Applications of the theory of Ihara zeta function in biomedicine—the case of protein interaction networks

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RESUMEN

Network representations are popular tools for characterizing and visualizing patterns of interaction between the micro-constituents of large complex synthetic, social or biological systems. They reduce the full complexity of such systems to topological properties of their associated graphs, which are more amenable to analysis. In particular, the cyclic structure of complex networks is receiving increasing attention, since the presence of cycles affects strongly the behaviour of processes supported by these networks.

In biology, proteomic and gene regulatory networks are the infrastructure of cellular signalling. Errors in cellular signalling are responsible for many diseases, such as cancer, autoimmunity or diabetes, therefore understanding how the structure of signalling networks affects the flow of information is a very important question. Also here short cycles are the main local network modules, so any realistic model for signalling networks should incorporate cycles as key observables. Networks with short loops are quite difficult to handle, hence most modelling in this field has so far been limited to locally tree-like graphs with controlled degree statistics and correlations. The next step would be to define and analyze random graph ensembles where also the number of short cycles is controlled. However, evaluating the number of cycles of a given length for an arbitrary graph is a non-trivial problem. Indeed, many studies focus instead on closed paths, whose number follows for any graph from the trace of powers of the connectivity matrix, or equivalently from the spectral density, which can be computed at a much lower computational cost. In this talk it is survey the analysis of cyclic properties of networks, and in particular the use of Ihara’s zeta function for counting cycles in networks and introduced the application of this formalism to the protein interaction networks.

Referencias


