Robustness of heterogeneous complex networks

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ABSTRACT

In this paper we study the robustness of heterogeneous preferential attachment networks. The robustness of a network measures its structural tolerance to the random removal of nodes and links. We numerically analyze the influence of the affinity parameters on a set of ensemble-averaged robustness metrics. We show that the presence of heterogeneity does not fundamentally alter the smooth nature of the fragmentation process of the models. We also show that a moderate level of locality translates into slight improvements in the robustness metrics, which prompts us to conjecture an evolutionary argument for the existence of real networks with power-law scaling in their connectivity and clustering distributions.

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1. Introduction

A complex network is a set of nodes and connecting links with a non-trivial topology [1]. Networks pervade all domains of science: natural [2], social [3], technological [4] and cultural [5]. With the aim of achieving a single unifying framework of the mechanisms underlying complex systems, network theory has focused on a uniform description of the relationships between interacting elements instead of their low-level dynamics. Through a combination of analytical insight, numerical simulation and empirical observations, complex networks have been subject to intensive research during the last few years [6,7].

Dynamical network models [8] are stochastic discrete-time dynamical systems that prescribe the evolution of a network by the iterated addition/subtraction of nodes/links. These regard topology as an emergent property of network evolution, focusing on the mechanisms that concur on such process. The preferential attachment (PA) model by Barabási and Albert (BA) [9] is a minimal account of sufficient mechanisms for the emergence of scale-free networks [10]. These networks are characterized by a power law scaling in the distribution of their connectivity degrees, $P(k) \sim k^{-\gamma}$, and exhibit a high degree of robustness against random errors, i.e. local failures rarely compromise their integrity [11]. Such tolerance, however, comes at the price of a high vulnerability to attacks, the removal of nodes with highest degrees.

Heterogeneous PA models [12] are a generalization of the Barabási–Albert model to heterogeneous complex networks. Elements in a heterogeneous network can be described by states that induce specific affinities in their interaction. In its simplest instance, the threshold model is based on the assumption that the affinity between nodes follows an inverse relationship with regards to the distance between their states. In this paper we present a study of the robustness of the

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threshold model to the random removal of nodes and links. While robustness has generally a dynamical component, the study focuses on its topological aspects. We numerically analyze the influence of the affinity parameters on the structural integrity of the network when a fraction of the network nodes (and the links connected to them) are randomly removed.

2. Heterogeneous preferential attachment

In this section we briefly discuss the BA model and its extension to heterogeneous networks. In the BA model [9,13] the process starts with a seed of arbitrary size and topology, and a new node is added to the network with each iteration. Each incoming node has a fixed number m of links attached, which are connected to the already existing nodes following a so-called *attachment rule*. The rule states that the linking probability of a network node v_i is proportional to its connectivity degree k_i. The addition of nodes is iterated until a network with a desired size N is achieved. The evolution model is purely topological, as just the connectivity degrees determine the probability distribution of the potential links destination. Nevertheless, the assumptions implicit in the BA model are not valid for a wide class of complex systems. Often, interactions between elements are mediated by intrinsic properties that induce specific affinities [14].

Heterogeneous PA models [12] explicitly incorporate the influence of such affinities in the network evolution while preserving the basic mechanisms of the original model. These models define node properties as fixed states in an arbitrary space and introduce an affinity function that biases the attachment rule depending on these states. In order to analyze the network tolerance we need to specify particular models within this general class. The so-called *threshold model* [15] is a simple case of heterogenous PA based on the assumption that the affinity between nodes is inversely related to the distance between their states as defined by a certain space metric. The rationale for this choice is that the inverse relationship between affinity and state distance may be a reasonable proxy for many real networks where PA can be considered as the most relevant linking mechanism, such as protein interactions, web page hyperlinks, scholar citations or social relationships.

The threshold model is defined by a triple (R, ρ, σ), where: (1) R is an arbitrary metric space. The elements $x \in R$ are the node *states*. (2) ρ is a nonnegative real function with unit measure over R referred as *node state distribution*. (3) $\sigma : [0, d_{max}] \mapsto [0, 1]$ is a nonnegative real function referred as *affinity* of the interactions and defined for $0 < \mu \leq d_{max}$, $0 \leq \epsilon \leq d_{max}$ as:

$$\sigma(x_i, x_a) = \begin{cases} 1 & \text{for } 0 \leq d \leq d_0 \\ 1/2 + (\mu - d)/\epsilon & \text{for } d_0 < d < d_1 \\ 0 & \text{for } d_1 \leq d \leq d_{max}, \end{cases} \tag{1}$$

where $d = d(x_i, x_a)$ is a metric on R, $d_{max} = \sup_{x_1, x_2 \in R} d(x_1, x_2)$, $d_0 = \max(0, \mu - \epsilon/2)$ and $d_1 = \min(d_{max}, \mu + \epsilon/2)$.

The evolution of a network in the threshold model is according to the following rules:

(i) The nodes v_i are characterized by their state $x_i \in R$. The node states describe intrinsic properties deemed constant in the timescale of evolution of the network. The links e_i are not characterized by any state.

(ii) The growth process starts with a seed composed by N_0 nodes and L_0 links. The seed nodes v_i are assigned arbitrary states $x_i \in R$.

(iii) A new node v_a (with m links attached) is added to the network at each iteration. The number m is common for all the added nodes and remains constant during the evolution of the network. The newly added node is randomly assigned a state x_a following the distribution $\rho(x)$.

(iv) The m links attached to v_a are randomly connected to the network nodes following a distribution $\{\Pi(v_i)\}$ given by an extended *attachment rule*,

$$\Pi(v_i) = \frac{\pi(v_i)}{\sum_j \pi(v_j)}, \quad \pi(v_i) = k_i \cdot \sigma(x_i, x_a). \tag{2}$$

The visibility π of a node v_i in the attachment rule is given by the product of its degree k_i and its affinity σ with the newly added node v_a. Steps (iii) and (iv) are iterated until a desired number of nodes has been added to the network.

The affinity σ of the interaction between nodes v_i and v_a in the threshold model is thus a function of the distance between their states x_i and x_a. The affinity is maximum when d is minimum, and vice versa. The transition between the minimum and maximum affinity values takes place linearly along a region defined by the middle value μ (*interaction threshold*) and the width ϵ (*transition width*). These two parameters are common to all the nodes and govern the form of the affinity σ in the attachment rule, thus the degree of heterogeneity in the network evolution. Local interactions are highly dependent on the different node states, while increasingly global interactions are progressively less dependent on such states and effectively hide the network heterogeneity. Henceforth we will focus on the unidimensional threshold model over the real line, thus we will choose the interval $R = [0, 1]$ as state space and the Euclidean distance $d = |x_i - x_a|$ as metric on R. The affinity parameters μ and ϵ of the model will therefore range in the interval $[0, 1]$.