Scale-free networks which are highly assortative but not small world

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(Received 19 October 2007; revised manuscript received 6 May 2008; published 20 June 2008)

Uncorrelated scale-free networks are necessarily small world (and, in fact, smaller than small world). Nonetheless, for scale-free networks with correlated degree distribution this may not be the case. We describe a mechanism to generate highly assortative scale-free networks which are not small world. We show that it is possible to generate scale-free networks, with arbitrary degree exponent $\gamma>1$, such that the average distance between nodes in the network is large. To achieve this, nodes are not added to the network with preferential attachment. Instead, we greedily optimize the assortativity of the network. The network generation scheme is physically motivated, and we show that the recently observed global network of Avian Influenza outbreaks arises through a mechanism similar to what we present here. Simulations show that this network exhibits very similar physical characteristics (very high assortativity, clustering, and path length).

DOI: 10.1103/PhysRevE.77.066112 PACS number(s): 89.75.Hc

I. INTRODUCTION

Over the past two decades, complex networks have been intensively investigated [1–3], especially small-world [4] and scale-free networks [5] and during this time the Barabási and Albert (BA) model of preferential attachment has become the standard mechanism to explain the emergence of scale-free networks. Nodes are added to the network with a preferential bias toward attachment to nodes which already have a high degree. This naturally gives rise to hubs with a degree distribution following a power law (i.e., the frequency of nodes whose degree is k) $P(k)\sim k^{-\gamma}$.

Many authors have sought, and found evidence of, small-world and scale-free networks in a wide variety of settings [6]. For most of these examples, the preferential attachment model provides a good explanation of the mechanism underlying the origin of the scale-free structure observed in the network. However, the preferential attachment model does lack one feature common in real world data: there is no bias for highly connected nodes to be connected to one another, or for poorly connected nodes to be associated with other poorly connected nodes [7,8]. In the case of our own work, we have frequently observed scale-free networks with strong assortativity and large average path length [14,15]. Networks from both of these sources will be considered in more depth in Sec. IV.

In [9], Cohen *et al.* reported that uncorrelated scale-free networks are "ultrasmall." Despite the title of that paper, this is only necessarily true for networks that are uncorrelated (the assortativity is zero). In the existing literature there is very little attention focused on modeling complex networks by enhancing assortativity. One notable contribution focuses on enhancing assortativity of an existing scale-free network through rewiring two links between four end points [10]. In contrast, our model is a method to grow a scale-free network that is generated as assortatively as possible based on a greedy algorithm (it may even be possible to combine both methods to further accentuate the resulting assortativity).

In contrast, disassortative networks have recently received some attention. Klemm and Eguíluz [11] introduced a novel network growth algorithm that accentuates clustering and lead to strong disassortativity (that is, negative assortativity coefficient). They showed that by allowing a small changing group of nodes to be "active," and by biasing preferential attachment to select these nodes, one leads to a highly clustered and disassortative network, which under some circumstances also exhibits a large average path length [11]. The network growth algorithms leads to the low degree nodes connected to multiple discrete high degree hubs. In contrast our model has large degree nodes collected together, rather than isolated. Surprisingly, we still observe a very large average path length.

Following a similar rationale to the idea of [11], Gómez-Gardeñes and Moreno [12] introduce an "affinity" parameter to the network growth algorithm and allow nodes to preferentially attach to others with similar affinity. Affinity could represent any physical quantity, and in our algorithm would be analogous to node degree. Nonetheless, the algorithm portrayed in [12] also generates disassortative networks and the average path length grows slower than, but proportional to, the standard BA algorithm (it is still smaller than small world). In a recent corollary to this work, Moreno and Vásquez [13] explored the spread of a contagion on such a network. They showed that in such a networ susceptible-infected-susceptible (SIS)-type infections did exhibit a nonzero threshold. In light of this result, and our own recent finding that the global Avian Influenza pandemic exhibits scale-free but not small-world characteristics [14], we propose a model for generation of a scale-free network with large average path length and show that the physical motivation and topological characteristics of this network closely match the network observed from global Avian Influenza (AI) data [14].

This paper is organized as follows. We first introduce the modeling mechanism in Sec. II; then the analysis of the key characteristics for our models is illustrated (Sec. III), especially the average path length (Sec. III D); finally, we sum-

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marize some significant properties of this algorithm so as to draw a comparison between the usual BA network and our models (Sec. IV). We also estimate the same ensemble of topological characteristics for the global spatiotemporal network of Avian Influenza outbreaks [14] (Sec. IV D). We find that this network matches very closely to the mechanism proposed here. Finally, in Sec. V we conclude.

II. SCHEME

In this paper we propose the following scheme to construct a network given the degree distribution $P(k) \sim k^{-\gamma}$ (although the algorithm is not necessarily confined to power-law form). Note that, in contrast to the BA model, we must specify the degree distribution *a priori*. This has the advantage of allowing arbitrary choice. Moreover, there is abundant evidence for the ubiquity of the power-law distribution in natural and physical systems, and we feel that it is therefore not unreasonable to make such a choice [17].

Step 1. Determine the sizes of the original and expected final network. A fully connected network with m_0 nodes is used to initiate the model; a new node is added to the network each time until the expected size of the network is reached, say N.

Step 2. Choose a function for the degree distribution of the model. In order to generate a scale-free network, we consider the probability density function (PDF) of the degree distribution as $P(k)=ck^{-\gamma}$ [where c is a corresponding positive constant for predetermined N and γ satisfying $\Sigma_{k=1}^{N} P(k)=1$]. Then $c(N,\gamma)=\frac{1-\gamma}{N^{1-\gamma}-1}$ can be calculated directly to ensure that $\Sigma_{k=1}^{N} P(k) \approx 1$.

Step 3. Establish the degree of a new node.

Step 3.1. At each time t, we take the degree of the (m_0+1)th node randomly from the set $\{k | 1 \le k \le \min\{m_0+t-1, k_{\max}\}\}$, where $k_{\max}$ is the maximum degree obtained by a "natural" cutoff [the critical maximum degree that satisfies $NP(k) \ge 1$]. For convenience, we choose a random number satisfying $P(k)=c(N,\gamma)k^{-\gamma}$.

Step 3.2. Before adding a new node, determine whether the chosen degree is already saturated. That is, determine whether the current sample value

$$\hat{P}(k) = \frac{\mathcal{N}(\text{nodes with degree } k)}{\mathcal{N}(\text{nodes})}$$

satisfies $\hat{P}(k) > P(k)$. If this is the case, generate another new degree according to step 3.1; otherwise take it as the degree of the new node.

Step 4. Connect each new node to the existing network as assortatively as possible. By applying a greedy principle, we first connect the new node to the existing nodes which have the same degree. If none exist, we connect it to the nodes whose degree is higher or lower by $n=1$. If it fails again, increase the value of n by 1 and repeat.

Because new nodes are wired into the existing network one at a time, this algorithm guarantees that the resultant network is connected and that multiple distinct edges connecting two nodes will not occur. This scheme naturally leads to two different types of networks, depending on whether the wiring of new nodes to the existing structure (when more than one node in the current network has the appropriate degree) is done strictly sequentially (unshuffled) or randomly (shuffled).

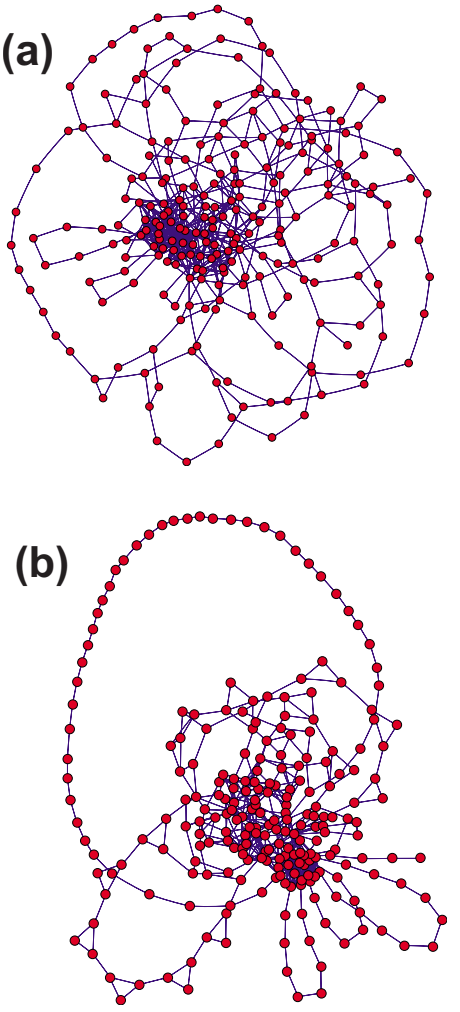

FIG. 1. (Color online) Shuffled (a) and unshuffled (b) models with $m_0=6$, $\gamma=2$ and the size $N=250$.

A. Shuffled version

In step 4, the set of existing nodes which is chosen to link the new node may not be unique, so we randomly choose one of them to be connected to the new node. When the network is generated by randomly choosing a node from among those that match the criteria in step 4, we call this the *shuffled* scheme. Figure 1(a) plots the shuffled model with $\gamma=2$, $m_0=6$, and $N=250$. A counterpart to this scheme can be found in social networks, which possess strict hierarchical social structure and are assortative within different layers [8]. For example, assume that a social community has a strict hierarchical structure (high assortativity) and the number of friends of each person obeys a power-law distribution. The shuffled model means that under the circumstance, a newcomer selects his friends randomly from the persons who have a similar number of friends in this community. A new "salesman" will be friends with other salesman that are

equally gregarious. Conversely, a new "physicist" will likely become connected with other equally solitary individuals.

B. Unshuffled version

In contrast to the shuffled model, we also define the *unshuffled* (or *preferential*) model, shown in Fig. 1(b), in which the existing nodes are chosen to connect to the new nodes in sequence. This model can be explained by the phenomenon that in some social communities senior individuals have priority when all other conditions are equal. That is, newcomers will attempt to connect with existing members of the community with equal degree, but will always connect preferentially with those that have been established in the community for longer.

At this point it is possible to suggest a pseudoanalytic justification for the non-small-world nature of networks constructed with this scheme. As Fig. 1(b) suggests this unshuffled algorithms leads to long chains of sparsely connected nodes. The reason for this is that when a node with high degree is randomly drawn, it is immediately closely packed with the other hub nodes, and this is done sequentially. Moreover (and more importantly for the discussion of path length), low degree nodes also wire themselves to the network sequentially and therefore form long chains. The length of these chains depends on the relative probability of lowly connected nodes occurring. The path length therefore is related to the frequency with which nodes of low degree are drawn from the power-law distribution. The long chains of degree 2 nodes are evident in Fig. 1 and these play a dominant role in the average path length. The average path length is therefore proportional to the expected number of nodes of degree 2 to appear in these networks. The occurrence of chains of degree 3 nodes (evident at the bottom of the illustration in Fig. 1) complicates this argument. We now turn to consider the structural properties of these networks in more detail.

III. NETWORK PROPERTIES

We now present a numerical study of the main measures of network geometry: assortativity (Sec. III A); rich-club prevalence (Sec. III B); clustering (Sec. III C); and average path length (Sec. III D). Of these statistics it is average path length which is of greatest interest to us, and so it is this quantity which we study closest. A summary of these various properties will be presented in Table I.

A. Assortativity

Assortativity by degree refers to the characteristic that nodes tend to connect to other nodes with similar degree. The preference for a network's nodes to attach to others that are similar in degree are often found in the mixing patterns of social networks [2,8]. The assortativity coefficient is given by

TABLE I. Properties of the three models with $N=1000$, $m_0=6$, and $m=6$. Here, APL, CC, and AC represent sample average path length, clustering coefficient, and assortativity coefficient, respectively. For the two AI networks $N=3346$.

	γ	APL	CC	AC
BA model	3	2.83 ± 0.01	0.047 ± 0.002	-0.042 ± 0.008
Shuffled	2	7.21 ± 0.37	0.052 ± 0.002	0.676 ± 0.027
Unshuffled	2	32.58 ± 7.21	0.202 ± 0.016	0.693 ± 0.034
AI (dated)	1.2[a]	47.23	0.285	0.715
AI (undated)	0.4[b]	16.46	0.870	0.784

[a]According to the calculation presented in [14].
[b]The statistical fit in this case is weak. The data is insufficient to conclude that the network actually *is* scale-free.

$$r = \frac{M^{-1}\sum_{i=1}^{N} j_i k_i - \left[M^{-1}\sum_{i=1}^{N} \frac{1}{2}(j_i + k_i)\right]^2}{M^{-1}\sum_{i=1}^{N} \frac{1}{2}(j_i^2 + k_i^2) - \left[M^{-1}\sum_{i=1}^{N} \frac{1}{2}(j_i + k_i)\right]^2},$$

where j_i and k_i are the degrees of the two end points of ith edge, M is the total number of edges in the network. If $r>0$, then the network is assortative; while $r<0$ represents a disassortative network. The BA scale-free network has assortativity coefficient $r=0$ [2]. Figure 2 shows the assortativity coefficients of our shuffled and unshuffled model, respectively. Compared to $r=0$ for the BA network, the assortativity coefficients of the two models are much larger and, moreover, increasing with the network size. Our two models exhibit a similar level of assortativity since the mechanism of greedily assortative mixing at each step is similar for both models.

B. Rich clubs

Rich-club connectivity describes the characteristic that highly connected nodes tend to be connected with other high

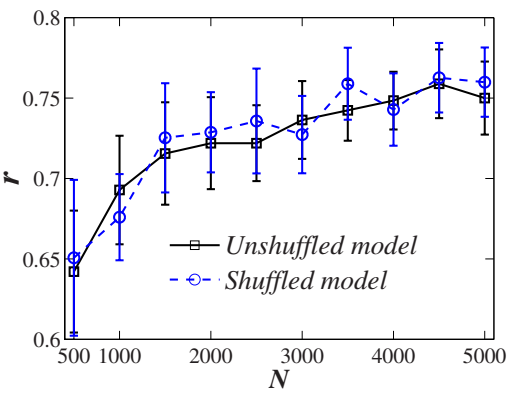

FIG. 2. (Color online) Assortativity coefficients of the shuffled and unshuffled models. Both models have similar values which are much larger than $r=0$ of the BA scale-free model and are growing as the size of the network model expands.

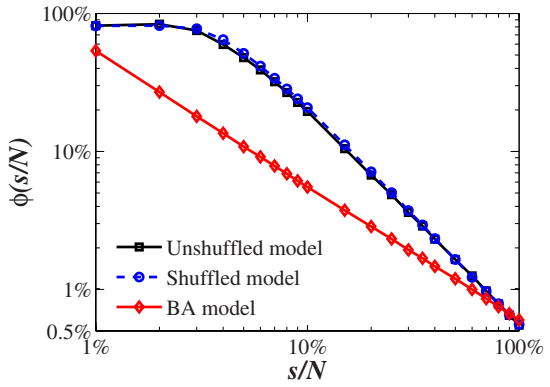

FIG. 3. (Color online) Rich-club coefficients of the shuffled, unshuffled, and BA scale-free network models with $m_0=6$, $m=3$, and $N=1000$. The rich-club coefficients of the new models are much larger than that of the BA network model for small fractions s/N and the three curves converge only gradually.

degree nodes. The rich-club connectivity coefficient of the s richest nodes is depicted by

$$\Phi(s/N) = \frac{R}{s(s-1)/2},$$

where R is the actual edges between the most s richest nodes. Figure 3 is obtained by choosing the network sizes $N=1000$ and $m_0=6$, $m=3$ for the BA network model to guarantee nearly the same numbers of edges. From Fig. 3, it can be concluded that the rich-club coefficients of the shuffled and unshuffled models are the same and they are both much higher than that of the BA network. This is natural since our method is greedily assortative mixing while the schemes of BA network modeling include preferential attachment. Besides, the assortative attaching mechanism leads to about 3% of the richest vertexes tending to be connected with each other and having significantly less links to other "poorer" ones. The low-degree nodes, since they prefer to link to themselves, form loops among themselves in the two new models. The presence of these loops contributes further to the elevated rich-club coefficients of our models.

C. Clustering

The clustering coefficient is defined as the average value of all the clustering coefficients of a single node, which means the ratio of the total number of links between the immediate neighbors of a node to the maximum possible number of links between these neighbors [4]. Clustering coefficients of the BA network and the shuffled and unshuffled models are depicted in Fig. 4. The clustering coefficient of the unshuffled model assumes a much higher value than the other two. Since older nodes have the priority to obtain links each time, the nodes which are chosen to link a new node have a high probability to have been joined together. Thus the neighbors of a new node are most likely to be connected to each other. On the other hand, the difference of the curves between the BA model and the shuffled model is due to the assortative mixing mechanism.

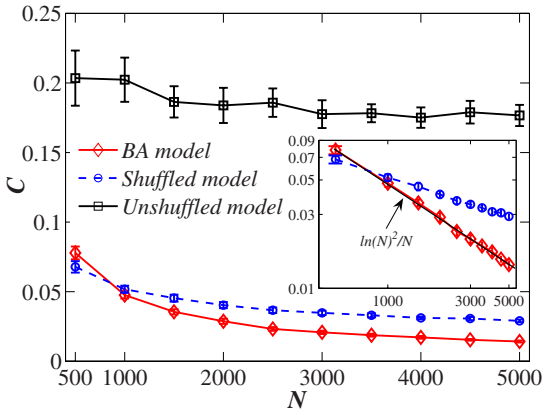

FIG. 4. (Color online) Clustering coefficients of the shuffled, unshuffled, and BA network models. The clustering coefficient of the shuffled model is a little higher than the BA network model, while that of the unshuffled model is substantially higher. The inset shows the same data plotted on the log-linear scale. For comparison we also plot the expected (for the BA model) $\ln N^2/N$ curve.

D. Path length

Finally, average (characteristic) path length is the most important measure of the efficiency of information or mass transport on a network. Moreover, it is this characteristic (or rather the trend of this characteristic) that is used to define a network as small world. It is defined as the average number of steps along the shortest paths for all possible pairs of network nodes [1], denoted L. Figure 5(a) reveals the average path lengths of a BA network and the shuffled and unshuffled models. Simulations demonstrate that L_{BA}, L_{shuf}, and L_{unshuf} scale as $\frac{\ln N}{\ln \ln N}$, $\ln N$, and N, respectively, as can be seen in Fig. 5.

Networks are said to show the small-world effect if L scales no more than logarithmically with network size N for a fixed mean degree [7]. Obviously, the new unshuffled model displays no small-world characteristic. In the shuffled model, for $P(k)=\frac{N}{N-1}k^{-2}$, we have $k_{\max}=\lfloor\frac{N}{\sqrt{N-1}}\rfloor$, where $\lfloor\cdot\rfloor$ represents the floor function, and then we have $\ln k_{\max}\sim\ln N$. Besides, it is shown that

$$\langle k\rangle = \sum_{1}^{k_{\max}} kP(k) = \frac{N}{N-1}\sum_{1}^{k_{\max}} k^{-1} \sim \ln k_{\max},$$

where $\langle k\rangle$ is the mean degree of the whole network. As a result, we get that $\langle k\rangle\sim\ln N$. According to the small-world effect, it can be seen that if the mean degree increases, a network exhibits small-world characteristic whose average path length L should scale strictly less than logarithmically with N. Therefore our shuffled model shows small-world (but not "ultra-" small-world) behavior.

The fact that the unshuffled model has a much higher average path length than the shuffled model is due to the higher clustering in the unshuffled model. In the unshuffled model, new nodes are added systematically to the earliest node in the current network which matches the required criterion (that is, have the right degree). Hence successive new nodes are often added to adjacent nodes (or at least nearby regions) of the existing network, and so are more likely to be

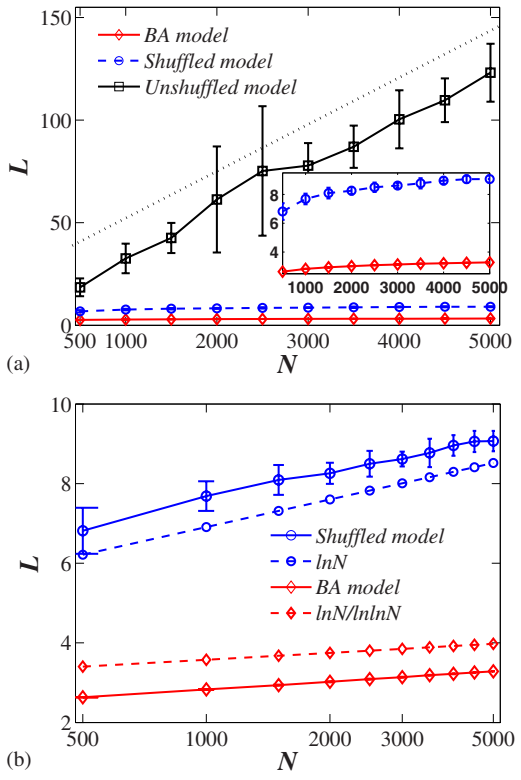

FIG. 5. (Color online) Average path length in the BA network, the shuffled, and unshuffled model. It is obvious that $L_{unshuf} \sim N$ (a). In (b) simulation shows that $L_{BA} \sim \ln N / \ln \ln N$ and that $L_{shuf} \sim \ln N$.

neighbors themselves. Hence the unshuffled network has a higher level of clustering than the shuffled model. Finally, this increased clustering means that there are fewer long-range links and therefore the average path length is larger. The consequence of this construction can clearly be seen in Fig. 1.

This feature has an intuitive analog in experimental networks. In the social community, for example, the fact that senior people have priority introduces societal inequality and can (necessarily) make society less efficient, and this lead to longer paths to transport information. On the contrary, randomly selecting makes the society more fair and equitable and then information transports quicker. By forming cliques of mutually connected individuals this necessarily generates chains of those that have relatively low degree (this can be seen in Fig. 1). Consequently, these chains contribute significantly to increasing the overall path length of the network.

IV. EXTANT NETWORKS

In the previous sections we introduced our network generation scheme which allows for the generation of scale-free networks which are not small world. To the contrary, networks generated with this algorithm can have very large average path lengths. In this section we compare the behavior of our algorithm to other algorithms for generating correlated scale-free networks. We also compare our algorithm to experimentally generated data from two sources: time series analysis and disease outbreak records. In Sec. IV A we compare our algorithm to techniques proposed in [11–13]. In Sec. IV B we analyze networks derived from time series (as described by [15]) and in Sec. IV C we provide an analysis of the Avian Influenza transmission path network described in [14].

The comparison to other networks we present here is far from comprehensive. To provide an exhaustive study of the statistical properties of these networks is beyond the scope of the main message we wish to present. We include these data based networks only to illustrate that scale-free networks which are not small world do actually occur in practical situations. The questions of whether these networks were actually generated with precisely the scheme we propose in this paper is far more subtle and complicated.

A. Alternative algorithms

The algorithm introduced by Gómez-Gardeñes and Moreno [12] does not show anything other than an increase in path length by a constant factor (depending on their algorithmic parameter μ). In [12] (Fig. 2 of that paper) they show that their algorithm produces scaling of path length (with parameter μ) that is proportional to the Barabási-Albert model, and is independent of network size. That is, the Gómez-Gardeñes-Moreno network produces a path length which is approximately proportional to $\frac{\ln N}{\ln \ln N}$. In contrast, the path length of networks produced with our algorithm is proportional to either $\ln N$ or N.

In [11] Klemm and Eguíluz describe an algorithm for which the average path length scales like $\ln N$ except for the special case where networks are constructed without long range connections ($\mu=0$ in the nomenclature of Klemm and Eguíluz). When this is the case ($\mu=0$), the network structure is disassortative and no longer small world (see Fig. 6). In contrast to the correlated but ultra-small-world model of Gómez-Gardeñes and Moreno [12] the algorithm proposed by Klemm and Eguíliuz [11] can actually be made to yield scale-free networks which are not ultra-small-world. However, our network is both scale-free and highly assortative. As we illustrate in Fig. 6, the network of Klemm and Eguíliuz is disassortative. Hence while Klemm and Eguíliuz achieve a large path length by stretching out their network, our network remains densely packed. The large average path length in our network is perhaps even more surprising in light of the very strong assortativity.

B. Time series networks

Zhang and Small [15] describe a method to represent an oscillatory time series as a complex network. The procedure, essentially, is the following. One partitions the time series into discrete cycles and measures the correlation between all pairs of cycles. Each cycle then represents a node of a complex network, with a link between two nodes if the correlation is sufficiently high (or equivalently, if the phase space distance is sufficiently low). The details of the procedures described in [15] and the corresponding results are beyond the scope of the current work. What is relevant here is that if this procedure is performed on chaotic time series, the cor-

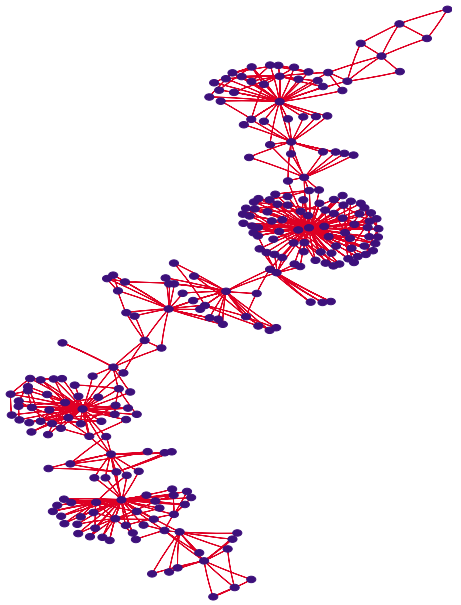

FIG. 6. (Color online) The complex network generated via the method describe by Klemm and Eguíliuz. We display 250 nodes of a network generated with the scheme described in [11] with $m=2$. The highly disassortative structure of this network is evident (assortativity estimated to be approximately −0.297). The structure of this algorithm stands in stark contrast to the detailed features presented in Fig. 1.

responding network is complex and exhibits a power-law distribution of vertex strength. Nonetheless, for a given connection threshold [18] the networks are also highly assortative (by construction this should be obvious) and may not exhibit a very short average path length. This is due to the dynamics of the system underlying the time series from which the network is generated. Similarly, cycles will be similar to one another and therefore the network is highly assortative. Conversely, dissimilar cycles correspond to nodes which are separated by a large number of intermediaries. Essentially two nodes which are similar to a third can only differ by a relatively small amount (dictated by the triangle inequality) and therefore two highly dissimilar nodes must be widely separated in the network.

In Fig. 7 we illustrate the highly assortative (and in this case without a scale-free degree distribution) structure of a complex network generated from the Rössler flow. The network exhibits assortativity and path-length characteristics of those generated with the algorithm we describe in this paper.

C. Avian Influenza

We now consider the real network of connections between outbreaks of Avian Influenza. The data and construction of the network are detailed in [14], briefly, each outbreak of Avian Influenza since 2003 is represented by global coordinates (latitude and longitude) and time. Two outbreaks are connected if they are close in both time and space. The network has been observed to be scale-free, highly assortative, and not small world [14]. In Fig. 8(a) the general structure of this network is depicted. The very large average path length

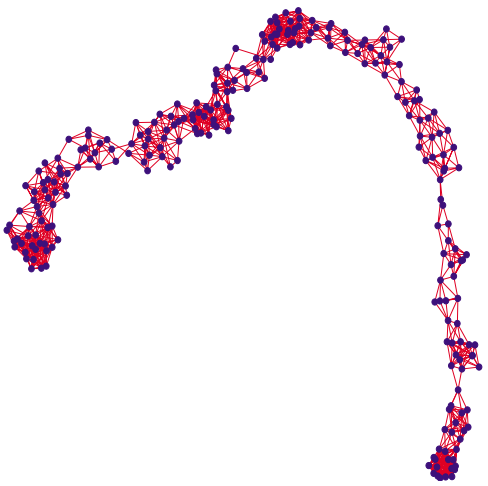

FIG. 7. (Color online) Complex network generated from cycles of a time series of the Rössler system. In this illustration, 250 successive cycles where compared via cross correlation and thresholded to produce an adjacency matrix which is then interpreted as a complex network. Although this example is too short to assert that the degree distribution of the underlying network is scale-free (and we believe that it may not be), this complex network clearly exhibits strong assortativity (assortativity coefficient estimated to be 0.595), in contrast to the illustrations of [11].

of the network is evident from its spindly "twig-like" structure. This is because the metric we employ limits the distance between connected nodes and prevents the occurrence of "short-circuit" links between distant parts of the network. The highly clustered and assortative connection between outbreaks is evident from Fig. 8(b) where we depict the network as a series of discrete pieces.

D. Summary

Table I summarizes the main numerical results discussed above. We compare the average path length, clustering coefficient, and assortativity of the BA model as well as our shuffled and unshuffled models for scale-free networks. Our method drastically increases path length and assortativity. The assortativity of both the shuffled and unshuffled model are comparable The unshuffled model also has a significantly raised clustering coefficient. We find that the AI network shares these topological characteristics exhibited by our model. It is highly assortative, highly clustered, and exhibits a large path length. Moreover, the relative magnitude of these numbers match fairly closely. To mimic the behavior of the shuffling algorithm we ignore the effect of the date of outbreaks of Avian Influenza cases. We find that this small change decreases the path length by approximately the same magnitude as the change from the shuffled to unshuffled network generation scheme. A more complex network generation scheme for time series data [15], when applied to chaotic time series (see Sec. IV B), also yields highly assortative networks (in Fig. 7 the assortativity coefficient is about 0.595). For example, a weighted complex network deduced from the x component of the Rössler system exhibits a power-law distribution of vertex strength when the system is

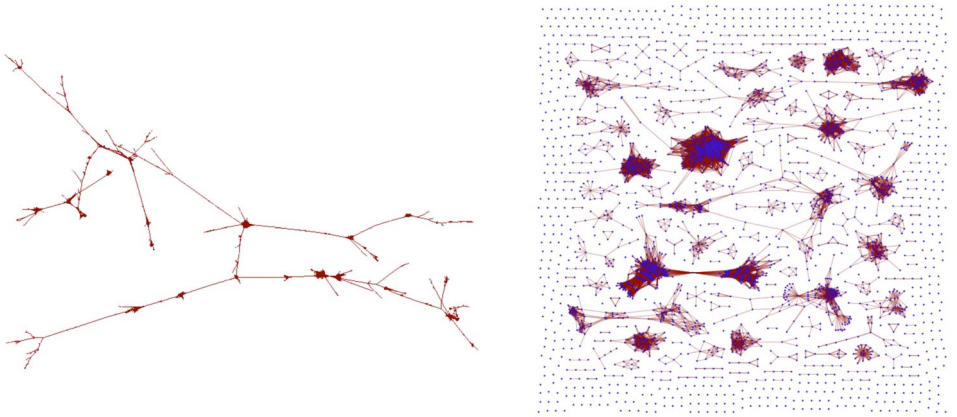

FIG. 8. (Color online) Temporally ordered AI network (see [14]) (a) and depiction of clusters within that network (b). In (b) the network from (a) has been divided into discrete chunks, such that the connection between those chunks [shown in (a)] consists of only single links. That is, in (b) we have removed the solitary connecting links from (a) to emphasize the assortative character of the remaining clusters.

chaotic, but not when the system is periodic. The network is also observed to not exhibit a short average path length (for a given connection threshold) and assortativity. In both the case of the AI network [14] and the chaotic time series network [15] the underlying network generation mechanism can be reduced to the formation of selectively assortative connections, just as with the current algorithm.

V. CONCLUSION

We have proposed a mechanism to model scale-free networks without small-world characteristics by greedy assortative mixing. The mechanism for biasing attachment so that new nodes connect to existing individuals with a similar number of acquaintances is natural in society: most friends have a similar number of friends. It is natural to presume that the most efficient "networkers" (the individuals with the highest degree) would be highly connected to one another. Nonetheless, a surprising consequence of this constraint is that the average path length is increased. This can be explained by observing that the average path length from the network's "networkers" to the rest of the network is relatively small, but the path length from nodes with relatively few links is appreciably increased. That is, in comparison to a BA network, the highly connected nodes benefit from the structure discussed in this paper, but the less highly connected individuals (and the network as a whole) suffer increased average path length.

The physically motivated algorithm presented in this paper generates scale-free networks with a high degree of assortativity that are not small world. This algorithm generates a network structure very similar to that found in the AI network and therefore provides an explanation for the emergence of strong clustering observed in this real world disease network. In an extension of this work we are now exploring the application of the ideas presented here to generate highly assortative networks with degree distributions other than power law [16].

ACKNOWLEDGMENTS

This work, and Xu Xiaoke, were supported by a grant from the Health, Welfare and Food Bureau of the Hong Kong SAR Government. Zhou Jin was supported with the funding of a Competitive Earmarked Research Grant (Grant No. PolyU 5268/07E) from the University Grants Council of the Hong Kong government. This paper has also benefited significantly from many useful comments and suggestions from the two patient and anonymous reviewers.

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[17] We also note that we do not include the commonplace, but extraneous, constraint that "usually $2 \leq \gamma < 3$" in our definition of power law. In fact, we are unsure as to the meaning or origin of this caveat, commonly imposed in the literature.
[18] That is, for a particular value of the cutoff parameter which dictates whether two nodes are connected.