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Protein-Protein interaction networks: why static MpK model works and preferential attachment does not JINGSHAN ZHANG, EUGENE SHAKHNOVICH, Harvard University — Various approaches have been proposed to explain the observed scale free structure $p(k) \sim k^{-\gamma}$ of protein-protein interaction networks. We argue that the preferential attachment coming from gene duplication[1] is questionable. A static “MpK” model produces the scale free structure via computer simulations[2] for unexplained reasons. On the other hand, it was analytically proved[3] that deterministic threshold models produce scale free networks (with $\gamma \equiv 2$) if fitness distributions are exponential. We study the static MpK model further and find the above analytical proof applicable with extensions, and γ dependent on the threshold parameter. This work not only predicts the dependence of γ on protein concentrations, but also provides a generic mechanism of scale free networks. The clustering coefficient distribution in the model is interpreted by a simple picture.

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