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Network Evolution Model with Preferential Attachment at Triadic Formation Step

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Abstract: It is recognized that most real systems and networks exhibit a much higher clustering with comparison to a random null model, which can be explained by a higher probability of the triad formation—a pair of nodes with a mutual neighbor have a greater possibility of having a link between them. To catch the more substantial clustering of real-world networks, the model based on the triadic closure mechanism was introduced by P. Holme and B. J. Kim in 2002. It includes a "triad formation step" in which a newly added node links both to a preferentially chosen node and to its *randomly* chosen neighbor, therefore forming a triad. In this study, we propose a new model of network evolution in which the triad formation mechanism is essentially changed in comparison to the model of P. Holme and B. J. Kim. In our proposed model, the second node is also chosen *preferentially*, i.e., the probability of its selection is proportional to its degree with respect to the sum of the degrees of the neighbors of the first selected node. The main goal of this paper is to study the properties of networks generated by this model. Using both analytical and empirical methods, we show that the networks are scale-free with power-law degree distributions, but their exponent γ is tunable which is distinguishable from the networks generated by the model of P. Holme and B. J. Kim. Moreover, we show that the degree dynamics of individual nodes are described by a power law.

Keywords: triadic closure; social networks; preferential attachment; complex networks; high clustering; growth model; community structure; edge clustering

MSC: 05C82; 05C90; 90B15; 91D10; 37M10

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1. Introduction

The structure and properties of many real networks cannot be meticulously captured by random graph models that cannot generate networks with complex cluster and community patterns. In social graphs, a simple yet realistic mechanism known as triadic closure is considered to be an important factor in producing high clustering and complex community structures. Triadic closure refers to the phenomenon where new links are formed between nodes that have a common neighbor, resulting in the closing of triads. This concept, first introduced by Rapoport in 1953 [1], highlights the tendency of real networks to exhibit a much higher likeliness of forming links between pairs of nodes that share a mutual neighbor compared to a random null model.

By leveraging the triadic closure effect, researchers and analysts can gain valuable insights into the organization and dynamics of complex networks. This knowledge can be utilized to facilitate the identification and analysis of communities within the network, enabling a better understanding of the collective behavior and interactions of its constituents. Furthermore, the study of triadic closure can inform the development of strategies for community detection, network growth modeling, and targeted interventions aimed at fostering collaboration and cooperation within these networks.

The triadic closure (TC) model developed in the study [2] uses the growth and preferential attachment mechanisms that are core to the Barabási–Albert (BA) model [3]. Moreover, the authors of [2] showed that the TC model generates networks that have a scale-free structure and whose degree distributions follow a power law. However, the TC model offers an additional feature that induces higher clustering compared to the BA model. This makes the networks obtained using the triadic closure model more similar to real social networks in terms of their clustering properties.

In the triadic closure model, when a new vertex is attached to the graph, it forms a link with an present vertex chosen based on preferential attachment. Preferential attachment is a mechanism where the probability of selecting a node to form a link with is proportional to its degree (i.e., the number of connections it already has).

In addition to the preferential attachment mechanism, the new node also forms other $m-1$ links. The probability of these links being formed with an existing node is determined by a parameter p. If $p=1$, then the new node joins a randomly selected neighbor of the first chosen node. This process, known as triad formation, strengthens the clustering in the network. On the other hand, if $p=0$, then the new node simply forms links based on the preferential attachment mechanism.

The triadic closure model allows one to generate graphs with different average clustering by changing the value of p. On the other hand, the resulting degree distributions in the networks generated by the TC model are exactly the same as in the BA model, following a power law with $\gamma=-3$ and do not depends on the value of p.

In the model proposed in [2], when a triad is formed, a new edge is attached to a random neighbor of a node, chosen *uniformly* from the nodes that were already selected in the previous step using the *preferential* attachment rule. However, in some complex networks, it appears that the selection of the second link is also performed using the *preferential* attachment rule, as follows:

- In social networks, when a person becomes a friend with someone, they also tend to be a friend of the most popular individual in the group. Most social networks are clustered, so dealing with a large volume of emerging new information in various types of networks requires selecting relevant information from the ever-increasing data pool. This significantly increases the costs of data selection. Due to the difficulty of making choices, network participants will rely on the opinions of experts as the most authoritative members of these networks;
- In citation networks, when an article cites a paper, it tends to cite the most cited items from the paper references as well;
- If an Internet page links to an existing page, there are great chances that it also links to the most popular pages to which the existing page is pointed to;
- In criminal structures: the tendency of two individuals to commit a crime together if they have a common accomplice.

In this paper, we present an enhancement to the triadic closure model by incorporating preferential selection of nodes during the triadic formation step. Unlike the basic model, where nodes are chosen uniformly, our proposed model allows for selective node choice. However, the dynamic nature of such models poses challenges in obtaining analytical descriptions and accurately identifying the network features that can be directly attributed to triadic closure.

To assess the effectiveness of our enhanced model, we conducted both analytical and empirical investigations into the geometric properties of the networks generated. Our findings demonstrate that a network simulated by the proposed model is scale-free, and is characterized by a power-law degree distribution. However, the exponent of the power-law, denoted as γ, can be adjusted or tuned in our model.

This distinction highlights the flexibility and versatility of our enhanced triadic closure model, as it allows for fine-grained control over the degree distribution exponent. Such control over the degree distribution exponent can have significant implications for network analysis and understanding real-world networks.

The paper is organized as follows. Section 2 presents a short review of recent studies on the topic. In Section 3, we introduce an extension of the triadic closure model based on the model of P. Holme and B. J. Kim. Moreover, in Section 3.2 we study the degree dynamics of a node in the networks generated by the extended triadic closure model. Finally, in Section 4 we show that the extended triadic closure model induces scale-free networks. Moreover, we show that the proposed model generates networks with tunable scale-free behavior (with its exponent γ depending on p and m), which differs from the behavior of the BA or the triadic closure models. The model under consideration generates networks with different levels of power-law exponent as well as clustering by varying p and m. Note that networks simulated by the triadic closure model exhibit a power-law degree distribution with exponent $\gamma = -3$ for any $0 \leq p \leq 1$.

2. Related Studies

Triadic closure is widely acknowledged as an essential mechanism in the formation of structural patterns in social networks. Numerous models of network formation have been proposed that incorporate triadic closure, typically as part of a growth or rewiring process.

This phenomenon is particularly pronounced in social networks, where individuals often tend to connect with others who are already connected to their acquaintances. Many studies show that this process of triadic closure leads to the formation of tightly-knit communities within the larger network, characterized by strong social ties and frequent interactions, including the following:

- The patterns of the temporal behavior of triads in social networks have been studied in paper [4]. The authors state that triads are common in social groups and propose a probabilistic factor graph model that captures the dynamic information in the triadic closure process.
- Paper [5] states that the community structure is an important property of complex social networks, while the triadic closure naturally implies the presence of community structure. The authors use a fitness-based link attractivity defined for a vertex to obtain a phase transition in which communities disappear.
- The study [6] deals with the problem of community formation in online social networks. The paper focuses on the triad formation mechanism and uses data sets based on a large microblogging network. The study shows that the triadic closure depends on user demographics, network characteristics, and social properties. The authors propose a a probabilistic graphical model to predict the triad formation in dynamic networks.
- The formation of social triads in social groups has been analyzed in paper [7]. The author conducted an empirical study based on data sets of two real social complex networks and they propose a method to predict inferring triadic tie strength dynamics.

- The paper [8] deals with the problem of predicting missing links in the complex network using triadic closure theory. The work is aimed at quantifying the common neighbor influence on creating the link between nodes. It is shown that the proposed algorithm a sufficient accuracy and is stable and robust. Moreover, the authors propose an ensemble link prediction algorithm which is based on some local characteristics.
- The paper [9] examines the temporal data sets taken from Flickr and Epinions. The study shows that the triad formation has a crucial role in the evolution of networks. Moreover, the authors developed a network evolution model which uses the preferential triadic closure. Numerical experiments show that the proposed model is capable in reproducing some global properties of real social networks.
- The authors of paper [10] applied Relational Event Modeling (REM) to a dataset from online discussions. The paper examines social interaction based on micro-level temporal patterns.
- The work [11] studies the effect of microstructures on the appearance of communities in networks. The authors use four community-detection approaches and three different generative network models including triadic closure.
- Paper [12] proposes local closure coefficient to quantify the phenomenon of edge clustering in real social networks. The authors show that the use of the closure coefficient may improve link prediction in real network dynamics.

However, triadic closure is not solely limited to social networks. It also manifests in other types of networks, including knowledge networks, citation networks, and research collaboration networks, among many others. These networks often demonstrate a similar propensity for establishing connections between nodes that have mutual connections, suggesting the presence of underlying community structures, including the following:

- The paper [13] proposes models of network growth in which the emergence of an edge between nodes is more likely if they have a common neighbor. Simulations have demonstrated that networks built using these models reproduce a number of features of real social networks, including high levels of clustering.
- A large group of articles is devoted to citation networks, in which, as empirical studies show, the probability of triangle formation is high. Thus, the work [14] proposes a model for the evolution of scientific citation networks. The model takes into account both the loss of relevance of articles over time and the formation of triangles.
- Another paper, [15] examines the citation network of scientific papers and proposes a stochastic model incorporating the triadic closure mechanism, statistics of links to scientific articles, as well as the dynamics of their citations. The authors substantiate the model using the example of citation dynamics for physics articles, identifying nonlinear citation dynamics, the nonlinearity of which is closely related to the network topology.
- Citation networks were also the subject of research in [16], which analyzed co-citations on the Web of Science citation dataset. The model proposed by the authors takes into account the frequency of co-occurrence of the first author, the frequency of co-occurrence of other authors, network density, as well as triadic closure in the co-citation graph. The model allows one to predict the appearance of co-authors in the co-authorship network.
- The study [17] notes that when modeling citation networks, it is necessary to take into account their high clustering. The authors propose a new model to explain the emergence of high clustering in such networks. The authors analyzed several real-life citation networks and showed that the proposed model adequately reproduces the power-law degree distribution and high clustering observed in these real-life networks.
- The authors of paper [18] look at knowledge networks and show that triadic closure and topographical closeness increase the likelihood of creating connections, but do not affect their sustainability. The authors analyze the influence of endogenous network effects and how the cognitive proximity of actors influence the process of cluster creation.

- The study [19] notes that the clustering coefficient does not reflect common interpersonal interpretations of triadic closure. In this regard, the study introduces a measure of triadic closure, which is used in the study of three empirical social networks.
- Note that in some real networks the process of triangle formation is counterintuitive. The paper [20] examines the network of co-inventors and empirically finds that two inventors are less likely to form a first research partnership if they have mutual partners.

Many recent studies examined the triadic closure mechanism (the tendency for individuals with a common friend to become friends themselves) with respect to homophily in complex networks (the habit for individuals to build connections with others who are similar to them), including the following:

- The paper [21] investigates the formation and nature of social networks in the context of Social Internet of Things (SIoT). The authors utilizes large datasets, including anonymized call detail records, to analyze triadic closure patterns and homophily in homophilic social networks. It proposes three social triad classes and explores the correlation between triads and homophily. The study concludes that there is a positive connection between homophily and a specific social triad class. Overall, this research contributes to the understanding of social networks in the SIoT context.
- The study [22] explores the concept of homophily and its impact on social segregation. The authors challenge the belief that triadic closure and homophily work together and demonstrate through network analysis and empirical investigation that triadic closure can actually help reduce segregation. The findings are supported by real-world networks, strengthening the validity of the study. The authors suggest practical interventions to alleviate segregation in settings where triadic closure and homophily interact, as well as insights for designing interventions in online communities. Overall, this work makes a significant contribution to understanding social segregation and offers potential solutions.
- The paper [23] examines how homophily (common interests) and triadic closure (mutual connections) affect the reciprocation benefit for content providers in social media. Using data from YouTube video providers, the researchers find that reciprocation is generally beneficial for the initiator, but content similarity and common ties can reduce the growth in subscribers. They also discover a positive interaction effect between content similarity and common ties. Overall, these findings provide practical implications for content providers and social media platforms seeking to optimize reciprocal promotion. The study sheds light on the complex dynamics of reciprocation in social media content promotion.
- The study [24] examines the relationship between triadic closure and choice homophily, in social networks. Using a dynamic model, the researchers demonstrate that these factors contribute to induced homophily in real-world social networks. They estimate the degree to which triadic closure amplifies observed homophily in friendship and communication networks, and show that this augmentation can bring to the core-periphery structure of networks and the persistence of homophilic constraints. The study also highlights that even small individual biases can have significant network-level effects, such as segregation or the dominance of a core group. This paper highlights the importance of considering the broader dynamics of society when studying individual-level mechanisms in social networks.

The article [25] analyzes the friendship paradox as a property of triadic closure in networks, and some works explore empirical studies on triadic closure in real social networks in the context of innovation [20], the acting environment [26], as well as the criminal world [27], to simulate real processes of collaboration development.

Models of complex networks using the triadic closure mechanism studied by various researchers, have shown that their properties vary from those of the well-known BA and TC models (the Barabási–Albert (BA) model and the triadic closure (TC) model), as follows:

- A static triadic closure (STC) model has been proposed in [28] for generating growth clustered networks. The author show that the proposed model is quite realistic and simple enough to obtain some of properties analytically.
- The authors of paper [29] introduce an extension of the triadic closure model in which the number of attached links selected randomly. They show that the model simulates more realistically the dynamics of generated networks.
- An interesting model that captures the dissimilarities between the incoming and outgoing network degrees has been analyzed in [30]. The model uses three different mechanisms including directed triadic closure. The authors empirically validate the model on real datasets.
- A nonlinear coevolving voter model with triadic closure local rewiring has been developed and studied in [31]. The model is capable of explaining some properties of real adaptive social networks such as the reproduction of isolated parts and a high clustering.
- The work [32] introduce a hierarchy of network evolution models based on triadic closure mechanism. The author uses a chemical kinetics framework to show that models reproduce an apparent metastability property of the microscale system.
- The authors of paper [33] propose a Triangle Generalized Preferential Attachment Model and investigate the clustering properties of simulated networks. They show that this model generate networks with a power law degree distribution.

The works [34–38] present heuristic algorithms, e.g., for maximizing influence in graphs with a triadic closure mechanism (TC-IM).

3. The Extended Triadic Closure Model

3.1. The Model Description

The triadic closure model developed by P. Holme and B. J. Kim [2] is based on the well-known Barabási–Albert model [3] (the preferential attachment model). In this section, we describe and study a development of triadic closure model proposed by P. Holme and B. J. Kim [2]. The authors of [39] develop a model describing the growth of a network, in which one node and two links are added at each iteration, and this node is connected by two links with neighboring nodes. In this section, we will extend this model in two ways. First, we will add $m \geq 2$ links at each iteration. Secondly, we will form a triad with the probability p (as it is in the classical triadic closure model).

In this model, when a new vertex is attached to the graph, it joins an existing node with a probability depending on the degree of that node, which is called the *preferential attachment* mechanism. Next, the remaining $m-1$ edges of the new node can be established with a certain neighbor of that node with probability p (so-called *triad formation*), or with probability $1-p$, the new node can connect with any node in the network selected using preferential attachment rule.

At each iteration one node appears and is added to the network. For simplicity, we will use integer i to mark the node that appeared at the corresponding iteration i.

Let $N(t)$ and $M(t)$ be the number of nodes and the number of edges at iteration t, respectively.

Denote $k_j(t)$ the degree of node j at iteration t. Let

$$p(j,i) = \begin{cases} 1, & \text{if the link } (j,i) \text{ exists,} \\ 0, & \text{otherwise.} \end{cases}$$

Then, we have

$$k_i(t) = \sum_{j=1}^{N(t)} p(j,i).$$

Let $s_i(t)$ denote the total degrees for all neighbors of node i at iteration t:

$$s_i(t) = \sum_{j=1}^{N(t)} p(i,j)k_j(t). \quad (1)$$

In the network evolution model, the process develops step by step as follows:

1. (*Growth*) At every iteration t, one new vertex t is attached;
2. At each stage, the network is replenished with m new connections, and each new node t joins m existing nodes, taking into account the following rules:
   (a) (*Preferential attachment*)
   Node t links to one of the existing nodes i of the network with a probability depending on the degree of the node $k_i(t)$;
   (b) Each of the remaining $m-1$ edges of the new node t is established as follows:
   - *(b1)* (*Triad formation*)
     With probability p, new node t is linked to one of the neighbors j of node i selected at the previous stage, proportional to the degree of the vertex $k_j(t)$. Therefore, the probability of choosing neighbor j of node i is $p\frac{k_j(t)}{s_i(t)}$, where $s_i(t)$ is defined in Equation (1).
   - *(b2)* With probability $1-p$, a link is established with one of the network nodes s (not necessarily adjacent to node i) with a probability proportional to the degree of this node $k_s(t)$.

The proposed model is extension of the growth network model presented in paper [39]; if we take $m=2$ then we obtain the model studied in [39] as a particular case of our model.

3.2. Degree Dynamics

In this model, every node i in the network has the possibility to increase the number of its links, i.e., its degree, at each iteration. This can happen in three different ways: at steps 2(a), 2(b1), and 2(b2).

When a new node is added to the network, it connects to one of the existing nodes. In step 2(a), the probability of choosing a node of degree k at time t is

$$\frac{k}{\sum_{j=1}^{N(t)} k_j(t)} = \frac{k}{2M(t)}, \quad (2)$$

where $N(t)$ denotes the number of nodes in the network, and $M(t)$ is the number of links at time t. It is clear that $N(t) = N_0 + (t-1)$ and $M(t) = M_0 + 2m(t-1)$, where N_0 and M_0 are the numbers of nodes and links of the initial graph (before the first iteration), respectively.

If we consider the degree k_i as a continuous quantity that represents the average of a set of random growth processes, as well as the rate at which node i acquires new connections as a result of new nodes joining it at iteration t involving steps 2(a), 2(b1), and 2(b2), then these processes will correspond to a certain equation, where $p_a(i)$, $p_{b1}(i)$, and $p_{b2}(i)$—the probability of choosing node i at the corresponding steps.

If we represent the degree k_i of node i as a continuous value, which is the average value for a set of random growth processes, and also take into account the rate at which node i acquires new links due to the addition of new nodes to it at iteration t, including steps 2(a), 2(b1), and 2(b2), then we can write the following equation

$$\frac{dk_i(t)}{dt} = p_a(i) + p_{b1}(i) + p_{b2}(i), \quad (3)$$

in which $p_a(i)$, $p_{b1}(i)$, and $p_{b2}(i)$ represent the probabilities of choosing node i at the corresponding steps. We obtain

$$p_a(i) = \frac{k_i(t)}{2M(t)} \sim \frac{k_i(t)}{2mt}. \quad (4)$$

Let $\gamma_i(t)$ be defined as follows:

$$\gamma_i(t) := \sum_{j=1}^{N(t)} p(j,i) \frac{k_j(t)}{s_j(t)}, \quad (5)$$

where $s_j(t)$ is defined in Equation (1).

To find the probability that vertex i is chosen at step 2(b1) we should calculate the sum (taken over all neighbors j for node i) each term of which is the multiplication of the following:

- The expectation of picking node j at step 2(a), which is equal to $\frac{k_j(t)}{2M(t)}$;
- The product of the number of trials $m-1$ and the expectation of triad formation p;
- The probability of picking vertex i among $k_j(t)$ neighboring nodes of vertex j, which is equal to $\frac{k_i(t)}{s_j(t)}$.

Thus, we obtain

$$p_{b1}(i) = p(m-1) \sum_{j=1}^{N(t)} p(j,i) \frac{k_j(t)}{2M(t)} \frac{k_i(t)}{s_j(t)} =$$
$$p(m-1) \frac{k_i(t)}{2M(t)} \sum_{j=1}^{N(t)} p(j,i) \frac{k_j(t)}{s_j(t)} \sim p(m-1) \frac{k_i(t)}{2mt} \gamma_i(t), \quad (6)$$

where $\gamma_i(t)$ is defined in (5).

We have

$$p_{b2}(i) = (1-p)(m-1) \frac{k_i(t)}{2M(t)} \sim (1-p)(m-1) \frac{k_i(t)}{2mt}. \quad (7)$$

It follows from (3), (4), (6), and (7) that $\bar{k}_i(t) := \mathbb{E}(k_i(t))$ satisfies

$$\frac{d\bar{k}_i(t)}{dt} = \left(1 + p(m-1)\gamma_i(t) + (1-p)(m-1)\right) \frac{\bar{k}_i(t)}{2mt}. \quad (8)$$

If we integrate Equation (8), we have the following dynamics for large t:

$$\bar{k}_i(t) \sim c \left(\frac{t}{i}\right)^{\frac{1+(1-p)(m-1)}{2m}} \exp\left(\frac{p(m-1)}{2m} \int \frac{\gamma_i(t)}{t} dt\right), \quad (9)$$

where c is a constant satisfying the initial condition $k_i(i) = m$.

Equation (9) shows the expected temporal trajectory for the degree of an individual node i. If $m = 2$ and $p = 1$, then we obtain the dynamics (11) of the simple model described in paper [39]. The exponents β_i have disparate values, which is completely different for the Barabási–Albert model.

Using simulations we will demonstrate that the trajectory of the expected degree for node i can be represented by a power law with exponent β_i that depends on i:

$$\bar{k}_i(t) \sim c\left(\frac{t}{i}\right)^{\beta_i}. \tag{10}$$

A complete graph of five vertices was taken as an initial graph. This number of nodes in the initial graph is sufficient for the first iteration, since we take as $m = 5$ as the amount of edges added at each iteration. Then 200,000 iterations of the proposed triadic closure model were applied to the initial graph. Thus, in each experiment a graph of size 200,000 was constructed using the triadic closure mode with the preferential attachment at triadic formation step (as it is described in Section 3.1).

At certain iterations of the graph evolution, the values of the degrees for four fixed vertices were calculated as $i = 2$ (the vertex from the initial complete graph), and $i = 10, 50, 100$.

We took $m = 5$ at the experiments. The probability p of triad formation was specified by the three different model parameters $p = 0.75$, $p = 0.5$, and $p = 0.25$. For each of chosen values of m and p we carried out 100 experiments. Thus, we obtained the values of $k_i^{[j]}(t)$ and the degree of node $i = 2, 10, 50, 100$ at iteration $t = 1, \ldots, 2 \cdot 10^5$ obtained in simulation $j = 1, \ldots, 100$.

Then, the degrees of vertices were averaged over the 100 simulations at fixed iterations of graph construction; i.e., we calculate

$$\bar{k}_i(t) = \frac{1}{100}\sum_{j=1}^{100} k_i^{[j]}(t).$$

The resulting dynamics of vertex degrees averaged over 100 simulated graphs are presented in Figure 1a,b ($p = 0.75$), Figure 1c,d ($p = 0.5$)), and Figure 1e,f ($p = 0.25$) .

Model-based network simulations show that the temporal behavior of the degree of each individual node is not the same for all nodes. Although it obeys a power law, its exponent depends on the iteration in which the node appears in the network. In other words, the growth of every node's degree follows a power-law, but its exponent β_i depends on i (its value is close to 1 for node $i = 2$, and β_i quickly decreases to $\frac{1+(1-p)(m-1)}{2m}$ with increasing i). Thus, the temporal behavior of node degrees in the proposed model differs significantly from the corresponding dynamics in networks constructed using the BA or TC models, for which node degree dynamics follow a power-law growth with the same exponent $\frac{1}{2}$.

Model-based network simulations show that there is a limit of $\gamma_i(t)$ as $t \to \infty$, $\gamma_i := \lim_{t\to\infty} \gamma_i(t)$. Consequently, the asymptotic behavior for large t satisfies the equation

$$k_i(t) \sim m\left(\frac{t}{i}\right)^{\frac{1+(1-p)(m-1)+p(m-1)\gamma_i}{2m}}. \tag{11}$$

Equation (11) specifies the expected degree trajectory of an individual node over time. Experiments have shown that the exponents β_i depend on the time of node appearance. It is known that in networks built using the Barabási–Albert model, the degree exponents are the same for all nodes.

Thus, the degree dynamics of an individual vertex i of the network follows the power law (10) with β_i that depends on i. The normalization condition is

$$\frac{2M}{N} = \frac{1}{N}\sum_{i=1}^{N} k_i \sim \frac{1}{t}\int_1^t m\left(\frac{t}{x}\right)^{\beta(x)} dx = 2m,$$

since the average degree over all the vertices is $\frac{2M}{N} = 2m$.

Equation (10) allows us to obtain several properties as follows:

- First, the expectation of a fixed node's degree increases as the network grows. This growth follows a power law with exponent β_i, the value of which varies for different nodes.
- Secondly, the smaller i, the higher the exponent β_i. Consequently, the growth of node degrees in this model occurs faster for nodes that appear in the early stages of the network's existence. As a result, the hubs in this model are larger compared to BA or TC models.

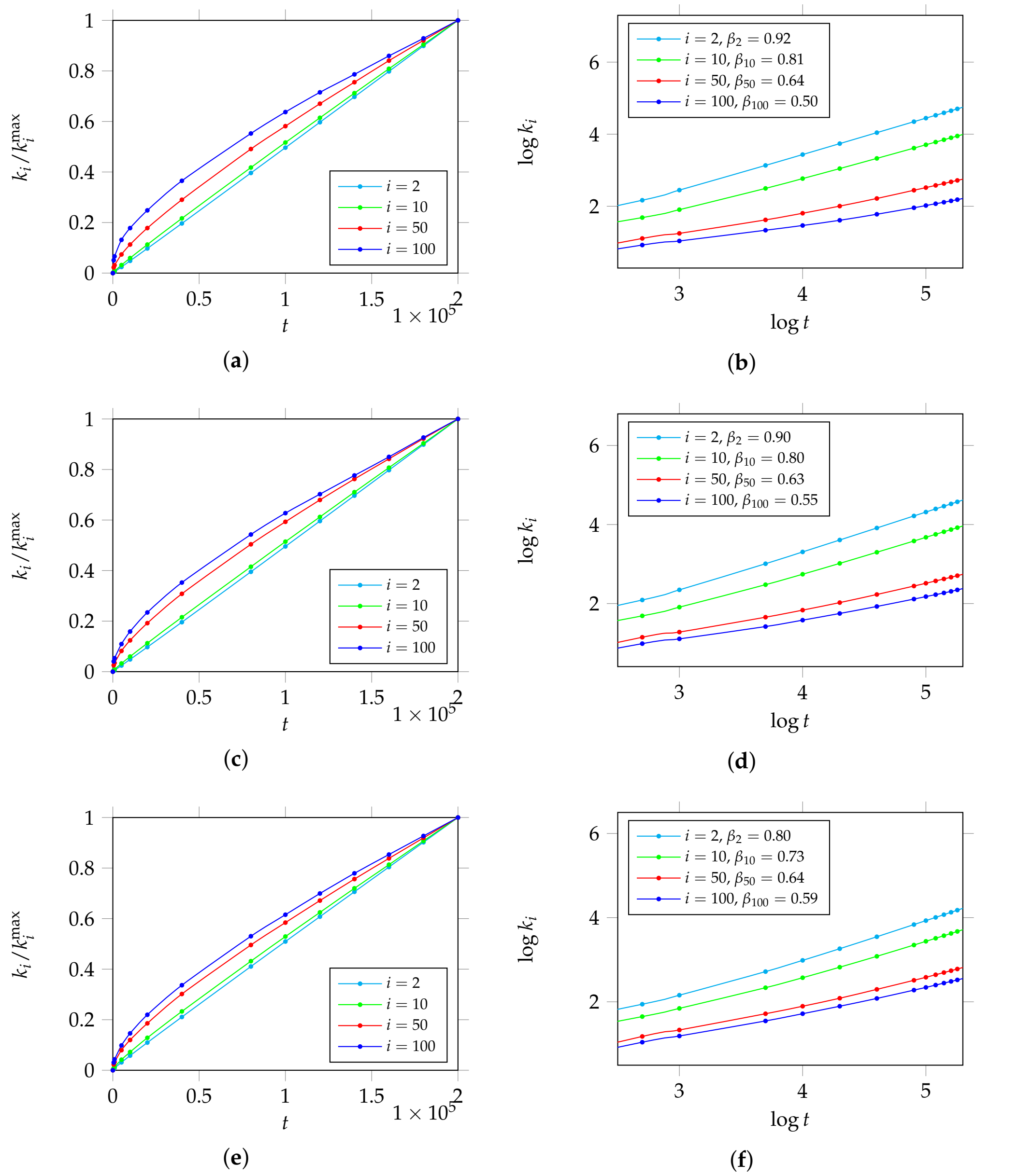

Figure 1. Degree dynamics of nodes $i = 2, 10, 50, 100$ (**a**) $p = 0.75$, (**c**) $p = 0.5$ and (**e**) $p = 0.25$. We normalized the data to a common scale by dividing each value by the maximum degree of a node. We then plotted the trajectories of the degrees for different nodes $i = 2, 5, 10, 50, 100$ obtained for (**b**) $p = 0.75$, (**d**) $p = 0.5$, and (**f**) $p = 0.25$ in the log–log scale. For each log–log plot, we also calculated the slope using the linear regression method. The results are averaged over 100 independent runs for graphs of the same size where $N = 200{,}000$.

3.3. Additional Properties of γ_i's

After t iterations, the algorithm described in Section 3.1 with parameters m and p produces a network of size $N(t) \sim t$. Denote $\Gamma_{m,p}(t)$ the mean value of $\gamma_i(t)$ over i at iteration t, i.e.,

$$\Gamma_{m,p}(t) := \frac{1}{N(t)} \sum_{i=1}^{N(t)} \gamma_i(t). \quad (12)$$

We have

$$\Gamma_{m,p}(t) = \frac{1}{N(t)} \sum_{i=1}^{N(t)} \sum_{j=1}^{N(t)} p(j,i) \frac{k_j(t)}{s_j(t)} = \frac{1}{N(t)} \sum_{j=1}^{N(t)} \frac{k_j(t)}{s_j(t)} \sum_{i=1}^{N(t)} p(j,i) = \frac{1}{N(t)} \sum_{j=1}^{N(t)} \frac{k_j^2(t)}{s_j(t)}. \quad (13)$$

The mean value of $\gamma_i k_i$ over i,

$$\begin{aligned} \frac{1}{N(t)} \sum_{i=1}^{N(t)} \gamma_i(t) k_i(t) = \frac{1}{N(t)} \sum_{i=1}^{N(t)} \sum_{j=1}^{N(t)} p(j,i) k_i(t) \frac{k_j(t)}{s_j(t)} = \\ \frac{1}{N(t)} \sum_{j=1}^{N(t)} \frac{k_j(t)}{s_j(t)} \sum_{i=1}^{N(t)} p(j,i) k_i(t) = \frac{1}{N(t)} \sum_{j=1}^{N(t)} \frac{k_j(t)}{s_j(t)} s_j(t) = \\ \frac{1}{N(t)} \sum_{j=1}^{N(t)} k_j(t) = \frac{2M(t)}{N(t)} = 2m, \end{aligned} \quad (14)$$

i.e., it is equal to the mean value of k_i over i, i.e., $2m$.

Theorem 1. *$\Gamma_{m,p}(t)$ tends to a constant as $t \to \infty$.*

The proof of Theorem can be found in Appendix A.

Figure 2 shows the dynamics of $\Gamma_{m,p}(t)$ (with different choices of m and p) over t and that $\Gamma_{m,p}(t)$ tends to a constant depending on m and p as $t \to \infty$.

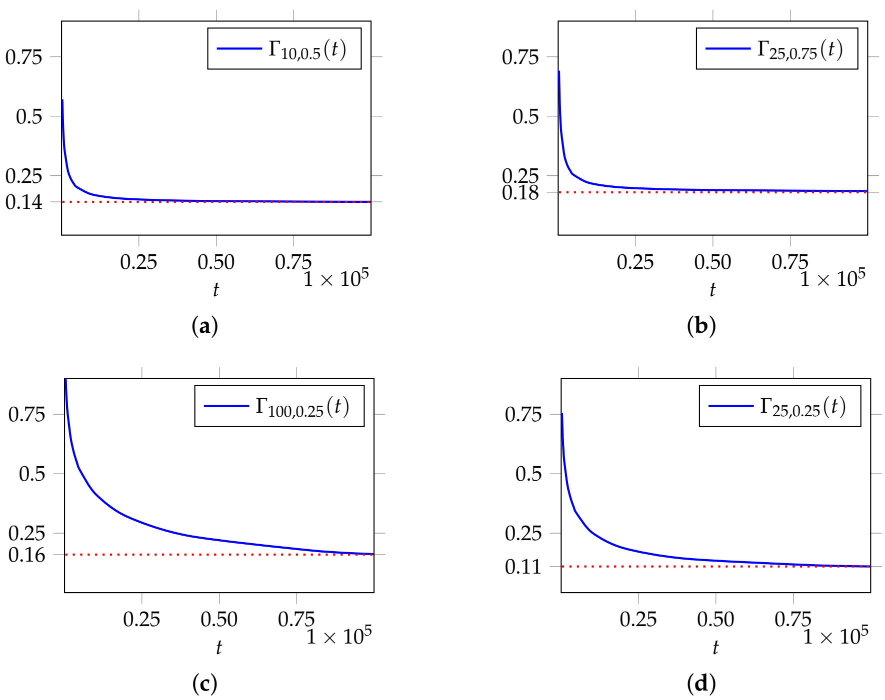

Figure 2. The dynamics of $\Gamma_{m,p}(t)$ over time for (**a**) $m = 10$, $p = 0.5$, (**b**) $m = 25$, $p = 0.75$, (**c**) $m = 100$, $p = 0.25$, and (**d**) $m = 25$, $p = 0.25$.

We built networks of size $N = 100{,}000$ using the proposed model for various values of the model parameters m and p. During each experiment, for fixed parameter values, we built 10 networks, for each of them we found a value $\Gamma_{m,p}(N)$ using Equation (13), and then we recorded their average values in Table 1.

Table 1. The empirical values of $\Gamma_{m,p}$ obtained for different p and m. The values were calculated for networks of size $N = 100{,}000$.

$p \setminus m$	2	5	10	25	50	100
0.25	0.41	0.20	0.11	0.11	0.13	0.16
0.5	0.33	0.14	0.14	0.15	0.16	0.17
0.75	0.27	0.17	0.18	0.18	0.18	0.20
1	0.27	0.20	0.19	0.19	0.19	0.20

Theorem 2. *The values of $\{\gamma_i(t)\}$ have the following properties:*

- $\mathbb{E}(\gamma_1(t)) \geq \mathbb{E}(\gamma_2(t)) \geq \ldots \geq \mathbb{E}(\gamma_i(t)) \geq \mathbb{E}(\gamma_{i+1}(t)) \geq \ldots$*;*
- $\mathbb{E}(\gamma_i(t)) \to 0$ *for as $i \to \infty$, i.e., $\mathbb{E}(\beta_i(t)) \to \frac{1+(1-p)(m-1)}{2m}$ as $i \to \infty$;*
- *The expected initial value of $\gamma_i(i)$ at iteration i is equal to*

$$\mathbb{E}(\gamma_i(i)) = \frac{1}{2M(i)} \sum_{r=1}^{i-1} \Big(1 + (1-p)(m-1) + p(m-1)\gamma_r(i)\Big) \frac{k_r^2(i)}{s_r(i)}.$$

The proof can be found in Appendix B.

4. Scale-Free Behavior

We study the stationary degree distribution as the number of iterations $t \to \infty$. Let us calculate the difference in the number of nodes with degree k after adding one node at the iteration t (and m links are added connecting the newborn node with existing vertices).

Let $q_t(s,k)$ denote the probability that vertex s has degree k at iteration t.

Let $p_k(t)$ denote the probability that a randomly chosen node of the graph (at iteration t) has degree k. In another words, $p_k(t)$ is the share of nodes with degree k among all nodes of the network at iteration t.

By definition of $q_t(s,k)$ we have

$$\frac{1}{t} \sum_{s=1}^{t} q_t(s, k-1) = p_{k-1}(t), \tag{15}$$

$$\frac{1}{t+1} \sum_{s=1}^{t+1} q_{t+1}(s,k) = p_k(t+1), \tag{16}$$

$$\frac{1}{t} \sum_{s=1}^{t} q_t(s,k) = p_k(t). \tag{17}$$

Since every new node obtains degree m, we have

$$q_{t+1}(t+1,k) = \delta_{k,m},$$

where $\delta_{k,j}$ is the Kronecker delta, i.e.

$$\delta_{k,j} = \begin{cases} 1, & k = j, \\ 0, & k \neq j. \end{cases}$$

Node s will have degree k at iteration $t+1$ if the following occur:

- The degree of vertex s is equal to $k-1$ at iteration t and it adds up by 1 at time $t+1$;
- The degree of node s at iteration t is k and it does not change at iteration $t+1$.

The probability that the degree of vertex s is equal to $k-1$ at iteration t and the node is chosen at step 2(a) of iteration $t+1$ is

$$q_t(s,k-1)\frac{k-1}{2M(t)}.$$

The probability that the degree of node s is equal to $k-1$ and the node is chosen at step 2(b1) of iteration $t+1$, is

$$p(m-1)q_t(s,k-1)\sum_{j=1}^{N(t)} p(s,j)\frac{k_j}{2M(t)}\frac{k-1}{s_j}.$$

The probability that node s has degree $k-1$ and the node is chosen at step 2(b2) of iteration $t+1$ is

$$(1-p)(m-1)q_t(s,k-1)\frac{k-1}{2M(t)}.$$

The probability that node s has degree k and the node is not chosen at iteration $t+1$ is

$$q_t(s,k)\left(1-\frac{k}{2M(t)}-p(m-1)\sum_{j=1}^{N(t)} p(s,j)\frac{k_j}{2M(t)}\frac{k}{s_j}-(1-p)(m-1)\frac{k}{2M(t)}\right).$$

Then,

$$\begin{aligned}
q_{t+1}(s,k) &= q_t(s,k-1)\frac{k-1}{2M(t)}+ \\
& p(m-1)q_t(s,k-1)\sum_{j=1}^{N(t)} p(s,j)\frac{k_j}{2M(t)}\frac{k-1}{s_j}+(1-p)(m-1)q_t(s,k-1)\frac{k-1}{2M(t)}+ \\
& q_t(s,k)\left(1-\frac{k}{2M(t)}-p(m-1)\sum_{j=1}^{N(t)} p(s,j)\frac{k_j}{2M(t)}\frac{k}{s_j}-(1-p)(m-1)\frac{k}{2M(t)}\right).
\end{aligned} \tag{18}$$

If we sum up the left- and right- hand sides of (18) over $s=1,\ldots,N(t)$, we obtain by using of Equations (15)–(17) that

$$\begin{aligned}
(t+1)p_k(t+1)-\delta_{k,m} &= tp_{k-1}(t)\frac{k-1}{2M(t)} \\
&+ p(m-1)\frac{k-1}{2M(t)}\sum_{s=1}^{N(t)} q_t(s,k-1)\sum_{j=1}^{N(t)}\frac{k_j(t)}{s_j(t)}p(s,j) \\
&+ (1-p)(m-1)tp_{k-1}(t)\frac{k-1}{2M(t)}+tp_k(t)-tp_k(t)\frac{k}{2M(t)} \\
&- p(m-1)\frac{k}{2M(t)}\sum_{s=1}^{N(t)} q_t(s,k)\sum_{j=1}^{N(t)}\frac{k_j(t)}{s_j(t)}p(s,j) \\
&- (1-p)(m-1)tp_k(t)\frac{k}{2M(t)}.
\end{aligned} \tag{19}$$

Denote $p_k=\lim_{t\to\infty} p_k(t)$ the limit probability, then

$$(t+1)p_k(t+1)-tp_k(t)\to p_k,\ t\to\infty.$$

Using approximations $N(t) \sim t$, $M(t) \sim mt$ and Equation (19) we obtain

$$2mp_k = \Big(1 + (1-p)(m-1)\Big)((k-1)p_{k-1} - kp_k) \\ + p(m-1)\lim_{t\to\infty}\frac{1}{t}\sum_{s=1}^{t}\gamma_s(t)\Big((k-1)q_t(s,k-1) - kq_t(s,k)\Big), \quad (20)$$

where $\gamma_s(t)$ is defined in (5).

Tending t to infinity we obtain

$$\lim_{t\to\infty}\frac{1}{t}\sum_{s=1}^{t}\gamma_s(t)((k-1)q_t(s,k-1) - kq_t(s,k)) = \\ A_{m,p}\lim_{t\to\infty}\left(\frac{1}{t}\sum_{s=1}^{t}\gamma_s(t)\right)\left(\frac{1}{t}\sum_{s=1}^{t}((k-1)q_t(s,k-1) - kq_t(s,k))\right) = \\ A_{m,p}((k-1)p_{k-1} - kp_k)\Gamma_{m,p}, \quad (21)$$

where $A_{m,p}$ is a constant and

$$\Gamma_{m,p} := \lim_{t\to\infty}\Gamma_{m,p}(t).$$

It follows from (20) and (21) that

$$2mp_k = (k-1)\Big(1 + (1-p)(m-1)\Big)p_{k-1} - k\Big(1 + (1-p)(m-1)\Big)p_k \\ + A_{m,p}p(m-1)(k-1)p_{k-1}\Gamma_{m,p} - A_{m,p}p(m-1)kp_k\Gamma_{m,p}. \quad (22)$$

It follows from (22) that

$$p_k = \frac{(k-1)\Big(1 + (1-p)(m-1) + A_{m,p}p(m-1)\Gamma_{m,p}\Big)}{2m + k\Big(1 + (1-p)(m-1) + A_{m,p}p(m-1)\Gamma_{m,p}\Big)}p_{k-1}, \quad (23)$$

and therefore

$$p_k = ck^{-\gamma_{m,p}}, \quad \gamma_{m,p} = 1 + \frac{2m}{1 + (1-p)(m-1) + A_{m,p}p(m-1)\Gamma_{m,p}}, \quad (24)$$

i.e., the degree distribution of the network follows the power law with its exponent $\gamma_{m,p}$ depending on m and p.

Table 2 shows the dependence of exponent $\gamma_{m,p}$ on different m and p obtained empirically in a series of experiments. In each experiment we generate ten networks of the same size where N =100,000 with the use of the proposed model. Then, we averaged results over these networks. Table 2 demonstrates that exponents of degree distribution depend on the model parameters m and p.

Table 2. The empirical values of the degree distribution exponent $\gamma_{m,p}$ obtained for different p and m. The values were calculated for networks of size $N = 100{,}000$.

$p \setminus m$	2	5	10	25	50	100
0.25	2.71	3.05	3.25	3.40	3.47	3.50
0.50	2.84	3.35	3.66	3.94	4.08	4.14
0.75	3.03	3.60	3.96	4.38	4.61	4.79
1.00	3.42	3.86	4.46	4.50	4.79	5.10

Figure 3 presents the log–log plots of degree distributions for networks generated for different m and p. The plots show that the degree distributions follow the power law with the corresponding exponents that are present in Table 2.

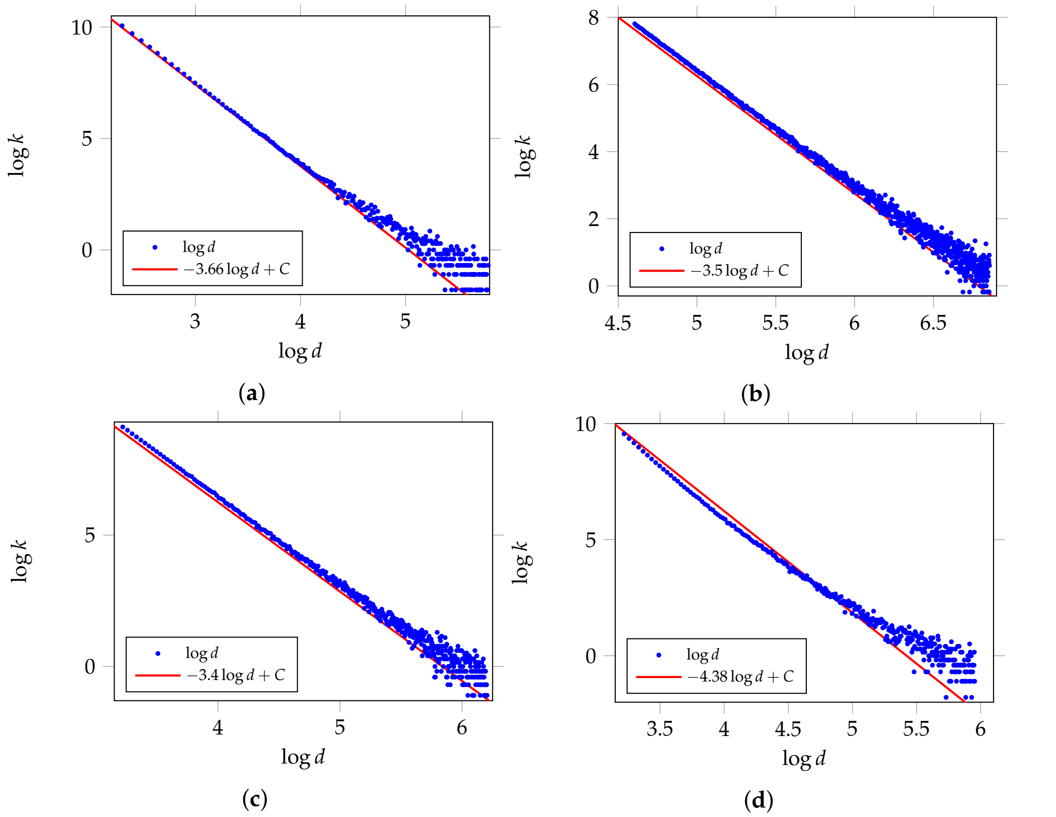

Figure 3. Log–log plots of degree distributions for networks generated with parameters (**a**) $m = 10$, $p = 0.5$; (**b**) $m = 100$, $p = 0.25$; (**c**) $m = 25$, $p = 0.25$; (**d**) $m = 25$, $p = 0.75$

5. Conclusions

In this paper, we consider the development of the triadic closure model, in which all nodes at each iteration are selected based on the preferential attachment mechanism. The results show that the stationary degree distribution follows a power law, but the value of the exponent is significantly different from the value of the exponent for the basic triadic closure model.

The model has the attractive feature of allowing networks to be created with different power law exponents for the degree distribution depending on the choice of model parameters. Moreover, the model allows one to generate networks with more realistic clustering that is inherent in real networks. However, issues related to the study of the behavior of local clustering coefficients, as well as the dynamic behavior of global clustering indicators, remained beyond the scope of this work. We believe that the study of these characteristics is a fairly important problem in the context of analyzing the capabilities and limitations inherent in the proposed network generation model.

We have shown that changing the mechanism of triad formation during network growth leads to significant changes in the structure of the generated networks. It would be interesting to study the influence of other mechanisms of triangle formation on the characteristics of the resulting networks. In addition, it is also important to ensure that these mechanisms lead to the creation of networks whose properties are close to those of real social networks.

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Appendix A. The Proof of Theorem 1

Proof. We will prove the statement in case of $m = 2$ and $p = 1$. The other cases can be proved in an analogous way.

We will show that the expected values of increments

$$\Delta\Gamma(t+1) = \Gamma(t+1) - \Gamma(t)$$

are non-positive. Then, Lemma follows from the fact that $\Gamma(t) > 0$ for all t.

For simplicity we let $N(t) = t$. The following terms in the sum (13) are changing with the transition from t to $t+1$:

- All terms $\frac{1}{t}\frac{k_j^2(t)}{s_j(t)}$ in $\Gamma(t)$ are replaced by $\frac{1}{t+1}\frac{k_j^2(t)}{s_j(t)}$ in $\Gamma(t+1)$, therefore the difference is

$$\sum_{j=1}^{t}\left(\frac{1}{t+1} - \frac{1}{t}\right)\frac{k_j^2(t)}{s_j(t)} = -\sum_{j=1}^{t}\frac{1}{t(t+1)}\frac{k_j^2(t)}{s_j(t)}; \tag{A1}$$

- New $(t+1)$-term is adding to $\Gamma(t+1)$:

$$\frac{k_{t+1}^2(t+1)}{(t+1)s_{t+1}(t+1)} = \frac{4}{(t+1)s_{t+1}(t+1)}, \text{ since } k_{t+1}(t+1) = 2.$$

- With probability $\frac{k_j(t)}{4t}$ new node $t+1$ increases the degree of node j by 1 and the value of $s_j(t)$ by 3, therefore the difference between the corresponding term in the sum $\Gamma(t+1)$ and j-term in $\Gamma(t)$ is

$$\frac{(k_j(t)+1)^2}{(t+1)(s_j(t)+3)} - \frac{k_j^2(t)}{ts_j(t)} + \frac{k_j^2(t)}{t(t+1)s_j(t)} = \frac{s_j(t)(2k_j(t)+1) - 3k_j^2(t)}{(t+1)s_j(t)(s_j(t)+3)},$$

  Where term $\frac{1}{t(t+1)}\frac{k_j^2(t)}{s_j(t)}$ is added to annihilate the corresponding term in (A1);
- If node j is chosen at step 2(a), then for each of its neighbors l the value of s_l increases by 1, while their degrees remain the same, i.e., the difference is (with probability $\frac{k_j(t)}{4t}$)

$$\sum_{l=1}^{t} p(l,j)\left(\frac{k_l^2(t)}{(t+1)(s_l(t)+1)} - \frac{k_l^2(t)}{s_l(t)} + \frac{k_l^2(t)}{t(t+1)s_l(t)}\right) = -\sum_{l=1}^{t} p(l,j)\frac{k_l^2(t)}{(t+1)s_l(t)(s_l(t)+1)},$$

where the last term is added to annihilate it in (A1);

- The probability that node i (one of the neighbors of node j chosen at step 2(a)) will be chosen at step 2(b) is $\frac{k_i(t)}{s_j(t)}$ and the changes caused by this choice are:
  - New node $t+1$ increases the degree of node i by 1 and the value of $s_i(t)$ by 3:

$$\frac{(k_i(t)+1)^2}{(t+1)(s_i(t)+3)} - \frac{k_i^2(t)}{ts_i(t)} + \frac{k_i^2(t)}{t(t+1)s_i(t)} = \frac{s_i(t)(2k_i(t)+1) - 3k_i^2(t)}{(t+1)s_i(t)(s_i(t)+3)},$$

  - Each neighbors r of node i increases its value of s_r by 1, while their degrees remain the same:

$$\sum_{r=1}^{t} p(r,i)\left(\frac{k_r^2(t)}{(t+1)(s_r(t)+1)} - \frac{k_r^2(t)}{ts_r(t)} + \frac{k_r^2(t)}{t(t+1)s_r(t)}\right) = -\sum_{r=1}^{t} p(r,i)\frac{k_r^2(t)}{(t+1)s_r(t)(s_r(t)+1)}.$$

Then,

$$\begin{aligned}\Delta\Gamma(t+1) = \Gamma(t+1) - \Gamma(t) = -\frac{1}{t(t+1)}\sum_{j=1}^{t}\frac{k_j^2(t)}{s_j(t)} + \frac{4}{(t+1)s_{t+1}(t+1)} + \\ \sum_{j=1}^{t}\frac{k_j(t)}{4t}\left(\frac{s_j(t)(2k_j(t)+1) - 3k_j^2(t)}{(t+1)s_j(t)(s_j(t)+3)} - \sum_{l=1}^{t} p(l,j)\frac{k_l^2(t)}{(t+1)s_l(t)(s_l(t)+1)} + \right. \\ \left.\sum_{i=1}^{t} p(i,j)\frac{k_i(t)}{s_j(t)}\left(\frac{s_i(t)(2k_i(t)+1) - 3k_i^2(t)}{(t+1)s_i(t)(s_i(t)+3)} - \sum_{r=1}^{t} p(r,i)\frac{k_r^2(t)}{(t+1)s_r(t)(s_r(t)+1)}\right)\right).\end{aligned} \quad (A2)$$

It follows from

$$\sum_{j=1}^{N(t)} p(j,i)k_j(t) = s_i(t) \text{ and } \sum_{j=1}^{N(t)} p(j,i)\frac{k_j(t)}{s_j(t)} = \gamma_i(t)$$

that

$$\begin{aligned}\Delta\Gamma(t+1) = \Gamma(t+1) - \Gamma(t) = -\frac{1}{t+1}\Gamma(t) + \frac{4}{(t+1)s_{t+1}(t+1)} + \\ + \frac{1}{2(t+1)}\Gamma(t) - \frac{3}{4(t+1)}\sum_{j=1}^{t}\frac{k_j^2(t)}{s_j(t)(s_j(t)+3)} + \\ \frac{1}{4t(t+1)}\sum_{j=1}^{t}\frac{k_j(t)}{s_j(t)+3} - \frac{3}{4t(t+1)}\sum_{j=1}^{t}\frac{k_j^3(t)}{s_j(t)(s_j(t)+3)} - \\ \frac{1}{4(t+1)}\Gamma(t) + \frac{1}{4t(t+1)}\sum_{j=1}^{t}\frac{k_j^2(t)}{s_j(t)(s_j(t)+1)} + \\ \frac{1}{2t(t+1)}\sum_{i=1}^{t}\gamma_i(t)\frac{k_i^2(t)}{s_i(t)} - \frac{3}{4t(t+1)}\sum_{i=1}^{t}\gamma_i(t)\frac{k_i^2(t)}{s_i(t)(s_i(t)+3)} + \\ \frac{1}{4t(t+1)}\sum_{i=1}^{t}\gamma_i(t)\frac{k_i(t)}{s_i(t)+3} - \frac{3}{4t(t+1)}\sum_{i=1}^{t}\gamma_i(t)\frac{k_i^3(t)}{s_i(t)(s_i(t)+3)} - \\ \frac{1}{4t(t+1)}\sum_{r=1}^{t}\left(\sum_{i=1}^{t}\gamma_i(t)p(r,i)k_i(t)\right)\frac{k_r^2(t)}{s_r(t)(s_r(t)+1)}.\end{aligned} \quad (A3)$$

Since the degree of every node is at least 2, then for every node j the average degree of its neighbors $s_j(t)/k_j(t) \geq 2$. Therefore, $k_j(t) \leq s_j(t)/2$. Then, we can evaluate some positive terms in (A3) from the above as follows:

$$\frac{4}{(t+1)s_{t+1}(t+1)} \leq \frac{1}{t+1}, \text{ since } s_{t+1}(t+1) \geq 4,$$

$$\frac{1}{4t(t+1)}\sum_{j=1}^{t}\frac{k_j(t)}{s_j(t)+3} \leq \frac{1}{8t(t+1)}\sum_{j=1}^{t}\frac{s_j(t)}{s_j(t)+3} \leq \frac{1}{8(t+1)},$$

$$\frac{1}{4t(t+1)}\sum_{j=1}^{t}\frac{k_j^2(t)}{s_j(t)(s_j(t)+1)} \leq \frac{1}{16t(t+1)}\sum_{j=1}^{t}\frac{s_j^2(t)}{s_j(t)(s_j(t)+1)} \leq \frac{1}{16(t+1)},$$

$$\frac{1}{2t(t+1)}\sum_{i=1}^{t}\gamma_i(t)\frac{k_i^2(t)}{s_i(t)} \leq \frac{1}{4t(t+1)}\sum_{i=1}^{t}\gamma_i(t)k_i(t) \leq \frac{1}{t+1}, \text{ (with the help of (14))},$$

$$\frac{1}{4t(t+1)}\sum_{i=1}^{t}\gamma_i(t)\frac{k_i(t)}{s_i(t)+3} \leq \frac{1}{8t(t+1)}\sum_{i=1}^{t}\gamma_i(t)\frac{s_i(t)}{s_i(t)+3} \leq \frac{1}{8(t+1)}\Gamma(t).$$

Then, neglecting some negative terms in (A3), the difference $\Delta\Gamma(t+1)$ can be estimated from above as follows:

$$\Delta\Gamma(t+1) \leq \frac{7}{2(t+1)} - \frac{3}{4(t+1)}\Gamma(t).$$

The solution of the differential equation

$$\frac{df(t)}{dt} = \frac{7}{2(t+1)} - \frac{3}{4(t+1)}f(t)$$

is a constant function. Thus, $\Delta\Gamma(t+1) \leq 0$. □

Appendix B. The Proof of Theorem 2

Proof. We have

$$\gamma_i(t) = \sum_{j=1}^{N(t)} p(j,i)\frac{k_j(t)}{s_j(t)} = S_{1,i}(t) + S_{2,i}(t) + S_{3,i}(t), \tag{A4}$$

where

$$S_{1,i}(t) := \sum_{j=1}^{i-1} p(j,i)\frac{k_j(t)}{s_j(t)}, \quad S_{2,i}(t) := p(i+1,i)\frac{k_{i+1}(t)}{s_{i+1}(t)}, \quad S_{3,i}(t) := \sum_{j=i+2}^{N(t)} p(j,i)\frac{k_j(t)}{s_j(t)}.$$

First, we find the expectation $\mathbb{E}(S_{1,i}(t))$ of the first term at time t. Denote $j_1(i)$ the node to which the node i was attached at step 2(a) of iteration i. Let $j_2(i)$ and $j_3(i)$ denote nodes to which vertex i was linked at step 2(b1) and 2(b2) of iteration i, respectively. Note that the iteration i is the moment of the appearance of node i, so $j_1(i), j_2(i), j_3(i) < i$. Then, the first sum consists of three terms corresponding to the three nodes $j_1(i)$, $j_2(i)$, and $j_3(t)$. The expectation of the first sum in (A4) at t can be estimated as follows:

$$
\begin{aligned}
\mathbb{E}(S_{1,i}(t)) = \sum_{r=1}^{i-1} p(j_1 = r)\frac{k_r(t)}{s_r(t)} + \\
p(m-1)\sum_{r=1}^{i-1} p(j_1 = r)\sum_{l=1}^{i-1} p(j_2 = l|j_1 = r)\frac{k_l(t)}{s_l(t)} + (1-p)(m-1)\sum_{r=1}^{i-1} p(j_3 = r)\frac{k_r(t)}{s_r(t)} \\
= \sum_{r=1}^{i-1}\frac{k_r(i)}{2M(i)}\frac{k_r(t)}{s_r(t)} + p(m-1)\sum_{r=1}^{i-1}\frac{k_r(i)}{2M(i)}\sum_{l=1}^{i-1} p(l,r)\frac{k_l(i)}{s_r(i)}\frac{k_l(t)}{s_l(t)} + \\
(1-p)(m-1)\sum_{r=1}^{i-1}\frac{k_r(i)}{2M(i)}\frac{k_r(t)}{s_r(t)} = (1+(1-p)(m-1))\sum_{r=1}^{i-1}\frac{k_r(i)}{2M(i)}\frac{k_r(t)}{s_r(t)} + \\
p(m-1)\frac{1}{2M(i)}\sum_{l=1}^{i-1}\left(\sum_{r=1}^{i-1} p(l,r)\frac{k_r(i)}{s_r(i)}\right)k_l(i)\frac{k_l(t)}{s_l(t)} \\
= \frac{1+(1-p)(m-1)}{2M(i)}\sum_{r=1}^{i-1} k_r(i)\frac{k_r(t)}{s_r(t)} + \frac{p(m-1)}{2M(i)}\sum_{l=1}^{i-1}\gamma_l(i)k_l(i)\frac{k_l(t)}{s_l(t)} = \\
\frac{1}{2M(i)}\sum_{r=1}^{i-1}\Big(1+(1-p)(m-1)+p(m-1)\gamma_r(i)\Big)\frac{k_r(t)}{s_r(t)}k_r(i). \quad \text{(A5)}
\end{aligned}
$$

It follows from Equation (9) that

$$
\mathbb{E}(S_{2,i}(t)) = \Big(1+(1-p)(m-1)+p(m-1)\gamma_i(t)\Big)\frac{k_i(i+1)}{2M(i+1)}\frac{k_{i+1}(t)}{s_{i+1}(t)}. \quad \text{(A6)}
$$

It follows from Equation (A5) that

$$
\mathbb{E}(S_{1,i+1}(t)) = \frac{1}{2M(i+1)}\sum_{r=1}^{i}\Big(1+(1-p)(m-1)+p(m-1)\gamma_r(i+1)\Big)\frac{k_r(t)}{s_r(t)}k_r(i+1). \quad \text{(A7)}
$$

It follows from (A5)–(A7) that

$$
\mathbb{E}(S_{1,i+1}(t)) < \mathbb{E}(S_{1,i}(t)) + \mathbb{E}(S_{2,i}(t)), \quad \mathbb{E}(S_{2,i+1}(t)) + \mathbb{E}(S_{3,i+1}(t)) < \mathbb{E}(S_{3,i}(t)),
$$

therefore,

$$
\mathbb{E}(\gamma_i(t)) > \mathbb{E}(\gamma_{i+1}(t)),
$$

and the first statement of the theorem is proved.

The second follows from (A5) as $i \to \infty$. The third statement of the theorem follows from (A5) with $t = i$. □

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