Workshop on

Mechanisms underlying local to global signals in networks

19th and 20th May 2016-05-03

IXXI-ENS Lyon

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IXXI-ENS Lyon, 46 allee d'Italie, Site Monod, Lyon 69007

Speakers

- Márton Karsai, ENS Lyon / INRIA / IXXI, marton.karsai@ens-lyon.fr

Top-down and bottom-up approaches in modelling temporal networks

- Remy Cazabet, IXXI-ENS Lyon, remy.cazabet@ens-lyon.fr

Taking into account nodes' properties to better understand the topology of networks

- Anton Korniienko, EC-Lyon, AMPERE Laboratory, anton.korniienko@ec-lyon.fr

Local and Global Behavior, Robust Control System point of view

- Xavier Bombois, EC-Lyon, AMPERE Laboratory, xavier.bombois@ec-lyon.fr

Identification for control. From a single controlled system to the interconnection of controlled systems

- Paulo Gonçalves, INRIA, ENS-Lyon, Paulo.Goncalves@ens-lyon.fr

A possible isometric shift operator for signal processing on graphs

- Rodrigo Dorantes Gilardi, LAMA- Université de Savoie Mont-blanc, IXXI-ENS Lyon, rodrigo.dorantes-gilardi@ens-lyon.fr

Amino-acid network as a model of the protein's structure, an in silico investigation

- Laurent Vuillon, LAMA, Université de Savoie Mont-blanc, Laurent.Vuillon@univ-smb.fr

Similarity measures on amino-acid networks

- Nicolas Schabanel, LIAFA-Paris Diderot, nicolas.schabanel@cnrs.fr

Folding Turing is hard but feasible

- Bernadette Charron-Bost, LIX, charron@lix.polytechnique.fr

Influence Systems: an Algorithmic Approach to Collective Behavior

- Claire Lesieur, AMPERE Laboratory, IXXI-ENS Lyon, claire.lesieur@ens-lyon.fr

Influences versus Connections

Programme

Time	Thursday 19 May 2016	Friday 20th May 2016
9:00-9:55		Claire Lesieur
10:00-10:55	Marton Karsai	Rodrigo Dorantes Gilardi
11:00-11:55	Remy Cazabet	Laurent Vuillon
12:00-12:55	LUNCH	Nicolas Schabanel
13:00-13:55	Anton Korniienko	LUNCH
14:00-14:55	Xavier Bombois	-discussion
15:00-15:55	Paulo Gonçalves	
16:00-16:55	Bernadette Charron	
18:00-20:00	Visite Traboules Croix Rousse (to be confirmed)	
20:00-22:00	Diner Bouchon Lyonnais	

Thursday : salle des conseils MONOD (2 etage, ENS-Lyon, Monod)
Friday : salle de conférence du CBP (bâtiment LR6)

Meeting 5 min before beginning of the day IXXI-ENS-Lyon (46 allee d'Italie, 2 etage, site Monod)

Márton Karsai
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Top-down and bottom-up approaches in modelling temporal networks

In the last ten years the access to high resolution datasets from mobile devices, communication, and pervasive technologies has propelled a wealth of developments in the analysis of social networks. Particular efforts have been devoted to characterise how their structure influences the critical behaviour of dynamical processes evolving on top of them. However, the large majority of the approaches put forth to tackle this subject utilise a time-aggregated representation of the interactions and neglect their time-varying nature. Indeed, the concurrency, and time ordering of interactions, even if the social network contains stable relationships, are crucial and may have considerable effects.

In this talk we will take a short overview about some recent works identifying, characterising, and modelling structural and temporal correlations which influence the evolution of social communication networks and ongoing processes. We will take a special focus (a) on a top-down reference model approach to detect important correlations influencing the speed of information spreading; and (b) on a simple generative model of temporal interactions to study the effect of time-varying interactions and various social mechanisms on the spreading of contagion processes. The model integrates key mechanisms that drive the formation and maintenance of social ties – like memory, social reinforcement, focal closure and cyclic closure, which have been shown to give rise to weight heterogeneities, community structure, weight-topology correlations, and small-world connectedness in social networks. We compare the emerging characteristics of the proposed temporal model network with real-world time-varying networks, and through data-driven simulations we validate the effects of different social mechanisms.

Remy Cazabet
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Taking into account nodes' properties to better understand the topology of networks

Networks are often used to model a set of entities and their interactions.
To study the topological properties of a network (clustering, centrality, mesoscopic organization (communities), Assortativity, etc.), these properties are usually compared to those obtained in a randomly rewired version of the network, called a Null Model. The most commonly used Null Model is called the configuration model, and rewire edges randomly while keeping the degree distribution.

In networks for which numeric variables are associated to nodes (spatial situation, age, etc.), we can determine if these attributes play a role in the topology structure by computing a deterrence function.
We can use this deterrence function to create a Null model of the network neutralizing the effect of these variables.

I'll explain this process and its applications using a concrete case on Lyon's Bicycle Sharing System.

Anton Korniienko
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Local and Global Behavior, Robust Control System point of view

In this talk, we present and explore a control system point of view on the relation between local and global system behavior. Our vision is illustrated on the example of Phase Locked Loop (PLL) network from Microelectronics. This network can be described by a Linear Time Invariant (LTI) dynamical system. Each module (PLL) has to be designed such that it ensures both local and global properties enforcing global network synchronization. Of course the design problem as such is a complex problem, even in LTI case, giving a complex structure of network and big number of modules. Our strategy is then to transform the global design problem into (several) local one(s). The local design problem(s) can be easily solved (by H-infinity design technics for example) however in order to achieve the global network objective the link between local and global behavior should be investigated.

Xavier Bombois
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Identification for control. From a single controlled system to the interconnection of controlled systems

Modeling is a crucial task in modern engineering: in particular, for control engineering where models of dynamical systems are used to optimize the performance of these systems. Since engineering systems are nowadays very complex, it is an illusion to obtain a perfect model. However, for a given control objective, only few of the system properties are really relevant to model. Consequently, for that control objective, one should seek a model with a small uncertainty for those important system properties while a large uncertainty can be allowed for all the other properties. In this talk, we will discuss techniques to obtain such a appropriate model for control using system identification. System identification is an efficient technique that allows to derive models based on data collected on the to-be-modelled system. First, the input of the system is excited using an excitation signal and the corresponding output signal is measured. Second, these data are used to determine, in a certain class of models, that model that is best able to explain the data. In a nutshell, we derive techniques in order to design excitaion signals that allow to obtain appropriate models for control at a reasonable cost.

We first consider independent systems. Subsequently, we will spend attention to the case of interconnected systems and to their specificities. Control systems indeed become more and more interconnected (i.e. formation control of drones/satellites, automated highway systems, clock synchronization via PLL networks in computer systems). In these types of systems, the reference of the individual control systems is computed based on information transmitted from the neighboring control systems. Due to this interconnection, the uncertainty in each system has influence on the performance of the other systems in the network. Moreover, as far as identification is concerned, excitation signals and perturbation signals related to one individual loop have also influence on each of the other loops in the network.

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A possible isometric shift operator for signal processing on graphs

Graph signal processing (or signal processing on graphs) is an emerging area of numerical analysis. Its development is prompted by the proliferation of measurements issued from agents that interact geometrically, statistically, functionally or in any other behavioural way, even featureless. Thus, to better understand, model, predict and then control the characteristics / actions of individuals at the community scale, it is important to develop numerical methods and algorithms able to fully integrate into the data analysis, the discrete, possibly non-euclidean, nature of the measuring support. At the intersection of graph theory, harmonic analysis and statistical learning, this new trend aims at extending common concepts and operations well defined for samples lying on regular lattices (e.g. time series or images) to datasets supported on discrete structures such as arbitrary graphs.

Rodrigo Dorantes Gilardi
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Amino-acid network as a model of the protein's structure, an in silico investigation

Amino-acid networks are widely used to model protein structure; but so far little has been attempted to question the biological relevancy of such modeling. We present an in silico investigation that compares structural and functional changes of the PSD-95 protein on a large set of mutations, using the amino-acid network approach. We show how both changes correlate well for functionally sensitive positions but not for functionally tolerant positions; this, in accord with the robustness and adaptability of proteins.

Laurent Vuillon
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Similarity measures on amino-acid networks

We investigate the topology of amino-acid networks associated with natural proteins. We first compute the assortativity measures on these networks and define interesting sub-networks. In a second time we study the regularity of these networks and compute some similarity measures. We discuss the interpretation of similar amino-acids and compute a sub-network with a kind of robustness property.

Nicolas Schabanel
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Folding Turing is hard but feasible
Joint work with: Cody Geary, Pierre-Étienne Meunier and Shinnosuke Seki

We introduce and study the computational power of Oritatami, a theoretical model to explore greedy molecular folding, by which the molecule begins to fold before waiting the end of its production. This model is inspired by our recent experimental work demonstrating the construction of shapes at the nanoscale by folding an RNA molecule during its transcription from an engineered sequence of synthetic DNA. While predicting the most likely conformation is known to be NP-complete in other models, Oritatami sequences fold optimally in linear time. Although our model uses only a small subset of the mechanisms known to be involved in molecular folding, we show that it is capable of efficient universal computation, implying that extensions of this model will have this property as well.

We develop several general design techniques for programming these molecules. Our main result in this direction is an algorithm in time linear in the sequence length, that finds a rule for folding the sequence deterministically into a prescribed set of shapes depending of its environment. This shows the corresponding problem is fixed-parameter tractable although we proved it is NP-complete in the number of possible environments. This algorithm was used effectively to design several key steps of our constructions.

Bernadette Charron-Bost
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Influence Systems: an Algorithmic Approach to Collective Behavior

Algorithms offer a rich, expressive language for modeling biological and social systems. They lay the grounds for numerical simulations and, crucially, provide a powerful tool for their analysis. In this framework, influence systems model how influence, broadly defined, spreads across a dynamic network of autonomous agents and how collective structure emerges from the decentralized interaction of the agents. We examine the merits and challenges of this algorithmic approach to the analysis of the behaviors of multi-agent systems arising in biology and social dynamics.

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Influences versus Connections

Proteins are nanosize objects made of atoms in interactions. As all naturel systems, proteins are robust, adaptable and only rarely fragile. These properties rely on the topological and structural plasticity of the system.
The structural plasticity can be measured as a path of atomic motions going from a local site of perturbation to the rest of the protein. The path of motions can cover distances much longer than typical scales of atomic interactions, following a cascade mechanism. Let's investigate the role of the site of perturbation neighbors on the cascade mechanism.