

CA 18232: ONLINE WG3 MEETING
PROGRAM AND ABSTRACTS

15TH OF APRIL 2021

The Program

9.15 - 9.30	Welcome meeting	
9.30 - 10.00	Juris Viksna Hybrid system models of gene regulatory networks and network behaviour analysis	page 10
10.00 - 10.30	Rodica Ioan A mathematical approach of muscle tendon function and of robotic assisted liver tumor	page 4
10.30 - 11.00	Michał B. Paradowski Applications of network science to language phenomena: Social diffusion of linguistic innovation, second language acquisition via peer interaction, and remote (language) teaching and learning during the pandemic coffee break	page 8
11.30 - 12.00	Discussion panel: WG3 perspectives	
12.00 - 12.30	Ivica Nakić H_∞ analysis of cooperative multi-agent systems	page 6
12.30 - 13.00	Harun Šiljak Long-scale language dynamics as a reaction-diffusion system: mesoscopic analysis lunch break	page 9
14.30 - 15.00	Delio Mugnolo Random evolution equations on graphs and beyond	page 5
15.00 - 15.30	Serge Nicaise Stabilization results for a generalized telegraph equation on star shaped networks	page 7
15.30 - 16.00	Besiana Cobani Inverse scattering, important issues on an interior transmission problem	page 3

Inverse scattering, important issues on an interior transmission problem

Besiana Cobani

University of Tirana, Tirana, Albania

Nowadays inverse scattering is a special field of interest for many mathematicians who deal with partial differential equations theory and it is in continuous progress. The nature of the inverse problem is generally ill-posed, more specifically the third condition fails (the solution does not depend on the initial data), this means that the solution of the problem is not easy to find. Here, we present a given interior problem with non-homogeneous boundary conditions. Its homogeneous version is referred to as the transmission eigenvalue problem. The TEP (transmission eigenvalue problem) is non linear and not self-adjoint.

We show the discreteness of the transmission eigenvalues and the existence of real transmission eigenvalues. Both these issues are important for solving the inverse scattering problem since they provide information on refractive index n of the scattering media.

A mathematical approach of muscle tendon function and of robotic assisted liver tumor

Rodica Ioan

Spiru Haret University and Romanian Academy, Bucharest, Romania

One of the goals of this study is to give a model of the muscle-tendon function as observed in human walking. A network of eight elastic springs ensures the elastic behavior inside each segment and a perfect correlation among human walking phases, in order to describe the action of a unit muscle-tendon in a gait cycle of human walking.

Another goal is to obtain the optimization of the collision-free trajectory of the surgical needle, that is carrying drugs into the tumoral target, with fulfillment of all surgical constraints. We obtain the optimum needle free-collision trajectories using the particle swarm optimization algorithm.

Keywords: Muscle-tendon function, walking, elasticity, minimally invasive surgery, trajectory optimization, particle swarm optimization

Random evolution equations on graphs and beyond

Delio Mugnolo

University of Hagen, Hagen, Germany

We begin our talk by studying diffusion-type equations supported on an interval with boundary conditions that are randomly varying in time. We hence follow the evolution of a system along the path of a random walk whose states are diffusion equations driven by Laplacians with switching boundary conditions; this is only a special case of a large class of abstract evolution equations with random switching behavior. After settling the issue of well-posedness, we focus on the asymptotic behavior of solutions and provide sufficient conditions for almost sure convergence of the propagator towards a deterministic steady state.

This talk is based on joint articles with Stefano Bonaccorsi (Trento) and Francesca Cottini (Milano-Bicocca).

H_∞ analysis of cooperative multi-agent systems

Ivica Nakić

University of Zagreb, Zagreb, Croatia

In this talk we study a class of cooperative multi-agent systems described as a network of agents on a graph with the 2nd order dynamics and with decentralized output-feedback policy designed to achieve network synchronization.

We are interested in the following question: if one is to disturb (or bolster) one or more agents in order to undermine (or enhance) efforts of other agents or of the entire team, which agent(s) to choose?

Stabilization results for a generalized telegraph equation on star shaped networks

Serge Nicaise

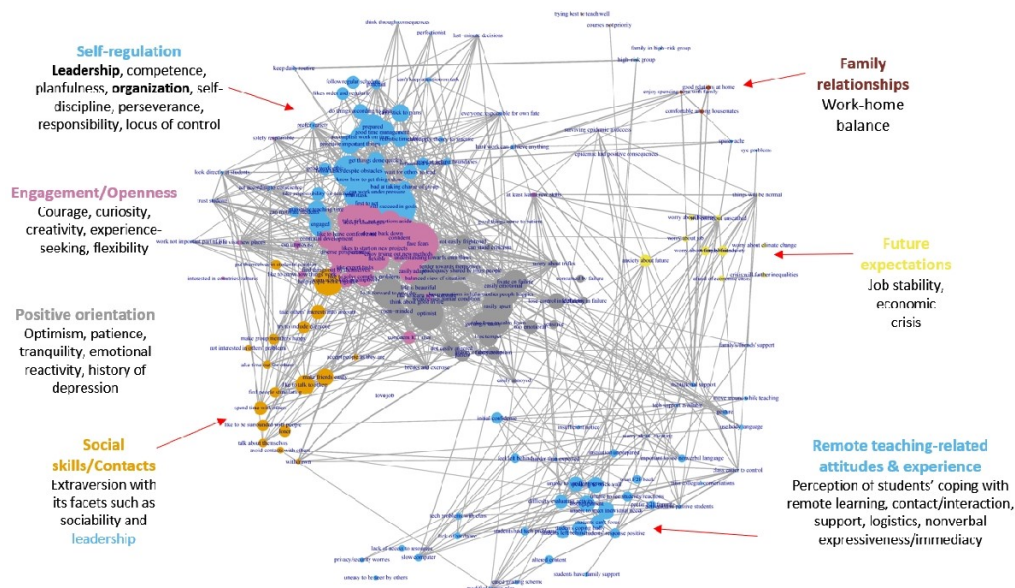
Polytechnic University of Hautsde-France, Valenciennes, France

The well-posedness, strong and exponential stability of a generalized telegraph equation set on one dimensional star shaped networks will be presented. It is assumed that a dissipative boundary condition is applied at all the external vertices and an improved Kirchhoff law at the common internal vertex is considered. The stability results are based on a frequency domain approach: Arendt-Batty's theorem for the strong stability and Huang-Prüss's theorem combined with a multiplier technique for the exponential stability result.

Applications of network science to language phenomena:
Social diffusion of linguistic innovation,
second language acquisition via peer interaction, and
remote (language) teaching and learning during the pandemic

Michał B. Paradowski
University of Warsaw, Warsaw, Poland

Social networks play a vital role in the attainment of individuals. The talk will present the results of three projects applying network science to language phenomena. The first one involved exploring the spread of neologisms in a microblogging site. The second looked at the influence of peer interactions among second language learners on their language progress. From a slightly different angle, the third project investigated (language) teachers' and learners' adaptation to emergency remote instruction during school closures; here, we show how network data science helps reveal easily interpretable clusters of naturally correlating variables, corroborating the potential of cluster detection algorithms for large sets of ordinal questionnaire responses, and the advantage of network visualisation over other hierarchical methods (such as correlation matrices and PCA scatterplots) in terms of ease of recognition of the relationships, their filtering and interpretation, due to the former's spatial graphical layout.



Long-scale language dynamics as a reaction-diffusion system: mesoscopic analysis

Harun Šiljak

Trinity College Dublin, Dublin, Ireland

Mathematical models of the cultural evolution of language are typically formulated either on a macroscopic level of abstraction, permitting the analytical solution of the model's governing equations or, more commonly, on a microscopic level, requiring simulation on the computer. In this presentation, we consider the formulation of such models on an intermediate mesoscopic level, where the model remains mathematically tractable (numerically soluble) but complex enough to approximate the complex real-life dynamics of human language in a meaningful way. Our model takes into account four known processes-population dynamics, diffusion dynamics, mutation dynamics and interaction dynamics.

Hybrid system models of gene regulatory networks and network behaviour analysis

Juris Viksna

University of Latvia, Riga, Latvia

We present a hybrid system based framework for modelling gene regulatory networks and methods for analysis of stability and other behavioural properties of the modelled systems. The emphasis is to start model development with very limited initial assumptions about parameter values, and then add constraints on these parameters that have significant impact on network dynamics.

The framework can be used for networks with up to few tens of genes; currently we have developed models for several phage viruses and for circadian cycle networks. The most detailed analysis has been done on lambda phage model, for which the model state space contains only two stable regions that well correspond to biologically known behaviours. The model also allows to propose changes in gene regulation that would lead to measurably different behaviour and in principle could be validated by biological experiments.