Dynamics On and Of Complex Networks V

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Technical Schedule and Abstracts

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Technical Schedule

14th September

Session 1: Social network analysis-I

8.45
Opening Session
9.00
“Community shared bicyles Velo'v: How to catch users with lasso”
Pierre Borgnat, ENS Lyon, CNRS, France
9:30
“Towards social network-based Sybil tolerant systems”
Krishna Gummadi, Max Planck Institute for Software Systems, Germany
10.00
“Geography and communities in mobile phone networks”
Vincent D. Blondel, Universite Catholique de Louvain, Belgium
10.30
“Generalized voter models on networks”
Romualdo Pastor-Satorras, Universitat Politecnica de Catalunya, Spain
11.00-11.15 Coffee Break

Session 2: Social network analysis-II

11.15
“Phylogenetic patterns in science evolution”
David Chavalarias, CREA (CNRS/Ecole Polytechnique), France
11:45
“Link creation and profile alignment in the aNobii social network”
Alain Barrat, CNRS, France
12.15
“Performance enhancement of wireless networks”
Sourav Kumar Dandapat, IIT Kharagpur, India
12.45-14.00 (Lunch break)

Session 3: Spreading in networks-I

14.00
“Information spreading on dynamic complex network”
George Kampis, Eotvos University, Hungary
14.30
“Rumour spreading in social networks”

Alessandro Panconesi, Sapienza Universita, Italy
15.00
“Simulating an epidemic process on an empirical temporal network of human contact”
Ciro Cattuto, ISI Foundation, Italy
15.30
“Detecting diffusion traces in large communication datasets”
Lionel Tabourier, Universite Pierre et Marie Curie, France
16.00-16.30 (break)

Session 4: Spreading in networks-II

16.30
“Pervasively overlapping network communities, dynamic network centralities and saltatoric information transmission: lessons from billion year-successes of biological networking strategies”
Dávid Gyurkó,Semmelweis University, Hungary
17.00
“Assortativity effects on diffusion-like processes in scale-free networks”
Guido Caldarelli, Institute of Complex Systems CNR, Italy
17.30
“Coverage maximization in complex networks”
Subrata Nandi,NIT Durgapur,India

15th September

Session 5: Information and Technological network

9.00
“Dynamics of the ego-centred views of the internet topology”
Clemence Magnien, LIP6 (UPMC/CNRS), France
9.30
“Alternative local routing for the Internet based on complex networks”
Pau Erola, Universidad Rovira i Virgili, Spain
10.00
“On the stability of network analysis algorithms”
Sanjukta Bhowmick, University of Nebraska, USA
10.30
“Designing global information grid”
Arunabha Sen, Arizona State University, USA
11.00-11.15
Coffee Break

Session 6: Network dynamics-I

11.15

"Network Meso-dynamics: How modular topology and hierarchical organization affect behavior of networks",

Sitabhra Sinha,Institute of Mathematical Sciences, India

11.45

"Dynamics on and of subway networks"

Camille Roth, CAMS (CNRS/EHESS), France

12.15

"Alphabetic bipartite networks: Theory and Applications"

Animesh Mukherjee, IIT kharagpur, India

12.45-14.00 (Lunch break)

Session 7: Network dynamics-II

14.00

"Global synchronization induced by network dynamics in excitable systems"

Claudio J. Tessone, ETH, Zurich

14.30

"Dynamics on networks for communities, centralities and consensus"

Jean-Charles Delvenne, Universite Catholique de Louvain, Belgium

15.00

"Constructing and sampling direct graphs with given degree sequence"

Charo I. Del Genio, Max Planck Institute for the Physics of Complex Systems, Germany

15.30

"Temporal effects in the growth of networks"

Matus Medo , Physics Department, University of Fribourg, Fribourg, Switzerland

16.00

Closing

Abstracts

Community shared bicyles Vélo'v: How to catch users with lasso

Pierre Borgnat , ENS Lyon, CNRS, France

Vélo'v is the community shared bicycle system in Lyon city. As a fully automated system, the uses of the bikes are all recorded and provide an exhaustive digital footprint of the moves done through the city with these bikes. As such, they can be used to reveal part of the activity of the city and, most specially, the patterns of movements of bike users. Following first works on this subject that probed the nonstationary dynamics of this system [1, 2], and its spatial aspects exhibiting some properties of complex networks (e.g., evidence of community grouping of stations) [3, 4], we are now dealing with the study of the users of the Vélo'v system and their social or demographic traits.

For that, a large-scale statistical analysis of the trips made using Vélo'v is conducted. The objective to relate, through a statistical regression model, the numerous social, demographic and economical data (available from the french INSEE, institute on statistcs) of the various neighborhoods of the city with the actual trips made from and to the different parts of the city. To deal with this large number of variables, parsimonious linear regression methods with positivity constraints are revisited. The lasso solution using the LARS algorithm [5, 6] is found to be not fully adequate for the present problem. Indeed, it is not possible to interpret in these results whether there is a clear dependence of the usage made of bikes on the time of the day and on the populations in the various parts of the city, dependences that qualitative analysis were able to suggest.

To remedy this problem of the lasso, a further specificity of the data is introduced in the problem of regression: real data on demand are truncated because of a constraint of capacity in bikes at the stations [7]. Indeed, a given station has a fixed number of stands and can only welcome a finite number of bikes. Moreover, depending on the part of the city, some stations may be found almost empty in the morning (hence, with no bikes available) or almost full (no vacancy for any incoming trip).

We show how to adapt the LARS algorithm to this situation of truncated observations. A study of the proposed new algorithm is conducted and it is found to perform well in controlled simulations, estimating well the linear model used to generate truncated observations. Some conclusions are then drawn from the application of this method to the Vélo'v data.

References

[1] P. Borgnat, P. Abry, P. Flandrin. "Modélisation statistique cyclique des locations de Vélo'v a Lyon", Symposium GRETSI-09, Dijon, FR (Sept., 2009).

[2] Borgnat, P., Abry, A., Flandrin, P., and Rouquier, J.-B. "Studying Lyon's Vélo'v: A Statistical Cyclic Model", Proceedings of ECCS'09, Warwick, UK (Sept., 2009).

[3]Borgnat, P., Fleury, E., Robardet, C., and Scherrer, A, "Spatial analysis of dynamic movements of Vélo'v, Lyon's shared bicycle program", Proceedings of ECCS'09, Warwick, UK (Sept., 2009).

[4]P. Borgnat, C. Robardet, J.-B. Rouquier, P. Abry, E. Fleury, and P. Flandrin. "Shared Bicycles in a City: A Signal Processing and Data Analysis Perspective", Advances in

Complex Systemes, 14:3, p. 415-438 (2011).
[5] R. Tibshirani. "Regression shrinkage and selection via the lasso", J. Roy. Statist. Soc. Ser. B, 58, p. 267-288 (1996).
[6] B. Efron, T. Hastie, I. Johnstone and R. Tibshirani. "Least Angle Regression". The Annals of Statistics, 32:2, p. 407-499 (2004).
[7] L. Merchez et J.-B. Rouquier. "L'usage des vélos en libre service (VLS) comme révélateur des rythmes urbains : le cas des stations de Vélo'v", submitted to Données Urbaines (2010).

Towards social network-based Sybil tolerant systems

Krishna Gummadi, Max Planck Institute for Software Systems, Germany

There has been a flurry of research on leveraging social networks to defend against multiple identity, or Sybil, attacks. Most existing proposals rely on analyzing the social network's structure in order to label nodes as Sybils ('evil') or non-Sybils ('good '), an approach I term Sybil detection. However, recent studies have shown that the effectiveness of this approach on real-world social networks is limited.

In this talk, I will advocate a fundamentally different approach: Sybil tolerance. Rather than focus on identifying nodes as Sybils, we focus on designing systems that strictly bound the impact of Sybil nodes. I will propose a general methodology for designing Sybil tolerant systems using credit networks. Credit networks provide a way to model trust between entities and support payments between arbitrary nodes. I will first show that credit networks are Sybil tolerant, meaning an attacker cannot gain additional credit by creating additional identities. I will then discuss approaches for mapping a range of applications onto credit networks. To demonstrate the general applicability of our approach, I will present the design of Genie, a new system that allows social networking sites to thwart large-scale crawls of their networks by attackers with multiple identities.

Geography and communities in mobile phone networks

Vincent D. Blondel, Universite Catholique de Louvain, Belgium

Many complex networks have their nodes distributed in space. In this talk, we describe some recent results for spatially distributed networks. In particular, we describe results obtained from a community detection method on a large network constructed from communications between millions of mobile phone users in several European countries. We quantify the decrease with distance of connection probability between mobile phone users, we describe a conjecture about a possible explanation for the observed decrease and we identify natural decompositions of the countries into socially cohesive regions. If time permits, we will also describe some recent results on privacy issues in data collection in large social networks.

Generalized voter models on networks

Romualdo Pastor-Satorras, Universitat Politecnica de Catalunya, Spain

A topical problem in the statistical physics approach to social and evolutionary dynamics is the study of the mechanisms ruling the formation of consensus in an initially disordered population, in situations implying the opinion about a certain issue, the intention of voting in an election, or the evolutionary competition of different species striving for the same ecological resources. Several stochastic copying/invasion processes have been proposed to represent this kind of problems, the simplest being the voter model and the Moran process. While simple voter-like models are well understood on regular lattices in terms of exact solutions, they become more relevant in social and evolutionary contexts when considered on top of complex networks, which act as more realistic representations of social or ecological contact patterns. Several studies have pointed out the relevance of the network connectivity heterogeneity in voter-like models, reflected on relevant quantities such as the exit probability or the time to reach consensus. However, not only the connectivity heterogeneity plays a natural role in ordering processes, but also the intrinsic heterogeneity of the individual, as measured by their propensity to interact with peers, and change state accordingly. Here we will discuss some generalizations of voter-like dynamics taking into account individual heterogeneity, parametrized in terms of topological features of the substrate network. Applying a heterogeneous mean-field approximation, we will be able to derive approximate expressions for relevant observables, which compare well with the result of direct numerical simulations.

Phylogenetic patterns in science evolution

David Chavalarias, CREA (CNRS/Ecole Polytechnique), France

Science is one of the core cultural production of mankind. If theories about science evolution - how theories are born, how ideas spread have flourished during the XX century, the possibility to propose large scale pictures of science evolution through the analysis of science productions is quite recent. The availability of vast digitalized scientific corpora combined with the development of complex network theory and text-mining methods make it possible nowadays to sketch the ever-fluctuating landscapes of science through the analysis of its digital traces. The phylogenetic networks obtained deliver new insights in science evolution, highlighting strong regularities in the evolution of scientific topics.

Link creation and profile alignment in the aNobii social network

Alain Barrat, CNRS, France

We investigate the structural and dynamical properties of aNobii (www.anobii.com), a social bookmarking system designed for readers and book lovers. Users of aNobii provide information about their library, reading interests and geographical location, and they can establish typed social links to other users. We perform an in-depth analysis of the system's social network and its interplay with users' profiles. We describe the relation of geographic and interest-based factors to social linking. Furthermore, we perform a longitudinal analysis to investigate the interplay of profile similarity and link creation in the social network, with a focus on triangle closure. We report a reciprocal causal connection: profile similarity of users drives the subsequent closure in the social network and, reciprocally, closure in the social network induces subsequent profile alignment. Access to the dynamics of the social network also allows us to measure quantitative indicators of preferential linking.

Performance enhancement of wireless networks

Sourav Kumar Dandapat, IIT Kharagpur, India

Wireless technology has gained huge popularity over last decade. In year 2010, wireless traffic contributes 37% of overall Internet traffic and it is being predicted that by 2015 wireless traffic will account for 54% of overall traffic. Wireless resources like bandwidth, battery power are very costly and sub-optimal utilization of these resources result in degradation of overall system performance. To handle this increased traffic, efficient utilization of resources and infrastructure becomes a necessity. Hence the objectives of our work can be listed as i) efficient utilization of resources and infrastructure ii) mitigating wireless Internet traffic iii) handling mobility and churn of devices.

Information spreading on dynamic complex network

George Kampis, Eotvos University, Hungary

We developed and analyzed an agent-based model for the study of information propagation in dynamic networks. We represent information as a state of a node in the network that can be probabilistically transferred to an adjacent node in a single time step. The model is based on a closed (yet large enough) population (i.e., network) that can support various dynamics processes both on and of the network. As dynamics of the network, we consider various network creation strategies (i.e., processes to add and remove links). By dynamics on the network, we study a spreading process where information is available in a fixed time window only. This can be seen as a variant of the SIR model of epidemics, where after a certain period, the 'infection' disappears (i.e., ceases to be transferable). This models the decay in the information's freshness as well as the node's limited effort in spreading it.

In our work, we study the interaction between the two types of dynamics and investigate the percentage of nodes receiving the information from a randomly initialized cascade (i.e., a few

random nodes receiving the information). It is important to emphasize that in this analysis we understand the cascade in a cumulative fashion, i.e., counting all nodes that ever received the information, independent of their current status of willing to transfer it further.

In our previous work we have studied what kind of networks (i.e., degree distributions) emerge from various network creation dynamics. Here we are interested in the interplay of these with the dynamics of information spreading processes on the network. In short, this extension is concerned with the interplay between the dynamics on and the dynamics of the network.

Rumour spreading in social networks

Alessandro Panconesi, Sapienza Universita, Italy

Gossip, as we all know, spreads like wildfire. What is the property of social networks that makes this possible? We show in a mathematically precise way that it all boils down to an empirical property of social networks, known as (high) conductance.

Simulating an epidemic process on an empirical temporal network of human contact

Ciro Cattuto, ISI Foundation, Italy

The spread of infectious diseases crucially depends on the contact patterns among individuals. Knowledge of these patterns is important to inform modeling and computational efforts. However, few empirical studies provide estimates for the number and duration of contacts in social groups, and typically data are not explicit at the individual level and the dynamical aspects of contacts are disregarded. Here we aim at assessing the role of temporal features on the spread of a simulated epidemic. We consider high-resolution data on the interactions between the attendees of a conference, collected by using a wireless network of wearable sensors. We simulate a SEIR process over both the dynamical network of contacts and over two aggregated versions of such network. We show that, for realistic values of the epidemic parameters, an aggregated network taking into account the daily duration of contacts is a good approximation to the full temporal network, whereas a homogeneous representation of the contact network fails to reproduce the size of the epidemic. These results have implications in understanding the level of detail that is needed to correctly inform computational models for the study and management of epidemics.

Detecting diffusion traces in large communication datasets

Lionel Tabourier, Universite Pierre et Marie Curie, France

The content of phone calls is in general out of reach for confidentiality reasons. In addition, the massive amount of information exchange in large communication networks makes in practice impossible to analyze it in order to identify how information flows. That is why it would be of great importance to design 'content-free' methods to identify where and when information propagation takes place.

Here we propose a method to address this issue that combines dynamical measurement tools with appropriate comparison models. It relies on the assumption that intentional information propagation, which can be expected from the caller to the callee, implies causality effects. These effects can be detected using measurements which take into account the dynamical nature and the directedness of such data.

We used for this study a large cellphone record providing who calls whom and when. We then run on this database a set of statistical tools and enumerate several dynamical patterns, such as loops or cascade-like mo- tifs, which may be seen as proxies of information propagation processes. By comparing these measures with those obtained on null models, we claim that we can detect traces of diffusion phenomena. We show that causality effects are only visible as local phenomena and during short time-scales in this context no more than a few hours. It is indeed possible to discover very specific motifs, such as star-like and cycle-like communication patterns, which are underestimated by the model, and we can assess the probability that such patterns are related to a diffusion process.

The method that we propose is thus a step forward in locating where and when information flow happens in a phone call dataset without resorting to the content of the calls. As it only relies on having a large sequence of timestamped events, we suggest that such analysis could be used in other contexts of information spreading over large communication datasets, such as emails exchanges or instant messaging networks.

Pervasively overlapping network communities, dynamic network centralities and saltatoric information transmission: lessons from billion year-successes of biological networking strategies

Dávid Gyurkó, Semmelweis University, Hungary

In the last decade several analogies have been uncovered between the topology and dynamics of complex social and biological networks [1]. Our studies on community-based, perturbation-based and spatial game-based centralities showed that inter-modular nodes and links play a key role in information transmission, and led us to suggest a novel information transmission mechanism of complex networks.

Moduland is a novel method family to detect pervasively overlapping communities (www.linkgroup.hu/modules.php, [2]). In the ModuLand framework local influence zones of each links (or nodes) are defined first. Next, a community landscape is constructed, where the

horizontal plane corresponds to a 2D visualization of the network, while the vertical scale is the sum of the influence zones containing the given link (or node). The value of the vertical scale is called as community centrality, since it characterizes the influence reaching the given link or node from any other links (or nodes) the whole network. The overlapping modules are the ‘hills‘ of the community landscape. The method also constructs a hierarchical, coarse-grained representation of the network, where the nodes of the upper level correspond to the modules of the original network, and the link-weights of the upper level denote the overlaps of the modules. This coarse-graining can be continued recursively, until the whole original network coalesces into a single node.

Our studies on changes of protein-protein interaction networks during abrupt changes of the environment (stress) [3] showed that the overlap of modules decreases, and modules became partially disintegrated as an initial response to stress. The stress-induced decrease of inter-modular connections is beneficial, since it A.) allows a better focusing on vital functions, and thus spares resources; B.) localizes damage (e.g. of free radicals) to the affected modules; C.) reduces the propagation of noise; D.) allows a larger ‘degree of freedom’ of the individual modules to explore different adaptation strategies; and E.) helps the ‘mediation of inter-modular conflicts’ during a period of violent intra-modular changes. Modular overlaps emerged as keys of adaptive processes in cells-and in all complex systems including social networks.Changes in community centrality identified key players of the response to the cellular challenge.

Turbine ([4], www.linkgroup.hu/Turbine.php) is a widely applicable, Matlab-compatible tool to assess the propagation of perturbations in any cellular networks. In these studies intermodular nodes emerged as highly efficient transmitters of perturbations.

Based on our earlier studies on spatial games (where agents playing repeated rounds of social dilemma-type games, like the prisoner's dilemma game, can play only with their neighbors), we constructed the spatial game framework, NetworGame ([5], www.linkgroup.hu/NetworGame.php), which is a versatile program package to model any types of two-agent games (with 2 to 5 strategies) in any real world, or model networks using any types of strategy update rules, update dynamics and starting strategy distributions. The NetworGame program interprets game centrality as the ability of a networked agent (or a link of two agents) with a single initial defective strategy to change an overall initial starting cooperation to defection (and vice versa: a cooperative strategy of a linked node-pair or triangle changing overall defection to cooperation). Spatial games can also be rationalized in networks of non-conscious agents, such as amino acids, or proteins [6]. Our game centrality measures correctly identified the major decision makers of social cooperation in benchmark networks, such as the Zachary karate club network or Michael's strike network, and pinpointed key ‘actors’ determining the cooperation of biological networks.

Recently we summarized the features of particularly dynamic central elements, and called them as ‘creative elements’ [7]. These elements bridge Ronald S. Burt's ‘structural holes’, and provide a key subset of Mark Granovetter's ‘weak links’. Active centers and binding sites of proteins often occupy such a position in protein structure networks. As the complexity of the system increases (as we examine protein-protein interaction networks, networks of neurons, or social networks), the mobility of creative elements expands, and covers more and more the entire network [7].

Based on our earlier studies demonstrating the partial disassembly of networks as a response to stress [3], recently we proposed that information transmission of 'cumulus-type' networks (which have a limited overlap between their modules and a more compact, rigid module structure) can be described by an 'energy transfer' mechanism. In 'stratus-type' networks (having a significant overlap between their modules) the information transfer utilizes multiple trajectories. These signaling trajectories converge at modular boundaries. Bridging nodes may have a decisive role in the regulation of signal transmission from one network module to another [8]. Such inter-modular nodes, called as cross-talks in cellular information transfer networks, are key players of biological information transmission [9-11].

References:

[1] P. Csermely, Weak links: The universal key to the stability of networks and complex systems. Springer Verlag, 2009. www.weaklink.sote.hu/weakbook.html

[2] I. A. Kovács, R. Palotai, M. S. Szalay, P. Csermely, Community landscapes: a novel, integrative approach for the determination of overlapping network modules. PLoS ONE 7, 2010, e12528.

[3] R. Palotai, M. S. Szalay, P. Csermely, Chaperones as integrators of cellular networks: changes of cellular integrity in stress and diseases. IUBMB Life 60, 2008, pp. 10-18.

[4] M. A. Antal, C. Böde, P. Csermely, Perturbation waves in proteins and protein networks: Applications of percolation and game theories in signaling and drug design. Curr. Prot. Pept. Sci. 10, 2009, pp. 161-172.

[5] S. Wang, M. S. Szalay, C. Zhang, P. Csermely, Learning and innovative elements of strategy update rules expand cooperative network topologies. PLoS ONE 3, 2008, e1917.

[6] P. Csermely, R. Palotai, R. Nussinov, Induced fit, conformational selection and independent dynamic segments: an extended view of binding events. Trends Biochem. Sci. 35, 2010, pp. 539-546.

[7] P. Csermely, Creative elements: network-based predictions of active centres in proteins, cellular and social networks. Trends Biochem. Sci. 33, 2008, pp. 569-576

[8] P. Csermely, K. S. Sandhu, E. Hazai, Z. Hoksza, H. J. M. Kiss, F. Miozzo, D. V. Veres, F. Piazza, R. Nussinov, Disordered proteins and network disorder in network representations of protein structure, dynamics and function. Hypotheses and a comprehensive review. Curr. Prot. Pept. Sci. 12, 2011, in press. http://arxiv.org/abs/1101.5865

[9] T. Korcsmáros, I. J. Farkas, M. S. Szalay, P. Rovó, D. Fazekas, Z. Spiró, C. Böde, K. Lenti, T. Vellai, P. Csermely, Uniformly curated signaling pathways reveal tissue-specific cross-talks, novel pathway components, and drug target candidates. Bioinformatics 26, 2010, pp. 2042-2050.

[10] I. J. Farkas, T. Korcsmáros, I. A. Kovács, Á. Mihalik, R. Palotai, G. I. Simkó, K. Z. Szalay, M. Szalay-Bekó´, T. Vellai, S. Wang, P. Csermely, Network-based tools in the identification of novel drug-targets. Sci. Signal. 4, 2011, pt3.

[11] T. Korcsmáros, M. S. Szalay, P. Rovó, R. Palotai, D. Fazekas, K. Lenti, I. J. Farkas, P. Csermely, T. Vellai, Signalogs: orthology-based identification of novel signaling pathway components in three metazoans. PLoS ONE 8, 2011, e19240.

Assortativity effects on diffusion-like Processes in scale-free networks

Guido Caldarelli, Institute of Complex Systems CNR, Italy

We study the variation in epidemic thresholds in complex networks with different assortativity properties. We determine the thresholds by applying spectral analysis to the matrices associated to the graphs. In order to produce graphs with a specific assortativity we introduce a procedure to sample the space of all the possible networks with a given degree sequence. Our analysis shows that while disassortative networks have an higher epidemiological threshold, assortative networks have a slower diffusion time for diseases. We also used these networks for evaluating the effects of assortativity in a specific dynamic model of sandpile. We show that immunization procedures give different results according to the assortativity of the network considered.

Coverage maximization in complex networks

Subrata Nandi, NIT Durgapur, India

Random walk has been thoroughly studied in the domain of physical sciences, where the speed of the walk is the primary concern. However, in recent years, random walk has been widely used in the domain of distributed systems e.g. unstructured search, information dissemination etc. In such applications, each hop of a random walker consumes some bandwidth which is a valuable resource and therefore, needs to be used judiciously. Hence the random walk phenomena have to be probed from quite a different perspective with an objective to ensure both speed and efficiency. However, the inherent trade-off between speed and efficiency makes the problem non-trivial. Being inspired by the study of walker dynamics on regular grids, we design a time varying regulated proliferation-based random walk strategy for that essentially fulfils the objective .

Dynamics of the ego-centred views of the internet topology

Clemence Magnien, LIP6 (UPMC/CNRS), France

I will present in details the dynamics of a specific case: the ego-centred views of the internet's topology. The internet, which is composed of routers linked at the IP level, has been widely studied during these last few years. Since no official map of its topology is available, the information about the nodes and links it is composed of must be acquired by measurement operations, often based on the traceroute tool. This tool discovers, under certain assumptions, the nodes (IP addresses) and links composing the path between a given source computer and a target computer.

Obtaining a map of the internet in this way is long and costly, and some results point towards the fact that the obtained map may be biased, i.e. not share the statistical properties of the original topology.

Measuring the dynamics of the internet topology is therefore both very costly (the measurements should be repeated periodically) and prone to bias. I will present an orthogonal approach to this question, called "a radar for the internet". It consists in focusing on what a given computer can see of the topology, which we call ego-centred views. This is an object that is well defined, and with a small size, which allows to measure it periodically with a high frequency.

Conducting such measurements however requires some care, as having a too high frequency and/or attempting to observe too many IP adresses may overload the network, causing a decrease in the quality of the obtained data. A careful analysis of the different measurement parameters must therefore be conducted.

I will then present an analysis of the collected data, beginning with the general characteristics of these measurements. We will in particular see that the ego-centred views evolve at a much faster rate that what could have been expected.

I will then focus on the study of the stability of the nodes. We will see that some of the nodes observed in the measurement are seen consistently throughout the whole measurement, while others are very volatile and are observed only a few times.

I will conclude the analysis of the data by highlighting two phenomena that play a key role in the observed dynamics: load-balancing, which consists in using more than one route to transfer the information between a given source and a given destination in order to lessen the load on each of these routes, and the evolution of the topology.

Finally, I will present some directions for modelling the network and its dynamics. We will see that by proposing simple models for the topology, its dynamics, and the load-balancing, we can reproduce many of our observations. This shows that in our case simple phenomena interact to produce a complex global behavior. We will also see that some phenomena cannot be reproduced in this way, which calls for further analysis.

I will also present an insight of some other questions linked to the study of network dynamics. The first question is whether one can trust the observed properties of the dynamics, i.e. whether the measurement procedure induces a bias in the data, is a fundamental one. Another important question is whether there are some moments at which a network's dynamics is significantly different from the usual dynamics, i.e. whether we can detect events in the dynamics.

Alternative local routing for the Internet based on complex networks

Pau Erola, Universidad Rovira i Virgili, Spain

Internet is one of the largest synthetic complex system ever built. It consists in a collection of more than 30,000 networks each one known as an Autonomous System. In the last few years, Internet is experiencing an explosive growth that is compromising its navigation scalability due to its dependence on the Border Gateway Protocol (BGP). The BGP routing protocol requires to maintain an updated view of the network topology, involving a huge amount of data exchange and significant convergence times. The scale-free topology of Internet makes

the complex network theory the natural framework to analyze its problems and propose solutions. Here, we present a local alternative to this routing protocol based on complex networks with close to optimal results.

On the stability of network analysis algorithms

Sanjukta Bhowmick, University of Nebraska, USA

Algorithms for analyzing large complex networks, such as those for community detection, are mostly based on combinatorial techniques. Traditionally combinatorial algorithms assume that the input is exact. However, real world networks are derived from subjective or experimental data and therefore inherently contain some degree of approximation. In this presentation,we will discuss how this inexactness of input affects the stability of network analysis methods and present some methods for improving the algorithmic stability.

Designing global information grid

Arunabha Sen, Arizona State University, USA

The newly emerging discipline of Network Science attempts to model the structure and dynamics of large-scale complex systems both natural and man-made. Natural systems such as the genetic pathways and man made systems such as the WWW are often given as examples of such complex networks. In this presentation, we discuss a part of another man made complex system - the Global Information Grid (GIG), an all-encompassing communications project undertaken by the U.S. department of defense (DoD). The GIG is defined as a "globally interconnected, end-to-end set of information capabilities for collecting, processing, storing, disseminating, and managing information on demand to war fighters, policy makers, and support personnel." The goal of the GIG is to encompass all communication assets of the DoD covering space, air, land and sea. One can recognize the complexity of this system by noting the fact that it involves seven million computers connected over twenty thousand commercial telecom circuits with twenty thousand Air Force satellite terminals and nearly five thosand manned airborne platforms. In this talk we will focus on the aerial layer networking aspects of the GIG. The airborne network formed by a large number of heterogeneous airborne networking platforms is dynamic in nature - that is the topology changes frequently with time. We discuss challenges of designing a time varying network with time invariant properties. In particular, we discuss the design aspects of an dynamic airborne network with time invariant connectivity and coverage.

Network Meso-dynamics: How modular topology and hierarchical organization affect behavior of networks

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It has been known for some time that the topological organization of a network can critically affect its function, e.g., by controlling its dynamical robustness or the response to external perturbations. However, till quite recently the focus had been on either microscopic properties (such as degree or centrality of nodes) or macroscopic features (such as average path length or clustering). It is only recently that we have become aware of the important role that mesoscopic features, such as modularity and hierarchy, play in network dynamics. In this talk we review our recent work in this area, showing how modularity and hierarchically arranged modular organization can introduce several distinct time-scales in a system. This results in the emergence of novel dynamical features in networks - such as the enhancement of global stability of attractors in models of associative memory and the occurrence of novel phases in spin models at optimal levels of modularity. We also look at a plausible model for the generation of such mesoscopic features in networks.

Dynamics on and of subway networks

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Subway networks shape, to some extent, the structure of movements of individuals across a city; similarly, they are being partially shaped by the presence of these individuals in the city. This talk will present two complementary studies describing the dynamic processes which subway networks both host and undergo.

The first analysis focuses on dynamics processes occurring on the subway network of a large city (London) in terms of its commuting patterns. It uses the large scale, real-time electronic ticketing data from the Oyster Card system, introduced less than a decade ago, to reveal a part of the structure and organization of the city. More precisely, this study shows that patterns of intraurban movement are strongly heterogeneous in terms of volume, but not in terms of distance travelled, and that there is a polycentric structure composed of large flows organized around a limited number of activity centers. For smaller flows, the pattern of connections becomes richer and more complex and is not strictly hierarchical since it mixes different levels consisting of different orders of magnitude.

The second study investigates the temporal evolution of the major subway networks in the world over the last century. The main result is that most of these networks tend to converge to a shape which shares some generic features, despite their geographical and economical differences. These features include a core with branches radiating from it to cover about twice the average radial extension of the core. The core generally includes about 60% of the network stations and exhibits an average degree of order 2.5. Interestingly, core and branches define two distinct and universal regimes in terms of the number of stations at a given distance from the barycenter. This result which was difficult to interpret in the framework of fractal geometry finds here a natural explanation.

More broadly, these two types of studies open the way to more integrated analyses of the coevolution between the dynamics on and of subway networks.

Alphabetic bipartite networks: Theory and Applications

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Life and language are discrete combinatorial systems (DCSs) in which the basic building blocks are finite sets of elementary units: nucleotides or codons in a DNA sequence and letters or words in a language. Different combinations of these finite units give rise to potentially infinite numbers of genes or sentences. This type of DCS can be represented as an Alphabetic Bipartite Network (α-BiN) where there are two kinds of nodes, one type represents the elementary units while the other type represents their combinations. There is an edge between a node corresponding to an elementary unit u and a node corresponding to a particular combination v if u is present in v. Naturally, the partition consisting of the nodes representing elementary units is fixed, while the other partition is allowed to grow unboundedly. The evolution equations for α-BiNs under different growth rules are derived, and the corresponding degree distributions computed. It is shown that asymptotically the degree distribution of α-BiNs can be described as a family of beta distributions. The one-mode projections of the α-BiNs and their asymptotics is also studied theoretically and further supported through simulations.

Global synchronization induced by network dynamics in excitable systems

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Synchronisation is the emergence of common dynamics in a set of iteracting units. This phenomenon is pervasive in biological, technological, chemical, and social systems. Which mechanisms underly the emergence of synchronisation beyond that of strong coupling, constitutes an active area of research. The phenomenology of synchronisation in excitable systems is quite different than that of oscillatory ones: for example, it was found that noise, heterogeneity and repulsive interactions may enhance synchronisation in excitable systems. In this contribution we study a new source of synchronisation in excitable systems: the network dynamics.

In many cases of interest, the structure describing the interaction network evolves over time. However its full --often complex-- structure is apparent only when seen over long time-scales, in many cases much larger than those associated with the internal dynamics of the elements represented by the nodes. Take a social network as a prototypic example: individuals can interact only with a very limited subset of their acquitances over a given period of time (because of limited capacity, for example). Then, if we take a snapshot over a short interval of the actual social contacts, the network would look rather sparse. Despite of this, several dynamical processes are able to survive and spread though real-world networks, such as diseases and opinions. In particular, we study a sparsely connected network of excitable units in which the edges randomly rewire at a given rate λ. Indeed, at any time, there are exactly **N/2** isolated components, each node being connected to exactly one another --constituting a

so-called *monogamous network*--. We show that, contrary to intuition, a **globally** synchronised state can be induced solely by the network dynamics. If the rewiring rate is too slow, no emergent dynamics appear. There exists an intermediate range of values of λ where all the units fire in a synchronised fashion. In the limit of very fast rewiring, which induces a fully connected -like coupling, the phenomenon dissapears again. This shows that this phenomenon is not a trivial one induced by global coupling, but the outcome of an interplay between node dynamics and the time-scale of the global dynamics. We provide a semi-analytical treatment that allows for a qualitative understanding of the phenomenon.

Dynamics on networks for communities, centralities and consensus

Jean-Charles Delvenne, Universite Catholique de Louvain, Belgium

Dynamical systems taking place on networks, such as opinion dynamics, synchronisation, consensus or random walks, reveal a lot about their structure. In particular we show, through a dynamical reinterpretation of well-known concepts, how centrality measures and community detection quality functions are intimately related. The dynamical interpretation allows to design new centrality or community detection measures tailored for every particular application. We also show how a dynamical distance measure between nodes allow to represent evolving networks easily. We illustrate this on the evolution of the European trade network before and after the introduction of the Euro.

Constructing and sampling direct Graphs with given degree sequence

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The interactions between the components of complex networks are often directed. Modeling such systems often requires the construction of ensembles of directed graphs with a given sequence of in- and out-degrees. As the number of simple labeled graphs with a given degree sequence is typically very large even for short sequences, sampling methods are needed for statistical studies. One of the existing methods first generates a restricted class of graphs, then uses a Markov Chain Monte-Carlo algorithm based on edge swaps to generate other realizations. As the mixing time of this process is at best unknown, and at worst very long, the independence of the samples is not well controlled. Another class of methods is based on the Configuration Model, which, however, leads in many cases to uncontrolled biases or at least unacceptably many sample rejections due to self-loops and multiple edges. We present an algorithm that can construct all possible realizations of a given bi-degree sequence by simple digraphs, is rejection free, guarantees the independence of the constructed samples, and provides their weight. The weights can then be used to compute statistical averages of network observables as if they were obtained from uniform or arbitrarily distributed sampling.

The mathematical foundations of our method have their roots in the realization that not all the sequences of integer pairs (bi-degree sequences) constitute the in- and out-degrees of a directed graph. The ones that do are called graphical sequences. Also, even if a bi-degree sequence is graphical, not every connection is guaranteed to yield a digraph in the end: a careless placement of links can break graphicality and bring a construction to a forced stop.

The Fulkerson theorem provides a way to test for the graphicality of a given bi-degree sequence. However, the theorem is not constructive, and as such it does not provide a way to build a graph from the sequence. This is an issue because of the possibility of breaking graphicality mentioned above. On the other hand, a constructive graphicality test is the Kleitman-Wang (KW) theorem. However, the KW mechanism cannot access the entirety of the space of the graphs realizing a given sequence.

In order to create a method that overcomes the theoretical and practical limitations of the current approaches, we prove a theorem characterizing the graphicality of a bi-degree sequence in the presence of star-constraints, i.e., a set of forbidden nodes to which connections cannot be placed. Given a node i, this result allows the creation of its "allowed set", i.e., the set of all nodes to which i can be connected without breaking graphicality. In its turn, this enables the creation of a sampling algorithm that places connections systematically from each node before passing to the next. At each step, the algorithm constructs the allowed set for the first node, then extracts a random node from it and places the connection, repeating this procedure until the out-degree of the first node has vanished. Repeating these steps for all the nodes yields a directed graph realizing the given bi-degree sequence.

To create the allowed set one could perform repeated applications of the star-constrained di-graphicality theorem. However, this is not needed, as we show the existence of a fail-node that allows an immediate discrimination between allowed and not-allowed nodes. In order to find the fail-node, we study the properties of a particular derivative sequence, obtained from the one being sampled. We find that the fail-node can be readily identified via comparison of the left-hand-sides and right-hand-sides of the Fulkerson inequalities for this particular sequence.

The algorithm generates an independent sample every time it runs. However, the samples are not generated with a uniform probability. Nevertheless, we give an expression for the relative probability for each sample to occur, which allows the calculation of observables as if they were obtained from a uniform or arbitrary distribution.

Finally, we estimate a theoretical upper bound for the worst case complexity of the algorithm. We show that all the non-trivial steps in the placement of a link can be completed in linear time. In particular, we express the left-hand-sides and the right-hand-sides of the Fulkerson inequalities in terms of recurrence relations. Since the procedure must be repeated for each edge in the digraph, the maximum complexity of the algorithm is cubic.

In summary, we develop a graph construction and sampling method to construct simple directed graphs realizing any given sequence of in-degrees and out-degrees. Such constructions are needed in many practical modeling situations, ranging from epidemics and opinion spreading through food webs to transcriptional regulatory networks. Unlike existing methods, which are plagued by biases and unacceptably long running times, our algorithm is unbiased, rejection-free, can generate all the possible realizations of a bi-degree sequence and guarantees the independence of the samples. In proving our results we also provide a recurrence-relation formulation of the necessary and sufficient conditions for graphicality of a bi-degree sequence, giving the possibility of efficient, linear-time, tests whose scope of application is fully general and goes beyond the present algorithm.

Temporal effects in the growth of networks

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We show that to explain the growth of the citation network by preferential attachment (PA), one has to accept that individual nodes exhibit heterogeneous fitness values that decay with time. While previous PA-based models assumed either heterogeneity or decay in isolation, we propose a simple analytically treatable model that combines these two factors. Depending on the input assumptions, the resulting degree distribution shows an exponential, log-normal or power-law decay, which makes the model an apt candidate for modeling a wide range of real systems.