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Incompatibility networks as models of scale-free small-world graphs

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Abstract. We make a mapping from Sierpinski fractals to a new class of networks, the incompatibility networks, which are scale-free, small-world, disassortative, and maximal planar graphs. Some relevant characteristics of the networks such as degree distribution, clustering coefficient, average path length, and degree correlations are computed analytically and found to be peculiarly rich. The method of network representation can be applied to some real-life systems making it possible to study the complexity of real networked systems within the framework of complex network theory.

PACS. 89.75.Hc Networks and genealogical trees – 05.45.Df Fractals – 02.10.Ox Combinatorics; graph theory – 89.75.Da Systems obeying scaling laws

1 Introduction

The main advantages of the flexibility and generality for representing real systems have made complex networks become a focus of attention from the scientific community [1–5]. The empirical analysis of various real networks has uncovered the presence of several typical properties: scale-free nature of degree distribution [6], small-world effect including large clustering coefficient and small average path length (APL) [7], degree correlations, i.e., the degrees at both end points of any given edge are not usually independent. These quantities have important effects on the dynamical processes taking place on top of complex networks, such as epidemic spreading [8], percolation [9,10], synchronization [11], and games [12].

The empirical discovery of such distinguished properties of real networks has spawned a truly cross-disciplinary study in an effort to design models that exhibit the newly-discovered properties, among which Watts and Strogatz's (WS) small-world network model [7] and Barabási and Albert's (BA) scale-free network model [6] are the most well-known. Enlightened by the two pioneering models [6,7], a wide variety of models has been proposed resulting in great progresses in the research of network topology [13–22]. Thanks to both the advances in network theory and the increasing amount of network data available, authors are beginning to reveal many different processes that may lead to above striking generic characteristics. It is of current interest to model complex networks with general structural features [1–4].

In this paper, on the basis of the famous deterministic fractal — Sierpinski gasket, we introduce for the first time a family of nontrivial networks, named incompatibility networks (INs). This new family of networks, can be either determinist or stochastic, are maximal planar graphs, show scale-free degree distribution, exhibit small-world effect, and display disassortative degree-degree correlations. These incompatibility networks provide a paradigm of representation for the complexity of many real systems in biological and information fields, which have been studied to a much lesser extent from the perspective of IN.

2 Network construction

To define the network, we first introduce the classical fractal, Sierpinski gasket, also known as Sierpinski triangle. This well-known fractal denoted as S_t after t generations, is constructed as follows [23,24]: start with an equilateral triangle, and denote this initial configuration as S_0. Perform a bisection of the sides forming four small copies of the original triangle, and remove the interior triangles to get S_1. Repeat this procedure recursively in the three remaining copies to obtain S_2, shown in Figure 1. In the infinite t limit, we obtain the famous Sierpinski gasket S_t, whose Hausdorff dimension is $d_f = \frac{\ln 3}{\ln 2}$ [25]. In fact, this fractal can be generalized to other dimensions and expanded to random cases [26].

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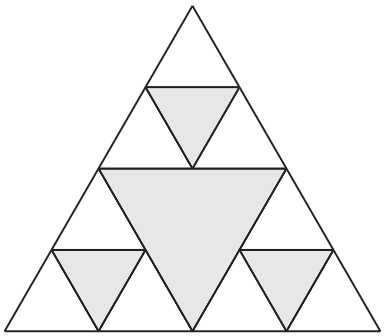

Fig. 1. The first two stages in the construction of the Sierpinski triangle.

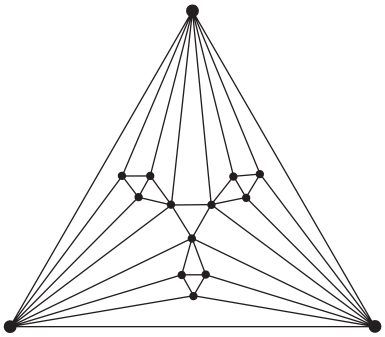

Fig. 2. The first two steps of construction of incompatibility network.

From Sierpinski gasket we can easily construct a network with sides of the removed triangles mapped to nodes and contact to edges between nodes. For uniformity, the three sides of the initial equilateral triangle of S_0 also correspond to three different nodes. Since the resulting network shown in Figure 2 is associated with contact relation, we call it an incompatibility network (IN). Analogously, one can establish a class of INs related to this family of Sierpinski fractals [26].

This introduced network representation is convenient for studying the complexity of some real systems and may have wider applicability. For instance, a similar recipe was recently adopted for investigating the navigational complexity of cities [27]; on the other hand, it is frequently used in RNA folding research [28,29]; moreover, earlier links associating INs with polymers have proven useful to the study of polymer physics [30,31], thus IN may find application in investigating the complexity of traveling salesman problems (TSP) that has been conjectured to belong to the same universality class as dense polymers [32].

3 Iterative algorithm of the network

In the construction process of the classical Sierpinski gasket, for each equilateral triangle at arbitrary generation, once we perform a bisection of its sides and remove the central down pointing triangle, three copies of it are formed. When building the network, it is equivalent that for every group of three new added nodes, three new small

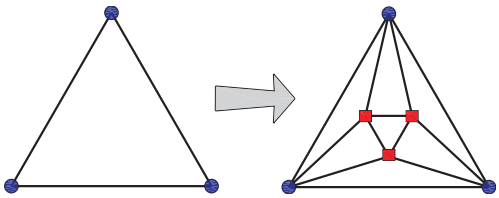

Fig. 3. (Color online) Iterative construction method for the network.

equilateral triangles are generated, each of which may create three nodes in the next generation. According to this, we can introduce a general algorithm to create the corresponding network, denoted by $H(t)$ after t generation evolutions.

The iterative algorithm for the network is as follows: for $t = 0$, $H(0)$ consists of three nodes forming a triangle. Then, we add three nodes into the original triangle. These three new nodes are linked to each other shaping a new triangle, and both ends of each edge of the new triangle are connected to a node of the original triangle. Thus we get $H(1)$, see Figure 3. For $t \geq 1$, $H(t)$ is obtained from $H(t-1)$. For each of the existing triangles of $H(t-1)$ that is created at step $t-1$ and contains only one newly emerging node at this step, we call it an active triangle. We replace each of the existing active triangles of $H(t-1)$ by the connected cluster on the right hand of Figure 3 to obtain $H(t)$. The growing process is repeated until the network reaches a desired order (node number of network). Figure 2 shows the network growing process for the first two steps.

Next we compute the order and size (number of all edges) of the network $H(t)$. Let $L_v(t)$, $L_e(t)$ and $L_\Delta(t)$ be the number of vertices, edges and active triangles created at step t, respectively. By construction (see also Fig. 3), each active triangle in $H(t-1)$ will be replaced by three active triangles in $H(t)$. Thus, it is not difficult to find the following relation: $L_\Delta(t) = 3\,L_\Delta(t-1)$. Since $L_\Delta(0) = 1$, we have $L_\Delta(t) = 3^t$.

Note that each active triangle in $H(t-1)$ will lead to an addition of three new nodes and nine new edges at step t, then one can easily obtain the following relations: $L_v(t) = 3\,L_\Delta(t-1) = 3^t$, and $L_e(t) = 9\,L_\Delta(t-1) = 3^{t+1}$ for arbitrary $t > 0$. From these results, we can compute the order and size of the network. The total number of vertices N_t and edges E_t present at step t is

$$N_t = \sum_{t_i=0}^{t} L_v(t_i) = \frac{3^{t+1}+3}{2} \tag{1}$$

and

$$E_t = \sum_{t_i=0}^{t} L_e(t_i) = \frac{3^{t+2}-3}{2}, \tag{2}$$

respectively. So for large t, the average degree $\overline{k}_t = \frac{2E_t}{N_t}$ is approximately 6, which shows the network is sparse as most real systems.

From equations (1) and (2), we have $E_t = 3N_t - 6$. In addition, by the very construction of the network, it is

obvious that arbitrary two edges in the network never cross each other. Thus our network is a maximal planar network (or graph) [33], which is similar to some previously studied networks [34–38].

4 Topological properties of the network

Now we study some relevant characteristics of the network $H(t)$, focusing on degree distribution, clustering coefficient, average path length, and degree correlations.

4.1 Degree distribution

When a new node i is added to the network at step t_i ($t_i \geq 1$), it has a degree of 4. Let $L_\Delta(i,t)$ be the number of active triangles at step t that will create new nodes connected to the node i at step $t+1$. Then at step t_i, $L_\Delta(i,t_i)=1$. From the iterative generation process of the network, one can see that at any subsequent step each two new neighbors of i generate two new active triangles involving i, and one of its existing active triangles is deactivated simultaneously. We define $k_i(t)$ as the degree of node i at time t, then the relation between $k_i(t)$ and $L_\Delta(i,t)$ satisfies:

$$L_\Delta(i,t)=\frac{k_i(t)-2}{2}. \tag{3}$$

Now we compute $L_\Delta(i,t)$. By construction, $L_\Delta(i,t) = 2\,L_\Delta(i,t-1)$. Considering the initial condition $L_\Delta(i,t_i)=1$, we can derive $L_\Delta(i,t)=2^{t-t_i}$. Then at time t, the degree of vertex i becomes

$$k_i(t)=2^{t-t_i+1}+2. \tag{4}$$

It should be mentioned that the initial three vertices created at step 0 have a little different evolution process from other ones. We can easily obtain that at step t, the degree of one of the initial three vertices and the number of active triangles involving it are 2^{t+1} and 2^t, respectively.

Equation (4) shows that the degree spectrum of the network is discrete. It follows that the cumulative degree distribution [3] is given by

$$P_{\rm cum}(k)=\sum_{\tau\leq t_i}\frac{L_v(\tau)}{N_t}=\frac{3^{t_i+1}+3}{3^{t+1}+3}. \tag{5}$$

Substituting for t_i in this expression using $t_i = t+1-\frac{\ln(k-2)}{\ln 2}$ gives

$$P_{\rm cum}(k)=\frac{3^{t+1}(k-2)^{-(\ln 3/\ln 2)}+3}{3^{t+1}+3}. \tag{6}$$

When t is large enough, one can obtain

$$P_{\rm cum}(k)=(k-2)^{-(\ln 3/\ln 2)}. \tag{7}$$

So the degree distribution follows a power law form with the exponent $\gamma=1+\frac{\ln 3}{\ln 2}$. Note that the same degree exponent has been obtained in some other deterministic models such as Apollonian networks [34,35,38] and pseudofractal scale-free web [39–41].

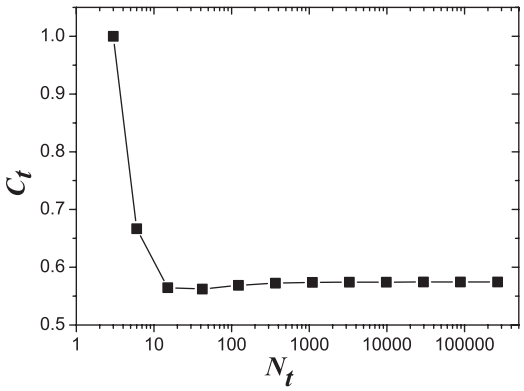

Fig. 4. Semilogarithmic plot of average clustering coefficient C_t versus network order N_t.

4.2 Clustering coefficient

The clustering coefficient [7] of a node i with degree k_i is given by $C_i = 2e_i/[k_i(k_i-1)]$, where e_i is the number of existing edges among the k_i neighbors. Using the connection rules, it is straightforward to calculate analytically the clustering coefficient $C(k)$ for a single node with degree k. When a node is added into the network, both k_i and e_i are 4. At each subsequent discrete time step, each of its active triangles increases both k_i and e_i by 2 and 3, respectively. Thus, $e_i = 4+\frac{3}{2}(k_i-4)$ for all nodes at all steps. So there is a one-to-one correspondence between the clustering coefficient of a node and its degree. For a node of degree k, we have

$$C(k)=\frac{2\left[4+\frac{3}{2}(k-4)\right]}{k(k-1)}=\frac{4}{k}-\frac{1}{k-1}, \tag{8}$$

which is inversely proportional to k in the limit of large k. The scaling of $C(k)\sim k^{-1}$ has been observed in many real-world scale-free networks [42].

After t generation evolutions, the clustering coefficient C_t of the network, defined as the average of $C_i^{'}s$ over all nodes in the network, is given by

$$C_t=\frac{1}{N_t}\sum_{r=0}^{t}\left[\left(\frac{4}{K_r}-\frac{1}{K_r-1}\right)L_v(r)\right], \tag{9}$$

where the sum runs over all the nodes and K_r is the degree of those nodes created at step r, which is given by equation (4). In the limit of large N_t, equation (9) converges to a nonzero value $C=0.5745$, as shown in Figure 4. Therefore, the network is highly clustered.

4.3 Average path length

Shortest paths play an important role both in the transport and communication within a network and in the characterization of the internal structure of the network. We represent all the shortest path lengths of $H(t)$ as a matrix in which the entry g_{uv} is the geodesic path from node u to

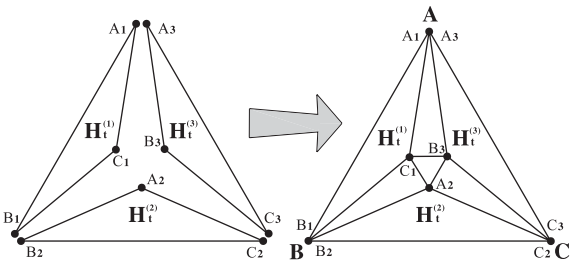

Fig. 5. Alternative construction of Sierpinksi network. H_{t+1} on the right may obtained by the juxtaposition of three copies of H_t denoted as $H_t^{(\varphi)}$ $(\varphi = 1, 2, 3)$.

node v, where geodesic path is one of the paths connecting two nodes with minimum length. A measure of the typical separation between two nodes in $H(t)$ is given by the average path length $\bar{d}_t$, also known as characteristic path length, defined as the mean of geodesic lengths over all couples of nodes. Thus

$$\bar{d}_t = \frac{D_t}{N_t(N_t-1)/2}, \tag{10}$$

where D_t denotes the sum of the total distances between two nodes over all pairs, that is

$$D_t = \sum_{u,v \in H_t} g_{u,v}\,. \tag{11}$$

We can exactly calculate $\bar{d}_t$. As shown in Figure 5, in addition to the above-mentioned iterative algorithm, $H(t+1)$ may be obtained by the juxtaposition of three copies of H_t, which we label $H_t^{(\varphi)}$, $\varphi = 1, 2, 3$. Thus, network $H(t)$ has a self-similar structure [43] which allows one to analytically compute the average path length $\bar{d}_t$ of $H(t)$. Then the total distance D_{t+1} satisfies the recursion relation $D_{t+1} = 3\,D_t + \Theta_t$, where Θ_t is the sum over all shortest paths whose endpoints are not in the same H_t branch. The solution of D_t is

$$D_t = 3^{t-1}\,D_1 + \sum_{m=1}^{t-1} \left(3^{t-m-1}\Theta_m\right). \tag{12}$$

The paths that contribute to Θ_t must all go through at least one of the six edge nodes (i.e. A (A_1, A_3), B (B_1, B_2), C (C_2, C_3), A_2, B_3, and C_1). To calculate Θ_t, we classify the interior nodes (excluding A, B, and C themselves) in H_t into six different sets P_1, P_2, $\cdots$, P_6, which are shown in Figure 6. Denote the shortest path lengths from v to A, B, C as x, y, and z, the classification of any node v is $P_1 : x < y = z$, $P_2 : y < x = z$, $P_3 : z < x = y$, $P_4 : x = z < y$, $P_5 : x = y < z$, and $P_6 : y = z < x$. Denote N_{t,P_r} the number of nodes in network H_t belonging to P_r, d_{t,P_r} the sum of f_v over all nodes belonging to Class P_r in H_t, where $f_v = \mathtt{min}\{x, y, z\}$ for any node v in H_t. Then

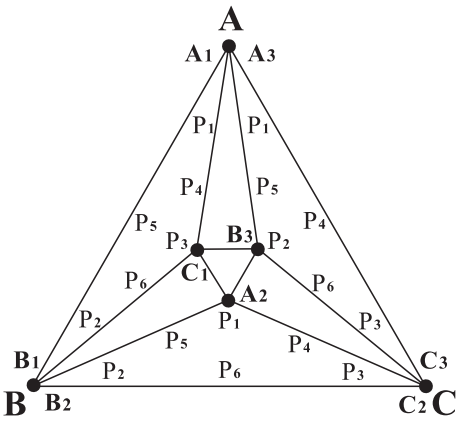

Fig. 6. Illustration of the classification of nodes in $H_t^{(1)}$, $H_t^{(2)}$, and $H_t^{(3)}$.

Θ_t can be expressed as [44]

$$\Theta_t = 3\sum_{i=1}^{6}\sum_{j=1}^{6}\left(N_{t-1,P_j}\,d_{t-1,P_i} + N_{t-1,P_i}\,d_{t-1,P_j} + N_{t-1,P_i}\,N_{t-1,P_j}\delta_{ij}\right) + 9\sum_{i=1}^{6} d_{t-1,P_i} + 18\,N_{t-1,P_1} + 9\,N_{t-1,P_4} + 9\,N_{t-1} - 18, \tag{13}$$

where δ_{ij} may equal to either 0 or 1, depending on whether the paths between two nodes in different $H(t-1)$ branches meet at one or two edge nodes. In equation (13), we have used the following equivalent relations: $N_{t,P_1} = N_{t,P_2} = N_{t,P_3}$, $N_{t,P_4} = N_{t,P_5} = N_{t,P_6}$, $d_{t,P_1} = d_{t,P_2} = d_{t,P_3}$, and $d_{t,P_4} = d_{t,P_5} = d_{t,P_6}$, which are easily obtained according to the network construction.

Clearly, $N_t = 3\,N_{t,P_1} + 3\,N_{t,P_4} + 3$. When merging three H_t into a H_{t+1}, one can obtain the recursive relations (see Fig. 6):

$$\begin{cases} N_{t+1,P_1} = 2\,N_{t,P_1} + 2\,N_{t,P_4}, \\ N_{t+1,P_4} = N_{t,P_1} + N_{t,P_4} + 1, \end{cases} \tag{14}$$

and

$$\begin{cases} d_{t+1,P_1} = \quad 2\,d_{t,P_1} + 2\,d_{t,P_4}, \\ d_{t+1,P_4} = d_{t,P_1} + d_{t,P_4} + N_{t,P_1} + 1. \end{cases} \tag{15}$$

Considering the initial conditions $N_{1,P_1} = 0$, $N_{1,P_4} = 1$, $d_{1,P_1} = 0$, and $d_{1,P_4} = 1$, equations (14) and (15) are solved inductively to obtain

$$\begin{cases} N_{t,P_1} = 3^{t-1} - 1, \\ N_{t,P_4} = \dfrac{1}{6}(3 + 3^t), \end{cases} \tag{16}$$

and

$$\begin{cases} d_{t,P_1} = \quad 2 \times 3^{t-3}(1+t), \\ d_{t,P_4} = 3^{t-2} + 3^{t-3}(1+t), \end{cases} \tag{17}$$

which hold for all $t \geq 2$.

Combine all the prior equations, the exact solution of APL can be obtained as

$$\bar{d}_t = \frac{27 + 22 \times 3^{1+t} + 91 \times 9^t + 4 \times 3^{1+t}(3^{1+t} - 2)t}{27 + 4 \times 3^{3+t} + 9^{2+t}}. \tag{18}$$

This analytic result has been successfully checked against numerical calculations for different network order up to $t = 9$ which corresponds to $N_{10} = 29\,526$. From equation (18), it is clear that the scaling of APL in the infinite limit of network order is $\bar{d}_t \propto \ln N_t$. This logarithmic scaling of d_t with network size N_t, together with the large clustering coefficient obtained in the preceding subsection, shows that the considered graph has a small-world effect.

4.4 Degree correlations

Degree correlation is a particularly interesting subject in the field of network science [45–50], because it can give rise to some interesting network structure effects. An interesting quantity related to degree correlations is the average degree of the nearest neighbors for nodes with degree k, denoted as $k_{\rm nn}(k)$, which is a function of node degree k [46,47]. When $k_{\rm nn}(k)$ increases with k, it means that nodes have a tendency to connect to nodes with a similar or larger degree. In this case the network is defined as assortative [48,49]. In contrast, if $k_{\rm nn}(k)$ is decreasing with k, which implies that nodes of large degree are likely to have near neighbors with small degree, then the network is said to be disassortative. If correlations are absent, $k_{\rm nn}(k) = {\rm const}$.

We can exactly calculate $k_{\rm nn}$ for the networks using equations (3) and (4) to work out how many links are made at a particular step to nodes with a particular degree. By construction, we have the following expression [51,52]

$$k_{\rm nn}(k) = \frac{1}{L_v(t_i)k(t_i,t)}\left(\sum_{t_i'=0}^{t_i'=t_i-1} 2L_v(t_i')L_\Delta(t_i',t_i-1)k(t_i',t) + \sum_{t_i'=t_i+1}^{t_i'=t} 2L_v(t_i)L_\Delta(t_i,t_i'-1)k(t_i',t)\right) + 2 \tag{19}$$

for $k = 2^{t-t_i+1} + 2$ and where $k(t_i,t)$ is the degree of a node i at time t that was born at step t_i. Here the first sum on the right-hand side accounts for the links made to nodes with larger degree (i.e. $t_i' < t_i$) when the node was generated at t_i. The second sum describes the links made to the current smallest degree nodes at each step $t_i' > t_i$. The last term 2 accounts for the two links connected to two simultaneously emerging nodes. After some algebraic manipulations, we can rewrite equation (19) in term of k to obtain

$$k_{\rm nn}(k) = \frac{\left[8\left(\frac{4}{3}\right)^t - 4\left(\frac{2}{3}\right)^t\right](k-2)^{\ln 3/\ln 2}}{k(k-2)} + \frac{6}{k} + \left(1 - \frac{2}{k}\right)\frac{\ln(k-2)}{\ln 2} - 1. \tag{20}$$

Therefore, for large t and k, $k_{\rm nn}(k)$ is approximately a power law function of k as $k_{\rm nn}(k) \sim k^{-\omega}$ with $\omega = 2 - \frac{\ln 3}{\ln 2} \simeq 0.415$, which shows that the network is disassortative. Note that $k_{\rm nn}(k)$ of the Internet exhibit a similar power-law scaling with exponent $\omega = 0.5$ [46].

5 Conclusion

In conclusion, based on the of Sierpinski gasket, we have introduced a class of incompatibility networks. According to the network construction we have proposed a generative algorithm creating the networks. We have shown that the networks share some important properties of real systems: power-law degree distribution, small-world effect, and negative degree correlations. In addition, the networks are maximal planar graphs, which may be helpful for designing printed circuits [33].

The connection between Sierpinski fractals and incompatibility networks investigated here could reveal important also in other related problems. One can use a similar mapping from road map of cities to the INs to quantify the information associated with locating specific addresses [27]. Another possible connection is to the TSP, the corresponding IN could serve as a checkpoint for the conjectured correspondence with dense polymers [32]. One can also establish link from a globular biopolymer, e.g. a folded protein, to an IN to study the complexity of real biological systems [31].

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