Whole Sampling Generation of Scale-Free Graphs

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Abstract

This paper presents the development of a new class of algorithms that accurately implement the preferential attachment mechanism of the Barabási–Albert (BA) model to generate scale-free graphs. Contrary to existing approximate preferential attachment schemes, our methods are exact in terms of the proportionality of the vertex selection probabilities to their degree and run in linear time with respect to the order of the generated graph. Our algorithms are based on a principle of random sampling which is called whole sampling and is a new perspective for the study of preferential attachment. We show that they obey the definition of the original BA model that generates scale-free graphs and discuss their higher-order properties. Finally, we extend our analytical presentation with computer experiments that focus on the degree distribution and several measures surrounding the local clustering coefficient.

Keywords: Preferential Attachment, Scale-Free Graphs, Barabási-Albert Model

1 Introduction

The Barabási–Albert (BA) model [1] is a growing preferential attachment mechanism that dictates the rules of connections among vertices when newborn nodes enter the network. Specifically, it requires that we select $m$ vertices from the graph population when a newborn node enters the network in such a way that the probability of selecting a vertex is proportional to its degree. By repeating this process, the model results in the generation of a scale-free graph of order $n$. According to the analytical arguments made in the original paper, the random sampling model involved in this growing process is a selection without replacement and with inclusion probabilities strictly proportional to the degree of the vertices. Consequently, a round of the BA model is defined as follows:

Definition 1. (A round of the BA model.) A new node is inserted into the graph. Then $m$ distinct existing nodes are randomly selected. The probability of each node to be selected is proportional to its degree.
Current state of the art preferential attachment models are typically efficient in terms of their running time but they are not equivalent to the exact model described by Barabási and Albert; they do not refer to the same simple graph without multiple edges, or the probability model employed is only an approximation of the original scheme.

One of the most popular theoretical models in the literature is the model of Bollobás [2], which employs a probability model that guarantees strict proportionality but results in a multigraph. Due to its simplicity and the rigorous analysis made in this work about various properties of this network, the model has since been adopted in the literature. Another example of a multigraph generator is mentioned in [3, Chapter 8], where the edges are added with intermediate weight updates with replacement, a scheme that results in possible multiple edges per node pair.

Other studies correctly treat the BA model as a simple graph but with a probability selection scheme that is only an approximation of the original model. For example, Hadian et al [4] define a simple graph generator but the probabilities of node inclusions are not exactly proportional to their degree due to rejections. This difference has been explained further in [5], where the distinction of inclusion and selection probabilities is made. Berger et al [6] attempt to make a distinction about different probability schemes (independent, conditional, sequential) but also refer to the Bollobás multigraph model.

Despite the models mentioned previously being both efficient and rigorously studied, they do not strictly abide by the definition of the original BA model. The definition requires a sampling scheme without replacement that generates simple graphs, and the inclusion probability of a vertex is strictly proportional to its degree. These requirements can be summarized into the strπps random sampling scheme, which refers to a weighted random sampling design without replacement with inclusion probabilities strictly proportional to degree, and is also known as the ratio estimator property [7, Section 1.4].

In this paper, we present a class of algorithms that obey the definition of the BA model strictly, both with respect to the type of the output graph and the interpretation of the probabilities being employed in the preferential attachment step being exactly proportional to the node degrees. Our algorithms also run in linear time with respect to \( n \), or in constant time for each time step, i.e., for each new node. It is worth noting that it is trivial to apply any strπps sampling method on each time step independently but that would result on quadratic complexity for the whole process. The computational complexity of the algorithm is of great importance since the sizes of the generated scale-free graphs are often very large, up to hundreds of thousands or even millions of nodes. To our knowledge, up to now there was no efficient sampling algorithm for running each step in \( O(1) \) with respect to \( n \). This could be a reason why current software libraries (e.g. networkx\(^1\), igraph\(^2\)) have opted for a related efficient weighted random scheme that only approximates the BA definition. To the best of our knowledge this is the first time that both a strict interpretation of the inclusion probabilities and a linear running time are satisfied.

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1https://networkx.org/
2https://igraph.org/
The basic principle of our algorithms can be demonstrated in the simple case where \( m = 2 \). During each time step, a random edge is selected and the newborn node is connected with the ends of that edge creating a triangle. The process is repeated until the graph is of the desired size. It is easy to show that on this sampling scheme, where each edge is guaranteed to connect two different nodes, each vertex exists in the edge set as many times as its degree and, therefore, its inclusion probability on any time step is exactly proportional to its degree, satisfying the \( \text{str}\pi\psi \text{ps} \) scheme. The closest concepts to our algorithms are, to our knowledge, the sampling methods of Jessen (Tableau based methods [8]) and the concept of whole sampling (ie., sampling the whole sample in one step [7 Section 1.7.1]), which are both in much earlier literature. Therefore our weighted random sampling procedures and the corresponding BA graph generators are a new approach in the domain of preferential attachment. The idea of sampling an edge has been mentioned before in [9], where the authors claim that “in a list of all edges created thus far, the number of occurrences of a vertex is equal to its degree, so that it can be used as a pool to sample from the degree-skewed distribution in constant time”. 

Based on the principle of this simple model, we generalize its operation for \( m > 2 \) by taking advantage of the operation of Jessen’s whole sampling algorithm [8], a weighted \( \text{str}\pi\psi \text{ps} \) random sampling scheme, and adjust its operation to fit the preferential attachment problem by introducing auxiliary data structures. Similarly to the simple \( m = 2 \) model where selections of pairs of nodes are made, our generalization allows the selection of \( m \)-tuples by parallelizing the list of edges with a list of hyperedges of an implicit \( m \)-uniform hypergraph. We prove that our approaches satisfy the \( \text{str}\pi\psi \text{ps} \) model and show their running time to be linear with respect to \( n \).

Our contribution can be summarized as follows:

1. We present a new algorithmic approach of scale-free graph generators that is based on the concept of whole sampling.

2. Our methods obey the strict inclusion probability scheme required by the definition of the BA model while running in linear time with respect to \( n \).

2 Algorithms

We begin the presentation of our methods with the simple \( m = 2 \) algorithm that was previously described; we label this algorithm SE-A (Section 2.1). Although this algorithm works only for \( m = 2 \), it demonstrates the basic principle of our approach. A generalization is then given for \( m > 2 \) as the abstract algorithm SE (Section 2.2) that utilizes an auxiliary data structure \( H \) that resembles a \( m \)-uniform hypergraph. Due to the generalization being abstract, we propose two possible implementations that achieve the generation of scale-free graphs in slightly different ways. Algorithm SE-B (Section 2.3) is a more minimalistic approach towards the growth of the \( H \) data structure while algorithm SE-C (Section 2.4) performs more work, while still maintaining linear
complexity, in an attempt to reduce correlations among tuples of vertices in the resulting graph. Both SE-B and SE-C reduce to algorithm SE-A when \( m = 2 \). We prove that both algorithms are correct with respect to the \( str\pi ps \) probability model and have linear time worst case complexities.

Each algorithm is described as a growing process starting from an initial graph \( G_0 \) until it reaches the desired order \( n \). For simplicity, it is assumed that the starting graph is connected, otherwise unconnected graphs may be generated. A discussion surrounding the properties of initial graphs is given in Section 2.5.

### 2.1 Algorithm SE-A

The operation of algorithm SE-A can be summarized via its growth function. During the addition of one newborn node, one uniformly random edge is selected from the existing edge set and the new vertex is connected to the endpoints of that edge. A high level sketch of SE-A appears in Algorithm 2. All following algorithms are assumed to have an implicit random number generator input.

**Algorithm 2. Algorithm SE-A (high level sketch)**

**Input** An initial connected graph \( G_0(V_0, E_0) \) containing at least one edge and the desired number of vertices \( n \)

**Output** A scale-free graph \( G(V, E) \)

1: \((V, E) \leftarrow (V_0, E_0)\)
2: while \(|V| < n\) do
3: select one uniformly random edge \( e = (u, w) \in E\)
4: add new vertex \( v \) to \( V\)
5: add new edges \((v, u)\) and \((v, w)\) to \( E\)
6: return \( G(V, E)\)

The intuition of the method is that a vertex exists in the edge set as many times as its degree and no edge can contain the same vertex more than once. As a result, during a single uniform random edge selection, the inclusion probability of a vertex with degree \( d \) at any time is \( d/|E| \). Therefore, the probability of a vertex with degree \( d \) gaining an edge at any time after a newborn node has been added is exactly proportional to its degree, which proves the following theorem regarding the correctness of the algorithm:

**Theorem 3.** Algorithm SE-A satisfies the \( str\pi ps \) probability scheme and generates a simple graph according to the definition of the BA model.

### 2.1.1 Complexity

The work performed by algorithm SE-A during its growth function is one random edge selection, one vertex addition and 2 edge additions. Therefore, the whole process requires \( \sim n \) vertex additions,
~ 2n edge additions and ~ n random variates, leading to the following theorem:

**Theorem 4.** Algorithm SE-A runs in time $\Theta(n)$ to create a graph of $n$ vertices.

Here the tilde symbol is set to mean asymptotic equivalence [10, Section 1.4]. Algorithm SE-A does not require any additional memory other than the output graph and doesn’t use auxiliary data structures.

### 2.1.2 Clustering Coefficient

The simplicity of algorithm SE-A also allows us to analytically study several properties surrounding the local clustering coefficient. For the following analysis, it is assumed that the initial graph $G_0$ consists of 2 vertices an 1 edge, which is the smallest graph from which the operation can start. First, we state the following theorem regarding the correlation of the local clustering coefficient with the degree:

**Theorem 5.** The local clustering coefficient of a vertex with degree $d$ is $2/d$ at any time of the generation process.

**Proof.** The local clustering coefficient of a vertex $i$ at time $t$ is

$$C(d) = \frac{2E_i}{d_i(d_i - 1)},$$

where $E_i$ is the amount of edges among $i$’s neighbors and $d_i$ the degree of $i$. Therefore, when $i$ enters the network, its local clustering coefficient is 1, because $d = 2$ and $E_i = 1$. If $i$ does not acquire any new edges, its local clustering coefficient will not change, because none of the quantities $E_i$ or $d_i$ will change, since no edges are created among existing vertices. If $i$ obtains one edge, both its degree and $E_i$ will be increased by 1, because new vertices only connect to existing edge’s endpoints. Thus, $d$ and $E_i$ are always connected via the formula $d = E_i + 1$. Replacing in (1) gives

$$C(d) = \frac{2(d - 1)}{d(d - 1)} = \frac{2}{d}.$$  

It is easy to see that the formula also holds for the 2 vertices in the initial graph after the third node has entered. 

**Theorem 5** shows that the local clustering coefficient of a vertex depends only on its degree. As a result, the limit of the average local clustering coefficient can now be derived based on the expected power law degree distribution:

**Theorem 6.** The limiting average local clustering coefficient of a graph produced using the SE-A algorithm is $2\pi^2 - 19$. 

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Proof. The degree distribution of a graph generated using the \( \text{str\,ps} \) method when \( n \to \infty \) is given in [11, Equation 90]:

\[
P(d) = \frac{2m(m+1)}{d(d+1)(d+2)}, \quad d \geq m. \tag{3}
\]

By combining (2) and (3) and setting \( m = 2 \), we can get the average local clustering coefficient:

\[
C_{\text{avg}} = \sum_{d=2}^{\infty} \frac{2}{d} P(d) = \sum_{d=2}^{\infty} \frac{24}{d^2(d+1)(d+2)} = 2\pi^2 - 19 \approx 0.73921. \tag{4}
\]

Additionally, the local clustering coefficient distribution can also be formulated. Exchanging \( d \) with \( \frac{2}{c} \) and setting \( m = 2 \) in Equation (3), we get the local clustering distribution \( P_c \):

\[
P_c(c) = P\left(\frac{2}{c}\right) = \frac{6c}{(2/c)(2c+2)}. \tag{5}
\]

The value of the average limiting local clustering coefficient produced by algorithm SE-A is inline with empirical observations of real social networks [11, Table I]. Thus, the SE-A mechanism can simulate features of real social networks beyond the power law degree distribution. The operation of the algorithm can also be parallelized with [12], where the clustering coefficient is tunable by setting a probability of creating a triangle when new vertices enter the network. Here, this probability is 1 because the new vertex always connects with two endpoints of the same edge. As a result, the number of triangles in the final graph \( G \) is \( \text{tri}(G) = \text{tri}(G_0) + n - 2 \sim n \).

Finally, it is worth mentioning that the case of \( m = 1 \) is not discussed here as there is no distinction between the interpretation of the proportionality of the probabilities and, hence, existing mechanisms obey the \( \text{str\,ps} \) model for this particular case.

### 2.2 Generalized Abstract Algorithm SE

We present a new whole sampling method that perfectly fits the constrains and requirements of this problem and use it to generalize algorithm SE-A to efficiently handle any value \( m > 2 \). An early example of whole sampling is due to Jessen [8]. Jessen’s method builds a sample space (called tableau) according to the given inclusion probabilities as \( m \)-tuples of elements in an iterative way. Each element is assigned a balance quantity proportional to its inclusion probability which is reduced each time the element is used in a sample; the method terminates when all balances are depleted. It is then possible to select one \( \text{str\,ps} \) sample of \( m \) elements in constant time.

Here, we exploit the constant time selection and the growing nature of Jessen’s method to define the abstract algorithm SE. Algorithm SE maintains a tableau of possible samples as an auxiliary data structure \( H \), which comprises a list of \( m \)-tuples such that each node exists in as many tuples as its degree. Updating this data structure when newborn nodes enter the network can be performed by
increasing the balance of the newborn node and the selected vertices in the tableau without having to repeat the process. We note that for algorithm SE-A, the $H$ data structure is equivalent to the edge set of the network and, hence, not required concretely. The $H$ data structure resembles a $m$-uniform hypergraph, where each of the $m$-tuples of the list represents one hyperedge. The nature of the process allows multiple copies of the same hyperedge in $H$, similarly to Jessen’s method allowing for the same row in the tableau. As a result, $H$ may represent a non-simple hypergraph where repeated edges are possible. Note that even though the hypergraph is non-simple, the $m$-uniform property assures that each hyperedge contains exactly $m$ distinct vertices. Therefore, no loops are permitted. In the rest of the document, we refer to $H$ and its contents in the hypergraph terminology. A high level sketch of this abstract algorithm appears in Algorithm [7].

**Algorithm 7. Abstract Algorithm SE (high level sketch)**

**Input** An initial connected graph $G_0(V_0, E_0)$, the desired number of vertices $n$ and the desired number of edges added per step $m$

**Output** A scale-free graph $G(V, E)$

1: $(V, E) \leftarrow (V_0, E_0)$
2: init($H$, $G_0$) \hspace{1cm} $\triangleright$ initialize $H$ based on $G_0$
3: while $|V| < n$ do
4: select one uniformly random hyperedge $e = (e_1, e_2, \ldots, e_m) \in H$
5: add new vertex $v$ to $V$
6: add new edges $(v, e_1), (v, e_2), \ldots, (v, e_m)$ to $E$
7: update($H$, $v$, $e$) \hspace{1cm} $\triangleright$ update $H$ based on $v$ and the contents of $e$
8: return $G(V, E)$

Algorithm SE, as defined here, is abstract with respect to the update function, which can be implemented in numerous ways. This function corresponds to the maintenance of the $H$ hyperedge set when newborn nodes enter the network and is required to satisfy two invariants after the update function returns:

1. Each vertex may only exist at most once in a hyperedge.
2. Each vertex participates in as many hyperedges as its degree in $G$.

These invariants guarantee the correctness of any algorithm, as they are the only necessary conditions for the sampling scheme to be strips. These requirements are implicitly satisfied in the SE-A algorithm since the $H$ data structure is identical to the edge set. The invariants can be simplified by stating that

$H$ must be a (possibly non-simple) $m$-uniform hypergraph with the same degree sequence as $G$. 

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A general operation of the update function is to handle the updating of the $H$ data structure based on the newborn node addition. In particular, the vertices $e_1, e_2, \ldots, e_m$ and $m$ copies of the newborn node $v$ have to be added in $H$. These $2m$ items imply the addition of 2 new hyperedges in $H$. Since no more than 2 copies of $v$ can be added in 2 hyperedges, previously added hyperedges need to be adjusted as well to satisfy the invariants. Two possible methods of achieving this are described in Sections 2.3 and 2.4.

The init function represents the initialization of the $H$ data structure so that the invariants are satisfied during the start of the process. Directly following the definition of the invariants, it can be seen that the initial graph $G_0(V_0, E_0)$ needs to satisfy the divisibility $2|E_0|/m$ and no vertex can have degree higher than $2|E_0|/m$ for the $H$ data structure to be feasible. The requirements of the initial graph $G_0$, which are omitted from Algorithm 7 for brevity, are discussed in more detail in Section 2.5.

The init function is marked as abstract because it is possible to be implemented in various different ways. Here, we describe one possible implementation that distributes the vertices in $V_0$ randomly throughout $H$. The method, which we call random systematic partitioning, has been influenced by the random systematic sampling method [13], which we here adjust to partition the items instead of sampling them. This algorithm, which – to our knowledge – does not seem to have been described before in the literature, might be of independent interest. Random systematic partitioning accepts a bag of elements $x_1, x_2, \ldots, x_n$ where each element $x_i$ is characterized by its frequency $d_i$ (the degree in this context). The goal of the algorithm is to partition the bag into $s$ sets of $m$ elements, where no vertex can exist more than once in any of those $s$ sets. For a feasible outcome, it must hold that $s \cdot m = \sum_{i=1}^{n} d_i$ and the maximum frequency cannot be higher than $s$. If the frequencies are not known in advance they can be created in one pass over the population.

A high level sketch of random systematic partitioning can be seen in Algorithm 9. The algorithm initially shuffles the unique $x$ values and expands them into their frequencies into an implicit $s \times m$ matrix written by row. The output of the operation is the transpose of this matrix; each of the $s$ rows represents one group of the partition. The computational complexity of random systematic partitioning is $\Theta(sm)$ because of the encapsulated loops and is formalized in the following theorem:

**Theorem 8.** Given a multiset with $s \cdot m$ items with at most $s$ repetitions of each item, random systematic partitioning runs in time $\Theta(sm)$, and partitions the multiset into $s$ sets of $m$ items each.

**Algorithm 9.** Random Systematic Partitioning Algorithm (high level sketch)

**Input** A bag of elements $x_1, x_2, \ldots, x_n$ where each element $i$ appears with frequency $d_i$, the desired number of sets $s$, the desired number of elements in a set $m$, and a random number generator $R$.

**Output** A partitioning $H$ of the input bag into $s$ sets of $m$ elements randomly distributed across the data structure.

1: $H \leftarrow$ array of $s$ empty sets
2: $k \leftarrow 1$
3: shuffle $x$
4: for all $i \in [1, n]$ do
5: for all $\_ \in [1, d_i]$ do
6: add $i$ to $H_k$
7: $k \leftarrow (k \mod s) + 1$
8: return $H$

2.3 Algorithm SE-B

Algorithm SE-B is an implementation of algorithm SE with a minimal approach into implementing the update function. The main issue of distributing the $m$ copies of the newborn node $v$ is addressed by inserting one copy into each of the 2 new hyperedges and $m - 2$ copies into previously inserted hyperedges. In the latter case, one node from each of these $m - 2$ is swapped back into the new hyperedges. A high level sketch of the update function of algorithm SE-B is shown in Algorithm 10.

Algorithm 10. Algorithm SE-B – update function (high level sketch)

Input The existing hyperedge list $H$, the newborn node $v$ and the selected hyperedge $e$
Output The new state of the hyperedge list $H$

1: initialize two new hyperedges $h_x$ and $h_y$
2: divide the vertices of $e$ in $h_x$ and $h_y$
3: add $v$ in $h_x$ and $v$ in $h_y$
4: select $m - 2$ hyperedges from $H$: $h_1, h_2, \ldots, h_{m-2}$
5: for all $i \in [1, m - 2]$ do
6: $h_c \leftarrow$ a non-empty hyperedge in \{ $h_x, h_y$ \}
7: find an element $w$ of $h_i$ not present in $h_c$
8: add $w$ in $h_c$ and replace it with $v$ in $h_i$
9: add $h_x$ and $h_y$ on $H$
10: return $H$

First, the two new hyperedges $h_x$ and $h_y$ are initialized with the vertices from the randomly selected hyperedge $e$. Although this choice does not impact the correctness of the algorithm and can be executed arbitrarily, a sensible option is a half split, or a near-half split if $|e|$ is odd. One copy of the newborn node $v$ is then added to each of the $h_x$ and $h_y$ hyperedges as it cannot have been previously contained in either. The algorithm then selects $m - 2$ existing hyperedges to perform the swap of the $m - 2$ remaining copies of $v$. The selection of these hyperedges is also irrelevant to the correctness of the algorithm and can be performed arbitrarily but it is generally desirable or useful to randomize the selection. One possible algorithm is shown in [9, Section II.B, Alg. 3] that operates using a virtual shuffle and performs $m - 2$ selections without the possibility of collisions. This algorithm has the property that all higher-order inclusion probabilities are equal, i.e. all possible
Add all elements of \( e \) and \( m \) copies of \( v \) into the new hyperedges \( h_x \) and \( h_y \).

Satisfy the invariants by swapping two copies of \( v \) with vertices in existing hyperedges.

Final state of the \( H \) list after the swap.

**Figure 1**: Demonstration of the operation of Algorithm SE-B for \( m = 4 \). On the left, the contents of \( e \) and \( m \) copies of \( v \) are added in the new hyperedges temporarily. This step is not explicit in the algorithm, as normally only 2 copies of \( v \) would be added, and it simply aids the visualization. In the middle, \( m - 2 \) existing hyperedges have been selected and one value of each (\( h_1^4 \) and \( h_2^4 \)) is identified as swappable with the new hyperedges. The state to the right is the final state of the \( H \) data structure after swapping these values. The new node \( v \) is in \( m \) hyperedges, whereas nodes \( e_1 \ldots e_4 \) in one more hyperedge than before.

\( m - 2 \) groups of hyperedges are equiprobable to be selected. It is worth noting that \( e \) might be one of these \( m - 2 \) hyperedges. The algorithm selects one node from each of these \( m - 2 \) hyperedges that is not already present in either \( h_x \) or \( h_y \) and swaps its value with \( v \). This selection can also be done in different ways but one option consistent with the choices made previously is to traverse an existing hyperedge in random order until a node is found not to be contained in the new hyperedge. Finally, the new hyperedges \( h_x \) and \( h_y \) are appended into \( H \). Note that Algorithm SE-B reduces to Algorithm SE-A for \( m = 2 \), as no exchanges are taking place. A diagram of the operation of Algorithm SE-B for \( m = 4 \) is shown in Figure 1.

Algorithm SE-B satisfies the correctness invariants, as during the updating of the \( H \) hypergraph, the newborn node that has degree \( m \) gains exactly \( m \) hyperedges and each node in \( e \), whose degree is increased by 1, gains one more hyperedge. No additional insertions or removals are performed, except swaps, leading to the following theorem:

**Theorem 11.** Algorithm SE-B satisfies the \( \sigma \pi \rho s \) probability scheme and generates a simple graph according to the definition of the BA model.
The complexity of algorithm SE-B can be derived from the complexity of the update function in Algorithm 10. The initial steps are operations that can be performed in time proportional to \( m \), including the selection of the \( m - 2 \) existing hyperedges. In order to fill \( h_x \) and \( h_y \), there are

\[
2 \cdot \left( \frac{m}{2} + \left( \frac{m}{2} + 1 \right) + \left( \frac{m}{2} + 2 \right) + \ldots + \left( m - 1 \right) \right) = \Theta(m^2)
\]

operations required in the worst case when every element checked in the existing hyperedges except for the last exists in either \( h_x \) or \( h_y \). This leads to the following theorem:

**Theorem 12.** Algorithm SE-B runs in time \( O(nm^2) \) to create a graph of \( n \) vertices.

Despite algorithm SE-B running in linear time with respect to \( n \), the \( nm^2 \) complexity of the worst case is unlikely to occur in a typical instance of the problem. Given that as \( n \) increases, the probability of collisions when finding elements in the existing hyperedges not already present in \( h_x \) and \( h_y \) is being reduced, we conjecture that the average case complexity of algorithm SE-B is \( O(nm) \). This hypothesis is supported by experimental observations but should be pursued in future work.

### 2.4 Algorithm SE-C

Algorithm SE-B works correctly with respect to the probability model involved but has one inherent property regarding the higher-order inclusion probabilities in the preferential attachment step, which refers to the probability of certain groups of vertices to acquire common neighbors during the growing process. Specifically, groups of vertices that have been selected together in the past are more likely to also be selected together in the future, since the nodes inside \( e \) are used to populate the new hyperedges. This behavior is sometimes desired, for example real social networks are not typically uncorrelated and have some degree of underlying structure. In this section, we describe algorithm SE-C, which can be used in situations where the above behavior is not desired. Unlike algorithm SE-B, algorithm SE-C is tunable with respect to the randomization and shuffling of the vertices inside the \( H \) data structure and can potentially minimize the effects of the higher-order inclusion probability bias.

The core idea of algorithm SE-C is, instead of swapping only a single element of each of the \( m - 2 \) existing hyperedges to replace \( v \), to shuffle all copies inside the \( m - 2 \) existing hyperedges as well as \( h_x \) and \( h_y \) (\( m^2 \) elements in total). Random systematic partitioning (Algorithm 9) fits this concept perfectly, as it is guaranteed that no vertex will have more copies than the number of hyperedges (\( v \) being the maximum with \( m \) copies).

A high level sketch of the update function of algorithm SE-C is shown in Algorithm 13. Following the scheme of random systematic partitioning, the contents of the \( m - 2 \) existing hyperedges and \( e \) as well as \( m \) copies of \( v \) are inserted into the partitioning algorithm and the resulting groups are replacing their old records, comprising the new value of the \( H \) hypergraph. It is worth noting that the shuffling performed by algorithm SE-C can be tuned by increasing the number
of hyperedges inserted into random systematic partitioning, for example $2m$ (2 new and $2m - 2$ existing) instead of $m$.

**Algorithm 13.** Algorithm SE-C – update function (high level sketch)

**Input** The existing hyperedge list $H$, the newborn node $v$ and the selected hyperedge $e$

**Output** The new state of the hyperedge list $H$

1: initialize empty array $A$
2: select and remove $m - 2$ hyperedges from $H$: $h_1, h_2, \ldots, h_{m-2}$
3: add $m \cdot (m - 2)$ elements from $h_1, h_2, \ldots, h_{m-2}$ into $A$
4: add $m$ copies of $v$ into $A$
5: add all elements of $e$ into $A$
6: perform random systematic partitioning on $A$ with $s = m$
7: add the $m$ sets of $A$ to $H$
8: return $H$

Algorithm SE-C performs the same amount of additions as Algorithm SE-B. Therefore, there is no change in the correctness in relation to algorithm SE-B:

**Theorem 14.** Algorithm SE-C satisfies the $strps$ probability scheme and generates a simple graph according to the definition of the BA model.

Regarding its complexity, Algorithm SE-C is bounded by the random systematic partitioning that is applied on $m^2$ elements and, hence, considering Theorem 8, its running time is proportional to $nm^2$. Unlike Algorithm SE-B, the running time is not impacted by the random number generator and its asymptotic performance is always proportional to $nm^2$:

**Theorem 15.** Algorithm SE-C runs in time $\Theta(nm^2)$ to create a graph of $n$ vertices.

As a closing remark, it is interesting to note that algorithm SE-C demonstrates the close association between preferential attachment and the random sampling problem. In fact, three different random sampling methods are involved in the design of algorithm SE-C to solve a preferential attachment problem:

1. One sampling algorithm to select $m - 2$ existing hyperedges from the population of hyperedges in $H$.
2. Random systematic partitioning, which is influenced by systematic random sampling and is used to both initialize the $H$ array from $G_0$ and to shuffle the node copies inside the $m$ hyperedges.
3. Jessen’s whole sampling method to update the $H$ array in such a way that the inclusion probabilities are always proportional to the degrees of the vertices.
In this paper, we exploit this relation in order to develop an implementation of the growing preferential attachment mechanism that perfectly fits the requirements of the \textit{strps} probability scheme. Future integration between these two problems should also be pursued in the future.

### 2.5 Discussion: The Initial Graph

In this section, we discuss the options for the initial graph $G_0(V_0, E_0)$ that can be used in our algorithms, explain its requirements that were previously omitted for brevity, and propose methods to satisfy them.

The global features of the scale free graph are expected to be independent of the initial graph, as the BA model is typically regarded a stationary distribution model. However, the initial graph state influences features of the first nodes, for example the probability that a specific node will become the heaviest node in the social network. For consistency and completeness, we note that the initial graph constitutes a state of our methods (the first state) and, as such, needs to satisfy the invariants of Section 2.2 in order for the transformation into the hypergraph $H$ to be feasible. In particular:

1. The number of edges $|E_0|$ in the initial graph needs to satisfy the divisibility $2|E_0|/m$.

2. No vertex can have degree higher than $2|E_0|/m$.

It is worth noting that the complete graph of $m$ vertices, which is a typical initial graph used in the BA model, satisfies both of these conditions without any processing required.

Regarding requirement (2), and assuming that requirement (1) is satisfied, a vertex may not have degree that is bigger than $2|E_0|/m$, otherwise the number of hyperedges in the $H$ data structure will not be enough for the copies of this vertex; at least one hyperedge would have to contain multiple copies, which is not allowed. For example, in the star graph of 5 vertices and $m = 4$, the center node has degree 4 while the sum of the degrees is 8. Thus, there are 2 hyperedges in $H$ but the center node needs to have 4 copies in $H$, which is impossible. This situation highlights the inherent issue of infeasibility in random sampling when the \textit{strps} model is used \cite{14}. In the previous example, the inclusion probability of the center node is $(4/8) \cdot 4 = 2$ (200%). A straightforward approach is to accept the fact that the probabilities are infeasible and to bound all infeasible probabilities to be at most 1, until the probabilities gradually become feasible as the number of nodes $n$ increases. We do not further discuss this issue.

Regarding requirement (1), considering that $H$ needs to contain an integer amount of hyperedges, it follows that $2|E_0|$ needs to be divisible by $m$. For example, a complete graph of 6 nodes for $m = 4$ does not satisfy this property (30 node copies are not divisible by 4). In the rest of this section, we discuss two methods to address the limitations imposed by requirement (1), namely forcing the number of edges to a specific value that does not oppose the requirement and introducing a multiplication factor that enlarges the count of all entries of the problem.
Forcing the number of edges  Initially, $G_0$ can be transformed into a graph that satisfies requirement (1) by selecting an appropriate number of edges and using the $G(n, M)$ generator to produce the initial graph. The minimum number of edges in the initial graph such that it satisfies the requirement is

$$|E_0|_{\text{min}} = \frac{\text{lcm}(m, 2)}{2},$$

while the largest number of edges depends on $|V_0|$ and is

$$|E_0|_{\text{max}} = \left\lfloor \frac{|V_0| \cdot (|V_0| - 1)}{\text{lcm}(m, 2)} \right\rfloor \cdot \text{lcm}(m, 2).$$

Thus, it follows that

$$|V_0| \cdot (|V_0| - 1) - \text{lcm}(m, 2) \leq |E_0|_{\text{max}} \leq |V_0| \cdot (|V_0| - 1),$$

which implies that $|E_0|_{\text{max}}$ is within a margin of $m$ or $2m$ of the edges of the complete graph with the same number of vertices that is often used as input. Naturally, the $G(n, M)$ generator is still subject to requirement (2) and rejections should be used to ensure that.

Introducing a multiplication factor  Another way to address the limitation caused by requirement (1) is to setup a factor of multiplication for the entire process. The multiplication factor is

$$\lambda = \frac{\text{lcm}(2|E_0|, m)}{2|E_0|}$$

and denotes the factor with which all node copies are multiplied with. Hence, for the initial graph, instead of inserting $2|E_0|$ entries in $H$, which might not be divisible by $m$, we are inserting $2\lambda|E_0| = \text{lcm}(2|E_0|, m)$ entries, which is divisible by $m$. Similarly, for the duration of the process, instead of inserting $2$ hyperedges, we insert $2\lambda$ hyperedges, where the copies of the vertices are multiplied also by $\lambda$. While our algorithms are easy to be generalized to support this process and completely solve the limitation if such behavior is desired, this method costs in memory and design complexity and for most cases the solution of generating an initial $G(n, M)$ graph with the closest number of acceptable edges should be preferred.

3 Experimental Approach

In this section, we present some computer experiments that highlight the behavior of algorithms SE-A, SE-B and SE-C in practical situations for finite $n$. We focus on two properties that typically arise in social network analysis of scale-free graphs: the degree distribution and properties surrounding the local clustering coefficient. We specify that for all experiments the version of the SE-C algorithm refers to the algorithm that shuffles $m$ hyperedges (instead of more) while the random systematic
partitioning algorithm is used for the initialization of the auxiliary hypergraph $H$. Finally, the split of $e$ in the two new hyperedges is performed using the random method with equal split. The reference implementation of our algorithms is available online\textsuperscript{3}.

### 3.1 Degree distribution

For the experimental approach of the degree distribution of our algorithms we use $n = 300\,000$ in order to capture an approximation of the asymptotic state of the limiting distribution. By definition, the SE-A algorithm is only compatible with $m = 2$. For the SE-B and SE-C algorithms we use $m = 5$, as using $m = 2$ would result in identical behavior to SE-A, but within the limits of what is often used in practice. These are also the settings of $m$ that are used throughout this section. In terms of the initial graph, the complete graph of $|V_0| = m$ is used.

Figure 2 shows the experimental degree distributions of the three algorithms; from left to right SE-A, SE-B and SE-C. The plots were generated using 10\,000 iterations of the generation process to achieve statistical stability. The plots also contain the theoretical degree distribution (Equation 3) as a cyan line rendered on top of the data points. We note that, despite the theoretical distribution being a discrete probability distribution, it is rendered here as continuous in order to be visually distinguishable from the data points. The simulation shows that the resulting graphs are scale-free and an almost exact fit with the theoretical distribution. Although algorithms SE-A, SE-B and SE-C are different in their operation and their internal preferential attachment mechanism, they all result

\textsuperscript{3}https://github.com/gstatatelat/preferential-attachment-se
in scale-free distribution because they all satisfy the $st\pi ps$ property, as otherwise proven in [11].

### 3.2 Local clustering coefficient distribution

The local clustering coefficient is typically used in social network analysis in order to study the degree to which nodes in a graph tend to cluster together. Initially, we experimentally show the local clustering coefficient distribution for our three models. While the distribution is analytically found for the SE-A model (Equation 5), the experiment provides insight about this distribution in the SE-B and SE-C models, which might be more difficult to gain analytically. It should be noted that, while the degree distribution of the three models is identical in terms of its shape according to the $st\pi ps$ property, the same is not guaranteed in the experiments regarding the local clustering coefficient that follow.

Figure 3 shows our experimental results. The same $n$ and $m$ settings were used as in the degree distribution experiment; we also performed 10,000 iterations here for statistical stability. For the case of SE-A, the theoretical local clustering coefficient distribution is displayed (cyan line), with a strongly perceivable association with the experimental data points. In this case too, the theoretical distribution is displayed as a continuous distribution. For the SE-B and SE-C models, the distribution is more complicated and contains significant fluctuation noise; for this reason it is displayed here as a histogram of linearly binned data. The local clustering coefficient distributions of the SE-B and SE-C algorithms appear to be bitonic and resemble the log-normal distribution but this should be investigated further.
Figure 4: Average local clustering coefficient with respect to \( n \) for the SE-A, SE-B and SE-C models. The horizontal axis spans from 5 to 5000. While SE-A immediately converges to its theoretical average, the SE-B and SE-C models have declining behavior.

### 3.3 Average local clustering coefficient

Another perspective of the clustering properties of our algorithms is the average local clustering coefficient with respect to its size \( n \). While the results displayed in Figure 3 indicate that the average local clustering coefficient of SE-C is lower than this quantity for SE-B due to the distribution being more biased towards the lower \( x \) values, the plot does not show how the average is shaped over the duration of the generation process. For this analysis, we use the same settings for \( m \) as previously and increase \( n \) from 5 to 5000 in order to observe how the average local clustering coefficient behaves.

Figure 4 presents the results of the simulation of 1000 iterations of the experiment. It can be observed that Algorithm SE-A converges fast to its theoretical expectation given in Equation 4. For the SE-B and SE-C there is an apparent declining behavior with respect to \( n \) which is due to the initial graph being a clique with average local clustering coefficient 1. The average local clustering coefficients of both algorithms appear to converge with Algorithm SE-C having smaller values for graph sizes \( n \) up to 5000.

### 3.4 Degree correlation with local clustering coefficient

The convergence of the average local clustering coefficient of Figure 4 can be better understood via the correlation among the degree and the local clustering coefficient. The properties surrounding the connection between these two quantities for uncorrelated scale-free graphs have been studied before, for example in [15, Section 2.2], [16] and [17]. Due to our graph generators not being uncorrelated, we approach this association experimentally. The same settings of \( n = 300000 \) and \( m = 2, 5 \) are
Our results are illustrated in Figure 5. In this scatter plot, the horizontal component of each point represents the degree value and the vertical component represents the average local clustering coefficient of the vertices with that degree. The plots are averaged over the results of 20,000 iterations for the SE-B and SE-C figures and 1 iteration for the deterministic SE-A experiment. The theoretical correlation of the SE-A algorithm, given in Theorem 5 (2/d) is also presented in the figure as a continuous cyan line. A declining behavior is observed for all three methods, which is consistent with previous findings of uncorrelated graphs [15, 16, 17]. Moreover, the convergence of Figure 4 can be further explained. Following the process shown in Equation 4 and the declining nature of the degree-clustering correlation, it can be easily seen that the average local clustering coefficient converges to a non-zero constant for both SE-B and SE-C cases as $n \to \infty$.

### 3.5 Discussion: The higher-order case

The experimental simulations of this section also raise discussion regarding the high-order dynamics of the BA model and the preferential attachment mechanism in general. While the first-order properties define the probability that individual vertices are selected during a step of the preferential attachment process, the higher-order properties define the probability that groups of vertices are selected together during a single step of the growing process. The issue has been raised before [5], where it is claimed that the BA model is not one model but a family of models that respect the same first-order probability model but not necessarily the higher-order model. In the original works of
Barabási and Albert, it is shown that the degree distribution, and therefore the scale-free nature of the resulting graph, only depend on the first-order properties of the generator. Given that the scale-free nature of the BA model is regarded as the most interesting property of the model, the properties surrounding the higher-order case are less studied and known.

The algorithms SE-A, SE-B and SE-C presented in this paper are examples of the distinction between the first and higher order probabilities of the preferential attachment mechanism. While their degree distribution is identical (assuming the same value for \( m \)), our experiments indicate a significant difference on their higher-order properties. One such property is related to the clustering coefficient and the probabilities of certain groups of vertices to gain a common neighbor on each of the preferential attachment steps. This phenomenon, in turn, impacts the probabilities of triangle formations or the degree at which certain groups of vertices form stronger clusters. This situation is more prevalent and extreme in the SE-A algorithm, where pairs of vertices that are not connected via an edge will never gain a common neighbor. The quantities surrounding the higher-order properties of different scale-free graph generators are worth investigating and positioned in relation to each other in the future.

4 Conclusions

In this paper, we have utilized multiple random sampling schemes and methods to design a class of scale-free graph generator algorithms. Our models obey the dynamics of the preferential attachment scheme and the definition of the BA model. In particular, the algorithms are designed such that the inclusion probability of any vertex and at any time of the process is exactly proportional to its degree. This behavior is in contrast to existing methods where the inclusion probabilities are only approximately proportional to their degree. Our algorithms, that are primarily based on the concept of whole sampling, also run in linear time with respect to the desired graph size \( n \). This is, to the best of our knowledge, the first time that both strict probability interpretation and linear complexity are achieved in the literature for the generation of scale-free graphs via the preferential attachment mechanism.

Our analysis started with algorithm SE-A, the simple case for \( m = 2 \) that demonstrates the principle of our approach, where one uniform random edge is selected and a newborn node is connected with its endpoints. The correctness of this algorithm was shown by the fact that a vertex exists in the edge set as many times as its degree. The generalization of SE-A, algorithm SE, is proposed, that uses an auxiliary data structure \( H \) that resembles a \( m \)-uniform hypergraph and works for \( m \geq 2 \). While the operation of this algorithm is abstract, the necessary invariants are defined that guarantee its correctness. Finally, algorithms SE-B and SE-C implement algorithm SE more concretely by either exchanging the necessary values in \( H \) to ensure the invariants are satisfied or completely shuffling parts of \( H \) respectively. Our computer simulation experiments confirm the scale-free nature in the resulting graphs and raise interesting observations and future work directions.
about the higher-order properties surrounding the clustering features of the resulting scale-free graphs.

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