarchy (RH). The SH and CH treatments include two phases, named Phase I and Phase II, while the RH treatment only considers one phase, i.e. Phase II. During Phase I participants in the SH and CH treatments acquire a hierarchy playing a Public Goods Game. Participants playing the RH treatment begin the experiment directly at Phase II, with one of the four hierarchy profiles assigned to them at random. During Phase II participants play iterated Asymmetric Prisoner's Dilemma (APD) games.

Figure 1A shows the average contribution during Phase I. Participants cooperate sensibly more in the CH treatment with respect to the SH treatment in order to increase their group ranking position and thus obtain a higher hierarchy profile for Phase II. This is in agreement with theoretical predictions. Figure 1B depicts the average level of cooperation in APD games per round number. As is generally the case in these setups, the cooperation level is decreasing for all treatments as a function of the number of rounds. Participants' behaviors in the CH and RH treatments look very similar and rather different to the one observed in the SH treatment. This is to the fact that participants have been framed by the way in which hierarchy profiles are obtained and interpret them as a reputational label.

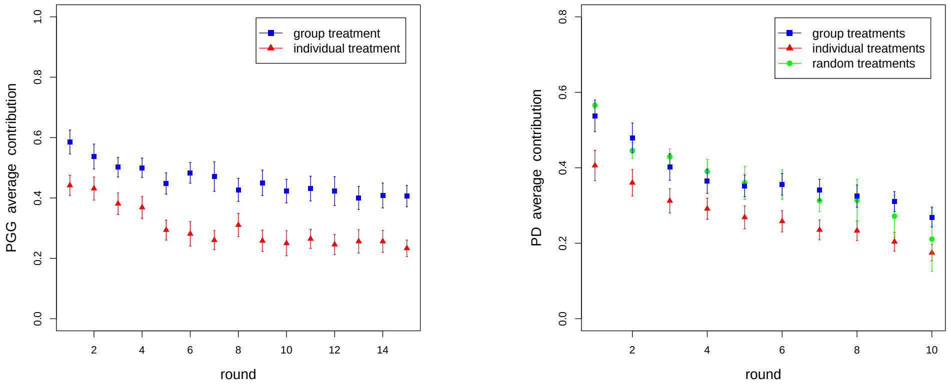

FIG. 1: (left) Public Goods Game average cooperation level (Phase I);
(right): asymmetric Prisoner's Dilemma games cooperation level (Phase II).

Criticality as key-concept to understand Social Norms' dynamics

Daniele Vilone[1,2], Giulia Andrighetto[1], John Realpe-Gómez[3]

October 10, 2017

[1] LABSS-ISTC, National Research Council (CNR), Rome, Italy.
[2] GISC – Departamento de Matemáticas, Universidad Carlos III de Madrid, Spain.
[3] Quantum Artificial Intelligence Laboratory, NASA Ames Research Center, CA-US

In a recent experiment [1], human subjects, put on a square lattice with 8 nearest neighbours, playing a weak Prisoner's Dilemma Game show three main possible strategies: always defection, always cooperation, or acting as a Moody Conditional Cooperator (MCC). The MCCs are the majority and behave according the following rules:

- If at the previous round the agent defected, now it cooperates with probability q;
- If instead it cooperated in the last round, now its probability to cooperate is $\Pi_{c\to c} = pK+r$, where K is the number of nearest neighbours which cooperated in the previous stage.

Therefore, we have here three parameters defining the model; p, q, r, whose empirical values, found fitting the experimental results, are

$$p \simeq 0.09; \quad q \simeq 0.2; \quad r \simeq 0.4 \ . \tag{1}$$

They appear to be at a critical point, that is, fixed for example q and r, the observed value of p is a critical value, as shown in Figure 1, where simulation results are reported. Other empirical results confirmed by simulations are the decreasing of cooperation rate from a higher initial value to a rate around 20% and the independence from the details of the network.

The fact that real MCCs are at a critical point can be explained by the fact that the global payoff reaches its maximum when the cooperation rate is also at its maximum, that is for $p \geq p^*$; on the other hand, evolutionary simulations show also that for $p > p^*$ MCC agents get rapidly extinct leaving absolute defectors alone. Therefore, only being at the critical point allows the system to maximize the global fitness.

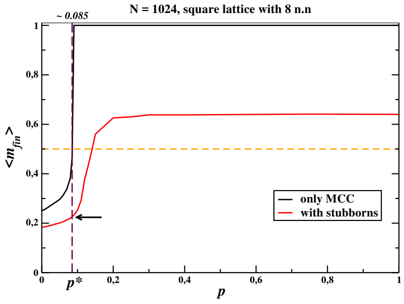

Figure 1: Final cooperation rate $\langle m_{fin} \rangle$ as a function of the parameter p, fixed q and r (see main text) for a system of $N = 1024$ agents. Black line: system with only MCC agents; red line: MCC agents mixed with stubborns (absolute cooperators and defectors in the proportions found in the experiment [1]). No evolutionary dynamics; for details on evolutionary simulations see main text. The arrow points out the state found empirically.

More details and deeper analyses to understand better this phenomenon are already on their way [2].

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Investigating the coevolution of institutions and social norms within game interactions on a multiplex network model

Francesca Lipari[1,2] and Alberto Antonioni[3,4,5]

[1] *LUMSA University of Rome, Italy*

[2] *National Research Council (CNR), Rome, Italy*

[3] *Department of Economics, University College London, UK*

[4] *Departamento de Matemáticas, Universidad Carlos III de Madrid, Léganes, Spain*

[5] *Instituto de Biocomputación y Física de Sistemas Complejos (BIFI), Universidad de Zaragoza, Spain*

Among other examples, we know that the same institutional change may have different effects according to the cultural environment and that social institutions, such as families, shape attitudes toward generalized morality and civic engagement. A social norm is a pattern of behavior such that individuals prefer to conform to it if 1) they believe that, 2) most people in their relevant network conform to it and 3) believe they ought to conform to it. Individual expectations are learnt and reinforced by actions coordination in their relevant network. Motivated by previous literature, we study socio-economic environments in which culture, expressed in terms of specific informal norms, and institutions jointly evolve and interact. We represent the society as a multiplex network structure in which all the players are positioned on its nodes. We investigate through computer simulations the evolution of the *cooperation* norm when players face a Prisoner's Dilemma game on the institutional layer and a pure coordination game on the institutional one. We find that the underlying network topology can drive the dynamics to more efficient and cooperative outcomes.

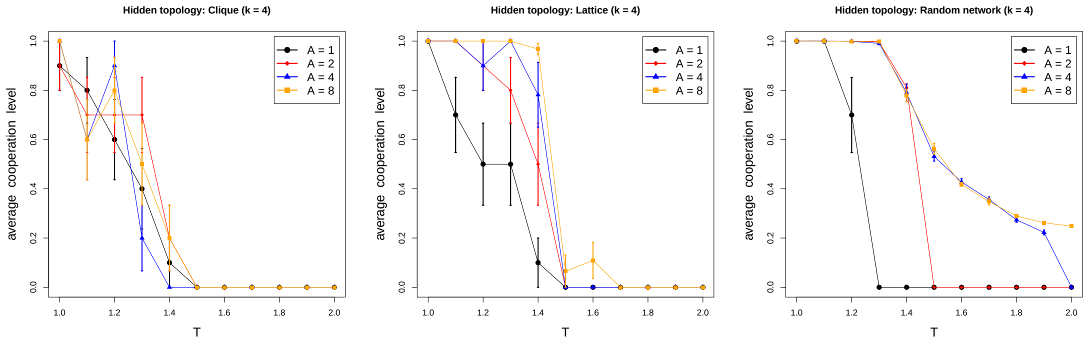

FIG. 1: Network influence as a function of the harshness of the Prisoner's Dilemma game, i.e. Temptation to Defect T, played on the social layer. Results for different institutional layers: clique, lattice and random network; and importance of the coordination game A played on the institutional layer.

Weighted openness coefficient as a measure of creative potential

Balazs Vedres
Central European University

How do network ties shape chances of creative success in a creative field, such as jazz music? Creativity needs network ties to provide access to cultural forms and to give insights into tacit knowledge on emerging styles and audience tastes. At the same time there is a risk of becoming locked into a cohesive network of groupthink, that stifles innovative agility. Workers of creative fields – jazz musicians in this case – need to maximize the benefits of both trusted partnerships, and fresh combinations of perspectives and musical styles.

In this article I propose a new measure for the creative potential of collaboration networks: the weighted openness coefficient. This coefficient measures the sum of geometric means of relative edge weights in open triads, normalized by the number of open triads.:

$$C_O = \frac{\sum_{\tau\Omega} \hat{w}_\Omega}{\sum \tau\Omega}, \qquad (1)$$

that captures weight of open triads independently of the proportion of triads that are open. C_O is set to zero for completely cohesive networks where $\sum \tau\Omega = 0$. (Graphs without any triads are excluded.)

Using data on the entire history of recorded jazz from 1896 to 2010 (175,000 jazz sessions) the paper presents evidence for a trade-off in the importance of the relative number of open triads, and weighted openness. The weighted networks at the level of a particular recording session indicate the number of past collaborations among musicians. Figure 1 shows predicted success by the proportion of open triads and weighted openness.

The results indicate that there are two paths to creative success: one is an open network, with weak ties and a high proportion of open triads. The other avenue to success is to have few open triads in the session, but with medium-high weights. One example for such a session was Miles Davis's "Kind of Blue" sessions in 1959.

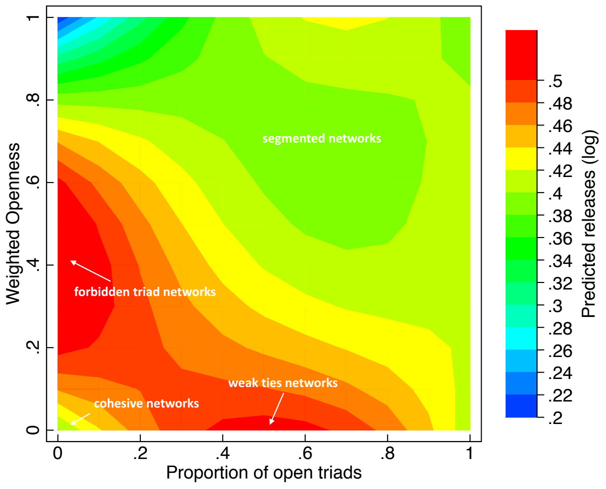

Figure 1: Predicted success (log number of releases) of a session by the proportion of open triads and weighted openness.

Understanding the dynamics of hashtags

Philipp Lorenz* and Philipp Hövel
Institute of Theoretical Physics, Technische Universität Berlin, Hardenbergstr. 36 D-10623 Berlin, Germany

Content in online media is highly dynamic, popularity of topics rises and falls within hours and this data becomes increasingly available. Hashtags as discrete and information-wise dense entities of online content are particularly usefull for the analysis of the general dynamics of topics on the web.

We consider various datasets, ranging from news blogs, twitter (both: snap.stanford.edu [1]) and image boards (pr0gramm.com) to fashion platforms (lookbook.nu). We find that the way hashtags gain and loose popularity follows similar distributions across all of them. In order to understand this common behavior we propose a model that incorporates following ingredients:

- Gaining interest follows a gradient-dependent preferential attachment (Fig. 1 left) [2].
- Borigness due to recent exposure within an attention span decrases fame (Fig.1 right).
- Ranked websites and limited attention capacity leads to competition among threads [3].

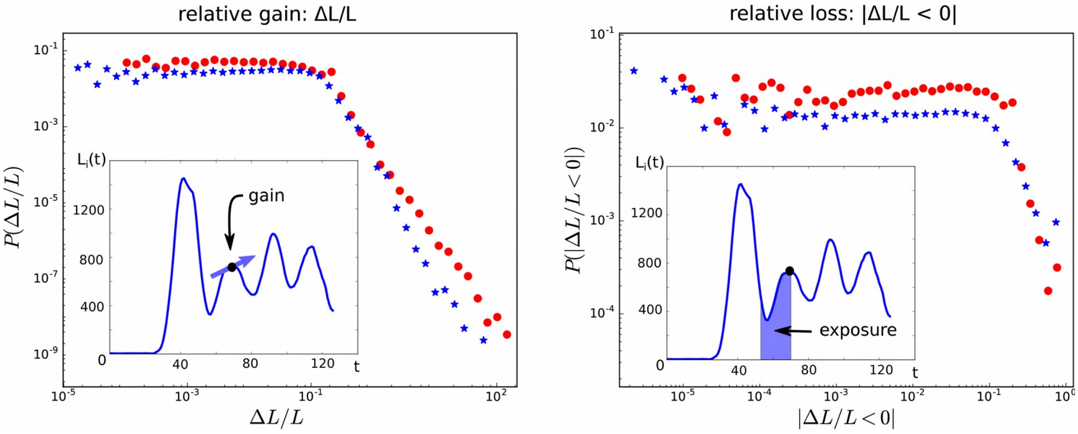

Figure 1: Comparison between the empirical distributions from twitter (red dots) of the relative gains ΔL/L (left) and the losses |ΔL/L < 0| (right) and the distributions from the simulated model (blue stars), which incorporates preferential attachment according to the current slope of the popularity curve and loss due to boringness from exposure during recent timesteps, as schematically shown in the corresponding inlets.

With this model we can reproduce the qualitative dynamics and the quantitative distributions of dynamical properties in the empirical observations, as shown in Fig. 1.

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*e-mail: philipp.lorenz@tu-berlin.de

Social Evolution of Structural Discrimination

Gorm Gruner Jensen[1], Stefan Bornholdt[1]
[1]Institute of Theoretical Physics, University of Bremen

Structural discrimination is a persistent phenomenon in social systems with crucial consequences for those whose lives it affects. It is often defined as discrimination when people are treated differently according to groups in which they are perceived to belong rather than individual qualities.

Classical economic game theory provide two main explanations of this fundamentally irrational discrimination. Either it is seen as an asymmetric Nash-equilibrium such as in the Hawk-Dove Game, or as a history-dependent selection between multiple Nash-equilibria in asymmetric games, such as employment situations, stabilized by collective reputation compensating incomplete individual information.

Both explanations, however, describes discrimination as rational decisions, in sharp contrast to the unconscious prejudice often described by sociologists and psychologists.

Here we outline the hypothesis that irrational discrimination can result from the evolutionary dynamics of the social system itself. We study the evolutionary dynamics of agents with neutral labels in a simple social game and find that if the selection pressure is high the labels are readily discriminated by the system although not being tied to the payoff matrix of the game. The sole property of being distinguishable leads to the subsequent discrimination, therefore suggesting an unexpected link between the emergence and freezing of social prejudice and intense competitiveness.

Preprint available on https://arxiv.org/abs/1703.06311

A networked voting rule for democratic representation

Alexis Hernández,[1,2] Carlos Gracia-Lazaro,[2] Edgardo Brigatti[1] and Yamir Moreno[2,3]

[1] Instituto de Física, Universidade Federal do Rio de Janeiro,
Rio de Janeiro, Brazil
[2] Institute for Biocomputation and Physic of Complex Systems (BIFI),
Universidad de Zaragoza, Zaragoza, Spain
[3] Department of Theoretical Physics, Faculty of Sciences,
Universidad de Zaragoza, Zaragoza, Spain

We introduce a general framework for exploring the problem of selecting a committee of representatives with the aim of studying a networked voting rule based on a decentralized large-scale platform, which can assure a strong accountability of the elected. The results of our simulations suggest that this algorithm-based approach is able to obtain a high representativeness for relatively small committees, performing even better than a classical voting rule based on a closed list of candidates. We show that a general relation between committee size and representatives exists in the form of an inverse square root law and that the normalized committee size approximately scales with the inverse of the community size, allowing the scalability to very large populations. These findings are not strongly influenced by the different networks used to describe the individuals interactions, except for the presence of few individuals with very high connectivity which can have a negative marginal effect in the committee selection process.

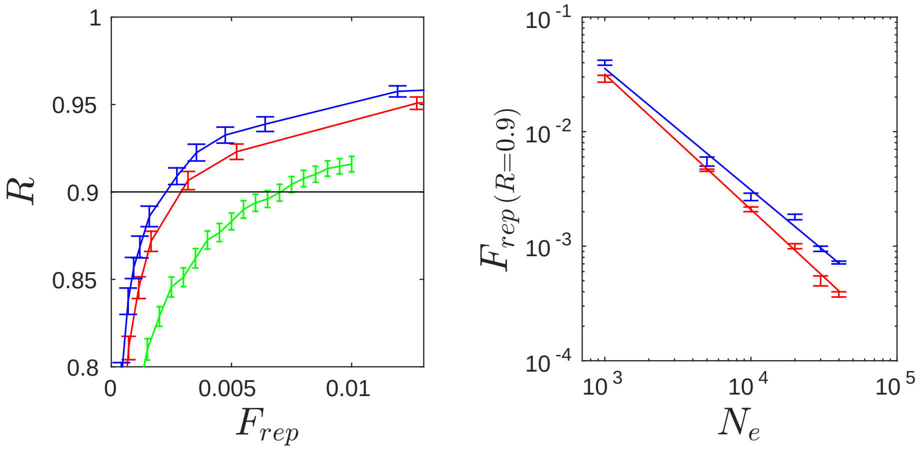

Figure 1: Left: Representativity vs the fraction of representatives for our model (blue curve), a model where a closed list of randomly selected politicians collect votes maximizing the overlap with the electorate (green curve) and a perfect voting rule (red curve). Right: logarithmic plot of the normalized committee size, for a representativity R = 0.9, as a function of the number of electors. Data are well approximated by a power-law fitting. The power-law exponent is 1.06 ± 0.05 for a Barabási-Albert network (Blue) and 1.18 ± 0.03 for a Erdös-Rényi network (Red).

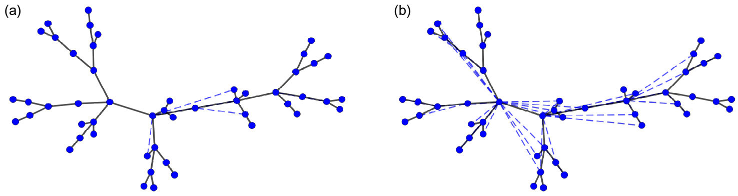

FIG. 1: Two instances of Node-Duplication networks of size $N = 50$, with $p = 0.1$ (a) and $p = 0.4$ (b). Both instances are formed around the same backbone tree (solid lines). Increasing p makes the network denser.

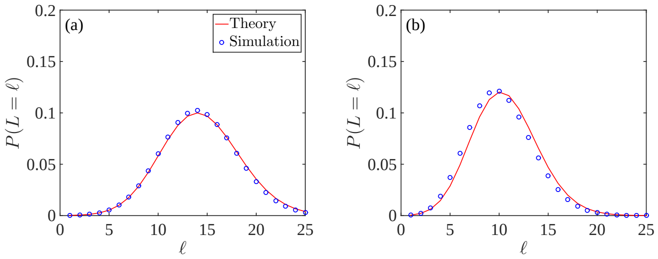

FIG. 2: The distribution of shortest path length of the Node-Duplication network of $N_t = 10^4$ nodes with (a) $p = 0.1$ and (b) $p = 0.3$. The theoretical results (solid lines) are found to be in very good agreement with the results of simulations (circles).

Distances in node-duplication networks

Chanania Steinbock, Ofer Biham and Eytan Katzav

Racah Institute of Physics, The Hebrew University, Jerusalem 91904, Israel,

To gain insight into the structure of complex networks, it is useful to study their growth dynamics. In general, it appears that many of the networks encountered in biological, ecological and social systems grow step by step, by the addition of new nodes and their attachment to existing nodes. In some networks, the new nodes emerge with no predefined connections, while in other networks the new nodes result from the duplication of existing nodes, followed by a stochastic readjustment of their links. The local structure of a network is captured by the degree distribution and by certain correlations between nearby nodes. The large scale structure is captured by the spectrum of path lengths between random pairs of nodes. The shortest path between each pair of nodes is of particular importance because it provides the strongest interaction and fastest response between these nodes.

The effect of node duplication (ND) processes on the structure of complex networks was studied using node duplication models. In a typical ND model at each time step a random mother node is selected for duplication. Its daughter node is added to the network, forming a link to the mother node, and with probability p to each one of its neighbors. Examples of the resulting network are shown in Fig. 1. The degree distribution of this network follows a power-law, making it a scale-free network. This model is suitable for the study of acquaintance networks, in which a newcomer who has a friend in a new community becomes acquainted with members of the friend's social group. In this model, the formation of triadic closures, which is an essential property of the dynamics of social networks, is built into the dynamics of the growing network.

In this talk I will present exact analytical results for the distribution of shortest path lengths (DSPL) in the ND model [1]. To this end we derived a master equation for the time evolution of the probability $P_t(L = \ell)$, $\ell = 1, 2, \dots,$ where L is the distance between a random pair of nodes and t is the time. Finding an exact analytical solution of the master equation, we obtained a closed form expression for $P_t(L = \ell)$. The mean distance is found to scale logarithmically with the network size, $\langle L\rangle_t \sim \ln N_t$, thus the ND network is a small world network. This result is in contrast to the "ultra-small" behavior observed in other scale-free networks, in which $\langle L\rangle_t \sim \ln\ln N_t$. In Fig. 2 we present the distribution $P_t(L = \ell)$ for an ensemble of ND networks of size $N_t = 10^4$, grown from a seed network of size $s = 2$, with $p = 0.1$ and 0.3. The analytical results are found to be in very good agreement with the results of simulations. The distribution turns out to be much broader than in other random networks.

In summary, I will present exact analytical results for the distribution of shortest path lengths in node duplication networks. These results provide insight into the large scale structure of ND networks and on the relation between the growth process and the resulting structure. Surprisingly, although the ND network is scale free, it is not ultra-small as usually assumed for scale-free networks, but rather only small-world. Interestingly, an exact result for the DSPL is achieved here for a non-equilibrium network model, while for the uncorrelated configuration model ensemble, which is considered to be much simpler, it is known only approximately.

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“Not to know is bad,
not to wish to know is worse”
Design: COSNET Lab

FLASH TALKS

Expectations, exerting influence through social norms, are a very strong candidate to explain how complex societies function. In the Dictator game (DG), people expect generous behavior from others even when they cannot enforce any sharing of the pie. Here we assume that people donate following their expectations, and that they update their expectation after playing a DG by reinforcement learning. With these assumptions, we construct a model that is able to explain the main experimental results in the DG: people expect reciprocity (donations higher than zero) and expectations (aspirations) are align to donations, as Fig. 1 shows for different parametrizations of the learning algorithm. Full agreement with the experimental results is reached when some degree of mismatch between expectations and donations is added into the model. These results are robust against the presence of envious agents, but affected if we introduce selfish agents that do not update their expectations. Our results point to social norms being on the basis of the generous behavior observed in the DG and also to the wide applicability of reinforcement learning to explain many strategic interactions.

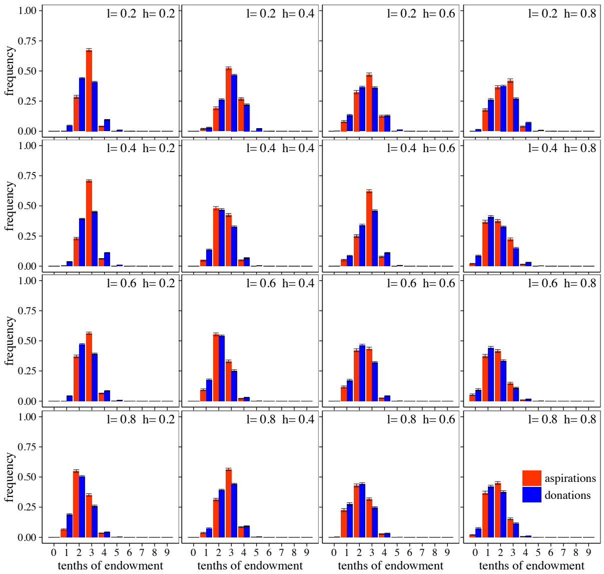

Figure 1: Final averaged distribution of aspirations and donations for $\varepsilon = 0.1$. Each subplot presents results for a combination of learning rate, l, (in increasing order from top to bottom) and habituation parameter, h, (in increasing order from left to right). Red bars, histograms of aspirations; blue bars, histograms of donations. Bins labelled n of the histograms count the frequency of donations with values verifying $(n/10) \leq D < (n+1)/10$. Error bars correspond to the standard deviation arising from averaging over 100 realizations.

Studying the effects of network nodes sensitivity in a model of brain dynamics poised at criticality

Rodrigo Pereira Rocha, Loren Kocillari, Samir Suweis, Amos Maritan
University of Padua, Department of Physics and Astronomy “Galileo-Galilei”

Large-scale neuronal dynamics models, i.e. whole-brain models, have attracted great attention of the scientific community to unveil key mechanisms about the relationship between brain function and brain structure. Despite the vast amount of whole-brain models found in literature with different degrees of complexity, some empirical signatures of brain at rest, such as the functional connections (FC) between brain regions and the emergence of resting state networks (RSNs) are only partially understood and still poorly reproduced. The increase in the predictive power of whole-brain models is a fundamental step that can trigger many fundamental applications, such as quantitative discriminations between healthy and lesioned subjects. It has been shown [1] that brain at rest may be poised near a critical state, defined as the special point in the space of parameters where the system displays the maximum susceptibility/complexity, i.e. it optimally and collectively responds to external inputs [2]. Exploiting this notion of criticality and following seminal work of Haimovici et al. [2], we propose a biological meaningful yet simple stochastic model which is able to predict the brain organization into resting state networks through only few independent parameters. In this study we developed biological meaningful parametrization of the structural connectivity matrix (SC) (i.e., the human connectome) that increases the match between simulated and empirical data. In addition, using our modeling approach we are able to distinguish between simulated healthy and lesioned brains.

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Deciphering a regulatory system beyond the transcriptional regulation performed by the FUR family in *Anabaena* based in protein-protein interactions.

Cristina Sarasa[1,2], Isabel Valero[1], M. Teresa Bes[1,2], Adrián Velázquez Campoy[1,2,3] , María F. Fillat[1,2], María Luisa Peleato[1,2], Emma Sevilla[1,2].

[1] Department of Biochemistry and Molecular and Cell Biology, University of Zaragoza. Zaragoza, Spain, 50009.
[2] Institute for Biocomputation and Physics of Complex Systems (BIFI), University of Zaragoza. Zaragoza, Spain, 50009.
[3] ARAID Foundation, Government of Aragón. Zaragoza, Spain, 50018.

The Ferric uptake regulator (Fur) protein is a global regulator found in most prokaryotes. Although Fur proteins are specifically known for the regulation of several iron responsive genes, they are involved in a variety of metabolic pathways. DNA sequence analysis of the *Anabaena* sp. PCC7120 genome confirmed the presence of three open reading frames: all1691 *furA*, all2473 *furB* (*zur*) and alr0957 *furC* (*perR*) containing the histidine-rich region characteristic of the FUR family. The three paralogues share different implications in several cellular processes in cyanobacteria. FurA takes part of a cross-talk between iron and nitrogen regulatory networks[1] and also participate in the close connection between iron homeostasis and oxidative stress, as in the case of FurB[2] and FurC[3]. FurC the least characterized of the three, has been related with a possible implication as a modulator of the DNA-binding activity of FurB and FurA[4]. The evidences were based in changes on FurA and FurB DNA-binding activities in the presence of FurC. In our work, we aimed to obtain more insights into this possible complex regulation of a system formed by the three fur paralogues in *Anabaena*. We studied the *in vitro* protein-protein interaction between FurC and FurA as well as with FurB using ITC (isothermal titration calorimetry). These experiments were confirmed with new EMSA assays, to elucidate whether there was a modulatory effect by FurC on the FurA and FurB DNA binding activity. In addition, transcriptional analyses of a *furC*-overexpression *Anabaena* strain were performed to study the expression levels of genes that are part of the FurA or FurB regulon.

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International Conference BIFI 2018

Abstract

J.J. Galano-Frutos[I,II], J. Sancho Sanz[I,II]

[I] Institute for Biocomputation and Physics of Complex System, Saragossa, Spain.

[II] Department of Biochemistry and Molecular and Cellular Biology of the University of Saragossa, Saragossa, Spain.

Title: Energetically validated structural model for the unfolded state of proteins.

A deep understanding of the principles governing protein stability[1] is required for applying quantitative methods to the description and control of biological and technological phenomena in which that stability plays a key role.[2] To understand well and address the protein stability issue a synergistic approach both from the experimental and computational point of views should be carried out. One of the biomolecular phenomena in which protein stability has a special relevance is the protein folding/unfolding. To the best of our knowledge, the possibility to computationally calculate the energetics associated to this process has not been exploited yet. Here, we show an *in silico* approach -including atomistic Molecular Dynamics- from which both the unfolding enthalpy variation and the unfolding specific heat capacity variation for two small, two-state proteins are accurately calculated: the *Bacillus amyloliquefaciens* barnase[3] and the *Staphylococcus aureus* nuclease.[4] It allowed us to estimate the associated Gibbs' free-energy through the integrated Gibbs-Helmholtz equation,[5] and also to propose a reliable structural model for the unfolded state of these two proteins, something that had not been shown before. Our results indicate that a fine atomistic model of the fully unfolded ensemble of a protein can be generated from its sequence, and at the same time demonstrate an impressive accuracy of the force fields used in this work to calculate thermodynamic parameters linked to protein folding/unfolding. Likewise, this work may open a way to compute protein folding energetics in larger, non-fully cooperative proteins with reasonable computational cost and to investigate the energetics of equilibria difficult to analyse experimentally.

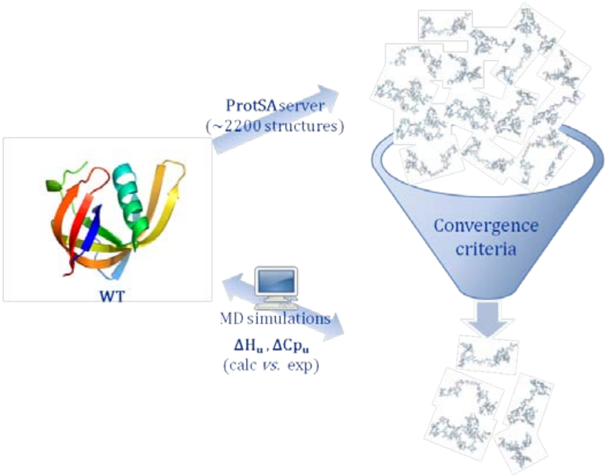

Figure 1. Methodological scheeme to develop our structural model for the unfolded state of proteins.

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Social Influence in Music Listenership: A Natural Experiment on 1.3 Million Last.fm Users

Taha Yasseri
Oxford Internet Institute, University of Oxford, Oxford, UK
Alan Turing Institute, London, UK
taha.yasseri@oii.ox.ac.uk

Social influence has been an important topic of research in the social sciences. We use Last.fm's song-listen data to quantify social influence on music listenership around live events. We study live events performed by “Hyped” (i.e. trending) and “Top” (i.e. most popular) artists. We analyse how listenership changes around the time of the live event both for users who attended the event, and more importantly, for those who did not, but are friends with someone who attended. We use three distinct types of data: (1) event attendance, (2) track listens, and (3) the Last.fm friends network.

We extracted all live events in 2013 and 2014 by the most popular Hyped and Top artists. We tracked listenership of 1.3 million users over a two-month time horizon—with one month of listenership data prior to the attendance of an event and one month of listenership data after the attendance of the event.

In order to assess the direct impact of live events on attendees' listenership, we use a regression discontinuity design. We find strong evidence of direct impacts on listenership among concert attendees of both Top and Hyped Artists. As seen in Figure 1, the impacts of the datasets are comparable—a Top Artist live event increases listenership by 1.13 of a song (z-test p-value<.001), while a Hyped Artist live event increases listenership by 1.05 of a song (z-test p-value<.001).

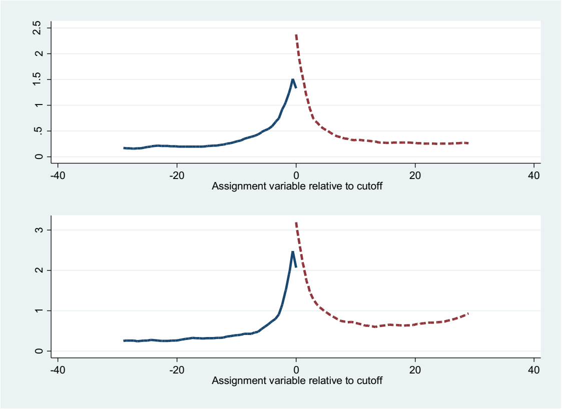

Figure 1: Graphical Depiction of the Regression Discontinuity Estimate of Impact of Live Event

To determine if the attendee then, in turn, influences their friends, who have *not* attended the same event, we apply the same regression discontinuity design to all friends of the attendees. The indirect effect on friends of Top Artist attendees is a 0.060 additional song plays, or more than 5% of the direct impact on listenership. While this is a trivial impact on its own, it is important to emphasize that the mean Top Artist attendee has 81.3 friends. This means that one user’s attendance translates to 4.8 more song plays on average. The indirect effect on friends of Hyped Artist attendees was not significant.

To determine whether the indirect impact increases as the number of friends who attended the event increases, we run a series of regression discontinuity analyses across non-attending users with various numbers of attending friends. We see that as the number of friends who attended the event increases, the influence on listenership increases monotonically. It is possible that individuals with more friends are simply more persuadable. To better discern if this pattern stems from multiple attendees exerting influence on the non-attender, we perform a permutation test. Namely, we look at the discontinuity estimates across number of attendee friends in our actual dataset and then compare these results to a synthetic dataset where we held the friend network constant but randomly assigned that non-attending friend to a different live event date of the same artist in the same 60 day period such that no participant in their friend network attended that live event. We observe that the indirect effects vanish in the shuffled network, confirming the presence of social influence within the friendship network.

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Analysis of citizen science publications at global scale

Fermín Serrano (1, 2)
Jesús Clemente (1,2, 3)
Alfredo Ferrer (2, 3)
Mari Carmen Ibáñez (1)
Maite Pelacho (1, 4)
Francisco Sanz (2,1,3)
Alfonso Tarancón (2, 3)

1 Ibercivis www.ibercivis.es
2 Instituto de Biocomputación y Física de los Sistemas Complejos de la Universidad de Zaragoza
3 Kampal Data Solutions
4 Universidad del País Vasco

Citizen science is gaining relevance in the last years because its potential to enrich both research and social aspects through public involvement in science. Contributions from the general public occur in all the steps of the the research cycle. This open paradigm is consolidated in some areas of knowledge such as biodiversity or environmental monitoring, and it is growing rapidly in other like digital humanities or physics behavior.

To understand the evolution of the citizen science concept, its impacts and formats, Ibercivis created in 2016 the Observatory of Citizen Science of Spain www.ciencia-ciudadana.es with the support of the FECYT. In this initiative, more than 150 practices have been catalogued and located in a Map. Also, a number of analysis, networking and dissemination activities take place regularly.

One of these activities is the analysis of the scientific publications containing ‘citizen science’ in it their title, abstract of keywords. With the support of the Kampal Data Solutions S.L. we have downloaded from the Web of Science hundreds of papers from thousands of authors*. Having this set of papers and authors as starting point, we have analyzed several qualitative and quantitative aspects, including the evolution of publications in number and JCR impact, the communities emerging from collaborations i.e. co-authorship, and gender issues among others.

We found some scientific papers in early 2000s but the number of publications is growing exponentially since 2012. We can observe prominent role of USA and UK communities behind projects such us eBird and Zooniverse, but the diversity of topics and formats under research is also growing significantly globally. The number of publications with citizen science as subject of research is also relevant representing the opportunity of this pardigm to observe and to understand general public motivations and performance.

Authors are aware that having this specific search based on the term ‘citizen science’ makes the study incomplete leaving out a great number of research practices which could be categorized as citizen science. However, this study is one of the earliest and greatest meta studies on citizen science trends and its taxonomies.

* At the moment of writing this abstract 710 papers with 2676, but we will update this study for the BIFI2018 Conference.

SBM is discrete surface tension

Zachary M. Boyd
University of California—Los Angeles

Community detection using stochastic block models (SBMs) is rapidly gaining popularity among network scientists because of its relatively high level of mathematical rigor, flexibility, and applicability to real data. Normally, SBMs are interpreted in a probabilistic framework and optimized using a variety of algorithms, such as belief propagation.

In my talk, I will show that, in the context of maximum likelihood estimation, SBMs have another interpretation in terms of surface tension. This reformulation yields three very different approaches to uncovering community structure that follow naturally from the surface tension viewpoint. The maximum likelihood estimation problem for a degree-corrected SBM, for instance, can be cast as the problem of minimizing the following function:

$$\sum_{\alpha,\beta=1}^{\hat{\text{n}}} \sigma_{\alpha\beta} \operatorname{Cut}(\alpha,\beta) + e^{-\sigma_{\alpha\beta}} \frac{\operatorname{vol}(\alpha)\operatorname{vol}(\beta)}{2m} \tag{1}$$

where $\sigma_{\alpha\beta}$ encodes the affinity between communities α and β, Cut denotes the graph cut, $\operatorname{vol}(\alpha) = \sum_{i\in\alpha} \operatorname{degree}(i)$ is the volume of cluster α, m is a normalizing constant, and $\hat{\text{n}}$ is the number of communities.

This is analogous to minimizing the continuum functional

$$\sum_{\alpha,\beta=1}^{\hat{\text{n}}} \sigma_{\alpha\beta} \operatorname{Per}(\alpha,\beta) + e^{-\sigma_{\alpha\beta}} \frac{\operatorname{vol}(\alpha)\operatorname{vol}(\beta)}{2m}, \tag{2}$$

where we interpret the parameters as follows: $\operatorname{Per}(\alpha,\beta)$ is the surface area between regions α and β, $\sigma_{\alpha\beta}$ encodes the surface tension density between the materials composing regions α and β, $\operatorname{vol}(\alpha)$ denoted ordinary volume or area, and m is, again, a constant. The analogy between Eqs. 1 and 2 is explained further in Fig. 1.

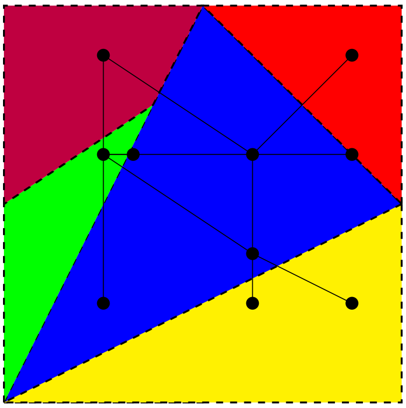

Figure 1: Comparison between continuum surface tension dynamics and SBM maximum likelihood estimation. The perimeters between the different regions are analogous to the graph cuts between subgraphs, and the surface tensions between the regions are analogous to the affinities between different communities.

Models such as Eq. 2 have been studied for many years in the partial differential equation (PDE) community [3], and breakthroughs on appropriate numerical methods for such problems are still happening [5]. My coauthors and I leveraged this connection to derive new, efficient numerical methods for maximum likelihood estimation on SBMs that are inspired by the PDE literature. We were able to show experimentally that three numerical solvers based on mean curvature flow, diffuse interfaces, and threshold dynamics, respectively, can be generalized to the case of networks, giving very competitive results. These include exact recovery of planted partitions, exact recovery when community sizes are highly uneven, and exact recovery when many communities are present. The speed of these methods is such that a simple MATLAB implementation is able to process a network with one million edges in seconds.

This is joint work with Mason Porter and Andrea L. Bertozzi. It was inspired by three related papers, which are worth noting. First, in [4] Hu et al. showed that modularity optimization can be cast as a total variation minimization problem, which is similar to perimeter minimization. Second, in [6], Newman showed that modularity optimization is a special case of maximum likelihood estimation. Third, in [2], the modularity criterion was again linked to total variation, but with a heavier emphasis on graph volumes. These works together suggested that the stochastic block model may have an interpretation in terms of surface areas and volumes, which our work shows to be the case.

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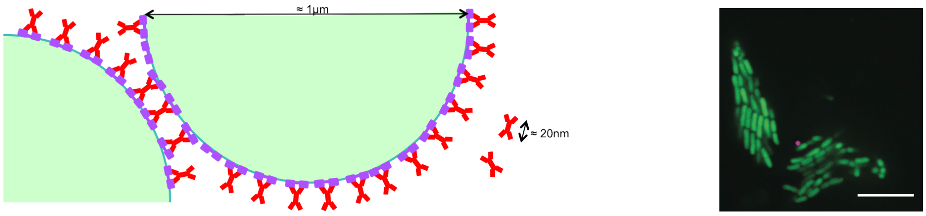
Modeling the physical mechanisms underlying immune system/bacteria interactions in the gut

F. Bansept[1], E. Slack[2], R. R. Regoes[3], R. Voituriez[1], C. Loverdo[1]
[1]Laboratoire Jean Perrin - CNRS - UPMC
[2]Institute of Microbiology - ETH Zürich
[3]Institute for Integrative Biology - ETH Zürich

While inside the organism, the immune system immediately recognizes bacteria as intruders to be eliminated, the situation is very different in the gut lumen. The digestive system microbiota – which is composed of even more microorganisms than the number of cells composing the human body [1] – is very useful to its host, helping for example in many digestive tasks. Yet, some bacteria are still pathogenic for the host if they proliferate in the intestine. The challenging task which falls to the immune system in this body part is thus to preserve the gut flora equilibrium essential to the host's health. However, little is known as to how it is able to discriminate between beneficial and noxious bacteria.

Inside the gut lumen, the main effector of the immune system is Immunoglobulin A (IgA), a specific kind of antibody secreted in high quantities if triggered by previous infection or vaccination [2]. IgA have been known for a long time to be able to bind bacteria together, due to their structure with several binding sites (see figure 1.). However, it had always been thought that the observed clusters were the result of random meetings of bacteria, which are actually very unlikely at the typical initial concentrations in the common case of food poisoning. We recently contributed to show in the mice that this clustering happens through enchained growth : dividing bacteria remain stuck together, hence forming clonal clusters of daughter-bacteria [3]. The bacteria once agglomerated are prevented from approaching the epithelium and colonizing the rest of the organism, and eliminated more easily [4].

We now argue that since enchained growth is a growth-dependent process triggering preferentially fast-growing bacteria – which are the most susceptible to disrupt the gut flora equilibrium and thus become pathogenic – it could be a mean for the immune system to regulate the microbiota composition. We therefore explore quantitatively this idea with various models of clustered growth and were indeed able to show that the number of free bacteria is drastically reduced for faster-growing bacteria in our models.



(a) (b)

Figure 1: **(a)** Schematic of bacterial agglomeration with Immunoglobulin A.
(b) Fluorescent microscopy image of live cecal content 5h post infection

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Using SOMbrero for clustering and visualizing large cattle-trading networks

M. Olteanu[1,2], G. Beaunée[3], C. Bidot[1], C. Laredo[1], E. Vergu[1]
1 - MaIAGE, INRA, Université Paris Saclay, 78350 Jouy-en-Josas, France
2 - SAMM (EA4543), Université Paris 1 Panthéon Sorbonne, 75013 Paris, France
3 - Bioepar, INRA, Oniris, La Chantrerie, 44307 Nantes, France

In the current world context, with a globalized production system and highly interconnected farms, understanding and controlling livestock diseases and their spreading are critical issues both for food industry and for public decision-makers. In order to prevent outbreaks, it appears essential to characterize and predict animal trade movements, as major pathogen-inducing pathways between farms.

A convenient way to grasp and explore the general structure of this complex system is to use a dynamic graph representation. Indeed, the vertices of this network are the farms (and also the commercial operators such as markets and assembly centers), while the edges represent animal exchanges between farms. This graph is directed (sellers send cattle to buyers), weighted (each edge is labelled with the number of exchanged animals), and time-varying (a transaction occurs at a given time-instant). Furthermore, additional information on the vertices, such as geographical situation, type of farm, ... is usually available. With this representation, mathematical models integrating the dynamics of the network, but also the epidemics spreading on the temporal network and the farmers' behaviour with respect to trading may be developed and investigated. However, one of the limits of these models is their scalability, whereas cattle-trading networks are usually of substantial size. For instance, the data at our disposal, concerning the exchanges involving French farms from 2005 until 2009 with a daily resolution level, contains millions of edges and hundreds of thousands of nodes. In this context, it is important to build a reduced version of this network, by identifying groups of vertices with common features (in a broad sense).

In this paper, we propose an exploratory study of the French cattle-trading network using self-organizing maps and, more particularly, the recently developed **R**-package **SOMbrero**, which implements both numerical and relational versions of the algorithm. The output consists in a clustering of the vertices and a nonlinear mapping of the graph, which is a reduced version of the original network. The SOM algorithm may be trained either on vector data, which may be numerical features extracted from the dynamical graph or from snapshots of it, or on relational data, which may be any kernel or dissimilarity computed on the vertices or on the edges, such as, for example, the dynamic shortest-path distance. We will illustrate both versions of the algorithm by providing some of the outputs (see Figures 1 and 2 for an example of the algorithm trained on numerical features extracted from one yearly snapshot of the network) and explaining the benefit of each of them in the process of understanding the inner mechanisms of the network.

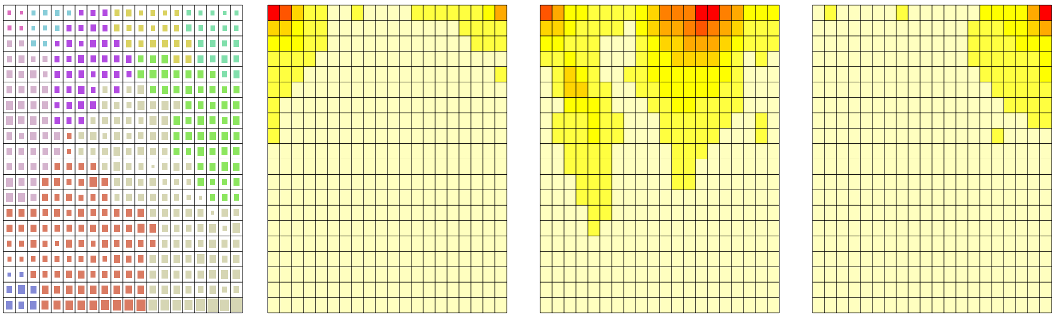

Figure 1: Output of a numerical SOM (grid of size 10x10), trained on the 2005 snapshot. Distribution of the ten final clusters (left image) and distribution of three of the numerical features (right images) used for training: number of sold animals, number of trading partners, suckler-cows farms. The orange/red cells correspond to high values of the features.

Soft Matter

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Bidirectional motion of filaments: the role of motor proteins and passive cross linkers

Subhadip Ghosh,[ab] V. N. S. Pradeep,[c] Sudipto Muhuri,[d] Ignacio Pagonabarraga[ef] and Debasish Chaudhuri *[ab]

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In eukaryotic cells, motor proteins (MPs) bind to cytoskeletal filaments and move along them in a directed manner generating active stresses. During cell division a spindle structure of overlapping antiparallel microtubules forms whose stability and dynamics under the influence of MPs have been studied extensively. Although passive cross linkers (PCLs) are known to provide structural stability to a filamentous network, consequences of the interplay between ATP dependent active forces of MPs and passive entropic forces of PCLs on filamentous overlap remain largely unexplored. Here, we formulate and characterize a model to study this, using linear stability analysis and numerical integration. In the presence of PCLs, we find dynamic phase transitions with changing activity exhibiting regimes of stable partial overlap with or without oscillations, instability towards complete overlap, and stable limit cycle oscillations that emerge *via* a supercritical Hopf bifurcation characterized by an oscillation frequency determined by the MP and PCL parameters. We show that the overlap dynamics and stability depend crucially on whether both the filaments of an overlapping pair are movable or one is immobilized, having potential implications for *in vivo* and *in vitro* studies.

1 Introduction

The cytoskeleton in eukaryotic cells is a complex network of interlinking filaments associated with motor proteins (MPs) and passive cross linkers (PCLs). It plays a central role in controlling the cell shape and motility apart from being also involved in intra-cellular transport. For example, the cytoskeleton controls mechanical processes in the essential mechanism of cell division. In fact, the process of chromosome segregation to daughter cells in eukaryotes is achieved by the formation of a spindle structure composed of overlapping microtubules (MTs).[1–3] In a spindle, interpolar MTs from two microtubule originating centers (MTOC) grow antiparallel to each other to interdigitate at the cell midzone. On the other hand, astral MTs grow towards the cell membrane, where active force generators like dynein capture these MTs and pull them towards the cell cortex.[4] The active dynamics of the spindle, and its positioning and oscillations controlled by motor proteins (MPs) have been studied in detail.[4–9] The Kinesin-8 family of MPs Kip3 has been identified for its role in active length control of MTs and generation of relative sliding force between MT pairs.[10,11] Experimental and theoretical studies showed how force generation by dynamic MTs together with MPs contributes to the positioning and morphology of spindles, microtubule originating centers and nuclei in cells.[12–17] The important role that collective dynamics of cytoskeletal MPs plays in intra-cellular transport has been studied using *in vitro* and *in vivo* experiments, and theoretical studies.[18–25,27]

A large body of experimental and theoretical work has focussed on active MP-filament systems,[26–28,35] *e.g.*, a filamentous actin–myosin complex that forms the cell cortex,[29–31] and MP driven active self-assembly of filamentous proteins.[32–34] These studies have clarified the subtle and rich interplay between filaments and MPs in the emergence and stability of the cytoskeleton, as well as qualitative differences of active complexes with respect to their equilibrium counterparts. Although the presence of PCLs in the cytoskeleton has been known for a long time, relatively less attention has been paid to their role in determining the various structural properties of the cytoskeletal network. Only recently has it become clear that they may also play an important role in the spindle formation during mitosis. For example, it has been shown that PCLs can increase sliding viscous friction between overlapping filaments,[36] and provide stability to the overlap.[37] In fact, it has been predicted that PCLs can stabilize the overlap of antiparallel MTs in the mitotic spindle, competing against MP pull.[38,39] Recent studies on *in vitro* motility assays have

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[a] *Institute of Physics, Sachivalaya Marg, Bhubaneswar 751005, India. E-mail: debc@iopb.res.in*
[b] *Homi Bhaba National Institute, Anushaktigar, Mumbai 400094, India*
[c] *Indian Institute of Technology Hyderabad, Yeddumailaram 502205, Telangana, India*
[d] *Department of Physics, Savitribai Phule Pune University, Ganeshkhind, Pune 411007, India*
[e] *Departament de Física de la Matèria Condensada, Universitat de Barcelona, Carrer Martí i Franques 1, ES 08028 Barcelona, Spain*
[f] *École Polytechnique Fédérale de Lausanne, Lausanne, Vaud, Switzerland*

Resilient Networks with Adaptive Capacity

Yukio Hayashi[1] and Naoya Uchiyma[1]

Japan Advanced Institute of Science and Technology, Ishikawa, Japan

Cascades of overload failures [1] cause a serious problem with large damage in sociotechnological networks such as power-grid (blackout), economic trading (bankruptcy), communication or traffic system (congestion or jamming), and so on. Not only the topological structure of network but also the change of routing to heterogeneously distributed load $\{L_i(t)\}$ is deeply related to the intrinsic dynamics of flow on the network and to the damage size of the consequence of propagation of overload failures. We propose a **congestion-aware routing** with random ordering of transfers but without rewiring cost [2] and intentional sacrifice of nodes [1] in order to drastically reduce cascading overload failures. Our **adaptive routing** which changes the policy from shortest-based to load-based selection of paths is superior to the conventional navigation strategy [3] on paths by avoiding passing through high degree nodes. Especially for the resilience in the meaning of adaptive capacity [4] to supplely absorb pressure of transfer load by our **distributed detour routing**, growing onion-like networks [5] have larger adaptation than scale-free (SF) networks found in many real systems. The adaption becomes more remarkable in the trigger of multiple atacks. At least, it has been known that onion-like networks with positive degree-degree correlations have optimal robustness of connectivity [6]. Thus, our obtained results will be useful for prospective topological design and furthermore control of flow in future infrastructural networks.

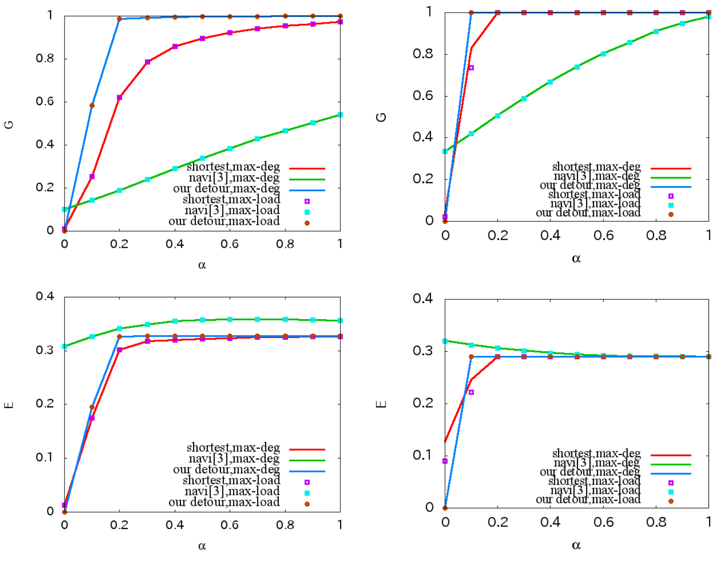

Fig. 1. Resilience against cascading failures triggered by a node of the maximum degree or load. Comparison of our adaptive congestion-aware detour routing with the conventional shortest-based one and navigation [3] by G: relative size of the giant component and E: efficiency w.r.t path lengths for the parameter α in $C_i \overset{\text{def}}{=} (1+\alpha)L_i(0)$. The change of routing policy distributes flow and inhibits cascading overload. (Left) SF, (Right) onion-like nets with $N = 1000$, $\langle k \rangle \approx 8$.

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COMPLEX ROAD
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Exploiting a cognitive bias promotes cooperation in social dilemma experiments

Marko Jusup[1] with Zhen Wang[a], Lei Shi[b],
Joung-Hun Lee[c], Yoh Iwasa[c], and Stefano Boccaletti[d]

[1]Center of Mathematics for Social Creativity, Research Institute for Electronic Science, Hokkaido University, Sapporo 060-0808, Japan; **presenter**
[a]Center for OPTical IMagery Analysis and Learning (OPTIMAL), Northwestern Polytechnical University, Xi'an 710072, China
[b]Statistics and Mathematics College, Yunnan University of Finance and Economics, Kunming 650221, China
[c]Faculty of Science, Kyushu University, Fukuoka 819-0395, Japan
[d]Institute of Complex Systems of the CNR, 50019 Florence, Italy

The decoy effect is a cognitive bias documented in behavioural economics by which the presence of a third, (partly) inferior choice causes a significant shift in people's preference. Resting on this bias is a critique of one of the cornerstones of decision theory, the so-called independence of irrelevant alternatives axiom. We performed an experiment with human volunteers who played a variant of the repeated prisoner's dilemma game with "reward" as a decoy option. Although this decoy gets largely ignored, it sparks a significant increase in overall cooperativeness and improves the likelihood of success for cooperative individuals. We trace these outcomes back to increased willingness of volunteers to cooperate in the first step of each game, and subsequent propagation of such willingness by (noisy) tit-for-tat (Fig. 1). Our study thus reveals an untapped potential of decoys to elicit prosocial action. Moreover, given the recent hypotheses on the evolutionary origins of cognitive biases, we discuss how human cooperation may have evolved as a largely accidental consequence of living in heterogeneous and autocorrelated environments.

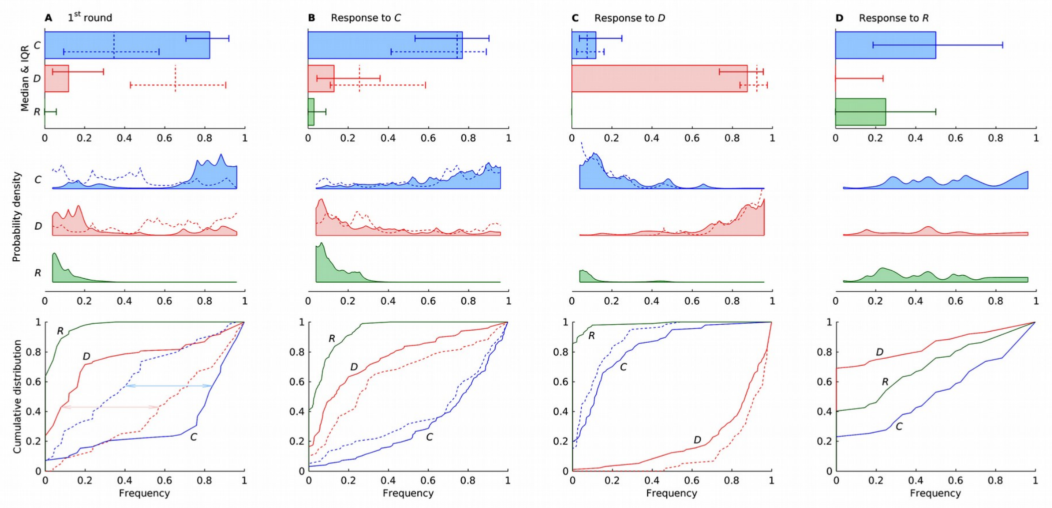

Fig. 1: As a cooperation promoter, reward is effective even before it can be used. ***A****, Median frequency of cooperation C in the first round of the decoy treatment (bars) is considerably higher than in the control treatment (dashed lines): 82.4% vs. 34.7%, respectively. The opposite is true of defection D: 12.0% vs. 65.3%, respectively. Probability densities show the frequency distributions, while cumulative densities reveal how distant these distributions are when decoy is compared to control (two-sample Kolmogorov-Smirnov test for C; K-S statistic 0.5772; p-value <* 10^{-10}*).* ***B–D****, Past the first round, response to C in the previous round is overwhelmingly C irrespective of the treatment (two-sample Kolmogorov-Smirnov test for C; K-S statistic 0.1184; p-value 0.6467), response to D in the previous round is overwhelmingly D irrespective of the treatment (two-sample Kolmogorov-Smirnov test for D; K-S statistic 0.1979; p-value 0.0958), while response to R in the decoy treatment is either C or to a lesser extent R. These results suggest that the presence or absence of decoy greatly affects the first round of an encounter. In the later rounds, by contrast, volunteers play what seems to be noisy tit-for-tat.*

Cooperative vs. defective pathogens, at evolutionary stationary state

Fakhteh Ghanbarnejad
fakhteh.ghanbarnejad@gmail.com
Institut für Theoretische Physik, Technische Universität Berlin, Berlin, Germany

In this work, we first extend the interacting SIS model [1]. Thus we consider each pathogen has two different strategies: cooperator or defector, see Fig. 1-b, and treat the dynamics in a mean field approximation. By scanning the parameter space as well as varying initial conditions we show where bi-stability can happen and which strain will prevail within each pathogen in the stable branches. In order to understand if the chosen strategy is stable in an evolutionary scenario, see Fig. 1-a,we then apply Hawk and Dove game to this spreading dynamics. We show that by cooperation pathogens can affect even larger amount of the host population at evolutionary stationary state (ESS). Also although in wide range of parameters cooperators are the winners at ESS but defectors have also the chance to take over in a small area of the parameter space and suppress the high influence of the cooperators in the host population.

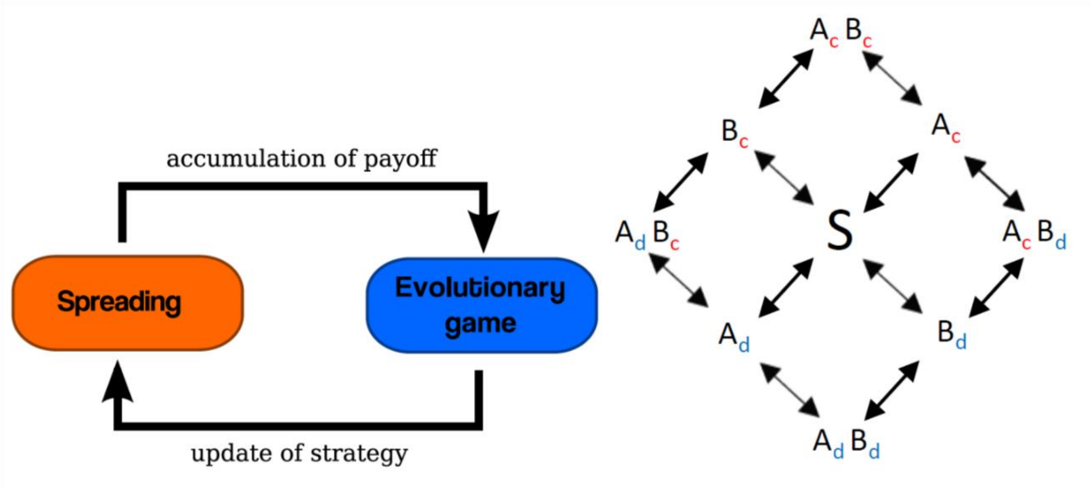

Fig. 1: Schematic representation of the coevolutionary dynamics between disease spreading and evolution of cooperation. Panel (a) shows the global evolutionary dynamics: The outcome of seasonal dynamics is used as initial condition for the other. The processes are applied in cascade several times until the evolutionary stationary state (ESS) is reached. Panel (b) represents schematically the seasonal dynamics, i.e. spreading dynamics: all the possible transitions among compartments in the multi disease propagation of diseases [A] and [B] while cooperation and defection are both present.

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Quantifying phase synchronization in global surface air temperature data

Dario Zappala[1], Marcelo Barreiro[2], Cristina Masoller[1]

1 Universitat Politecnica de Catalunya, Terrassa, Barcelona, Spain.

2 Universidad de la Republica,Montevideo, Uruguay

We analyze observed climatological data from a complex system perspective. Specifically, we apply the Hilbert transform to time series of daily surface air temperature (SAT, Fig. 1), covering a regular grid over the Earth surface, in a period of more than three decades. We quantify Hilbert phase synchronization between the different geographical regions by using the well-known Kuramoto parameter. We find strongly synchronized oscillations in the extra-tropics while there is low synchronization in the tropical region. These finding are interpreted as due to the different time-scales of main climatic phenomena: while ENSO (the well-known El Niño or La Niña, which occur in the tropics) has a characteristic time-scale of 3-6 years, the main modes of variability in the extra-tropics (Rossby waves) are much faster.

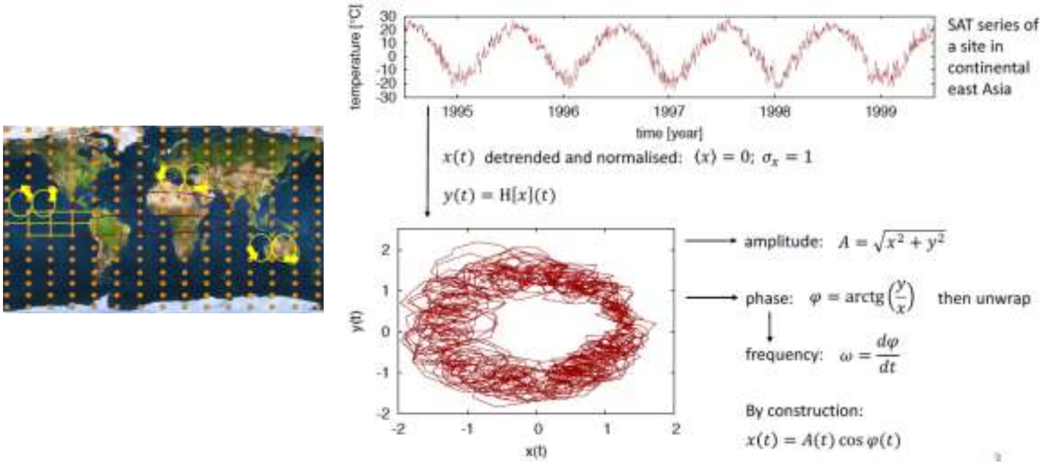

Fig. 1. Left: Schematic representation of the regular grid of geographical locations where phase synchronization is investigated. Right: procedure to extract Hilbert phases from observed SAT.

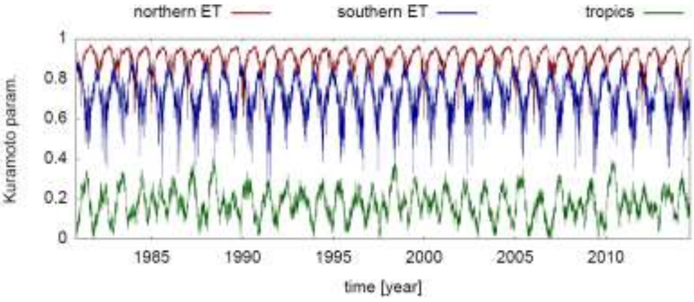

Fig. 2. Kuramoto parameter, computed from Hilbert phases, as a function of time. High synchronization is detected in the northern hemisphere (latitude above +30), lower synchronization in the southern hemisphere (below -30), and almost no synchronization in the tropical band (in between 30 and -30).

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Molecular basis of the interaction of the human Apoptosis Inducing Factor with its nuclear partners

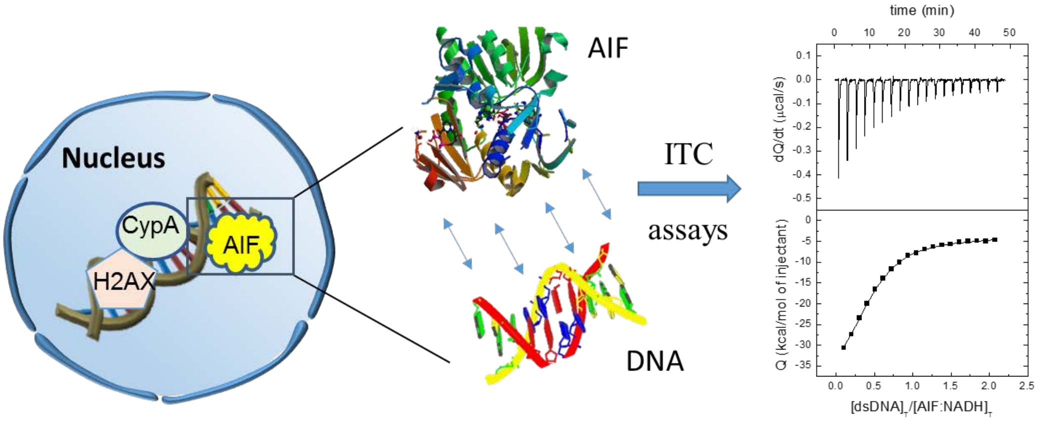
Silvia Romero-Tamayo[1], *Adrián Velázquez-Campoy*[1, 2], *Milagros Medina*[1], *and Patricia Ferreira*[1]

[1]*Department of Biochemistry and Molecular and Cellular Biology and Institute of Biocomputation and Physics of Complex Systems, University of Zaragoza, Spain.*
[2]*ARAID Foundation.*

The Apoptosis Inducing Factor (AIF) was first discovered as a caspase-independent cell death promoter that also played a vital role in mitochondria, where it is normally confined [1]. In healthy mitochondria, AIF contributes to the maintenance and stability of several respiratory chain complexes and is present in a monomer-dimer equilibrium regulated by NADH/NAD$^+$ levels. NADH reduction produces AIF dimerization as well as conformational rearrangements of the reductase and apoptotic domains. These observations suggest an interconnection between the mitochondrial and apoptotic activities of AIF, making worth the understanding the intriguing relationship between redox states and cellular activities [2].

After cell death induction, AIF is liberated into cytosol, and then translocated to the nucleus where induces DNA degradation into 50 kb fragments (typical chromatinolysis caspase-independent pattern) [3]. The interaction of human AIF (hAIF) with the DNA occurs in an independent manner based on electrostatic interactions [4]. To exhibit its lethal activity AIF requires the requitment of other nuclear proteins to form a degradasome, where AIF binds to an Histone and to nucleases, such as cyclophilin A (Cyp A) [5, 6].

In this contribution, we present the *in vitro* characterization of the interaction of hAIF with some of its nuclear partners (DNA, Cyp A and H2A), as well as the influence of the hAIF redox state in their modulation, by using gel-retardation and isothermal titration calorimetry (ITC) techniques.



Studying the interaction of hAIF with its physiological partners
in the nucleus by ITC technique. (PDB ID 1BNA, 4BUR)

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Combating bacterial multidrug resistance: new drugs against *Helicobacter pylori*

S. Salillas[1,2*], *M. Alías*[1,2], *V. Michel*[3], *J. Bueno*[4], *J. Arribas*[4], *A. Lucía*[5], *L. Rodrigues*[5], *A. Mahía*[1,2,6], *C. Sostres*[4], *J. A. Aínsa*[5], *J. A. Carrodeguas*[1,2], *J. Castillo*[4], *A. Lanas*[4], *M.D. Díaz-de-Villegas*[6], *E. Touati*[3], *A. Velázquez-Campoy*[1,2,7] *and J. Sancho*[1,2,*]

[1]University of Zaragoza. Department of Biochemistry and Molecular and Cellular Biology. Zaragoza, Spain. [2]Universitiy of Zaragoza. Biocomputation and Physics of Complex Systems Institute (BIFI). BIFI-IQFR(CSIC)-Joint Unit. Zaragoza, Spain. [3]Pasteur Institute. Unit of Helicobacter Pathogenesis, Department of Microbiology. Paris, France. [4]University Hospital Lozano Blesa. Service of Digestive Diseases. Zaragoza, Spain. [5]University of Zaragoza. Department of Microbiology, Preventive Medicine and Public Health. Zaragoza, Spain. [6]University of Zaragoza-CSIC. Department of Catalysis and Catalytic Processes. Institute of Chemical Synthesis and Homogeneous Catalysis (ISQCH). Zaragoza, Spain. [7]ARAID Foundation, Diputación General de Aragón, Zaragoza, Spain.

The increasing antibiotic resistance in *Helicobacter pylori* (*Hp*), whose infection is associated with chronic gastritis, peptic ulcers, gastric cancer and several extragastric diseases, results in a decreased eradication rate of the current treatments. That is why new specific therapies are required. The flavodoxin of *H. pylori* (*Hp*-Fld) is an electron carrier involved in the production of NADPH, which is an essential process for *Hp* viability. This protein has been identified as a target for the development of new antibiotics against this bacterium. Accordingly, several compounds were identified as inhibitors of the *Hp*-Fld. Some of its functional groups were modified by chemical synthesis in order to improve its *in vitro* (against three commercial *Hp* strains) and *in vivo* (in mice) properties, and also its affinity (measured by Isothermal Titration Calorimetry). Nowadays, we are studying the mechanism of action and the pharmacokinetic properties of the best developed compounds to obtain new specific antimicrobials against *Hp*.

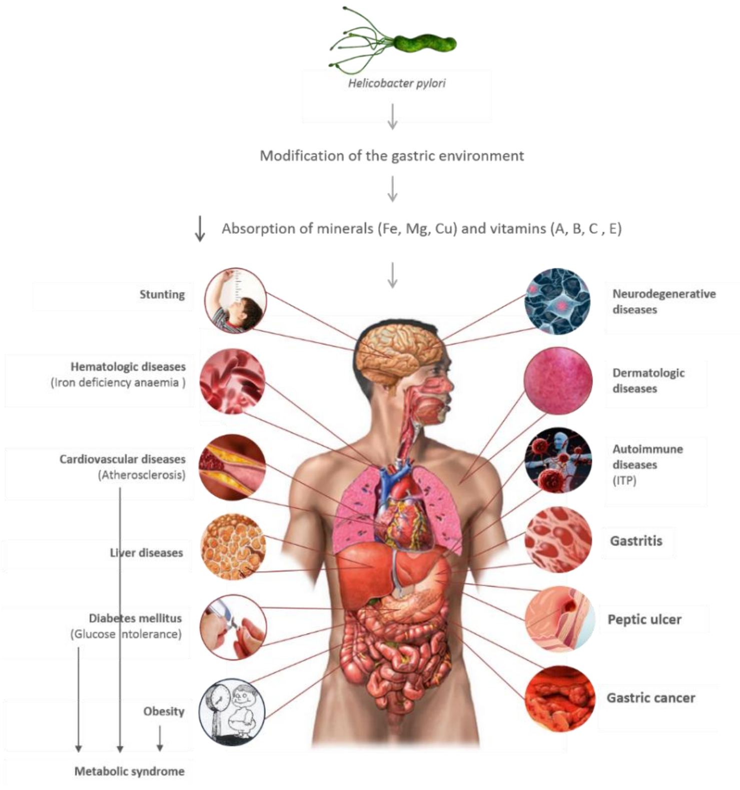

Figure 1. *Helicobacter pylori*-related diseases.

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*Correspondence: sandrasb@unizar.es / jsancho@unizar.es

Epidemic detriment driven by recurrent human mobility patterns

J. Gómez-Gardeñes[1,2], A. Arenas[3] and D. Soriano-Paños[1]
[1]Departamento de Física de la Materia Condensada, Universidad de Zaragoza, 50009 Zaragoza, Spain
[2] Instituto de Biocomputación y Física de Sistemas Complejos (BIFI), Universidad de Zaragoza, 50018 Zaragoza, Spain
[3]Departament d'Enginyeria Informàtica i Matemàtiques, Universitat Rovira i Virgili, 43007 Tarragona, Spain

During recent years, we have witnessed the outbreak of some important diseases such as the H1N1 pandemic in 2009, Ebola in 2014 and Zika in 2015. A common feature of these illnesses is that they were originated in a little region and then, after some elapsed time, they propagate at large scale to turn into worldwide epidemics. This fact have encouraged the researchers to do models capable of taking into account the contagious processes at a local scale and also the large scale mobility processes which lead to the global propagation. By this way, metapopulation models have emerged.

A metapopulation is a complex network where nodes are associated to places in which the agents live. These agents can move over the network, being their displacements determined by the links. Therefore, mobility patterns are encoded by links. Even though first metapopulation models relied on diffusion processes to represent the movements of the agents, we have chosen commuting proccesses to model the agents movement due to their higher degree of realism. In this sense, several articles have been written proposing models in order to face the large scale spread of a disease considering commuting processes [1-3]. Even though some interesting results have been obtained, all these models make some assumptions, mainly heterogeneous mean field, which limit their predictability.

In order to avoid this fact, we leave this assumption and make all the agents statistically independent. Under this premise and considering commuting processes, we propose a model (MIR Model) using a MMCA (Markovian Microscopic Chain Approach). In our model, each agent has a node associated to him. For each time step, agents decide whether staying in their node or going to another node with a probability p. If they decide to move, they choose their target in function of the weights of the mobility matrix $\mathbf{W}$. Once all the agents have moved, contagious processes take place. In order to characterise them, we consider a SIS model and also a well mixed population inside each node, so that each agent interacts with the rest who are inside his node. After all agents have updated their dynamical state according to the SIS model, we force the agents to return to their residence.

To check the validity of this new model, we compare its predictions about the global incidence of a disease over the city of Cali to numerical results from Monte Carlo simulations. In Fig.1 we can observe the accuracy of our model since there is an almost exact agreement between theory and simulations. Besides, we can notice there how mobility makes the epidemic spreading more difficult since the epidemic threshold increases with the mobility. To understand this phenomenon, we use a perturbation method[4] which reveals the existence of three regimes which correspond to continuous detriment, non-monotonous detriment and no detriment with the mobility.

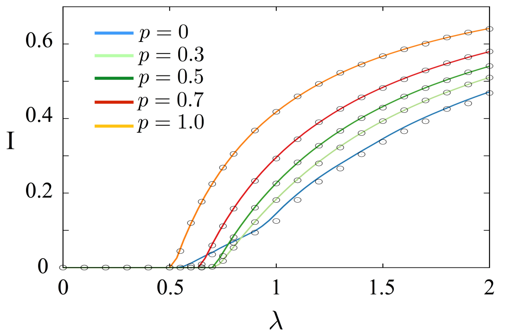

Figure 1: Total fraction of infected people I as a function of λ after the onset of a SIS disease over the city of Cali. Solid lines, whose colours represent different values of the mobility of the agents p, correspond to the predictions of our MIR model, whereas black dots are the numerical results from Monte Carlo simulations. The recovery rate μ is set to $\mu = 0.2$.

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Alternated model for the interplay between epidemics and awareness

Paulo Cesar Ventura da Silva[1,*], Francisco Aparecido Rodrigues[2] and Yamir Moreno[3]

[1]Instituto de Física de São Carlos - São Carlos, Brazil
[2]Instituto de Ciências Matemáticas e de Computação - Sâo Carlos, Brazil
[3]Institute for Biocomputation and Physics of Complex Systems - Zaragoza, Spain
[*]paulo.pc.vs@gmail.com

Abstract

The human behavior strongly influences the propagation of contagious diseases. Guided by the information, people adopt preventive methods such as vaccines, hand hygiene, contact prevention and others. Recent works have tried to model the interplay between human behavior and the epidemic spreading in society [Manfredi and D'Onofrio (2013)], including the influence of information about the diseases.

Multiplex networks are a very useful tool to model such interplay, as they allow us to capture the multiple structures of interaction present in society. In this work, we propose the use of multiplex networks to study the interplay between disease and information spreading in society, enhancing previous works on this subject [Granell et al. (2013, 2014)].

Our model considers a two-layer multiplex, with one layer propagating an SIS epidemic and the other a Maki-Thompson informational (rumor) spreading, where nodes can either be unaware (U), aware (A) or *stiflers* (R). The informational state influences the epidemic spreading as nodes that are aware of the disease avoid infection, reducing their contagion probability by an adjustable factor $\rho < 1$. Infected nodes can also become aware of the disease with a probability κ per time step. With probability γ, aware nodes loose interest in propagating the information and become *stiflers* when they contact other aware or stifler nodes.

We also include a stochastic alternation between informational and epidemic iterations. At each time step, the information process is updated with probability π, and the epidemic process is updated with probability $1 - \pi$. This feature allows us to simulate different time scales between the two processes.

We promote a Microscopic Markov-Chain Approach (MMCA) calculation to estimate the stationary prevalences of each state in this model. We study the epidemic curves (i.e., stationary fraction of infected nodes as a function of the transmission probability β_{ep}) for different values of the alternation parameter π. Our first results show that, for smaller values of π, the prevalence of infected nodes is smaller. However, the epidemic threshold is not affected by the value of π.

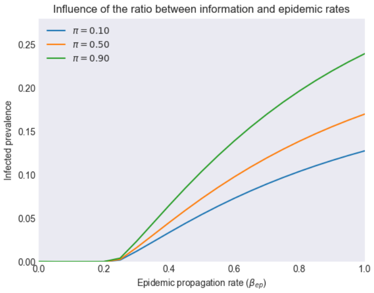

Figure 1: Stationary fraction of infected nodes as a function of the epidemic transmission probability, for different values of the alternation parameter π.

We also study the effects of degree-correlations between the two layers (inter-layer assortativity). For large values of the informational transmission probability β_r, the assortative case (positive correlations) always produces a smaller infected prevalence when compared to the neutral and dissortative cases. However, we show that, due to the inclusion of *stiflers* in the model, such behavior can be reversed for small values of β_r.

Acknowledgements

We thank Fapesp for the financial support (grant number 2016/24555-0).

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Coevolution of synchronization and cooperation in costly networked interactions

Alberto Antonioni[1,2,3] and Alessio Cardillo[4,3]

[1] *Department of Economics, University College London, UK*

[2] *Departamento de Matemáticas, Universidad Carlos III de Madrid, Léganes, Spain*

[3] *Instituto de Biocomputación y Física de Sistemas Complejos (BIFI), Universidad de Zaragoza, Spain*

[4] *Institut Català de Paleoecologia Humana i Evolució Social (IPHES), E-43007 Tarragona, Spain*

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. [Physical Review Letters (2017) 118: 238301]

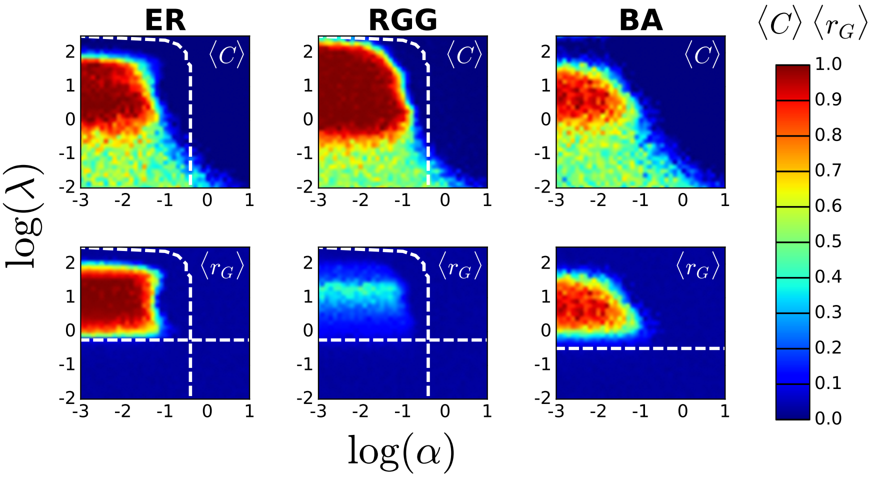

FIG. 1: Emergence of cooperation/synchronization at global scale. The top (bottom) row illustrates the average level of cooperation (synchronization) $\langle C \rangle$ ($\langle r_G \rangle$) as a function of the coupling λ and game relative cost α. Each column corresponds to a different topology, namely: ER, RGG and BA.

Matteo Morini*°, Sarah de Nigris#

* Université de Lyon, Inria, CNRS, ENS Lyon, UCB Lyon 1, Laboratoire de l'Informatique du Parallélisme UMR 5668, Institut Rhône-Alpin des Systèmes Complèxes, DANTE

° Department of Economics and Statistics, University of Torino

\# CNRS, Institut Rhône-Alpin des Systèmes Complèxes, ENS Lyon, Laboratoire de Physique UMR 5672

A Simple Model of Coevolution for Macroscopic and Microscopic Levels

Abstract:

In Thomas Schelling's famous segregation model, it is shown that the link between the individual characteristics of agents (micro) and the global states of the system (macro) is not trivial. By the use of statistical physics tools [1] it was possible, nevertheless, to establish an analytical link between these two levels, characteristics of agents (utility function) and global structures of segregation.

This work aims to build a similar conceptual model, but includes an important sociological ingredient: the evolution of individual characteristics. Economic models have often been subject to criticism (by sociologists, mainly) about their arbitrary and static set of individual characteristics.

In our approach we thus blend in the the standard segregation model a simple co-evolution mechanism of micro and macro levels in order to encompass, at least to some extent, the aforementioned limitation. More specifically, we add a feedback mechanism linking the agents' interactions and their individual characteristics.

The most dramatic departure from the standard model regards the movement rule as we endow the agents with the possibility of wisely deciding their relocation target and, moreover, this choice is informed both by their own personal preferences and by their social ties' ones.

In practice, instead of picking a different random empty cell on the lattice, unhappy agents move to the location which better suits their preferences, albeit with some noise. An adaptive decision mechanism is implemented in form of a per-agent "palatability" matrix pM_i, the size of the whole lattice, which is initialized with average values. As soon as agents appear in the model, they evaluate their location (standard Moore neighborhood) and establish links with their neighbors (proportional to their tolerance: 0 = same type only, 1 = equally split between types) on an undirected and unweighted graph. During each iteration of the model, each agent evaluates the option of either staying or leaving, given her tolerance threshold. In the latter case, the relocation target is decided mixing both the agent's personal preferences and its acquaintances': for instance, one possible strategy is to build a final decisional matrix $F(pM_i)$ from the personal matrix pM_i, and the connected agents' matrices, pM_j $(j = 1, ..., n)$, linearly weighted by a given "stubbornness" parameter $\alpha \in [0, 1]$, $F(pM_i) = \alpha pM_i + (1-\alpha)\sum_{j=1}^{n} pM_j/n.$

For the sake of simplicity, connected agents are averaged with equal weight. The absolute best tile is taken as the destination.

With this approach, we thus aim to study the co-evolution of preferences and global states in order to identify possible stationary states (at both levels).

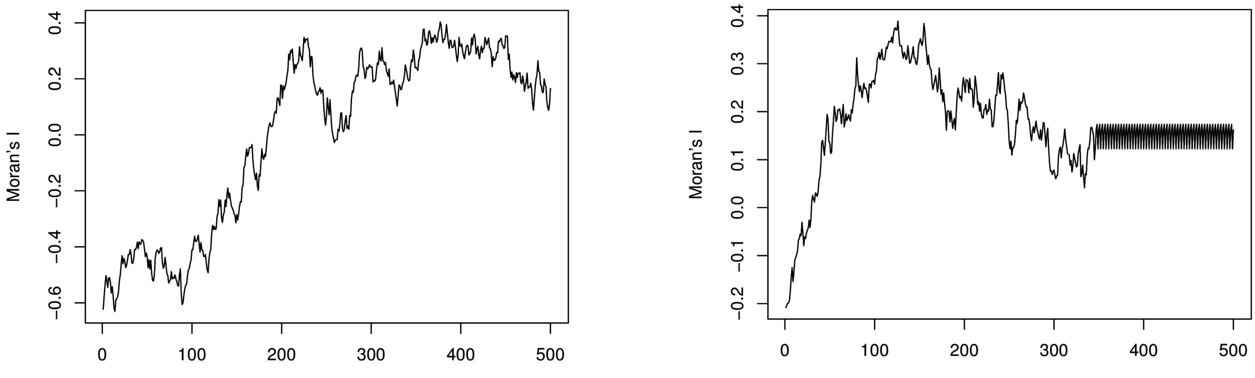

Figure: Spatial autocorrelation (Moran's Global I) time series without (left) and with (right) social influence.

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Intertemporal collective behavior in economics: allocations of time use at home

José Alberto Molina, University of Zaragoza, BIFI, IZA
José Ignacio Giménez-Nadal, University of Zaragoza, BIFI, CTUR
Jorge Velilla, University of Zaragoza

Abstract

The household had traditionally been as a whole unit, although this unitary approach raised several difficulties and limitations. The work of the 1992 Nobel prize Gary Becker (Becker, 1973, 1974, 1981) motivated the need of a new approach to the study of the family, and several collective models of household behavior appeared in the 1980s, but it was the generalized "collective" framework what supposed a change in the paradigm of how the household should be studied (Chiappori, 1988, 1992; Bourguignon et al., 1993; and Browning and Chiappori, 1998; Chiappori et al., 2002). This general collective framework explicitly considers the preferences of husbands and wives within households, and several studies have pointed toward the validity of this framework, subtracting relevance to the unitary approach. Despite of that, most of the literature has remained in the static field. In this paper, we propose a general collective model in an intertemporal framework, considering a household formed by two members $i = 1, 2$, living for T discrete periods of time. We consider two scenarios, one in which household members can commit to a time-fixed allocation plan and then reach Pareto-efficient outcomes, and another in which this allocation plan can be renegotiated. This model is based on the existence of an intra-household decision process, and a sharing rule to allocate household non-labor income. We identify this sharing rule, and thus it can be obtained from the partial derivatives of the labor supplies of household members. We then use the United States Panel Study of Income Dynamics (PSID) to estimate these labor supplies, and then the sharing rule, from a specific semi-logarithmic parametrization of husbands and wives labor supply functions.

Figure. Outline of the model

$$\text{For } i = 1, 2: \max_{\{h_{it}, c_{it}\}_{t=0}^{T}} E_0 \textstyle\sum_{t=0}^{T} u_i(c_{it}, 1 - h_{it})$$

$$\text{s.t.: } c_{it} + s_{it} = w_{it} h_{it} + \varphi_{it}, \ t = 0, \dots, T$$

$$h_{1t} = H^{1t}(w_{1t}, \varphi_t(w_{1t}, w_{2t}, y_t, s_{t-1}, \boldsymbol{z}, \boldsymbol{d}), h_{1t-1}, \boldsymbol{z}),$$

$$h_{2t} = H^{2t}(w_{2t}, y_t + s_{t-1} - \varphi_t(w_{1t}, w_{2t}, y_t, s_{t-1}, \boldsymbol{z}, \boldsymbol{d}), h_{2t-1}, \boldsymbol{z}).$$

Note: $u_i(.)$ represents member *i* individual preferences, as a utility function on consumption (c) and leisure ($1 - h$); s_{it} represents savings; *w* represents wage rates, and ϕ represents the sharing rule of household non-labor income, *y*. The family of individual labor supply functions $\{h_{1t}, h_{2t}\}$ represent the solution of the maximization problem, and the sharing rule ϕ_t can be derived from their partial derivatives, given a specific parametrization.

species i is λ_i, $M_{ij} > 0$ and $M_{ij} < 0$ denote symbiosis and competition between species i and j, respectively. U_i is usually defined in the positive orthant and we may restrict ourselves to it [8]. A generalization of these results to flows not recognizable as QP systems can be found in [6,7]. As examples of other transformations aiming to reduce the degree of non-linearity of a given system we cite the Carlemann procedure, in which a system of ODEs is led to an infinite dimensional linear system [9] and the Kerner procedure which relates the original system to quadratic forms [10]. More recently, a methodology to embed a multi-dimensional dynamics into a one dimensional case is presented in [11,12], which deals with the related concept to stability known as resiliency, or the ability of a system to return to equilibrium after a perturbation.

The fixed points U^* of (3) relate to those of (1), say x^*, through $U_i{}^* = \prod_{k=1}^{n} (x_k{}^*)^{D_{ik}}$, $i = 1, \ldots, n$. The following theorem was presented in [1–4]:

Theorem 1. *Given the QP system (1) and its associated $M = DC$ matrix, if M is admissible and the QP has an interior positive fixed point $x^* \in \Re^n_+$, then the function $V = \sum_{i=1}^{m} a_i(U_i - U_i^* \ln \frac{U_i}{U_i^*} - U_i^*)$ is a Lyapunov function for (1).*

The matrix M is said to be *admissible* if there exists $a_i > 0$, $i = 1, \ldots, n$, that satisfy [13]:

$$\omega^T\, Diag(a_i) M \omega \leq 0\,, \tag{4}$$

which is equivalent to $\sum_{i,j=1}^{n} a_i M_{ij} \omega_i \omega_j \leq 0$; $\omega \in \Re^n$. Here ω is a column vector, ω^T its transpose and $Diag(a_i)$ a diagonal matrix with elements a_i.

The necessary and sufficient conditions for a matrix to be admissible are not known. An algebraic and a numeric procedure was developed in references [1–4] providing a suitable methodology for obtaining sufficient conditions for stability in a given system. The algebraic procedure is based on the fact that (4) is a quadratic inequality in ω_1, thus, in order to satisfy eq. (4) for $\forall \omega \in \Re^n$ we must have:

$$a_1 M_{11} < 0, \text{ and } \beta(\omega_2, \cdots, \omega_n)^2 - 4 a_1 \gamma(\omega_2, \cdots, \omega_n) \leq 0\,, \tag{5}$$

or

$$a_1 M_{11} = 0 \Rightarrow M_{11} = 0, \text{ and } \beta(\omega_2, \cdots, \omega_n) = 0 \text{ and}$$
$$\gamma(\omega_2, \cdots, \omega_n) \leq 0. \tag{6}$$

As the inequalities (5) and (6) do not involve ω_1, the procedure can be iterated. In each step one set of conditions split in two and from a matrix M of dimension n we obtain 2^{n-1} independent sets of conditions. A numeric algorithm is presented in references [4,14]. It is an extension of a result presented in [15] and involves the resolution of a *linear programming problem*. In [4,14], some of the authors analyzed the inequality: $L(M, P) \equiv PM + M^T P \leq 0$, with $P > 0$ diagonal, known as a *linear matrix inequality*, the strict case $L(M, P) < 0$ often appearing in system and control theory [16].

3. Evolutionary stable states and game theory

Our purpose in this work is to link the concept of evolutionary stable states to stable fixed points in squared QP systems. Having defined the class QP system in previous section, here we make a brief overview of the main concepts of evolutionary games before presenting our main result in section 4.

Consider a given species possessing several different phenotypes in its gene pool. According to natural selection, the most adapted phenotype is the one capable to generate more offspring, all of them carrying its genes. In this way, after several generations, this phenotype becomes more frequent than others, ultimately leading to the extinction of other phenotypes. Maynard Smith was one of the pioneers in the use of game theory in the study of the dynamics of genes or phenotypes [17]. According to him the *payoff* for the *winner* of the game is a gain in *fitness* defined as an abstract potential or ability to generate an offspring.

Game theory tries to mathematically analyze conflict situations [18,19]. The game comprises a set of *movements*, in which the players choose a given *strategy* among a set of alternatives. The set of all the movements performed by the players that resulted in the present configuration is denoted the *state* of the game. The game is said to be of *perfect information* if the state of the game is known to all players. The game is *finite* if it involves only a finite number of movements over a finite number of choices. After the end of the game, it is usual to assign a payoff to the winner. Consider the following example of a game played by two participants J_1 and J_2 [18,19]. J_1 chooses among m numbers in the set a whose elements are a_i; $i = 1, \cdots, m$. Player J_2 chooses in its turn among n numbers in the set b with elements b_j; $j = 1, \cdots, n$. The game ends after these two movements (a finite game). Player J_2 pays to J_1 a given amount of money defined by the payoff $m \times n$ matrix of the game, say Y, where Y_{ij} represents the payoff to J_1 when J_2 chooses strategy b_j and J_1 chooses strategy a_i. When J_1 chooses the i-th strategy he knows he will receive at least $min_j Y_{ij}$. Knowing this he picks up i in order to maximize its gains to receive at least $max_i min_j Y_{ij}$. In the same way if J_2 chooses strategy j he knows to lose, at most, $max_i Y_{ij}$. Then his choice is dictated by the minimum of the latter $min_j max_i Y_{ij}$. A game has a saddle point Y_{ij} if $max_i min_j Y_{ij} = min_j max_i Y_{ij} \equiv \nu$, and in this case it is called a *strictly defined* game, with ν its *solution*. The particular case $\nu = 0$ is a *fair game*. Each action of J_1 or J_2 is a *pure strategy* [20].

It is of course possible that a matrix does not possess a saddle point. Even so a solution for the game can be obtained if we extend the concept of strategy. Suppose a given two person game is played repeatedly. Given the m pure strategies available to P_1, he can choose a different strategy each time the game is played with a given probability x_i. The *mixed strategy* is then defined as

$$x = (x_1, \cdots, x_m), \quad 0 \leq x_i \leq 1, \quad \sum_{i=1}^{m} x_i = 1.$$

Similarly J_2 adopts the mixed strategy $y = (y_1, \cdots, y_n)$, $0 \leq y_i \leq 1$, $\sum_{i=1}^{n} y_i = 1$. If J_1 uses a mixed strategy x and J_2 uses y, with the payoff matrix Y, the expected payoff to J_1 will be $P(x, y) \equiv \sum_{i=1}^{m} \sum_{j=1}^{n} x_i Y_{ij} y_j$.

Now let us suppose J_2 chooses a strategy y_0. Knowing this, J_1 seeks to maximize its gains, choosing x_0 such that $P(x_0, y_0) = max_{x \in X} P(x, y_0)$, where X denotes the set of all mixed strategies of J_1. Since J_2 expects J_1 to play exactly this way, the best to do is to choose y_0 such that [20]:

$$max_{x \in X} P(x, y_0) = min_{y \in \tilde{Y}} max_{x \in X} P(x, y),$$

where $\tilde{Y}$ is the set of all mixed strategies available to J_2. This reasoning can be reversed and it can be shown that, for every finite, two person, zero sum game, i.e. a game where the gain of J_1 equals minus the gain of J_2, we have [20,19]

$$min_{y \in \tilde{Y}} max_{x \in X} P(x, y) = max_{x \in X} min_{y \in \tilde{Y}} P(x, y) = \nu.$$

The mixed strategies thus solve the game and ν is its solution.

Now let us consider a game with n players and $\Gamma = (\gamma_1, \cdots, \gamma_n)$, where γ_i is a vector of dimension m denoting the mixed strategy i for the i-th player and m is the number of pure strategies. Γ is an equilibrium point of the n person game if, for every $i \in 1, \cdots, n$, and any γ_i', the payoff $P_i(\cdot)$ of player i is such that:

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Coexistence of multiple public goods in a bacterial colony.

Carlos Gracia-Lázaro,[1] Mauro Moreno,[1] Joaquín Sanz,[1,2] and Yamir Moreno[1,3,4]

[1] *Instituto de Biocomputación y Física de Sistemas Complejos (BIFI), Universidad de Zaragoza, 50018 Zaragoza, Spain*
[2] *CHU Sainte Justine Research Centre, Montreal, Canada*
[3] *Departamento de Física Teórica. University of Zaragoza, Zaragoza E-50009, Spain*
[4] *ISI Foundation, Turin, Italy*

Some aspects of the interactions between microorganisms (such as the siderophore production or the resilience to antibiotics) can be studied from the perspective of cooperation. Some microbes (producers or cooperators) pay a metabolic cost while non-producers or cheaters benefit from the public goods without paying that cost. In some theoretical models, ecological populations of microorganisms are operationally defined as groups of coexisting individuals that are highly clustered on the genotypic and phenotypic levels. In these models, each bacterium is characterized by the genes it possesses and has assigned a fitness related with the public good[1, 2].

In this work, we propose a theoretical model to study the effect of the Horizontal Gene Transfer mechanism HGT in a bacterial colony. As a novelty, we consider a variable number G of genes altogether, each one associated to a public good (e.g., iron scavenging molecules, an enzyme for digesting sucrose, resistance to antibiotics, proteins to extracellular protein digestion, etc). We assume that the G genes are intermediate frequency genes, which are susceptible to be acquired by HGT or also by asexual reproduction. Each bacterium has assigned a fitness related with the totality of the public goods.

The pay-off of bacterium i is calculated according to:

$$\pi_i = \left(\prod_{g=1}^{G} \frac{\sum_{j=1}^{N} A_{ij} u_j^g}{n_i}\right)^{1/G} - \frac{\epsilon}{G}\sum_{g=1}^{G} u_i^g \qquad (1)$$

where G represents the number of medium-frequency genes involved in public goods, u_i^g indicates the presence of gen g in bacterium i, and A_{ij} refers to the fact that the sum is carried out in its area of influence. The fitness of a bacterium is proportional to its payoff and takes into account the local carring capacity.

Once the population has reached the carrying capacity, and the ecological equilibrium associated with the strategic interactions, a mutation that involves an intrinsic evolutionary advantage is introduced in a random bacterium through a trait associated with a new medium-frequency gene u'. The presence of this new gene does not involves an associated metabolic cost.

We have found that, when more than a public good is considered, the appearance and spreading of a survival trait does not imply a shift from the previous strategic equilibrium: a small ratio of HGT is enough to not occur clonal sweeps. Furthermore, the greater the number of public goods involved, the lower the clonal sweep. For intermediate values of the HGT rate, this mechanism allows the spreading of necessary genes in the colonization phases, while for very low rates of HGT, a decrease in density is observed in the colonization phases, and only the producers genotypes survive. In addition, we have found that there is a range of the HGT ratio, compatible with the experimental values, that maximizes the biodiversity. In conclusion, we believe that these results can help to understand the genetic heterogeneity in bacterial populations.

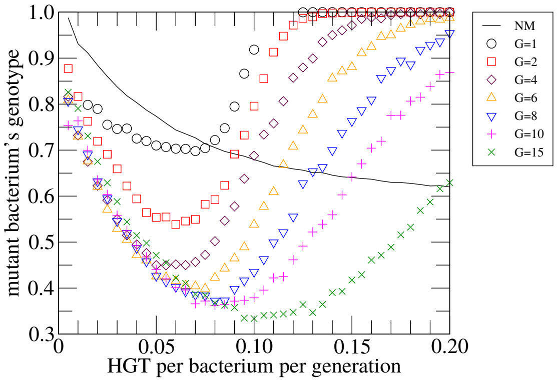

FIG. 1: **Genetic sweep.** As an observable of the genetic sweep, the figure displays the fraction of bacteria sharing the genotype of the bacterium in which appeared the evolutionary advantage Versus the horizontal gene transfer rate. Different symbols represent different number G of medium-frequency genes involved in the public good dynamics, while black line corresponds to the null model ($G = 0$).

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Exploring the Complex Dynamics of Business IT Alignment through the Analysis of a non-linear Model

Fabrizio Amarilli,
Fondazione Politecnico di Milano
fabrizio.amarilli@polimi.it

Abstract

Aligning Information Technology (IT) and business needs within organisations is widely acknowledged as a key driver for improving corporate performances. Despite an extensive scientific and practitioners' literature, spanning over three decades, business IT alignment is still considered an unachieved objective in corporate practice. The lack of a sound theoretical foundation for explaining the dynamics of alignment, i.e. how alignment occurs in organisations, is considered a key reason for justifying the difficulty in implementing alignment. A socio-technical interpretation of organisations where alignment is described as the result of the interplay of different actors, personnel and technologies, at different levels triggered a stream of research where the models and tools of complexity science have been adopted to investigate alignment. However, studies have mainly adopted a qualitative and descriptive approach and demonstrated the applicability of complexity science approaches of study or described the complex and non-linear evolution of alignment, rather than provide an explanation of the factors and rules that govern alignment. In our work we propose a first, simple model to explain the interaction of the variables influencing alignment. The study is based on an extensive literature review, covering three domains of research (Information Systems, Organisation Science, and Complexity Science) and on 4 case studies. The study of the literature allowed to select the relevant variables, pre-conditions, enablers, and inhibitors, determining alignment. The case studies provided insights on the interactions among the variables and on the mechanisms determining or influencing alignment. The developed model is in discrete time and describes the evolution of alignment in terms of the fraction of an organisation's personnel that is unsatisfied with IT. Alignment is explained as the result of company's effort to compensate the misalignment caused by the dynamic competitive environment companies operate in. The resulting dynamics is influenced by parameters such as the efficacy of the IT department, in terms of its capability to identify business needs and implement corrective actions; the IT investment policies; the capacity of the organisation to respond to changes and adapt to them (Fig. 1).

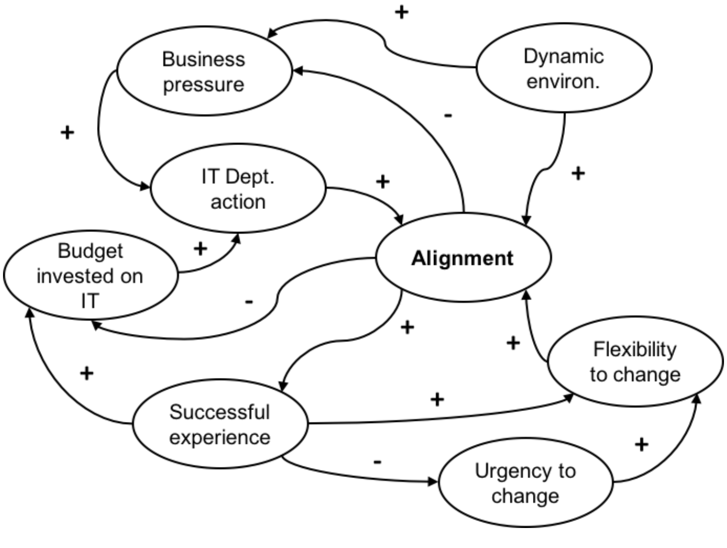

Fig. 1. Map of the factors influencing alignment

The analysis of the model exhibits behaviour that well fits the observed evolution of alignment in organisations. Critical conditions determining complex behaviour, such as the joint effect of turbulent environment and highly responsive organisations, are identified. The contribution of the study is both theoretical and operational. From a theoretical perspective, the model clarifies the complex relationship among variables influencing alignment, improving alignment theory beyond a linear, cause-effect vision. From an operational viewpoint, understating the complex dynamics of alignment represents a preliminary condition for implementing effective alignment strategies in companies.

Japan and Regional Trade Agreements; Understanding Trade Networks

Muhammad Mohsin Hakeem[1], and Ken-ichi Suzuki[2]

1. JSPS Postdoctoral Fellow, Graduate School of Economics and Management, Tohoku University, Japan
2. Associate Professor, Graduate School of Economics and Management, Tohoku University, Japan

Regionalism in Asia-Pacific can be explained by increase in Regional Trade Agreements (RTAs) among regional economies especially during last decade. While the global trade is experiencing an unexpected but a known phenomenon, the protectionist wave in large economies which can result in extreme reductions in trade volumes and probably a large dent on aggregate global output. The rise of regionalism in Asia-pacific opens up new opportunities for not only linked economies but depicts the positive move in broader context as well. The study analyses the trade network with consideration of Japan's bilateral, multilateral, or regional trade agreements with other economies by using network analysis. If we look at the region in terms of trade agreement, Singapore is a prominent member of this region with 33 active and in-process FTAs followed by China and Japan with 24 and 23 agreements respectively. We analyzed Japan's trade networks for multiple years from the CEPII dataset which contains bilateral trade relations of global trade network from 1948 to 2015. The descriptive analysis and variation in networks statistics explained the change within trade networks after introduction of policy change by Japanese government or major global events. Different bilateral or multilateral trade agreements impacted local as well as regional closely connected economies. We also incorporated "Gravity Model" proposed by Anderson and Wincoop (2003) to understand the findings of networks analysis in economic terms. Integrating outcomes of network analysis with gravity model gave us broader picture of regional trade and its global implications. The outcomes justified the concept of regionalism and its implications for Japan and other prominent Asian economies as well as global trade.

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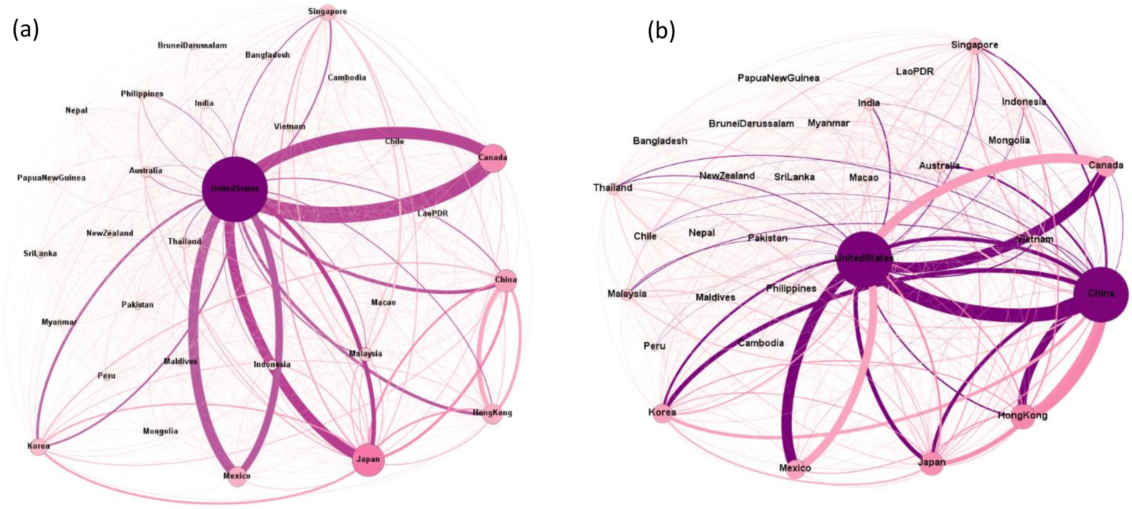

Aggregate Trade Volume Network for Asia-Pacific and Pacific-Rim countries for year 2000 (a) and 2015 (b)

DETECTION ALGORITHM OF CHAOTIC FAILURES IN A DIRECTED COUPLED MAP NETWORK.

Rodolphe Charrier *[1,2]

[1]Normandie Univ, France
[2]ULH, LITIS, F-76600 Le Havre, France

Given a directed network, whose nodes embed some dynamical state $x(t)$ governed by a non-linear map, like the logistic map, and coupled with other node states from a neighbourhood –that is a so-called Coupled Map Network (CMN)[2]–, we are interested in the following cascading failure scenario : at a given time step, as every state in the network is non-chaotic, one node in the network is chosen to become chaotic, that is its embedded state exhibits a chaotic time series (this is done by tuning the control parameter of the non-linear map governing the internal state of the node); then this chaotic dynamics spreads within the network through the directed links and the couplings between nodes. This generating phase may be fully predicted, while the network and couplings are known. In particular, we can know the sub-network potentially impacted by the chaotic perturbation, knowing the all network topology…

In a second phase, designed as the inverse problem, we don't know anything on the network, except the time series of every node. Issues here are firstly to identify the sub-network impacted by the chaotic perturbation, only by analyzing the time series, and secondly to detect the source of the chaotic perturbation by analysing the couplings within the impacted sub-network. To deal with these issues, we have designed a transfer-entropy based algorithm, which enables us to detect nodes impacted by the chaotic perturbation and to get the source of the perturbation with a good efficiency.

This algorithm has been tested on various kinds of complex network topology, like small-world or scale-free networks[1], and results show some specific evolution laws.

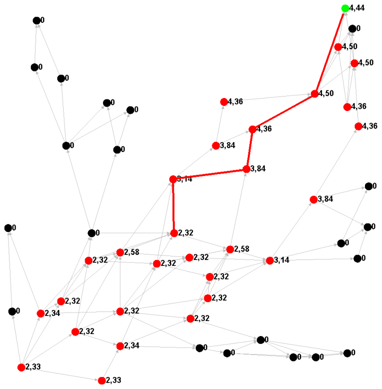

Figure 1: Example of a chaotic source detection in a network [3] on the red path. The source is in green, impacted nodes are in red, non impacted in black, labels are the calculated entropy values. The original underlying network is in gray.

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*Speaker : Rodolphe.Charrier@univ-lehavre.fr

Biodegradation of hexachlorocyclohexane isomers by *Anabaena* PCC 7120

Abizanda S, Guio J, Fillat MF, Peleato ML and Sevilla E.

Departamento de Bioquímica y Biología Molecular y Celular and Institute for Biocomputation and Physics of Complex Systems.

Lindane (γ-Hexachlorocyclohexane, γ-HCH) is a persistent pesticide that triggers environmental and health problems. Environments polluted with this compound are often contaminated with other hexachlorocyclohexane isomers such as α-HCH, β-HCH and δ-HCH. In spite of its molecular stability and persistence, some microorganisms are able to degrade these complex molecules. For example, *Sphingomonas paucimobilis* contains in its genome several enzymes involved in HCH degradation. These enzymes are encoded in the catabolic *lin* genes which are dispersed on the genome. It has been reported that this bacterium is able to catabolize not only γ-HCH but also α-HCH, β-HCH and δ-HCH with different degradation ratios. The cyanobacterium *Anabaena* PCC 7120 is another microorganism with proven capacity of performing lindane biodegradation. But to the date, if *Anabaena* PCC 7120 is able to catabolize the rest of HCHs isomers is unknown. In this work, the tolerance of *Anabaena* PCC 7120 to the presence of different HCH isomers has been evaluated since it has been reported that some isomers such as δ-HCH can be toxic to other microorganisms. On the other hand, the ability of this cyanobacterium to catabolize the four isomers (α-HCH, β-HCH, γ-HCH and δ-HCH) has been tested. The amount of HCH isomers and intermediate degradation products has been quantified in the extracellular medium as well as in the intracellular medium. Finally, in order to identify genes potentially involved in HCH degradation in *Anabaena* PCC 7120 *in silico* analyses have been carried out. The results showed three putative *lin* genes with high similarity to *linB*, *linE* and *linR* genes of *Sphingomonas paucimobilis*. The dynamics of expression of these three genes in response to the presence of different HCH isomers have been also evaluated.

A model of ecological and evolutionary effects of climate change

Evgeniia Alekseeva[1, *] and Iaroslav Ispolatov[2, †]

[1] *Skolkovo Institute of Science and Technology, Nobel str. 3, Moscow, Russia*
[2] *Departamento de Fisica, Universidad de Santiago de Chile, Casilla 302, Correo 2, Santiago, Chile*

(Dated: October 8, 2017)

The ecological consequences of climate change is a major concern for all of us. Living organisms cannot influence climate factors and the only way for species to survive is to adapt. We model evolutionary and ecological effects of climate change using the logistic model, where species, determined by several phenotypic coordinates, interact by competing for resources. To mimic the abiotic environmental changes caused by global warming, we modify the phenotypic position of the optimum of environmental carrying capacity. We observed that, in general, species evolve in phenotypic space following the carrying capacity, but lagging further and further behind it as the speed of environmental changes increases. Some species loose significant fraction of their population and even die out due to an unfavourable combination of the competition with their neighbours and unsupportive abiotic environment. Quantitatively, we have found that diversity of species and the total population of the system universally decreases with the speed of changes of environmental conditions for a wide range of system parameters. The speed of evolution, or phenotypic changes relative to the carrying capacity optimum, somewhat increases. We believe that our studies help to uncover microevolutionary mechanisms and peculiarities leading to detrimental macroevolutionary and ecological effects of rapid climate change.

Keywords: Evolution — Climate change — Extinction

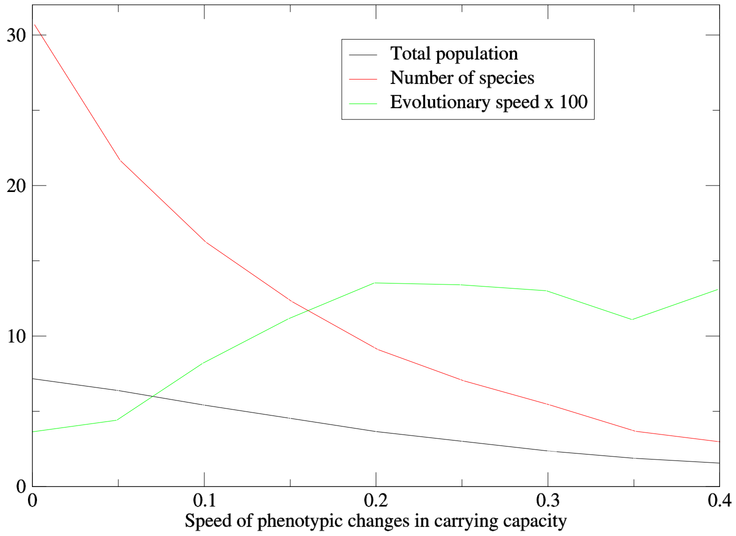

FIG. 1: Dependence of dynamic properties of evolving system on the speed of environmental change. The diversity of species and total population of entire system decrease with the speed of environmental change, while the speed of evolution somewhat grows.

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[*] Electronic address: evgeniia.alekseeva@skolkovotech.ru
[†] Electronic address: jaros007@gmail.com

Mean-field Analysis of Network Connectivity against Stochastic Node Removals

Department of Computer Science, Nagoya Institute of Technology
S. Takabe, T. Nakano, and T. Wadayama

Connectivity of networks is a fundamental graph property vastly studied in the literature of random graph theory. Recently, in theoretical computer science, connectivity of random graphs against stochastic node removals is proposed as a model of reliability of wireless sensor networks [1]. In the model, each node in a graph is removed independently with probability ϵ and the resulted induced subgraph is called a survival graph. The network breakdown probability is then defined as the average probability over random graphs that survival graphs are disconnected. Its upper bound for regular random graphs is shown in [1] while the asymptotic property is unrevealed. In this presentation, we give an approximation formula of the network breakdown probability using the mean-field approximation in statistical physics. The approximation formula is asymptotically correct as shown in Fig. 1 and can be used for random graphs with an arbitrary degree distribution. The phase transition in connectivity of random graphs with the stochastic node removal process is additionally studied as an asymptotic analysis of the approximation formula. It is revealed that the probability changes discontinuously at $\epsilon^* \in (0, 1)$ if the average degree is $\Theta(\log n)$.

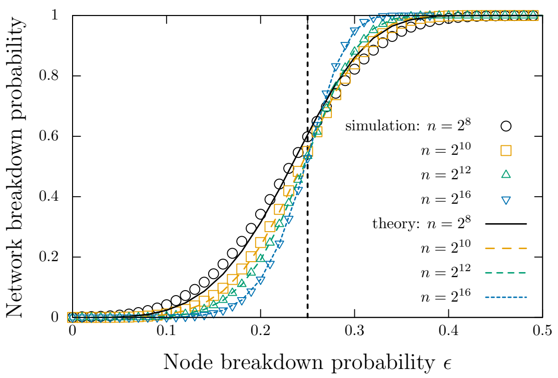

Figure 1: The network breakdown probability as a function of node breakdown probability ϵ for regular random graphs with size n and degree $0.5 \log_2 n$. Symbols and lines respectively represent numerical results and the approximation formula. A vertical dotted line is the threshold $\epsilon^* = 0.25$.

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A stochastic differential equation approach to the analysis of the UK 2016 EU referendum polls - An Abstract

Trevor Fenner trevor@dcs.bbk.ac.uk, Mark Levene (*Speaker*) mark@dcs.bbk.ac.uk, and
George Loizou george@dcs.bbk.ac.uk

Birkbeck, University of London, London WC1E 7HX, U.K.

Human dynamics and sociophysics suggest statistical models that may explain and provide us with better insight into social phenomena. Here we propose a generative model based on a stochastic differential equation that allows us to analyse the polls leading up to the UK 2016 EU referendum, known as the "Brexit" referendum. We provide empirical evidence that the beta distribution, which is a natural choice when modelling proportions, fits the marginal distribution of this time series. We also provide evidence of the predictive power of the proposed model.

In order to see the trends we inspect the moving average of the Brexit polls, as shown in Figure 1. In this case it is clear that, as the referendum date approached, the Leave vote was gaining traction and the proportion of Undecided votes was decreasing.

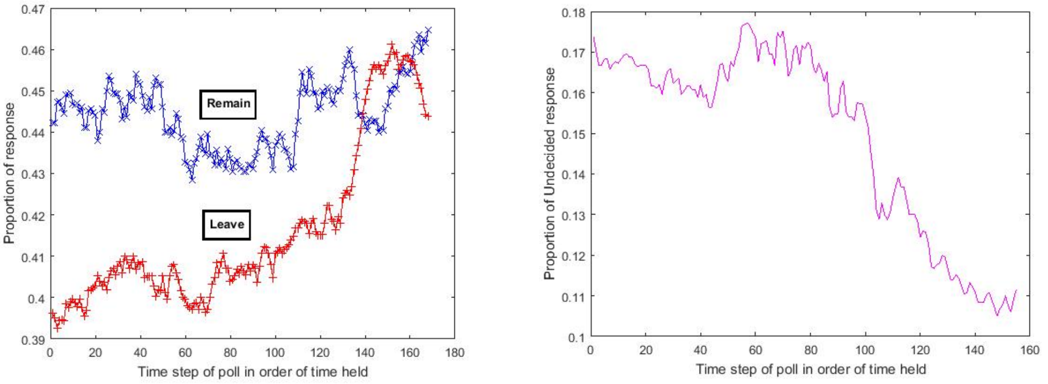

Figure 1: Moving average with a centred sliding window of 25 time steps for the Remain and Leave (left), and Undecided (right) poll results.

We model the time series of poll results by a *stochastic differential equation* (SDE), given by

$$\mathrm{d}X_t = \theta \left(\frac{\alpha}{\alpha+\beta} - X_t \right) \mathrm{d}t + \sqrt{\frac{2\theta}{\alpha+\beta}\, X_t \left(1 - X_t\right)}\, \mathrm{d}W_t, \tag{1}$$

where X_t is a random variable with $t \geq 0$ a real number denoting time, θ is the *rate parameter*, $\alpha, \beta > 0$ are the *shape* parameters of the beta distributions, and W_t is a Wiener process.

The maximum states of distribution in the ensemble of boolean networks

Jun Hu[1], Huijia Li[2], Zhen Wang[1]
[1]Northwest Polytechnical University
[2]Central University of Finance and Economics

Inference of gene regulation mechanism from gene expression patterns is getting more important especially due to the invent of DNA microarray technology. Thus, we need to get the distribution of the ensemble of Boolean networks, and can determine which states the genes are, which is very useful to study the expression profiles of several thousands of genes are being produced for further analyses. Specifically, in this paper, we study and calculate the distribution of the Boolean network's states. First we compute the probability of different BNs's states and get the value of \Omega, then we find the maximum probably distribution of the number of BNs's states. Furthermore, we calculate the fluctuation of the distribution. Finally, two representative experiments are given to verify the efficiency of the obtained results. Although the real genetic networks are different from the Boolean networks, the theoretical and practical results in this paper may be extended for more realistic models. Since the proposed algorithm is conceptually very simple, it is highly extensible for various situations.

Adaptive Landscape Mutation in the Eigen's Quasispecies Model

A.S. Bratus[1], I. Samohin[1], D. Yurchenko[2]

[1]Moscow State University, Moscow, Russia
[2]Heriot-Watt University, Edinburgh, UK

Consider a system of quisispecies u = (u1, u2, ..., un), that is described by the following set of differential equations:

$$du/dt = \exp(-\gamma \sum_{i=1}^{n} u_i) Q_m u - Du, \quad Q = \|q_{ij}\|, \quad q_{ij} = 1,2,\dots,n$$
$$Q_m = QM, M = diag(m_1, m_2, \dots, m_n), \sum_{i=1}^{n} m_i = const, D = diag(d_1, d_2, \dots, d_n), \gamma > 0 \quad (1)$$

where q_{ij} is the probability that under a replication of a macromolecule "i" a macromolecule "j" will appear, D - is the matrix of species mortality, M - a matrix that specifies the fitness landscape. The aim of the work is to derive a mathematical model that allows tracing the change in the adaptive landscape M, which arises as a response of the system to the change in mortality of species. According to the Darwin's natural selection theory, the evolutionary process is characterized by the principle that the average fitness of the system in the course of evolution should increase.

The paper proposes an algorithm for searching some changes in the fitness landscape in order to maximize the fitness of the system in a stationary equilibrium position of the system (1). The proposed algorithm is to consistently increase the fitness value by solving a sequence of linear programming problems. The action of the algorithm essentially depends on the step of the iterative process. In some cases, a change in the fitness landscape gives an advantage to a species whose mortality is minimal.

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[1] Normandie University, Le Havre, France

Impact of nervousness propagation on crowd dynamics

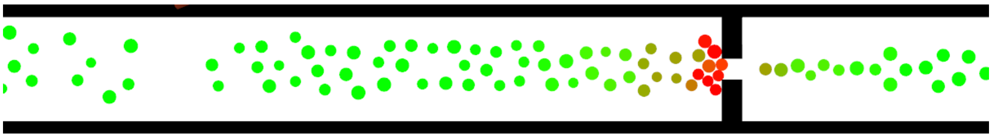
Julien Philippe[1], *RodolpheCharrier*[1], *CyrilleBertelle*[1]

Information is one of the key point when studying social phenomena, namely how crowds may behave in emergency situations. There are in litterature many model to simulate crowd dynamics, we have based our work on one of the most famous that is the Helbing's model of social forces, including nervousness[1]. Though nervousness is a component of this model, it's an individual property of each agent relying only on kinematic quantities. Or social psychology studies show that nervousness impacts crowd dynamics because of its social nature : "social contagion" is a strong assertion in the field[2] and lacks in many crowd dynamics models.

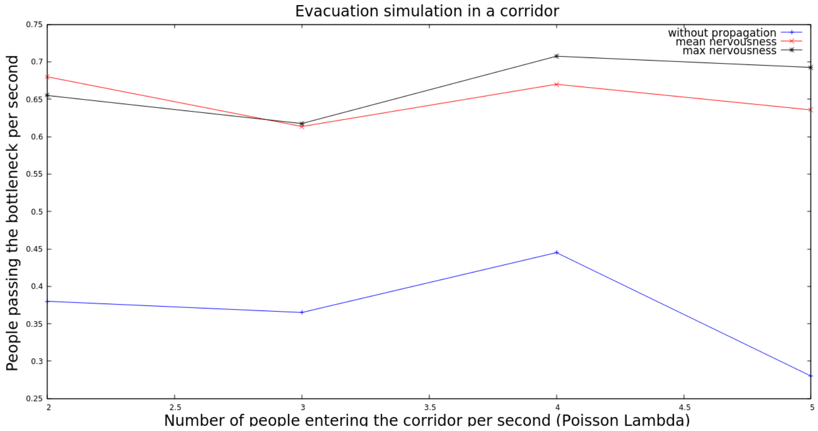
Our contribution is to add an information propagation network to the Helbing's model, in order to take into account this emotional contagion as a nervousness propagation.

Our goals consist in veryfing the impact of the nervousness propagation on the global crowd behaviour, especially in evacuation configuration for instance a corridor with a bottleneck. We aim also to show which kind of propagation mechanism may enhance evacuation efficiency.

Simulations results lead us to conclude that information propagation improves the evacution efficiency as shown in the figure below. Two ways to propagate nervousness are involved : one calculating the mean of nervousness int the perceived neighborhood, and the other calculating the maximum of nervousness. And we compare both to the standard Helbing model, without nervousness propagation.



(a) Simulation snapshot : agent's color depend on his nervousness, from quiet green to nervous red



(b) Number of people passing the bottleneck per second : simulations with propagation show better efficiency

Figure 1: Simulation illustration and results

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BACTERIAL COMMUNITIES AMPLICON PROFILES MODELLING BY MARKOV CLUSTERING AND NEURAL NETWORKS. DEFINING REFERENCE ANNOTATION SIGNATURES.

David Pérez-Villarroya 1 , Andrés Moya 2,3 , Giuseppe D'Auria 1,2.

1. Sequencing and Bioinformatics Service, Fundación para el Fomento de la Investigación Sanitaria y
Biomédica de la Comunidad Valenciana (FISABIO-Salud Pública), Valencia, Spain.
2. Centro de Investigación en Red en Epidemiología y Salud Pública CIBEResp
3. Genomics and Health Area, Fundación para el Fomento de la Investigación Sanitaria y Biomédica de
la Comunidad Valenciana (FISABIO-Salud Pública), Valencia, Spain; Integrative Systems Biology Institute, Universitat de València-CSIC

BACKGROUND: Association studies between taxonomy contingency tables and related metadata describing the origins or the state of the samples, are commonly carried out inferring statistical models. This process is usually carried out in a closed framework where only subject samples are statistically described in terms of case vs controls, physiological conditions, environmental/metabolic differences, etc.. While more and more amplicon surveys as well as metagenomic datasets are made available from almost all known environments, multiple sample comparisons methods and platforms become a hot issue to resume and categorize datasets towards biological comprehension. We can use already published and/or new datasets to create annotation profile models by the mean of supervised machine learning techniques. Thus, we can then classify new samples on the basis of the proper annotation signatures.

OBJECTIVES: In this work we employed unsupervised Markov cluster algorithm (MCL) to enrich authors provided metadata with formal samples categories. Neural networks (NNt) supervised machine learning techniques are then used to generate models from 16S taxonomy distributions suitable for further *de-novo* samples classification.

RESULTS: We found that using samples metadata coupled with MCL algorithm to define formal categories improve the NNt modeling showing higher sensitivity and specificity to classify samples.

CONCLUSIONS: The combination of MCL and NNt is a powerful approach to create databases of profile-models for further classification of new samples enriched with new profiles when the issued sample is not recognized.

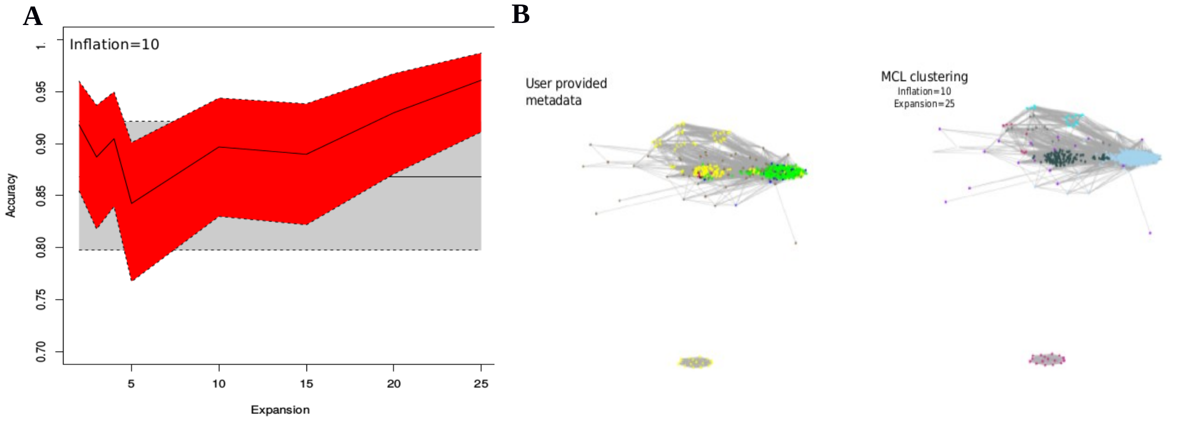

Figure 1. (A) In red color, resulting accuracy confidence interval for NNt classification models tested using MCL clustering groups for constant inflation parameter (10) and a range of expansion values. In grey color, accuracy confidence interval for NNt classification models using user provided metadata. As can been seen, The accuracy of NNt with MCL groups is generally greater than user provided metadata NNt . (B) Correlation networks between 16S amplicon samples abundances profiles and node colors based on user (left) or MCL (right) sample groups. This networks show well defined groups and better fitness between samples network position and the assigned group in MCL clustering results.

Authors: C. Casert, A.M. Belaza, J. Ryckebusch, T. Verstraelen

Collective motion is ubiquitous in nature and is universal in the sense that the same patterns of motion are found in very different situations. For this reason, it has attracted widespread interest over the past decades. The Vicsek model (VM) has provided a breakthrough in understanding the underlying dynamics (see e.g. [1,2,3]). In the VM, self-propelled particles tend to align their direction of motion to the one of their nearest neighbors. The model exhibits a discontinuous phase transition, as the system makes the transition from a disordered regime to one where collective motion appears when the noise level is sufficiently low. Recently, a model that generalizes the VM has been introduced for capturing the collective motion of passive Brownian particles [4]. While most natural systems that exhibit collective motion can be represented as active matter, it has been suggested that some "artificial" systems better follow the behavior of interacting passive Brownian particles. It is then vital to understand to what extent the self-propulsion of particles affects the emergence of collective motion and its patterns. Using Langevin dynamics we have conducted in-depth simulations for both passive and active matter [5]. By studying the relevant statistical measures – such as the cluster-size distributions, the particle diffusion properties, and the widths of the collectively moving bands that appear at the transition point – we can discern, in great detail, the underlying dynamics of the two models. Those models open opportunities to study the effect of self-propulsion in non-equilibrium systems.

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Collective social behavior in a crowd controlled game

Alberto Aleta[1,2]

1. Department of Theoretical Physics, University of Zaragoza, 50009 Zaragoza, Spain
2. Institute for Biocomputation and Physics of Complex Systems (BIFI), University of Zaragoza, 50009, Zaragoza, Spain

The characterization of the large-scale collective behavior that emerges from local interactions among individuals has several areas of interest: from pedestrian behavior to collective decision making or the dynamics that lead to opinion formation and social change. In this work we analyze a phenomenon that took place in February 2014 where thousands of users played the same online game for 16 days. The novelty of this event was that all of them were controlling the exact same character simultaneously. Due to the lack of a central authority, progress was usually much slower in this crowd controlled setting in comparison to what can be achieved by a single player as it was necessary to continuously reach consensus on what to do next. However, the objective for some users was not to complete the game. While some tried to hijack the efforts of the dedicated players, others created a very rich narrative around the game. Thus, this event represents a great opportunity to study crowd based movements like consensus, the emergence of naming conventions or crowd working. We classify users into different groups according to their behavior and we see how the community spontaneously split into two different groups. Then, we focus our attention on a specific part of the event and we try to find out if progress was mainly driven by chance or consensus, and by some groups of users or all of them. The results of this work shed some light on how crowds behave in the absence of authority and arise an interesting question, what if society has to keep moving before consensus can be achieved?

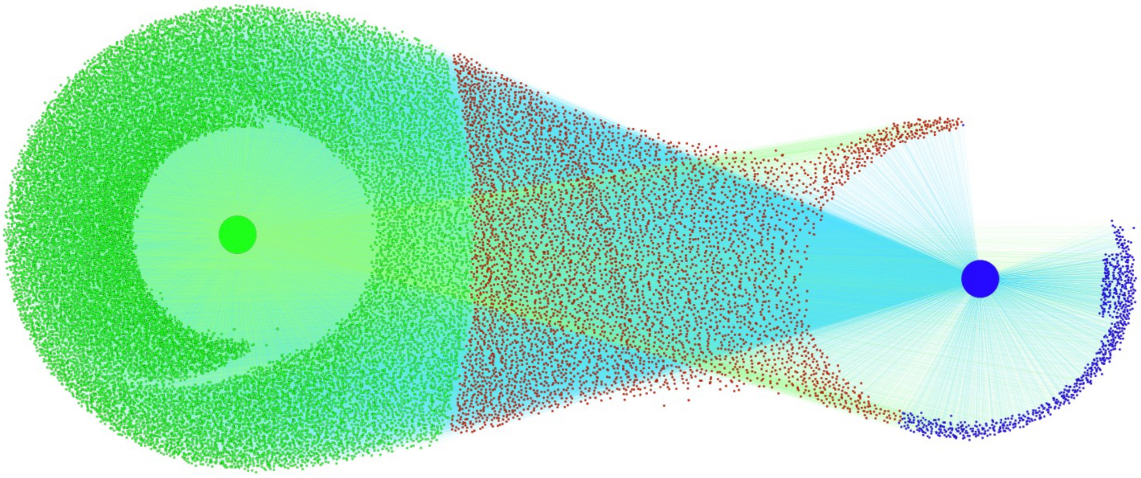

Figure 1: the green node on the left represents the messages directly related to controlling the game while the blue node on the right represents messages not related to the control of the game (the chit-chat of the crowd). Smaller nodes represent those users with more than 100 messages and their position is related to their behavior: the closer to the left the more “pure” players they are whereas the closer to the right the less dedicated to the progress of the game they are. It is possible to distinguish groups of users according to their behavior and use that information to model the behavior of the crowd.

Topical homophily in online social systems

October 10, 2017

Felipe M. Cardoso[1,2], Sandro Meloni[1,3], André Santanchè[2], Yamir Moreno[1,3,4]

[1] Institute for Biocomputation and Physics of Complex Systems, University of Zaragoza, Spain
[2] Institute of Computing, State University of Campinas, Brazil
[3] Department of Theoretical Physics, University of Zaragoza, Spain
[4] Complex Networks and Systems Lagrange Lab, Institute for Scientific Interchange, Turin, Italy

Understanding the dynamics of social interactions is crucial to comprehend human behavior. The emergence of online social media has enabled access to data regarding people relationships at a large scale. Twitter, specifically, is an information oriented network, with users sharing and consuming information. In this work, we study whether users tend to be in contact with people interested in similar topics, i.e., topical homophily. To do so, we propose an approach based on the use of hashtags to extract information topics from Twitter messages and model users' interests. Our results show that, on average, users are connected with other users similar to them and stronger relationships are due to a higher topical similarity. Furthermore, we show that topical homophily provides interesting information that can eventually allow inferring users' connectivity. Our work, besides providing a way to assess the topical similarity of users, quantifies topical homophily among individuals, contributing to a better understanding of how complex social systems are structured.

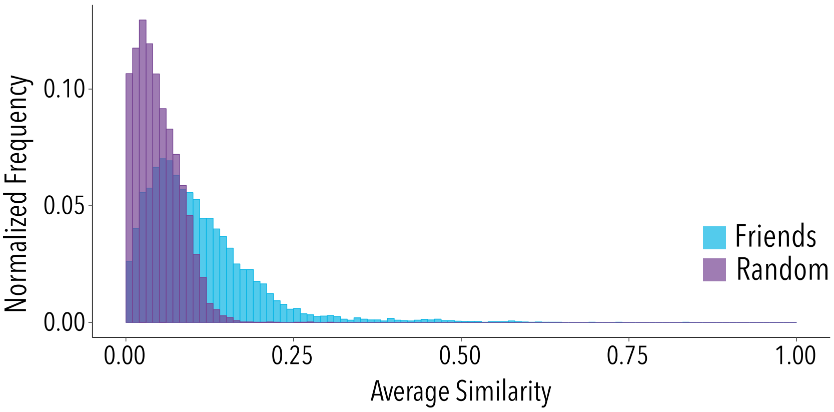

Figure 1: Distribution of average similarity between users and their friends (blue) and randomly selected groups of the same size (purple).

Cross-border Banking Crises: A Multilayer Network Perspective

Oscar M. Granados

Department of Economics and International Trade, Universidad Jorge Tadeo Lozano
Bogotá, Colombia | E-mail: oscarm.granadose@utadeo.edu.co | Speaker: Oscar M. Granados

Abstract

The network science as a characterization of societies has become a tool to understand the transformation of systems and has contributed to the understanding of the complex structure of the real world and random events [1, 2]. Banking systems proceed as an integrated scheme that cannot separate from their parts and they established a process of a complex adaptive system that acquires information both from their environment and from the interaction between the system and the environment. That is, banking systems are systems that learn and information is the element that becomes their genetic inheritance for their survival and evolution, identifying patterns to condense them into a model [3]. This is how banking crises, unpredictable events, are the result of the complexity of these interactions with impacts on the financial systems and, sometimes, the economy in general. Each crisis reveals topological information that can be the way to identify the characteristics of the banking system or establish patterns to make control. Current literature has used different methodologies, usually in recent crises but these researches have not yielded patterns that can facilitate the understanding of the characteristics of the interactions that vary according to market, asset, term, durability, etc. Then, could it be learning and understanding the patterns that allow creating tools to solve the interactions of the next banking crisis?

The present work evaluates some banking crises of global impact through a perspective of multilayer networks and the construction of data from primary sources that allow understanding the application of a model and the interpretations of parameters that emerge from the interactions. However, the definitions of centrality, clustering, assortativity or disassortativity, density and expected force can present in a simple layer but will be different in a multi-layer network because this set of networks differentiates financial assets markets and local markets from global markets. Moreover, because of banks participating differently in each of these markets and their influence or exposure may be different cross-borders markets. As result, I developed a multilayer network model that identifies the previous definitions in an elementary layer and determines their transformation into a multilayer network. In addition, the banking systems are closer to a proposal of free-scale networks, where a high degree of self-organization emerges and the continuous incorporation of new nodes into the system [4].

In this way, the assembling of a sequence of elementary layers allows a multilayered network from the combinations of the elementary layers [5]. The different types of participation and interactions of a bank *i* at time *t* are given by matrix formed by a set of elementary layers that represent the different markets (See Fig. 1). From this, I identified the banking agent's behavior, the evolutionary characteristics of the network structure and the impacts that have in its stability. The evidence is not far from the results that refer to more recent crises, but if it is possible to identify more precisely the definitions initially proposed and the patterns that make it easier to understand the robustness and stability of banking systems to develop a proposal for control of banking networks (See Fig. 1). I concluded that they are dynamic networks, but also temporary networks and there would be the possibility of asking if these networks are atemporal.

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Multifractal Spectrum Indicates Criticality in a Network of Integrate-and-Fire Neurons

Marzieh Zare[1], Mohammad Dehghani[2], Farhad Shahbazi[2,3]

[1]School of Computer Science, Institute for Research in Fundamental Sciences(IPM), Tehran 19395-5746

[2]Department of Physics, Isfahan University of Technology, Isfahan 84156-83111

[3]School of Physics, Institute for Research in Fundamental Sciences(IPM), Tehran 19395-5531

Keywords: Multifractal Spectrum, Criticality, Integrate-and-Fire Model

Abstract: Brain as a complex system is a source of non-stationary and nonlinear signals. The multifractal analysis used in interdisciplinary research [1] is deployed to explain whether a single exponent or a continuous spectrum of exponent is required to explain the system's behavior [3]. The fractal analysis also reveals long-range correlations indicated by scaling exponents. These exponents are signature of complexity, and reveal the underlying dynamics of the system producing these fluctuating signals. Moreover, there are widely empirical evidences showing that the resting brain works near criticality [4]. Power-law distributions are usually indicators of criticality, and some criticality indicators are suggested including neural avalanches [5], and temporal complexity [6]. We have previously shown the emergence of criticality for a range of control parameter in [6]. Here, however, using the leaky integrate-and-fire model (LIFM), we explore whether multifractal spectrum indicates criticality in a network of neurons residing on a regular lattice. We consider $N = X$ neurons, and the connection between neurons plays the role of the control parameter that is expected to generate criticality when the special value K_c is adopted.

To deploy the fractal analysis, we focus on the time distance between two consecutive firings, and use the Root-Mean-Square (RMS) technique, to define the multifractal patterns of the firing time-series. In order to quantify the difference between singularity spectrums, we calculate the width of singularity parabola, and found that for a range of cooperation strength, K, the singularity spectrum displays a wider distribution, while for values below and above that range, the spectrum shows a narrow parabola. This also indicates that at criticality, a fractal set of points is necessary to explain criticality in the neural network (Fig.1.).

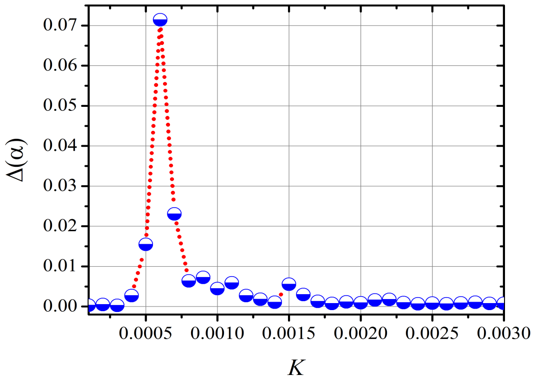

Fig.1. Width of Spectrum vs Cooperation Strength, K. The peak indicates criticality K_c.

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Causal Dynamicl Networks: dialectic complexity

M.M. Khoshyaran

Abstract.

The objective of this paper is to discuss the Causal Dynamical Network (CDN), [1], [2], [3], [4], [5] in relation to dialectic complexity. CDN is a connected graph. Connectivity is the result of dynamical interaction of cause-n-effect. Therefore CDN is time independent. Connection is turned "on" and "off" based on the existence of causality. One particularity of this system is the occurrence of disordering locality links, [6]. Disordering localities occur when there exists random cause-n-effect. CDN is called a complex system if there exists dialectic causality. Dialectic causality occurs when there are several causes for an effect and these causes seem to be contradictory from each other. In addition, there exists a certain dynamics among these causes. The same can be said about the effects. Each cause can have many effects, and these effects may seem to be contradictory from each other. In addition, there exists a certain dynamics among the effects. Each cause is considered to be a tensor, and each effect is in a tensor field,[7]. The number and thus the stability of the links of a CDN depend on the existence of dialectic causality. It is this dialectic causality that defines the level of complexity of CDN. In this context dialectic causality is synonymous with dialectic complexity. The degree of the complexity of the CDN varies depending on the existence of dialectic causality in regular and disordering locality links. The higher the dialectic complexity, the higher the entropy of CDN. Dialectic complexity can vary from high to medium to low levels. Dialectic complexity can be measured by calculating the entropy,[8] of the CDN. The entropy of CDN is measured using metric probability in the Universal Probability Space, (UPS) introduced in [9], and [10].

The schematics of the dynamics of dialectic complexity and entropy are shown in Figure 1. In Figure 1, The existence of dialectic causality leads to positive entropy ($H \geq 0$) which leads to an evolution in the CDN. If dialectic complexity is low, then eventually, the network can reach a local equilibrium, meaning that no new change is occurring locally in the network. This could eventually break down, and lead to new entropy and the cycle continues. Or on the other hand, local equilibrium can spread to a general equilibrium, ($H = 0$). General equilibrium leads either to a static state, which is a static network that stays fixed. On the other hand accidental or unexpected dialectic causality changes the state of the network back to entropic state and a new cycle begins. The overall objective is to explain the dialectic complexity in the context of the CDN, and to analyse it's characteristics.

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BIFI18 ABSTRACT:

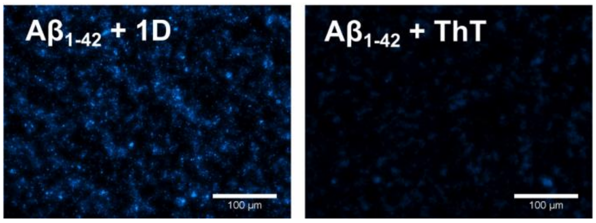
Design, synthesis and testing of a novel fluorescent probe for the staining of amyloid fibrils of A$\beta_{1\text{-}42}$ peptide, α-synuclein and amylin and for the detection of amyloid-nature *Staphylococcus aureus* biofilms

Alejandro Mahía[1,2], María Conde-Giménez[1], Sandra Salillas[1], Íñigo Lasa[3], Salvador Ventura[4], María D. Díaz-de-Villegas[2], José A. Gálvez[2], and Javier Sancho[1]

[1]Departamento de Bioquímica y Biología Molecular y Celular, Facultad de Ciencias, Universidad de Zaragoza, Pedro Cerbuna 12, 50009 Zaragoza, Spain. Biocomputation and Complex Systems Physics Institute (BIFI). Joint Unit IQFR-CSIC-BIFI, Joint Unit EEAD-CSIC-BIFI, Mariano Esquillor s/n, Edificio I+D, Zaragoza, Spain
[2]Instituto de Síntesis Química y Catálisis Homogénea (ISQCH), CSIC–Universidad de Zaragoza, Departamento de Química Orgánica, Pedro Cerbuna 12, 50009 Zaragoza, Spain
[3]Navarrabiomed, Universidad Pública de Navarra-Departamento de Salud, Pamplona-31008, Navarra, Spain
[4]Institut de Biotecnologia i de Biomedicina and Departament de Bioquímica i Biologia Molecular. Universitat Autònoma de Barcelona. E-08193 Bellaterra, Spain

Alzheimer´s disease (AD) is the main cause of dementia in humans. According to amyloid cascade hypothesis, aggregation of amyloid-beta peptide (Aβ) triggers the development of AD.[1] Furthermore, not only AD is caused by misfolding of functional proteins. Other diseases, such as Parkinson or Type II diabetes, derive from this aberrant mechanism. On the other hand, in some bacteria amyloid fibrils are produced under nonpathological conditions for different processes, such as formation of more resistant biofilm matrices.[2] At present, thioflavin T (ThT) is the typical fluorescent probe used for the detection of amyloid structures. Novel fluorescent markers with increased sensitivity or selectivity are needed.

We have designed, synthesized and tested four fluorescent compounds derived from a previously reported inhibitor of Aβ aggregation[3] that retain the interaction with the amyloid structure. One of them (compound 1D) has been probed to fluorescently stain amyloid fibrils of A$\beta_{1\text{-}42}$, α-synuclein and amylin. Interestingly, compound 1D is more sensitive than ThT. In addition, it also stains the amyloidogenic fibrils (composed of phenol soluble modulins) present in *Staphylococcus aureus* biofilm matrix, allowing the distinction, by direct staining, between *S. aureus* biofilms with amyloid nature and those without it.



Fluorescence microscope images of A$\beta_{1\text{-}42}$ fibrils incubated with Compound 1D or ThT.

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New antimicrobials targeting flavin homeostasis through FAD synthetase inhibition

Ernesto Anoz-Carbonell[1,2,3], María Sebastián[1,2], Ainhoa Lucía Quintana[3], Sandra Salillas[1,2], Javier Sancho[1,2], José Antonio Aínsa[1,3], Milagros Medina[1,2]

[1] Instituto de Biocomputación y Física de Sistemas Complejos (BIFI), Universidad de Zaragoza, Spain

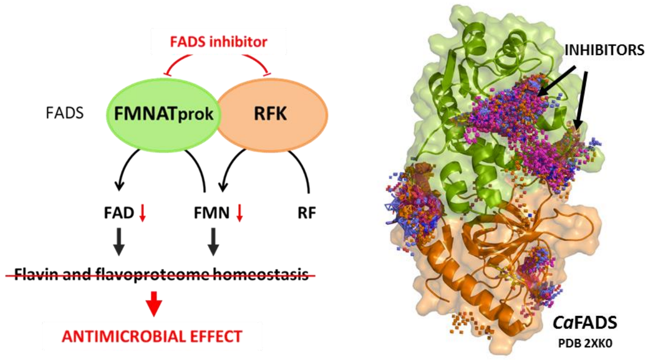
[2] Departamento de Bioquímica y Biología Molecular y Celular, Universidad de Zaragoza, Spain

[3] Dpto. Microbiología, Medicina Preventiva y Salud Pública, Universidad de Zaragoza and CIBER Enfermedades Respiratorias (CIBERES), Instituto de Salud Carlos III

Bifunctional FAD synthetases (FADS), prokaryotic enzymes that catalyze the biosynthesis of the essential cofactors flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD), are essential proteins in flavin and flavoproteome homeostasis [1]. This crucial role in cellular metabolism, together with the significant differences with their eukaryotic counterparts (monofunctional riboflavin kinases and FMN adenylyltransferases), converts the FADS in a promising drug target for the development of inhibitors with antimicrobial activity [2].

We have identified 40 potential inhibitors of *Ca*FADS and *Spn*FADS (FADS from *Corynebacterium ammoniagenes* and *Streptococcus pneumoniae*, representative members of the prokaryotic FADS) by the activity-based high-throughput screening of chemical libraries; that we have thoroughly characterized by the determination of their antimicrobial spectrum and their cytotoxic effect on eukaryotic cells. Only 5 compounds show antimicrobial activity against Gram-positives, and one of them against Gram-negative microorganisms as well. Nevertheless, their therapeutic application could be limited due to their cytotoxicity on eukaryotic cells at the concentrations required for the antimicrobial activity.

Both antibacterial and cytotoxic effects may be associated with the off-target alteration of other essential flavoproteins and flavoenzymes. In a further step, the molecular information of the antimicrobial mechanism will be used for the optimization of these compounds to generate second-generation antimicrobials with higher efficacy and less toxicity.



Proposed mechanism of action of FADS inhibitors leading to the antimicrobial effect, and *in silico* docking of the selected compounds against the crystallographic structure of *Ca*FADS (FADS from *Corynebacterium ammoniagenes*, PDB 2XK0).

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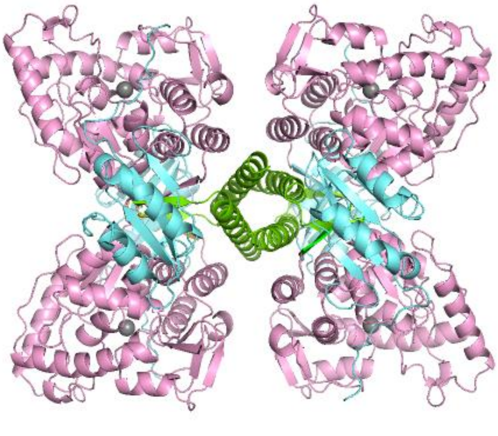
Development of novel stabilizing compounds of human phenylalanine hydroxylase for PKU patients

María Conde-Giménez^{1,2*}, *Sandra Salillas*^{1,2}, *Juan J. Galano-Frutos*^{1,2}, *María Galiana*^{1,2}, *Mº Dolores Díaz-de-Villegas*^{3}, *Javier Sancho*^{1,2}

1 Departamento de Bioquímica y Biología Molecular y Celular. Facultad de Ciencias. Universidad de Zaragoza (Spain)
2 Biocomputation and Physics of Complex Systems Institute (BIFI). BIFI-IQFR(CSIC)-Joint Unit. Universidad de Zaragoza (Spain)
3 Departamento de Catálisis y Procesos Catalíticos. Instituto de Síntesis Química y Catálisis Homogénea (ISQCH). Universidad de Zaragoza-CSIC (Spain)

Phenylketonuria (PKU) is a rare hereditary metabolic disorder due to mutations in the gene that encodes the human phenylalanine hydroxylase (PAH) enzyme [1]. Nowadays, there are more than 550 disease-causing PAH mutations identified and most of these mutations induce loss of conformational stability and decreased physiological enzymatic activity. Current therapies to treat this illness are not entirely effective so new therapeutic approaches are needed [2].

Based on different drug discovery methodologies, we have identified a group of novel stabilizing compounds chemically different to tetrahydrobiopterin, the unique approved drug for PKU patients. These compounds showed a thermal PAH stabilizing effect *in vitro* and we are evaluating if they can act as pharmacological chaperones *in vivo* (in human cell lines).



Composite structural model for human PAH (PDB codes: 2PHM and 2PAH). PAH is a tetramer with three domains: a regulatory domain (aquamarine), a catalytic domain (pink) and a short oligomerization domain (green). Each monomer requires the cofactor tetrahydrobiopterin, molecular oxygen and iron (grey sphere) for catalytic activity.

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*** Correspondence:** mcondeg@unizar.es

MEBS, a software platform to evaluate large (meta)genomic collections according to their metabolic machinery: unraveling the sulfur cycle

Authors

Valerie De Anda[1]*, Icoquih Zapata-Peñasco[2], Augusto Cesar Poot-Hernandez[3] Luis E. Eguiarte[1] , Bruno Contreras-Moreira[4,5]* and Valeria Souza[1]*

Affiliations:

[1]Departamento de Ecología Evolutiva, Instituto de Ecología, Universidad Nacional Autónoma de México, 70-275, Coyoacán 04510México D.F.

[2]Dirección de Investigación en Transformación de Hidrocarburos. Instituto Mexicano del Petróleo, Eje Central Lázaro Cárdenas, Norte 152, Col. San Bartolo Atepehuacan, 07730, México

[3]Departamento de Ingeniería de Sistemas Computacionales y Automatización. Sección de Ingeniería de Sistemas Computacionales. Instituto de Investigaciones en Matemáticas Aplicadas y en Sistemas.

[4]Estación Experimental de Aula Dei, Consejo Superior de Investigaciones Científicas (EEAD-CSIC), Avda. Montañana, 1005, Zaragoza 50059, Spain

[5]Fundación ARAID, calle María de Luna 11, 50018 Zaragoza, Spain.

Correspondence address: Valerie de Anda. Instituto de Ecología, Universidad Nacional Autónoma de México, 70-275, Coyoacán 04510; México D.F; Tel: (+52)5556229006; E-mail valdeanda@ciencias.unam.mx; Bruno Contreras Moreira. Estación Experimental de Aula Dei, Avda. Montañana, 1005, Zaragoza 50059; Spain; Tel:(+34) 976716089 ; E-mail bcontreras@eead.csic.es; Valeria Souza . Instituto de Ecología, Universidad Nacional Autónoma de México, 70-275, Coyoacán 04510; México D.F; Tel: (+52)5556229006; E-mail souza@unam.mx

Speaker: Valerie De Anda

BACKGROUND: The increasing number of metagenomic and genomic sequences has dramatically improved our understanding of microbial diversity, yet our ability to infer metabolic capabilities in such datasets remains challenging. FINDINGS: We describe the Multigenomic Entropy Based Score pipeline (MEBS), a software platform designed to evaluate, compare and infer complex metabolic pathways in large 'omic' datasets, including entire biogeochemical cycles. MEBS is open source and available through https://github.com/eead-csic-compbio/metagenome_Pfam_score. To demonstrate its use we modeled the sulfur cycle by exhaustively curating the molecular and ecological elements involved (compounds, genes, metabolic pathways and microbial taxa). This information was reduced to a collection of 112 characteristic Pfam protein domains and a list of complete-sequenced sulfur genomes. Using the mathematical framework of relative entropy (H'), we quantitatively measured the enrichment of these domains among sulfur genomes. The entropy

Complex network analysis of images of human retina

Pablo Amil[1], Irene Sendiña[2], and Cristina Masoller[1]

[1] Universitat Politecnica de Catalunya, Barcelona, Spain
`pa1000kmph@gmail.com`,
[2] Universidad Rey Juan Carlos, Madrid, Spain

Fundus images are color images taken from the posterior part of the eye (the retina). In this work we apply complex network tools to fundus images with the aim of automatically recover all the network structural information, which can yield information that can be useful to diagnose eye diseases.

We analyzed 45 publicly available fundus images [1] which are divided in 3 groups: healthy, glaucoma, and diabetes. An example is shown in figure 1, left. In order to enhance the contrast between the vessel network and the retina, we first perform a filtering processes. Then, by running a segmentation algorithm (adapted from Ref.[2]) a new image is obtained from where a list of nodes (bifurcation points and endpoints) with their locations can be extracted, as well as the path connecting the nodes. An example of the resulting image is shown in figure 1, right. From this information an adjacency matrix is obtained which is then used for characterization and analysis. Three sets of features can be extracted. The first set is obtained from each individual network: the number of nodes and links, and information-theory features that characterize the degree and distance distributions. A second set of features can be extracted from the comparison of pairs of networks via nonlinear dimensionality reduction algorithms. A third set of features can be extracted by comparing real networks with synthetic tree-like networks. Ongoing work is devoted to analyze this large set of features in order to determine which ones allow to classify the images in groups that more closely reflect the underlying ophthalmology classification.

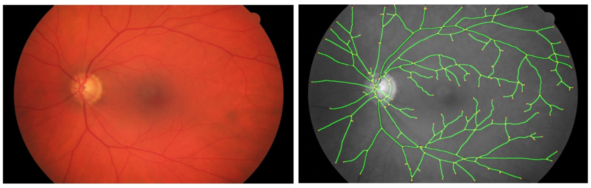

Fig. 1. Left: original image; right: after processing, a tree-like network is extracted.

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Fate of populations: Carrying capacity changes induced from mutants in a stochastic system

Hye Jin Park,[1] Yuriy Pichugin,[1] Weini Huang,[2] and Arne Traulsen[1]

[1]*Department of Evolutionary Theory,*
Max Planck Institute for Evolutionary Biology, 24306 Plön, Germany
[2]*Centre for Tumour Biology, Barts Cancer Institute,*
Queen Mary University of London, London, United Kingdom

Abstract

Trait variation emerging from mutation is common in nature. Since game dynamics can describe interactions between types, this emergence of new types can be interpreted as extending the payoff matrix. In our model, new payoff elements related to the mutant are drawn from an exponential distribution controlled by the mother type's payoff and the probability to have higher payoff than the mother type. Population dynamics under extended payoff matrix changes the equilibrium population size. Hence, in the long run, populations of finite sizes will go extinct or exponentially increase their population size. We examine conditions leading to extinction and quantify the extinction risk by using the mean time to extinction. Interestingly, results show that the extinction occurs much faster at the intermediary probabilities of increasing the payoff at mutation.

Heterogeneous Distributions in Academic Citations Patterns

Jinhyuk Yun, Sejung Ahn, June Young Lee

Korea Institute of Science and Technology Information
66 Hoegiro, Dongdaemun-gu, Seoul, 02456, Korea

Paper citation is an abundant source for investigating the knowledge structure of science and technology. It has been observed that citation of scientific literature follows a heterogeneous and fat-tailed distribution, and many of them suggest power-law distribution and its variants. However, many studies are limited to small-scale approaches, it is thus hard to conclude as a specific distribution. Tackling this issue, we investigate 21 years of citation evolution through systematic analysis entire citation history of 42,423,644 scientific literature published from 1996 to 2016. We tested six candidate distributions for the papers in three distinct levels of SJR(Scimago Journal & Country Rank) classification system. From this massive dataset, we observed the large disparity among the journals, which suggests that it is essential to remove the innate citation preference of different journals. By separating citation preference of individual article from the innate preference of journals, we observed an unexpected regularity on the normalized annual acquisitions of citation for the entire fields of science, regardless of its publication and citation year. Our result indicates that a fitness of an article also follows a fat-tailed distribution, specifically power-law with an exponent cutoff.

Analysis of the Free Energy Landscape of a small protein: a Markov State Model approach.

Pierpaolo Bruscolini
BIFI – University of Zaragoza

Many biological systems are characterized by a dynamics in high dimensional spaces, dominated by low frequency events, like barrier-crossing. Markov State Models are a useful tool to represent such dynamics; however, their analysis is often complicated by the huge number of states involved. Here we test the algorithm by Cameron [1] on the equilibrium folding-unfolding data obtained in a Monte Carlo simulation of the small protein gpW [2]. Preliminary results on the folded and unfolded basins, as well as the most likely folding pathway, are shown.

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