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The Modular Structure of Protein Networks HERNÁN D. ROZENFELD, DIEGO RYBSKI, Levich Institute, City College of New York, New York 10031, USA, SHLOMO HAVLIN, Minerva Center and Department of Physics, Bar-Ilan University, 52900 Ramat-Gan, Israel, HERNÁN A. MAKSE, Levich Institute, City College of New York, New York 10031, USA — The evolution of the human protein homology network (H-PHN) has led to a complex network that exhibits a surprisingly high level of modularity. Topologically, the H-PHN presents well connected groups (conformed by proteins of similar aminoacid structure) and weak connectivities between the groups. Here, we perform an empirical study of the H-PHN to characterize the degree of modularity in terms of scale-invariant laws using recently introduced box covering algorithms. We find that the exponent that determines the scale-invariance of the modularity is unexpectedly higher than the box dimension of the network. In addition, we perform a percolation analysis that gives insight into the evolutionary process that led to the modular organization and dynamics of the present H-PHN.

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