

UNIVERSITÁ DEL PIEMONTE ORIENTALE DIPARTIMENTO DI SCIENZE E INNOVAZIONE TECNOLOGICA

EVENTI DiSIT

Seminario | Seminar 27-11-2023 11:00-12:00 Aula 205 L'evento sarà trasmesso anche in streaming: https://meet.google.com/gvj-qojw-pgk

Redundancy in the Structure and Dynamics of Complex Networks

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Many advances in network science derive from the study of patterns of connectivity (network structure), which provides many insights into the organization of complex systems. Yet, a critical gap remains in understanding how the structure of networks affects the dynamics of complex systems. We have been addressing this gap from a complementary angle: in addition to patterns of connectivity and patterns of dynamics, there are important patterns of redundancy which dictate how interaction structure and logic shape network dynamics. We first characterize structural redundancy via the concept of distance backbone of a weighted graph: the sub-graph formed by all edges that obey a generalized triangle inequality for a given path length measure. We show that distance backbones are a parameter-free, principled method to obtain typically very small subgraphs that preserve all shortest paths and connectivity of the original networks across domains---and also preserve the modular and hierarchical structure of shortest distances. We illustrate the relationship to dynamics on networks by showing that the metric backbone is a primary subgraph for epidemic transmission based on pure diffusion processes. We further show that the (semi-triangular) edges that break the triangle inequality have highly variable importance in spreading dynamics. While all of them have null edge betweenness, a measure of how much they break the triangle inequality, the semi-triangular distortion, is highly correlated with edge relevance for spreading dynamics. Additionally, we discuss recent extensions to directed and multilayer graphs. Finally, we summarize the distinct concept dynamical redundancy in (discrete dynamical systems) models of biochemical regulation and signaling. We show that the redundancy found in biological models is much more pronounced than what is expected from random networks, and a major reason for them being much more ordered than what the current criticality hypothesis, or "edge-of-chaos" theory, predicts.

EVENTO APERTO A:

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SEMINARIO IN LINGUA: English

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