

Topological data analysis for complex systems

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The statistical mechanical approach to complex networks is the dominant paradigm in describing natural and societal complex systems. The study of network properties, and their implications on dynamical processes, mostly focus on locally defined quantities of nodes and edges, such as node degrees, edge weights and more recently correlations between neighboring nodes. However, statistical methods quickly become cumbersome when dealing with many-body properties and do not capture the precise mesoscopic structure of complex networks. Here we discuss recent progress coming from algebraic topology and the type of novel insights they provide. Topology is one of the oldest and more relevant branch of mathematics.

It studies the properties of spaces and maps between such spaces that are preserved under transformations that continuously deform the object under study. Besides being of theoretical interest in itself, topology has provided an expressive and affordable language which is progressively pervading many areas of mathematics, computer science and physics.

Indeed, these new goggles are able to extract information about the mesoscopic structures that are typically very hard to capture –if not invisible– to standard statistical and combinatorial tools. We will for example show that real-world networks divide themselves in two classes based on their homological properties, which cannot be reduced to known local or quasilocal properties.

We will then show that the homological information describes well the large-scale interaction between communities, e.g. research groups within and across scientific disciplines, and the spatial distribution of migrant communities within a large Italian city. In both cases the underlying reason is the capacity of topological tools to capture a notion of high-dimensional shape which eludes statistical mechanical tools.

We will then introduce an appropriate null model for simplicial complexes, which is akin to a configuration model and allows the validation of observed homological features. Finally, using examples from structural and functional brain networks, we will show how it is possible to encode the rich homological information in simplified network representations which localize homological features and facilitate the interpretation.

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