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The Blind Watchmaker Network: Scale-freeness and Evolution

P. Minnhagen^{1,2} and S. Bernhardsson^{1,2}

¹Department of Theoretical Physics, Umeå University, 901 87 Umeå, Sweden.

²Center for Models of Life, Blegdamsvej 17, 2100 Copenhagen, Denmark

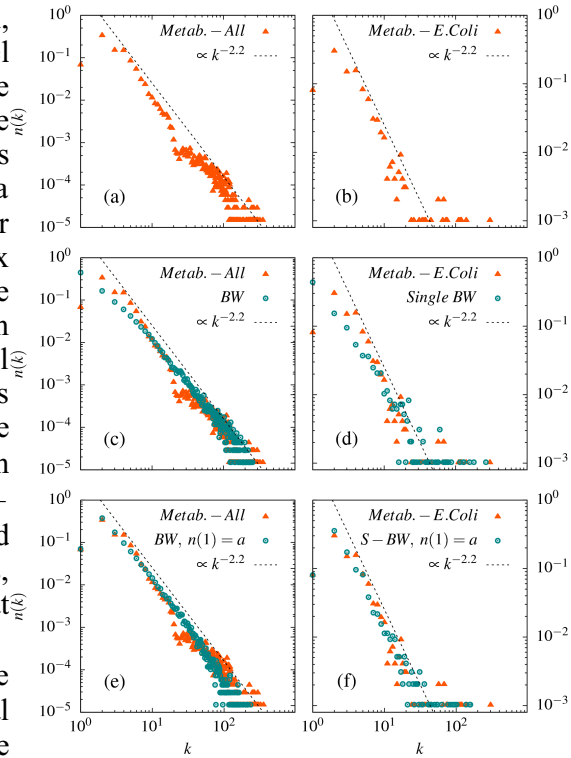
Introduction

To characterize the structure of a network, researchers often measure its degree distribution $N(k)$, the number of nodes with k links attached. Numerous studies have found that real-world networks often have very broad degree distributions for larger k , $N(k) \propto k^{-\gamma}$. These fat tailed distributions approximate a power law in their structure [1]. They are also called scale-free networks because a power-law tail indicates the lack of an intrinsic characteristic degree size. Biological networks are particularly interesting because the structure of these networks have, directly or indirectly, arisen through the process of evolution by natural selection. These networks have been constructed as if by a blind watchmaker, through the interplay between a random stochastic evolution and a natural selection process [2]. So what can we learn from the observation that a biological network such as the network of the metabolism of a cell has a power law distribution [3]? In order to answer this question we define and investigate a blind watchmaker network. In this paper [4] we demonstrate that the empirically observed degree distributions for networks of the cellular metabolism for simple organisms are good approximations of this random structure.

Results

We start from a simplified network model, the constrained-balls-in-boxes(CBB)-model [5]. Here, nodes are viewed as boxes and the link-ends attaching to these nodes are numerated (distinguishable) balls in this boxes. The balls in the boxes are given a ranking which can be seen as a time-order of the connections. We assume that each box has to have at least one ball and that the stochastic process behind the reorganization of the balls in the boxes have to pick a ball in order to pick a box. That is, each box is picked with the probability $p \sim k$. The number of possible states (Ω) is then given by the expression: $\ln \Omega = M \ln M - M - \sum N(k) \ln [N(k) - 1] - 2 \sum N(k) \ln k$, where N and M are the number of boxes and balls, respectively. The degree distribution that maximizes $\ln \Omega$: $N(k) = A \exp(-bk)/k^2$.

We also introduce an algorithm to solve the equation for $\ln \Omega_{max}$ with variational calculus through a random process. The algorithm goes as follows:



1. Pick two boxes (nodes) A and B randomly with probability $p \propto k^2$.
2. Pick a random ball in A and move to B.
3. If the attempted move is forbidden by a constraint choose another ball in A. Repeat until one ball is moved or until there are no more balls to choose from.

A comparison between the distributions of the Blind Watchmaker network and metabolic networks (data from Ref. [6]) are shown in the figure above. Fig. a) and b) are data for an average over 107 networks and the data for *E-Coli*, respectively. c) and d) show the same data but together with data constructed by the described algorithm. Finally, in e) and f) an additional constraint has been put in to the algorithm to fix the first data point ($N(I)$). The two data sets match extremely well.

Discussion

In the present work we focus on the different possible states a network can be found in. These network states distinguishes between the time order in which a node is connected to its neighbors. No *a priori* assumption of any growth mechanism or evolution process is made. We introduce the concept of *random with respect to the network states* and call the corresponding network *the blind watchmaker network*. It is found that the blind watchmaker network is scale-free and that metabolic networks to large extent are blind watchmaker networks. This means that the evolutionary path of the cell-metabolism, when projected onto a metabolic network representation, is statistically random with respect to a complete set of network states. This randomness emanates from the inherent randomness (the blind element) in Darwinian evolution and suggests that natural selection has had no or little effect on the network node degree distribution of metabolic networks.

The fact that also completely random networks may have scale-free node distributions gives a new perspective on the origin of scale-free networks in general.

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