

SCALING PROPERTIES OF INTRASPECIFIC AND INTER-SPECIFIC PHYLOGENIES IN THE TREE OF LIFE

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Many biological processes, from cellular metabolism to population dynamics, are characterized by allometric scaling (power-law) relationships between size and rate. During the last years different research groups [1,2] have developed statistical analysis tools, based on allometric scaling concepts, for the study of tree-like transportation networks (for example to characterize how branching properties change with network size). Among the biological processes naturally described in terms of a tree-like topology, the differentiation events happening during the evolution of the organisms are conveniently represented as phylogenetic trees. Here we introduce allometric scaling approaches for the statistical analysis of phylogenetic trees, and in a broader context, of the whole "Tree of Life".

Considering the "Tree of Life" or any other phylogenetic tree as a group of tips and nodes linked by branches, a node ultimately represents a diversification event. For each node i , a subtree S_i is made up of a root at node i and all the descendant nodes below i . That point of view allows us to understand how much the species diversify from i , through the subtree size A_i , and how is this diversity arranged, through several topological measures characterizing the shape of the subtree S_i . Universal scaling relationships between shape and size of phylogenetic trees are revealed and discussed.

[1] J. R. Banavar, A. Maritan and A. Rinaldo. Nature **399**, 130 (1999).

[2] D. Garlaschelli, G. Caldarelli and L. Pietronero. Nature **423**, 165 (2003).