

The evolution of metabolic networks: growth under constraints

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ABSTRACT

A cell is a complex system composed of numerous organic constituents thickly interwoven in a complex web of reactions. The processes underlying the life of the cell, which include the generation of mass and energy, and information transfer, are a result of these interactions [1].

One possible abstraction of this complexity is to represent the gamut of chemical reactions by a graph, where each node represents a chemical constituent of the cell and an arrow from constituent A to another B implies that B is a product of a reaction between A and other chemical constituents. Such a graph representation is referred to as a *cellular network*. A cellular network whose main function is metabolism is called a *metabolic network*.

It is possible to make a start towards the program of understanding the robust design principles underlying the functioning of a cell by studying similarities between the topologies of these graph representations.

Large scale sequencing projects have furnished integrated pathway-genome databases[2, 5, 3] from which these cellular networks can be inferred.

Recently, such an approach has been used [4, 6] to analyze the topological properties of the metabolic networks of 43 different organisms including *E-coli*(bacterium) and *Caenorh̄bditis elegans*(eukaryote). Quite strikingly they found remarkable similarities in the topological properties. In short they found that these metabolic networks were uniformly scale free with exponents between 2 and 3. Further they also found that the diameters (average shortest path between two nodes) of the networks were constant wrt size (number of nodes).

While models of preferential attachment (in which nodes having more links tend to attract more linkages) provide an explanation of the prevalence of scale-free networks, the models are largely endogenous and do not take account of global exogenous selection pressures which might shape the form of evolving and growing networks. Such selection pressures would be especially relevant in a biological context.

In this paper we consider the evolution of random graphs under the constraint that the diameter remain constant as the graph grows. We show if the graph maintains the form of its

link distribution it must be scale-free with exponent between 2 and 3. These uniqueness results may help explain the (apparently universal) scale-free nature of graphs, of varying sizes, representing the evolved metabolic pathways of different organisms. This is consistent with the experimental findings of [4].

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