Access time of an adaptive random walk on the world-wide Web

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We introduce and simulate the random walk that adapts move strategies according to local node preferences on a directed graph. We consider graphs with double-hierarchical connectivity and variable wiring diagram in the universality class of the world-wide Web. The ensemble of walkers reveals the structure of local subgraphs with dominant promoters and attractors of links. The average access time decays with the distance in hierarchy \( \Delta q \) as a power \(< t_{aw} > \sim (\Delta q)^{-\theta} \). The access to highly connected nodes is orders of magnitude shorter compared to the standard random walk, suggesting the adaptive walk as an efficient message-passing algorithm on this class of graphs.

Networks pervade all science making the problem of understanding the structure and dynamics of complex networks the greatest challenge today. Cellular and metabolic networks, chemical reactions, social collaboration, and science citation networks, and the world-wide Web are examples of networks that can be characterized by random graphs with individual dynamics and coupling architecture. In his inspiring paper Strogatz suggests that the inherent difficulty to understand networks lies in the intimate relationship between their structural complexity and evolution. To this end, the principle of universality that applies to systems with scale-free structures can play an important role in revealing those properties of the dynamics that are relevant for the universal behavior of a network. The world-wide Web belongs to the class of directed graphs with double-hierarchical organization of node ranks in which the wiring diagram rapidly changes in time. By exploiting the universality, the recently proposed model suggests minimum dynamic rules that are able to account for the complexity of the Web. So far other systems in this universality class are not known. It is tempting to believe that certain catalytic reactions in open environment can be represented by dynamic processes on directed graphs with variable wiring diagram.

Study of the response and relaxation of the network is the best way to understand how the structure affects function. Various dynamic processes, e.g., percolation and fragmentation by diluting links, core percolation by stripping leaves, and spreading of epidemics on networks of a given structure were examined.

In this work we study the random-walk dynamics on a directed graph. In particular, we consider a double-hierarchical directed graph in the universality class of the world-wide web, in which in- and out-links are governed by two distinct (and statistically dependent) power-law probability distributions. We introduce a random walker which copies its move strategies from the local node linking preferences. An ensemble of adaptive random walkers efficiently scans the connected subgraphs. The prominent feature of this class of hierarchically connected graphs is that the average access time to a node at distance \( \Delta q \) measured by in- or out-ranks decreases as a fractal power of the distance, indicating the presence of a peculiar structure with few dominant promoter and attractor nodes. The adaptive random walk suggests how an efficient message-passing algorithm can be constructed, that is driven by the properties inherent to this class of graphs. We demonstrate the advantages of the adaptive random walk by in parallel simulating the standard random walk on the same graph.

We consider a directed graph evolving from the dynamic rules which are recently suggested to mimic growth of the world-wide Web (the Web graph). The basic properties of the model are: (i) Directed linking, suggesting that at a node out- and in-links are not symmetric; (j) Growth and rearrangements (updates of links) at a unique time scale; and (k) Bias update and bias attachment of links, with probabilities specified below. At each growth step a new node is added to the network and the number of links changes by amount \( M(t) \). A fraction \( f_0(t) \equiv \alpha M(t) \) of new links are outgoing links from the new added node \( i = t \), whereas the remaining \( f_1(t) \equiv (1-\alpha)M(t) \) links are the updated links at other nodes in the network. Hence, the relevant parameter in the model is the ratio of updated and added links at each time step, i.e., \( \beta \equiv f_1(t)/f_0(t) = (1-\alpha)/\alpha \), which is independent of the actual increment \( M(t) \). Furthermore, the variations in \( M(t) \) are such that an average value \( M \equiv M(t) \) is finite, which can be considered as a constant in first approximation. In practice, the number of nodes and the number of links in the network increases with time, so that reasonable values for the average \( M \) are positive. For consistency, we keep \( M = 1 \) throughout this work (rendering reasonable computation time).

Bias activity of agents who create or update outgoing links from the Web pages (nodes) and bias (preferential) attraction of links can be formulated via following rules: At the growth step \( i \) an outgoing link is created from a node \( n \leq i \) with probability

\[
p_1(n,i) = \frac{\alpha M + \eta_{out}(n,i)}{(1+\alpha)M + i}.
\]
The link points towards the node $k$ with the probability
\[ p_2(k,i) = \frac{\alpha M + q_{in}(k,i)}{(1 + \alpha)M + i}, \] (2)
where $q_{out}(n,i)$ and $q_{in}(k,i)$ are current number of outgoing and incoming links at respective nodes at the growth step $i$. It is assumed that at the time of addition of a node $i$ to the network $q_{out}(i,i) = q_{in}(i,i) = 0$. Therefore, the biasing in the dynamics is linked to the time fluctuations of the node ranks. The effects of the attachment rule in Eq. (3) to the distribution of in-degree was studied analytically in Ref. [14]. For the values of the control parameter $\beta$ in the range $0 < \beta < \infty$, corresponding to $1 > \alpha > 0$, the network has the capability to rearrange its structure of links at the pace at which it grows. This property makes the Web substantially different from the networks that have static links. In our notation the networks with fixed links, e.g., science citation network [3], correspond to the limit $\beta = 0$ (i.e., $\alpha = 1$).

As discussed in detail in Ref. [2] the network that evolves according to the dynamic rules in Eqs. (2)–(4) shows a complex topology of links in which nodes are arranged hierarchically both according to ranks of outgoing and incoming links, in accordance with the data in the real Web [1]. The cumulative probability distributions that describe node ranks are [13]
\[ P(q_{out}) \sim q_{out}^{-(\tau_{out} - 1)}; \quad P(q_{in}) \sim q_{in}^{-(\tau_{in} - 1)}. \] (3)
The corresponding scaling exponent $\tau_{in}$ is given by the exact result [2] $\tau_{in} = 2 + \alpha$, whereas $\tau_{out} \approx 2 + 3\alpha$ [5] is approximately linear for $\alpha \leq 0.66$ and increases faster than linear for $\alpha \rightarrow \alpha_c < 1$. For $\alpha \rightarrow 1$ the distribution of outgoing links loses the scaling behavior and approaches random distribution. By comparison with the measured distributions of outgoing and incoming links in the real world-wide Web [1] the parameter $\alpha$ is estimated as [5] $\alpha = 0.22 \pm 0.1$, leading to $\beta$ in the range 3–4.

The topology of links in Eq. (3) affects the character of the dynamic processes on the Web graph and its relaxation properties. Next we study two types of random walks on the Web graph—a naive random walk and a walk with adaptive rules defined below. We first grow a network of $N$ nodes using the evolution rules in Eqs. (2)–(4). The walk then starts at time $t = 0$ from a randomly selected initial node, say node $n$. At this node we have $q_{out}(n) \equiv q_{out}(n,N)$ outgoing links. (It is assumed that the network does not grow during the walk, although this restriction is not essential for the results.) A naive random walker selects its next move along one of the outgoing links of the node $n$ with equal probability $w_0(n) = 1/q_{out}(n)$, say the link pointing to the node $k$ and moves there. At the next step it makes a similar selection among $q_{out}(k)$ links, and so on. In contrast to this standard random walk rules, the adaptive random walker at each node selects the link with certain statistical weight. Here we assume that the weights are correlated with the linking preferences in Eq. (3) of the visited node. In particular, the walker investigates target nodes $k_\ell$ at the other end of each the outgoing link $\ell$, $1 \leq \ell \leq q_{out}(n)$ of the visited node $n$ and assigns the weights $w_\ell$ to the corresponding links, where
\[ w_\ell \sim p_2(k_\ell,N), \quad \sum_{\ell=1}^{q_{out}(n)} w_\ell = 1, \] (4)
and $p_2(n,i = N)$ is given in Eq. (2) with the normalization in Eq. (4). Thus, the adaptive walker uses the same principle of selection that applied earlier to linking from the visited node. It should be noted that the weights $w_\ell$ are not necessarily identical to linking probabilities, both because they are evaluated in fully grown network and normalized. It this way, the adaptive random walker (ARW) utilizes the full information about local architecture of in- and out-degree of the graph, whereas the naive random walker (NRW) is driven exclusively by the out-degree distribution, thus exploiting only a part of the available information. The walk continues as long as $q_{out}(k) > 0$ at last visited node, and stops at a node with no out-links $q_{out}(k) = 0$ (border of the graph [4]).

Both ARW and NRW on the graph traverse along a connected path of nodes, that, in principle, is a subset of the set of all connected nodes (so called connected component, which is usually searched by the Web crawls). Similarly, the length of the walk is not equal to the depth of the connected component, because the walk can move backwards making loops of any size. Hence the random-walk path represents a local structure on the graph, that we discuss below. In the metabolic and catalytic reaction networks the path of the walk represents a possible relaxation process between two states corresponding to the departing and final node of the walk, respectively. In this context a naive random walk can not be considered as a process of choice, given that the presence of enzymes or catalysts inevitably selects the preferred reaction, much similar to our adaptive random walk.

It is interesting to define the distance traversed by a walker on the network in terms of the difference in node ranks $\Delta q$, in which the graph has a nontrivial topology. The distribution of such distances in principle depends on the time of the walk. In Fig. 1 we present the results of time-integrated distribution $W(\Delta q)$ of distances $\Delta q$ both for in- and out-links. Two bottom curves on the main figure represent the distribution for the adaptive random walk, whereas the curves above the dotted line are the corresponding distributions in the case of the naive random walk. As it is seen immediately from Fig. 1 the connected subgraphs visited by an ensemble of random walkers have topology that can be described by the power-law distributions
\[ W(\Delta q_{out}) \sim (\Delta q_{out})^{-\delta_{out}}; W(\Delta q_{in}) \sim (\Delta q_{in})^{-\delta_{in}}, \] (5)
with the distinct distribution of in- and out-degree, resembling the global structure of the graph in Eq. (3). For
the adaptive random walk the exponents $\delta_{in}$ and $\delta_{out}$ are close to $\tau_{in}$ and $\tau_{out}$ in Eq. (3), respectively, of the underlying graph structure (see inset to Fig. 1). In fact, the scaling exponents do depend on the size of the ensemble $N_a$ relative to the size of the network $N$. In the inset to Fig. 1 we have shown the exponents $\delta_{in}$ and $\delta_{out}$ measured by the ARW ensemble of the same size ($N_a = 2 \times 10^5$) as the distributions in the main Fig. 1, but at larger network $N = 10^6$. This measurements result in larger exponents compared to the slopes measured in smaller network $N = 10^4$ (cf. main Fig. 1). The exponents decrease with increasing ratio $N_a/N$. When a large enough ensemble of the adaptive random walkers is used the structure of selected subgraphs approaches the underlying topology of the entire graph (see caption to Fig. 1). Therefore, an ensemble of the adaptive random walkers on the Web graph can be used as a search algorithm for the structure of connected subgraphs.

In the case of naive random walk the distributions are qualitatively different from the global graph structure (see two top curves in main Fig. 1). While the distributions of in- and out-degree still differ each from other, the corresponding scaling exponents are $\delta_{in} < 2$ and $\delta_{out} < 2$. (Some consequences of this property will be discussed later.) The distributions $W(\Delta q)$ shown in Fig. 1 indicate that in the ensemble of naive random walkers several well connected nodes (i.e., for large $\Delta q$) are visited more frequently than in the ensemble of the same size made of the adaptive random walkers (frequency can differ up to four orders of magnitude for the simulated conditions, see Fig. 1). This suggests that a naive random walker is wasting time by walking in closed loops, which often pass through several highly connected nodes on the graph.

Direct measurements of the access time support this conclusion. We measure the average access time for a given distance $\Delta q$ in the ensemble of walkers corresponding to the distributions in Fig. 1. The results are shown in Fig. 2. The average access time for the naive random walker is generally higher than the one of the adaptive walker, the ratio reaching $< t_{rw} > / < t_{arw} > \sim 0.5 \times 10^2$ for large distances. The most remarkable feature of this class of networks is that the average access time decreases as a fractional power of the distance in hierarchy, i.e.,

\[ < t_{rw} > \sim (\Delta q)^{-\theta} \Phi(t/\Delta q), \]

for distances $\Delta q$ below the cut-off. On the double-hierarchical graphs that we study here, the Eq. (6) applies both for the random and for the adaptive walk, with different exponents $\theta_{arw}$ and $\theta_{nrw}$ as shown in Fig. 2. This implies that decrease of the access time with the ranks differences is an essential feature of these graphs that can be understood in the following way. Consider a node of in-degree $k$. It can be directly linked to a node of degree $k + Q$. Majority of nodes have a link with rather large rank difference $Q$—linking to a dominant attractor in view of the rule (4). The ARW, which is designed to follow such links, reaches quickly a locally dominant attractor. According to the fast decaying distribution $W(\Delta q)$ (we measured $\theta_{in}^{nrw} = 1.97 \pm 0.04$) there is a small number of attractors in the area scanned by the ARW. Hence, the access to any other node, including a node with a large out-degree often goes via a dominant attractor. The nodes with a large out-degree have the capacity to disperse the links throughout the network, because the probability to link back to the attractor decreases with the number of out-links (cf. Eq. (4)), i.e., they act as the promoters of the dynamics. In Fig. 2 the average time to access a dominant promoter is 2-20 steps for the ARW, compared with ~ 200-600 steps for the NRW, suggesting that the naive random walker makes up to 300 cycles containing locally dominant attractor and promoter node. Evidences of such structure in the real Web were recently discussed in Ref. [7].

The probability $P(t)$ that a walk survives for $t$ steps on the Web graph is a quantitative measure of relaxation of the graph. The simulated survival probability $P(t)$
shown in the inset to Fig. 2 indicate once again that the adaptive and naive random walk represent two types of relaxation processes. Although the fitted expressions are not definitive and require further theoretical analysis, they suggest that a random walk on this class of graphs corresponds to a stretch exponential relaxation, similar to relaxation in complex disordered systems, whereas the adaptive random walk dies off nearly exponentially.

As potential applications of these results we can mention the processes of message-passing and infection-spreading on the Web graph. Assuming that an infection can be transmitted with the walker, we find that both the complex architecture of the graph and the walk strategies are relevant for the spreading. Due to a slow relaxation and heavy tail of the distribution $W(\Delta q)$ of visited nodes ($\delta_{in} < 2$) in the case of the naive random walkers the epidemics is likely to spread over the entire graph. With the adaptive random walkers, on the other hand, the affected area remains restricted, however, locally dominant nodes are quickly affected. The adaptive random walk also offers an efficient algorithm of message passing to a given destination on the Web graph.

To explore the complex structure of the Web graph we proposed an adaptive random walk that learns its move strategies from the time varying local dynamic rules of the graph itself. The walker has a short access time to dominant nodes on the graph and affects a restricted area—the properties that are relevant for the potential applications. The adaptive random walk is a good candidate for a message-passing algorithm on the Web graph (and catalytic reactions in the same universality class), which builds its efficiency on fully exploiting the local graph structure with double-hierarchical connectivity.

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