UNIVERSITÀ
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DIPARTIMENTO DI SCIENZE
MATEMATICHE, FISICHE
E INFORMATICHE

Collective and Self- Organised Dynamics: Kinetic and Network Approaches

Kick off Meeting

Parma – 29 Giugno 2023

Centro S. Elisabetta, Aula Master, Campus "Parco Area delle Scienze", Università di Parma

Il meeting intende fornire contributi e momenti di discussione nell'ambito del progetto "*Collective and self-organised dynamics: kinetic and network approaches*" (Responsabile scientifico Prof.ssa Groppi Maria), finanziato dal Bando di Ateneo per la Ricerca 2022 - Azione A

PROGRAM

- **9.15 Opening**
- **9:30 Mattia Zanella (Università di Pavia)** *"Kinetic modelling and control of multiagent systems with missing information"*
- **10:15 Marco Mancastroppa (CNRS and Universitè Aix Marseille)** *"Hyper-core decomposition of hypergraphs: the role of hyper-cores in higher-order dynamical processes"*
- **11:00 Coffee Break**
- **11:30 Rossella Della Marca (SISSA, Trieste)** **"***SIR kinetic models tracking individuals' viral load"*
- **12:00 Nadia Loy (Politecnico di Torino)** *"Kinetic equations on graphs and multi-agent systems with multiple microscopic states"*
- **12:30 Cinzia Soresina (University of Graz)** *"Bifurcations and pattern formation in cross-diffusion models on networks"*
- **13:00 Lunch**
- **14:00-16:00 Discussion**

Organizers

- **Marzia Bisi**, Università di Parma - marzia.bisi@unipr.it
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SIR kinetic models tracking individuals' viral load

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In classical epidemic models, a neglected aspect is the heterogeneity of disease transmission and progression linked to the viral load of each infectious individual. Here, we attempt to investigate the interplay between the evolution of individuals' viral load and the epidemic dynamics from a theoretical point of view. In the framework of multi–agent systems [3], we propose a particle stochastic model describing the infection transmission through interactions among agents and the individual physiological course of the disease. Agents have a double microscopic state: a discrete label, that denotes the epidemiological compartment to which they belong, and a microscopic trait, representing a normalized measure of their viral load. Specifically, we consider Susceptible–Infected–Removed–like dynamics where the disease transmission rate [2] or the isolation rate [1] of infectious individuals may depend on their viral load. We derive kinetic evolution equations for the distribution functions of the viral load of the individuals in each compartment, whence, via suitable upscaling procedures, we obtain a macroscopic model for the densities and viral load momentum. We perform then a qualitative analysis of the ensuing macroscopic model, and we present numerical tests in the case of both constant and viral load–dependent model parameters.

This is a joint work with N. Loy and A. Tosin (Politecnico di Torino).

[1] Della Marca R., Loy N., Tosin A.: An SIR–like kinetic model tracking individuals' viral load. Netw. Heterog. Media **17** n.3, 467–494 (2022)

[2] Della Marca R., Loy N., Tosin A.: An SIR model with viral load–dependent transmission. J. Math. Biol. **86**, 61 (2023)

[3] Loy N., Tosin A.: Boltzmann–type equations for multi–agent systems with label switching. Kinet. Relat. Models **14** n.5, 867–894 (2021)

Kinetic equations on graphs and multi-agent systems with multiple microscopic states

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In this talk we present a class of kinetic models describing interactions among individuals having multiple microscopic states. In particular, we shall consider interacting agents who are divided into multiple sub-populations. As such, the agents are not indistinguishable, as classically assumed in kinetic theory, within the whole population. A general framework allowing to describe binary interactions and transfers among different sub-groups by deriving the model from microscopic stochastic processes will be presented. Moreover, we shall illustrate applications to compartmental models and to wealth exchange models with migration.

Hyper-core decomposition of hypergraphs: the role of hyper-cores in higher-order dynamical processes

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Many complex systems are composed of elements interacting in groups: these systems require to go beyond the network representation of binary connections, taking into account the higher-order nature of the interactions. This is crucial when considering self-organized and collective dynamics, since multi-body interactions can give rise to novel phenomena. *Hypergraphs* represent a powerful framework to describe these systems, representing a higher-order generalization of networks in which nodes can interact in hyperedges of arbitrary size [1]. These interactions induce novel structures, highlighting the need for new characterization techniques able to detect hierarchies and relevant substructures. However, concepts and tools to identify particularly cohesive structures or central nodes in hypergraphs are still missing.

We propose a procedure to decompose a hypergraph into *hyper-cores*, i.e. (k, m)-cores, that are subsets of nodes connected to each other through at least a certain number k of hyperedges of size at least m [2]. This procedure generates a hierarchy of subhypergraphs of increasing connectivity, composed of interactions of increasing size. We apply this procedure to several data sets, representing systems of interactions of different nature (from face-to-face to online interactions, from political to ecological systems). This allows us to identify non-trivial higher-order mesoscopic structures and to develop a new measure of centrality for nodes in hypergraphs, the *hyper-coreness*.

We investigate the role of these substructures in dynamical processes whose basic mechanisms are intrinsically higher-order. We consider two different contagion processes with higher-order infection mechanisms (e.g. group infections, non-linear infection rate) [3, 4]: we show that the spreading processes localize on hyper-cores of high connectivity and high interaction order; furthermore, if the seeding of the spreading process is within these cores, the total outbreak size is maximized. This suggests that cores sustain and drive higher-order contagion processes. We also consider a consensus formation process [5] for the self-organized emergence of social consensus in a population with a majority and a committed minority. We show that very few committed individuals with high hyper-coreness can rapidly overturn a majority convention, more efficiently than if the committed nodes were chosen randomly or with high strength-coreness in the projected graph.

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[1] Battiston, F. *et al.* Networks beyond pairwise interactions: Structure and dynamics. *Phys. Rep.* **874**, 1–92 (2020).

[2] Mancastroppa, M., Iacopini, I., Petri, G. & Barrat, A. Hyper-cores promote localization and efficient seeding in higher-order processes. *arXiv:2301.04235* (2023).

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[5] Iacopini, I., Petri, G., Baronchelli, A. & Barrat, A. Group interactions modulate critical mass dynamics in social convention. *Communications Physics* **5**, 64 (2022).

Bifurcations and pattern formation in cross-diffusion models on networks

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The concept of Turing instability, namely that diffusion can destabilise the uniform steady state, is well known either in the context of partial differential equations (PDEs) or in networks of dynamical systems. Currently, reaction-diffusion equations with cross-diffusion terms are investigated in different contexts (e.g. population dynamics, vegetation patterns, behavioural epidemiology), exhibiting an analogous effect called cross-diffusion induced instability. We extend this concept to networks of dynamical systems, showing that the spectrum of the graph Laplacian determines the instability appearance, as well as the spectrum of the Laplace operator in reaction-diffusion equations. We consider a particular network model for competing species with cross-diffusion, coming from the PDEs context. In particular, the influence of different topology structures on the cross-diffusion induced instability is highlighted, considering regular rings and lattices, and also small-world, Erdős-Réyni, and Barabási–Albert networks.
(joint work with C. Kuehn)

Kinetic Modelling and Control of Multiagent Systems with Missing Information

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Kinetic equations play a leading role in the modelling of large systems of interacting particles/agents with a recognized effectiveness in describing real world phenomena ranging from plasma physics to multi-agent dynamics. The derivation of these models has often to deal with physical, or even social, forces that are deduced empirically and of which we have limited information [1]. To produce realistic descriptions of the underlying systems, it is of paramount importance to manage efficiently the propagation of uncertain quantities across the scales [5].

We concentrate on the interplay of this class of models with collective phenomena in life and social sciences, where the assessment of uncertainties in data assimilation is crucial to design efficient interventions. Furthermore, to discuss the mathematical interface of this class of models with available data, we derive the evolution of observable quantities based on suitable macroscopic limits of classical kinetic theory [2]. Finally, we analyze how the introduction of robust control strategies leads to the damping of the uncertainties characterizing the system at the macroscopic level [4].

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