

The large-scale organization of metabolic networks

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In a cell or microorganism the processes that generate mass, energy, information transfer, and cell fate specification are seamlessly integrated through a complex network of various cellular constituents and reactions. However, despite the key role these networks play in sustaining various cellular functions, their large-scale structure is essentially unknown. Here we present a comparative mathematical analysis of the metabolic networks of 43 organisms representing all three domains of life. We show that, despite significant variances in their individual constituents and pathways, these metabolic networks display the same topologic scaling properties demonstrating striking similarities to the inherent organization of complex non-biological systems. This suggests that the metabolic organization is not only identical for all living organisms, but complies with the design principles of robust and error-tolerant scale-free networks, and may represent a common blueprint for the large-scale organization of interactions among all cellular constituents.