Evolving networks consist of cliques

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Abstract. Many real networks have cliques as their constitutional units. Here we present a family of scale-free network model consist of cliques, which is established by a simple recursive algorithm. We investigate the networks both analytically and numerically. The obtained analytical solution shows that the networks follow a power-law degree distribution, with degree exponent continuously tuned between 2 and 3, coinciding with the empirically found results. The exact expression of clustering coefficient is also provided for the networks. Furthermore, the investigation of the average path length reveals that the networks possess small-world feature.

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1. Introduction

Over the last few years, it has been suggested that a lot of social, technological, biological, and information networks share the following three striking statistical characteristics \[1, 2, 3, 4, 5, 6, 7\]: power-law degree distribution \[8\], high clustering coefficient \[9\], and small average path length (APL). Power-law degree distribution indicates that the majority of nodes in such networks have only a few connections to other nodes, whereas some nodes are connected to many other nodes in the network. Large clustering coefficient implies that nodes having a common neighbor are far more likely to be linked to each other than are two nodes selected randomly. Short APL shows that the expected number of links needed to pass from one arbitrarily selected node to another one is low, that is, APL grows logarithmically with the number of nodes or slower.

Mimicking such complex real-life systems is an important issue. A wide variety of models have been proposed \[1, 2, 3, 4, 5, 6, 7\], among which the most well-known successful attempts are the Watts and Strogatz’s (WS) small-world network model \[9\] and Barabási and Albert’s (BA) scale-free network model \[8\], which have attracted an exceptional amount of attention from a wide circle of researchers and started an avalanche of research on the models of systems within the physics community. After that, a considerable number of other models and mechanisms, which may represent processes more realistically taking place in real-life systems, have been developed. These include nonlinear preferential attachment \[10\], initial attractiveness \[11\], edge rewiring \[12\] and removal \[13\], aging and cost \[14\], competitive dynamics \[15\], duplication \[16\], weight \[17, 18\], geographical constraint \[19, 20, 21\], Apollonian packing \[22, 23, 24, 25, 26, 27\] and so forth.

The above mentioned models and mechanisms may provide valuable insight into some particular real-life networks. However, different networks have different creating mechanisms, it is almost impossible to mimic all real-life systems based on several special models. Thus, it is necessary that we should model peculiar networks according to their corresponding generating mechanisms.

In real-life world, many networks consist of cliques. For example, in movie actor collaboration network \[9\] and science collaborating graph \[28\], actors acting in the same film or authors signing in the same paper form a clique, respectively. In corporate director network \[29\], directors as members in the same board constitute a clique. Analogously, in public transport networks \[30\], bus (tramway, or underground) stops shape a clique if they are consecutive stops on a route, and in the network of concepts in written texts \[31\], words in each sentence in the text is added to the network as a clique. All these pose a very interesting and important question of how to build evolution models based on this particularity of network component—cliques.

In this paper, we suggest a growing evolution network model with cliques as its basic constitutional units, giving high general versatility for growth mechanisms. The model is governed by three tunable parameters \(p, q, \) and \(m\), which control the relevant
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network characteristics. Our networks have a power-law degree distribution with degree exponent changeable between 2 and 3, a very large clustering coefficient, and a small-world feature. The proposed model considers systematic reorganization of cliques as its building block, which is helpful for understanding development processes and controls in real-world networks.

2. Network construction

We construct the networks in a recursive manner and denote the networks after \( t \) generations by \( Q(q, t) \), \( q \geq 2, t \geq 0 \). Figure 1 shows the network growing process for a particular case of \( p = 1, q = 2, m = 2 \). The networks are constructed as follows: For \( t = 0 \), \( Q(q, 0) \) is a complete graph \( K_{q+1} \) (or \( (q + 1) \)-clique). For \( t \geq 1 \), \( Q(q, t) \) is obtained from \( Q(q, t-1) \). For each of the existing subgraphs of \( Q(q, t-1) \), with probability \( p (0 < p \leq 1) \), \( m \) (\( m \) is a positive integer) new vertices are created, and each is connected to all the vertices of this subgraph. The growing process is repeated until the network reaches a desired order.

There are at least three limiting cases of our model listed below. (i) When \( q = 2, p = 1, \) and \( m = 1 \), the networks are exactly the same as the pseudofractal scale-free web \([32]\). (ii) When \( q = 2, p \to 0 \) (but \( p \neq 0 \)), and \( m = 1 \), our model is reduced to the scale-free network with size-dependent degree distribution \([33]\). (iii) When \( q = 2, 0 < p \leq 1, \) and \( m = 1 \), our networks coincide with the stochastically growing scale-free network described in Ref. \([34]\). (iv) When \( q \geq 2, p = 1, \) and \( m = 1 \), our networks reduce to the recursive graphs discussed in Ref. \([35]\).

Next we compute the numbers of nodes (vertices) and links (edges) in \( Q(q, t) \). Let \( L_v(t) \), \( L_e(t) \) and \( K_{q,t} \) be the numbers of vertices, edges and \( q \)-cliques created at step
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t, respectively. Note that the addition of each new node leads to \( q \) new \( q \)-cliques and \( q \) new edges. So, we have \( L_v(t) = K_{q,t} = qL_v(t) \). Then, at step 1, we add expected \( L_v(1) = mpq(q + 1) \) new nodes and \( L_e(1) = mpq(q + 1) \) new edges to \( Q(q,0) \). After simple calculations, one can obtain that at \( t_i(t_i > 1) \) the numbers of newly born nodes and edges are \( L_v(t_i) = mpq(q + 1)(1 + mpq)^{t_i-1} \) and \( L_e(t_i) = mpq(q + 1)(1 + mpq)^{t_i-1} \), respectively. Thus the average number of total nodes \( N_t \) and edges \( E_t \) present at step \( t \) is

\[
N_t = \sum_{t_i=0}^{t} n_v(t_i) = \frac{(q + 1)[(mpq + 1)^t + q - 1]}{q}
\]

and

\[
E_t = \sum_{t_i=0}^{t} n_e(t_i) = \frac{(q + 1)[2(mpq + 1)^t + (q - 2)]}{2},
\]

respectively. So for large \( t \), The average degree \( \bar{k}_t = \frac{2E_t}{N_t} \) is approximately \( 2q \).

3. Topological properties

Topology properties are of fundamental significance to understand the complex dynamics of real-life systems. Here we focus on three important characteristics: degree distribution, clustering coefficient, and average path length, which are determined by the tunable model parameters \( p \), \( q \), and \( m \).

3.1. Degree distribution

When a new node \( i \) is added to the networks at step \( t_i \), it has degree \( q \) and forms \( q \) \( q \)-cliques. Let \( L_q(i,t) \) be the number of \( q \)-cliques at step \( t \) that will possibly created new nodes connected to the node \( i \) at step \( t + 1 \). At step \( t_i \), \( L_q(i,t_i) = q \). By construction, we can see that in the subsequent steps each new neighbor of \( i \) generated \( q - 1 \) new \( q \)-cliques with \( i \) as one vertex of them. Then at step \( t_i + 1 \), there are \( mpq \) new nodes which forms \( mpq(q - 1) \) new \( q \)-cliques containing \( i \). Let \( k_i(t) \) be the degree of \( i \) at step \( t \). We can easily find following relations for \( t > t_i + 1 \):

\[
\Delta k_i(t) = k_i(t) - k_i(t - 1) = mpL_q(i,t - 1)
\]

and

\[
L_q(i,t) = L_q(i,t - 1) + (q - 1)\Delta k_i(t).
\]

From the above two equations, we can derive: \( L_q(i,t + 1) = L_q(i,t)[1 + mpq(q - 1)] \). Since \( L_q(i,t_i) = q \), we have \( L_q(i,t) = q[1 + mpq(q - 1)]^{t - t_i} \) and \( \Delta k_i(t) = mpq[1 + mpq(q - 1)]^{t - t_i - 1} \). Then the degree \( k_i(t) \) of node \( i \) at time \( t \) is

\[
k_i(t) = k_i(t_i) + \sum_{t_h = t_i + 1}^{t} \Delta k_i(t_h) = q \left( \frac{[1 + mpq(q - 1)]^{t - t_i} + q - 2}{q - 1} \right).
\]

Since the degree of each node has been obtained explicitly as in Eq. (5), we can get the degree distribution via its cumulative distribution \( \mathcal{F} \), i.e., \( P_{\text{cum}}(k) \equiv \mathcal{F}(k) \).
Evolving networks consist of cliques. \[ \sum_{k' \geq k} N(k', t)/N_t \sim k^{1-\gamma}, \] where \( N(k', t) \) denotes the number of nodes with degree \( k' \). The detailed analysis is given as follows. For a degree \( k \)
\[ k = q \left( \frac{[1 + mp(q - 1)]^{t-s} + q - 2}{q - 1} \right), \]
there are \( L_v(s) = mp(q + 1)(1 + mpq)^{s-1} \) nodes with this exact degree, all of which were born at step \( s \). All nodes born at time \( s \) or earlier have this or a higher degree. So we have
\[ \sum_{k' \geq k} N(k', t) = \sum_{a=0}^{s} L_v(a) = \frac{(q + 1)((mpq + 1)^{s} + q - 1)}{q}. \]
As the total number of nodes at step \( t \) is given in Eq. (1) we have
\[ \left[ q \left( \frac{[1 + mp(q - 1)]^{t-s} + q - 2}{q - 1} \right) \right]^{1-\gamma} = \frac{(q+1)((mpq+1)^{s}+q-1)}{q}. \]
Therefore, for large \( t \) we obtain
\[ [1 + mq(q - 1)]^{t-s}]^{1-\gamma} = (1 + mpq)^{s-t} \]
and
\[ \gamma \approx 1 + \frac{\ln(1 + mpq)}{\ln[1 + mpq(q - 1)]}. \] (6)

Thus, the degree exponent \( \gamma \) is a continuous function of \( pq \), and \( m \), and belongs to the interval \([2,3]\). For any fixed \( q \), as \( p \) decrease from 1 to 0, \( \gamma \) increases from \( 1 + \frac{\ln(1 + mpq)}{\ln[1 + m(q - 1)]} \) to \( 2 + \frac{1}{m(q - 1)} \) (see Appendix A for the theoretic calculation of distribution for the particular case of \( m = 1 \)). In the case \( q = 2 \), \( \gamma \) can be tunable between \( 1 + \frac{\ln 3}{\ln 2} \) and 3. In some limiting cases, Eq. (6) recovers the results previously obtained in Refs. 32, 33, 34, 35.

Figure 2 shows, on a logarithmic scale, the scaling behavior of the cumulative degree distribution \( P_{\text{cum}}(k) \) for different values of \( p \) in the case of \( q = 2 \) and \( m = 1 \). Simulation results agree very well with the analytical ones.

3.2. Clustering coefficient

In the network if a given node is connected to \( k \) nodes, defined as the neighbors of the given node, then the ratio between the number of links among its neighbors and the maximum possible value of such links \( k(k - 1)/2 \) is the clustering coefficient of the given node [9]. The clustering coefficient of the whole network is the average of this coefficient over all nodes in the network, and can take on values between 0 and 1, the latter corresponding to a maximally clustered network where all neighbors of a node are linked to one another.

For our networks, the analytical expression of clustering coefficient \( C(k) \) for a single node with degree \( k \) can be derived exactly. When a node is created it is connected to all the nodes of a \( q \)-clique, in which nodes are completely interconnected. So its degree and clustering coefficient are \( q \) and 1, respectively. In the following steps, if its degree increases one by a newly created node connecting to it, then there must be \( q - 1 \) existing
Evolving networks consist of cliques of neighbors of it attaching to the new node at the same time. Thus for a node of degree $k$, we have

$$C(k) = \frac{q(q-1)}{2} + \frac{(q-1)(k-q)}{k(k-1)} \frac{2(q-1)(k-q)}{k(k-1)},$$

(7)

which depends on both $k$ and $q$. For $k \gg q$, the $C(k)$ is inversely proportional to degree $k$. The scaling $C(k) \sim k^{-1}$ has been found for some network models [22, 23, 24, 25, 26, 27, 32, 33, 34, 35, 36], and has also been observed in several real-life networks [36].

Using Eq. (7), we can obtain the clustering $\overline{C}_t$ of the networks at step $t$:

$$\overline{C}_t = \frac{1}{N_t} \sum_{r=0}^{t} \frac{2(q-1)(D_r - \frac{q}{2})L_v(r)}{D_r(D_r-1)},$$

(8)

where the sum runs over all the nodes and $D_r$ is the degree of the nodes created at step $r$, which is given by Eq. (5).

In the infinite network order limit ($N_t \to \infty$), Eq. (8) converges to a nonzero value $C$. Obviously, network clustering coefficient $\overline{C}_t$ is a function of parameters $p$, $q$, and $m$. If we fixed any two of them, $\overline{C}_t$ increases with the rest. Exactly analytical computation shows: in the case $q = 2$ and $m = 1$, when $p$ increases from 0 to 1, $\overline{C}$ grows from 0.739 [37] to 0.8 [32]; In the case $p = 1$ and $q = 2$, when $m$ increases from 1 to infinite, $\overline{C}$ grows from 0.8 [32] to 1; Likewise, in the case $p = 1$ and $m = 1$, $\overline{C}$ increases from 0.8 to 1 when $q$ increases from 2 to infinite, with special values $\overline{C}_t = 0.8571$ and $\overline{C}_t = 0.8889$ for $q = 3$ and $q = 4$, respectively. Therefore, the average clustering coefficient is very large, which shows the evolving networks are highly clustered. Figure 3 exhibits the
Evolving networks consist of cliques. Dependence of the clustering coefficient $C$ on $p$, $q$, and $m$, which agree well with our above conclusions.

From Figs. 2 and 3 and Eqs. (6) and (8), one can see that both degree exponent $\gamma$ and clustering coefficient $C_t$ depend on the parameter $p$, $q$, and $m$. The mechanism resulting in this relation should be paid further effort. The fact that a biased choice of the cliques at each evolving step may be a possible explanation, see Ref. [38].

3.3. Average path length

Denote the network nodes by the time step of their generations, $v = 1, 2, 3, \ldots, N - 1, N$. Using $L(N)$ to represent the APL of the our model with system size $N$, then we have following relation: $L(N) = \frac{2\sigma(N)}{N(N-1)}$, where $\sigma(N) = \sum_{1 \leq i < j \leq N} d_{i,j}$ is the total distance, in which $d_{i,j}$ is the shortest distance between node $i$ and node $j$. By using the approach similar to that in Refs. [21, 25, 26, 27], we can evaluate the APL of the present model.

Obviously, when a new node enters the networks, the smallest distances between existing node pairs will not change. Hence we have

$$\sigma(N + 1) = \sigma(N) + \sum_{i=1}^{N} d_{i,N+1}. \quad (9)$$

Equation (9) can be approximately represented as:

$$\sigma(N + 1) = \sigma(N) + N + (N - q)L(N - q + 1), \quad (10)$$

where

$$(N - q)L(N - q + 1) = \frac{2\sigma(N - q + 1)}{N - q + 1} < \frac{2\sigma(N)}{N}. \quad (11)$$

Equations (10) and (11) provide an upper bound for the variation of $\sigma(N)$ as

$$\frac{d\sigma(N)}{dN} = N + \frac{2\sigma(N)}{N}, \quad (12)$$
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![Graph showing APL vs network size N](image)

**Figure 4.** Semilogarithmic graph of the APL vs the network size $N$ in the special case of $m = 1$. Each data point is obtained as an average of 50 independent network realizations. The lines are linear functions of $\ln N$.

which yields

$$\sigma(N) = N^2(\ln N + \omega),$$

where $\omega$ is a constant. As $\sigma(N) \sim N^2 \ln N$, we have $L(N) \sim \ln N$.

Note that Eq. (12) was deduced from an inequality, which implies that the increasing tendency of $L(N)$ is at most as $\ln N$ with $N$. Thus, our model exhibits the presence of small-world property. In Fig. 4, we show the dependence of the APL on system size $N$ for different $p$ and $q$ in the case of $m = 1$. From Fig. 4 one can see that for fixed $q$, APL decreases with increasing $q$; and for fixed $p$, APL is a decreasing function of $q$. When network size $N$ is small, APL is a linear function of $\ln N$; while $N$ becomes large, APL increases slightly slower than $\ln N$. So the simulation results are in agreement with the analytical prediction. It should be noted that in our model, if we fix $p$ and $q$, considering other values of $m$ greater than 1, then the APL will increase more slowly than in the case $m = 1$ as in those cases the larger $m$ is, the denser the network becomes.

Here we only give an upper bound for APL, which increases slightly slower than $\ln N$. Especially, in the case of $p = 1$, the networks grow deterministically, and we can compute exactly the diameter, which is the maximum distance between all node pairs of a graph. In this particular case, the diameter grows logarithmically with the network size [24, 27].

4. Conclusion

In summary, we have proposed and studied a class of evolving networks consist of cliques, reminiscent of modules in biological networks or communities in social systems. We have obtained the analytical and numerical results for degree distribution and clustering coefficient, as well as the average path length, which are determined by the model
parameters and in accordance with large amount of real observations. The networks are power-law, with degree exponent adjusted continuously between 2 and 3. The clustering coefficient of single nodes has a power-law spectra, the network clustering coefficient is very large and independent of network size. The intervertex separation is small, which increases at most logarithmically as the network size. Interestingly, our networks are formed by cliques, this particularity of the composing units may provide a comprehensive aspect to understand some real-life systems.

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Appendix A. Exact degree distribution for some limiting cases

When \( p \to 0 \) (but \( p \neq 0 \)) and \( m = 1 \), our model turns out to be the graph which evolves as follows (see [34] for interpretation): starting with a \((q+1)\)-clique \((t = 0)\), at each time step, we choose an existing \( q \)-clique, then we add a new node and join it to all the nodes of the selected \( q \)-clique. Note that when \( q = 2 \), the particular model gives the network studied in detail in Ref. [33]. Since the network size is incremented by one with each step, here we use the step value \( t \) to represent a node created at this step. Furthermore, after a new node is added to the network, the number of \( q \)-cliques increases by \( q \). We can see easily that at step \( t \), the network consists of \( N = t + q + 1 \) nodes and \( N_q = qN - q^2 + 1 \) cliques.

One can analyze the degree distribution mathematically as follows. Given a node, when it is born, it has degree \( q \), and the number of \( q \)-clique containing this node is also \( q \). After that, when its degree increases by one, the number of \( q \)-cliques with this node as one of its components increases by \( q - 1 \), so the number of \( q \)-cliques for selection containing a node with degree \( k \) is \((q - 1)k - q^2 + 2q\). We denote by \( P_{k,N} \) the fraction of nodes with degree \( k \) when the network size is \( N \). Thus the number of such nodes is \( NP_{k,N} \). Then the probability that the new node happens to be connected to a particular node \( i \) having degree \( k_i \) is proportional to \((q - 1)k_i - q^2 + 2q\), and so when properly normalized is just \([((q - 1)k_i - q^2 + 2q]/(qN - q^2 + 1)\). So, between the appearance of the \( N \)th and the \((N + 1)\)th node, the total expected number of nodes with degree \( k \) that gain a new link during this interval is

\[
\frac{(q - 1)k - q^2 + 2q}{qN - q^2 + 1} \times NP_{k,N} \simeq \frac{q - 1}{q} kP_{k,N},
\]

which holds for large \( N \). Observe that the number of nodes with degree \( k \) will decrease on each time step by exactly this number. At the same time the number increases because of nodes that previously had \( k - 1 \) degrees and now have an extra one. Thus we can write a master equation for the new number \((N + 1)P_{k,N+1}\) of nodes with degree
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\[ (N + 1)P_{k,N+1} = NP_{k,N} + \frac{q-1}{q} [(k-1)P_{k-1,N} - kP_{k,N}] . \]  (A.2)

The only exception to Eq. (A.2) is for nodes having degree \( q \), which instead obey the equation

\[ (N + 1)P_{q,N+1} = NP_{q,N} + 1 - \frac{q-1}{q} qP_{q,N} , \]  (A.3)

since by construction exactly one new such node appears on each time step. When \( N \) approaches \( \infty \), we assume that the degree distribution tends to some fixed value \( P_k = \lim_{N \to \infty} P_{N,k} \). Then from Eq. (A.3), we have

\[ P_q = 1/q . \]  (A.4)

And Eq. (A.2) becomes

\[ P_k = \frac{k-1}{k+1 + \frac{1}{q-1}} P_{k-1} , \]  (A.5)

which can be iterated to get

\[ P_k = \frac{(k-1)(k-2) \ldots q}{(k+1 + \frac{1}{q-1})(k+1 + \frac{1}{q-1}) \ldots (q + 2 + \frac{1}{q-1})} P_q \]
\[ = \frac{(k-1)(k-2) \ldots (q+1)}{(k+1 + \frac{1}{q-1})(k+1 + \frac{1}{q-1}) \ldots (q + 2 + \frac{1}{q-1})} , \]  (A.7)

where Eq. (A.4) has been used. This can be simplified further by making use of a handy property of the \( \Gamma \)-function, \( \Gamma(a) = (a-1)\Gamma(a-1) \) with \( \Gamma(a) \) defined by:

\[ \Gamma(a) = \int_0^\infty x^{a-1} e^{-x} dx . \]  (A.8)

By this property and \( \Gamma(1) = 1 \), we get

\[ P_k = \frac{(q+1 + \frac{1}{q-1})(q + \frac{1}{q-1}) \ldots (2 + \frac{1}{q-1}) \Gamma(k)\Gamma(2 + \frac{1}{q-1})}{q(q-1) \ldots 1 \Gamma(k + 2 + \frac{1}{q-1})} \]
\[ = \frac{(q+1 + \frac{1}{q-1})(q + \frac{1}{q-1}) \ldots (2 + \frac{1}{q-1})}{q(q-1) \ldots 1} \frac{\Gamma(k)\Gamma(2 + \frac{1}{q-1})}{\Gamma(k + 2 + \frac{1}{q-1})} B \left( k, 2 + \frac{1}{q-1} \right) , \]  (A.9)

where \( B(a,b) \) is the Legendre beta-function, which is defined as

\[ B(a,b) = \frac{\Gamma(a)\Gamma(b)}{\Gamma(a+b)} , \]  (A.10)

Note that the beta-function has the interesting property that for large values of either of its arguments it itself follows a power law. For instance, for large \( a \) and fixed \( b \),
Evolving networks consist of cliques $B(a, b) \sim a^{-b}$. Then we can immediately see that for large $k$, $P_k$ also has a power-law tail with a degree exponent
$$\gamma = 2 + \frac{1}{q - 1}. \quad (A.11)$$

For $q = 2$, $\gamma = 3$, which has been obtained previously in Ref. [34].

Equation (A.9) is similar to the Yule distribution [39] called by Simon [40]. In fact, this particular case of our model can be easily mapped into the Yule process, which was inspired by observations of the statistics of biological taxa, from this perspective our model may find applications in biological systems.

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