

Abstract Submitted
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Unraveling the rules of evolution in the yeast protein-protein interaction network YULIANG JIN, HERNAN MAKSE, Levich Institute and Physics Department, the City College of New York, THOMAS WEINMAIER, DMITRIJ TURAEV, THOMAS RATTEI, Department of Computational Systems Biology, University of Vienna — A question of fundamental importance is to understand the dynamical principles according to which biological networks have acquired their topological structures and functional modules. Here, we perform an empirical study of the yeast protein-protein interactions (PPI), combined with theoretical modeling of the genomic duplication-divergence processes. Our duplication-divergence model agrees with experimental data, and provides a novel approach to reconstruct ancestral PPI networks. Following the phylogenetic tree, our analysis unravels that the ancient networks evolve into the present day yeast network by a multiplicative growth. The rule of multiplicative growth demonstrates the relationship between the topological exponents and the evolution growth rates of interactions. An important consequence of this evolutionary principle is the emergence of self-similar modular structure, which is confirmed by the analysis of functional modules of proteins.

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