# Generating graphs randomly<sup>1</sup>

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#### Abstract

Graphs are used in many disciplines to model the relationships that exist between objects in a complex discrete system. Researchers may wish to compare a network of interest to a "typical" graph from a family (or ensemble) of graphs which are similar in some way. One way to do this is to take a sample of several random graphs from the family, to gather information about what is "typical". Hence there is a need for algorithms which can generate graphs uniformly (or approximately uniformly) at random from the given family. Since a large sample may be required, the algorithm should also be computationally efficient.

Rigorous analysis of such algorithms is often challenging, involving both combinatorial and probabilistic arguments. We will focus mainly on the set of all simple graphs with a particular degree sequence, and describe several different algorithms for sampling graphs from this family uniformly, or almost uniformly.

#### 1 Introduction

The modern world is full of networks, and many researchers use graphs to model real-world networks of interest. When studying a particular real-world network it is often convenient to define a family, or ensemble, of graphs which are similar to the network in some way. Then a random element of the ensemble provides a  $null\ model$  against which the significance of a particular property of the real-world model can be tested. For example, a researcher may observe that their network contains what looks like a large number of copies of a particular small subgraph H, also called a "motif" in network science. If this number is large compared to the average number of copies of H in some appropriate ensemble of graphs, then this provides some evidence that the high frequency of this motif may be related to the particular function of the real-world network. (For more on network motifs see for example [94].)

In this setting, the null model is a random graph model, and it may be possible to analyse the relevant properties using probabilistic combinatorics. Where this is not possible, it is very convenient to have an algorithm which provides uniformly random (or "nearly" uniformly random) graphs from the ensemble, so that the average number of copies of H can be estimated empirically. Such an algorithm should also be efficient, as a large sample may be needed. (In this survey, "efficient" means "computationally efficient".) Another motivation for the usefulness of algorithms for sampling graphs can be found in the analysis of algorithms which take graphs as input, especially when the worst-case complexity bound is suspected to be far from tight in the average case.

The aim of this survey is to describe some of the randomized algorithms which have been developed to efficiently sample graphs with certain properties, with partic-

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ular focus on the problem of uniformly sampling graphs with a given degree sequence. We want to understand how close the output distribution is to uniform, and how the runtime of the algorithm depends on the number of vertices. Hence we restrict our attention to algorithms which have been rigorously analysed and have certain performance guarantees. In particular, statistical models such as the exponential random graph model (see for example [25, 69, 85, 118]), will not be discussed. Although we mainly restrict our attention to simple, undirected graphs, most of the ideas discussed in this survey can also be applied to bipartite graphs, directed graphs and hypergraphs, which are all extremely useful in modelling real-world networks.

It is still an open problem to find an efficient algorithm for sampling graphs with an arbitrary degree sequence. For bipartite graphs, however, the sampling problem was solved for arbitrary degree sequences by Jerrum, Sinclair and Vigoda [78], as a corollary of their breakthrough work on approximating the permanent. See Section 6.2 for more detail.

This is not a survey on random graphs. (Our focus is on *how* to randomly sample a graph from some family efficiently, from an algorithmic perspective, rather than on the properties of the resulting random graph.) However, some techniques are useful both as tools to analyse random graphs and as procedures for producing random graphs. There are many texts on random graphs [17, 52, 73], as well as Wormald's excellent survey on random regular graphs [120].

Before proceeding, we remark that in network science, the phrase "graph sampling algorithm" can refer to an algorithm for sampling vertices or subgraphs *within* a given (huge) graph (see for example [116]). For this reason, we will avoid using this phrase and will instead refer to "algorithms for sampling graphs".

#### 2 Preliminaries and Background

#### 2.1 Notation and assumptions

Let  $[a] = \{1, 2, \dots, a\}$  for any positive integer a.

A multigraph G = (V, E) consists of a set of vertices V and a multiset E of edges, where each edge is an unordered pair of vertices (which are not necessarily distinct). A loop is an edge of the form  $\{v, v\}$  and an edge is repeated if it has multiplicity greater than one. A graph is a simple multigraph: that is, a multigraph with no loops and no repeated edges. All graphs are finite and labelled, so V is a finite set of distinguishable vertices. A directed multigraph is defined similarly, except that edges are now ordered pairs. A directed graph is a directed multigraph which is simple, which means that it has no (directed) loops and no repeated (directed) edges.

Throughout, n will be the number of vertices of a graph, unless otherwise specified. We usually assume that the vertex set is [n].

Standard asymptotic notation will be used, and asymptotics are as  $n \to \infty$  unless otherwise specified. Let f, g be real-valued functions of n.

- Write f(n) = o(g(n)) if  $\lim_{n \to \infty} f(n)/g(n) = 0$ .
- Suppose that g(n) is positive when n is sufficiently large. We write f(n) = O(g(n)) if there exists a constant C such that  $|f(n)| \leq C g(n)$  for all n sufficiently large.

• Now suppose that f(n) and g(n) are both positive when n is sufficiently large. If f = O(g) and g = O(f) then we write  $f(n) = \Theta(g(n))$ .

We sometimes write  $\approx$  to denote an informal notion of "approximately equal". In pseudocode, we write "u.a.r." as an abbreviation for *uniformly at random*.

When calculating the runtime of algorithms, we use the "Word RAM" model of computation [51, 66]. In this model, elementary operations on integers with  $O(\log n)$  bits can be performed in unit time.

Randomised algorithms require a source of randomness. We assume that we have a perfect generator for random integers uniformly distributed in  $\{1, 2, ..., N\}$  for any positive integer N. Furthermore, we assume that this perfect generator takes unit time whenever N has  $O(\log n)$  bits.

#### 2.2 Which graph families?

It is very easy to sample from some graph families:

- Let S(n) denote the set of all  $2^{\binom{n}{2}}$  graphs on the vertex set [n]. We can sample from G(n) very easily: flip a fair coin independently for each unordered pair of distinct vertices  $\{j,k\}$ , and add  $\{j,k\}$  to the edge set if and only if the corresponding coin flip comes up heads. Every graph on n vertices is equally likely, so this gives an exactly uniform sampling algorithm with runtime  $O(n^2)$ .
- Next we might consider S(n, m), the set of all  $\binom{\binom{n}{2}}{m}$  graphs on the vertex set [n] with precisely m edges. A uniformly random graph from this set can be generated edge-by-edge, starting with the vertex set n and no edges. At each step, choose a random unordered pair of distinct vertices  $\{j, k\}$ , without replacement, and add this edge to the graph. When the graph has m edges, it is a uniformly random element of S(n, m). This algorithm has runtime  $O(n^2)$ . Letting  $G_i$  denote the graph obtained after i edges have been added, the sequence  $G_0, G_1, \ldots, G_m$  is known as the random graph process, with  $G_i$  a uniformly-random element of S(n, i) for all  $i \in [m]$ .

A uniform element from S(n,m) corresponds to the Erdős-Rényi random graph  $\mathcal{G}(n,m)$ , while the binomial random graph model  $\mathcal{G}(n,p)$  is obtained by adapting the process for sampling from S(n) described above, replacing the fair coin by a biased coin which comes up heads with probability p. These two random graph models have been the subject of intense study for more than 60 years, see for example [17, 46, 52, 61, 73]. However, since polynomial-time sampling is easy for both of these families (as described above), we will say no more about them.

Instead, our focus will be on algorithms for sampling graphs with a given degree sequence. More generally, we might be interested in bipartite graphs, directed graphs or hypergraphs with a given degree sequence. Alternatively, we may want to sample graphs with a given degree sequence and some other property, such as connectedness or triangle-freeness. There are many variations, but our main focus will be on sampling from the set  $G(\mathbf{k})$  defined below.

**Definition 2.1** A graph G on vertex set [n] has degree sequence  $\mathbf{k} = (k_1, \dots, k_n)$  if  $\deg_G(j) = k_j$  for all  $j \in [n]$ , where  $\deg_G(j)$  denotes the degree of j in G. Let  $G(\mathbf{k})$  denote the set of all graphs with degree sequence  $\mathbf{k}$ . A sequence  $\mathbf{k} = (k_1, \dots, k_n)$  of nonnegative integers with even sum is graphical if  $G(\mathbf{k})$  is nonempty. A graph with degree sequence  $\mathbf{k}$  is a realization of  $\mathbf{k}$ .

We do not assume here that the elements of k are in non-ascending order, though we will usually assume that all entries of k are positive. Unlike the binomial random graph model  $\mathcal{G}(n,p)$ , the edges of a randomly-chosen element of G(k) are not independent. This lack of independence makes sampling from G(k) a non-trivial task.

If  $\mathbf{k} = (k, k, \dots, k)$  has every entry equal to k, then we say that  $\mathbf{k}$  is regular. The set of all k-regular graphs on the vertex set [n] will be denoted by G(n, k) instead of  $G(\mathbf{k})$ .

We close this subsection with some more comments on graphical degree sequences. The characterisations of Erdős and Gallai [38] and Havel and Hakimi [68, 67] both give algorithms which can be used to decide, in polynomial time, whether a given sequence is graphical. The Erdős-Gallai Theorem says that if  $k_1 \geq \cdots \geq k_n$  then k is graphical if and only if  $\sum_{j=1}^{n} k_j$  is even and

$$\sum_{j=1}^{p} k_j \le p(p-1) + \sum_{j=p+1}^{n} \min\{k_j, p\}$$

for all  $p \in [n]$ . To avoid trivialities, we will always assume that the sequence k is graphical. The Havel–Hakimi characterisation also assumes that entries of k are in non-decreasing order, and states that k is graphical if and only if

$$(k_2-1,\ldots,k_{k_1+1}-1,k_{k_1+2},\ldots,k_n)$$

has no negative entries and is graphical. This leads to a greedy algorithm to construct a realisation of k in runtime  $O(n^2)$ : join vertex 1 to each of vertices  $2, \ldots, k_1+1$ , delete vertex 1, reduce the target degree of vertices  $2, \ldots, k_1+1$  by 1, sort the new degree sequence into nonincreasing order if necessary, and recurse. The runtime of this greedy algorithm is  $O(n^2)$ .

#### 2.3 What kind of sampling algorithm?

To be more precise about our goals, we need some definitions. Let  $(\Omega_n)_{n\in\mathcal{I}}$  be a sequence of finite sets indexed by a parameter n from some infinite index set  $\mathcal{I}$ , such as  $\mathcal{I} = \mathbf{Z}^+$  or  $\mathcal{I} = 2\mathbf{Z}^+$ . Asymptotics are as n tends to infinity along elements of  $\mathcal{I}$ . We assume that  $|\Omega_n| \to \infty$  as  $n \to \infty$ .

The reason that we consider a sequence of sets, rather than just one set, is that it makes no sense to say that the runtime of an algorithm is polynomial for a particular set  $\Omega$ . If the runtime of an algorithm for sampling from  $\Omega$  is T, then we could say that this is a constant-time algorithm with constant T, but then we learn nothing about how long the algorithm might take when given a different set as input. Having said that, in our notation we often drop the sequence notation and simply refer to  $\Omega_n$ .

As a general rule, we say that a (uniform) sampling algorithm for  $\Omega_n$  is efficient if its runtime is bounded above by a polynomial in  $\log(|\Omega_n|)$ , as it takes  $\log(|\Omega_n|)$  bits to describe an element of  $\Omega_n$ . However, the runtime of the algorithm may have a deterministic upper bound, or it may be a random variable, leading to the following paradigms:

- A Monte Carlo algorithm is a randomised algorithm which is guaranteed to terminate after some given number of steps, but has some probability of incorrect output. (The probability of incorrect output should be small.) A Monte Carlo sampling algorithm for  $\Omega_n$  is efficient if its runtime is bounded above by a polynomial in  $\log(|\Omega_n|)$ .
- A Las Vegas algorithm is a randomised algorithm which is guaranteed to provide correct output with probability 1, but may have no deterministic upper bound on its running time. A Las Vegas sampling algorithm for  $\Omega_n$  is efficient if its expected runtime is bounded above by a polynomial in  $\log(|\Omega_n|)$ .

Next, we focus on the output of the algorithm, and give three different definitions of "close to uniform". First we need a notion of distance for probability distributions.

**Definition 2.2** Let  $\sigma$  and  $\pi$  be two probability distributions on the finite set  $\Omega$ . The total variation distance between  $\sigma$  and  $\pi$ , denoted  $d_{TV}(\sigma, \pi)$ , is given by

$$d_{TV}(\sigma, \pi) = \frac{1}{2} \sum_{x \in \Omega} |\sigma(x) - \pi(x)| = \max_{S \subseteq \Omega} |\sigma(S) - \pi(S)|.$$

Here  $\sigma(S) = \sum_{x \in S} \sigma(x)$  for any event  $S \subseteq \Omega$ , and similarly for  $\pi(S)$ .

Suppose that some sampling algorithm over  $\Omega_n$  has output distribution  $\sigma_n$ , and let  $\pi_n$  denote the uniform distribution over  $\Omega_n$ , for any  $n \in \mathcal{I}$ .

- If  $\sigma_n = \pi_n$  for all  $n \in \mathcal{I}$  then we say that the algorithm is a uniform sampling algorithm or uniform sampler.
- If  $\lim_{n\to\infty} d_{TV}(\sigma,\pi) = 0$  then we say that the algorithm is an asymptotically uniform sampler. In this situation it is usually not possible to increase the accuracy by running the algorithm for longer, as the total variation distance depends only on n.
- If  $d_{TV}(\sigma_n, \pi_n) < \varepsilon$  for some positive constant  $\varepsilon$  then we say that the algorithm is an almost uniform sampler, and that the output is  $\varepsilon$ -close to uniform. Often,  $\varepsilon$  is provided by the user, and higher accuracy (smaller  $\varepsilon$ ) can obtained at the cost of a longer runtime.

The Markov chain approach to sampling, when successful, provides an algorithm called an FPAUS. See for example [74, Chapter 3].

**Definition 2.3** Let  $(\Omega_n)_{n\in\mathcal{I}}$  be a sequence of finite sets indexed by a parameter n from some infinite index set  $\mathcal{I}$ , such that  $|\Omega_n| \to \infty$  as  $n \to \infty$ . A fully-polynomial almost uniform sampler (FPAUS) for sampling from  $\Omega_n$  is an algorithm that, with probability at least  $\frac{3}{4}$ , outputs an element of  $\Omega_n$  in time polynomial in  $\log |\Omega_n|$  and

 $\log(1/\varepsilon)$ , such that the output distribution is  $\varepsilon$ -close to the uniform distribution on  $\Omega_n$  in total variation distance. (That is,  $d_{TV}(\sigma_n, \pi_n) < \varepsilon$  where  $\sigma_n$  is the output distribution and  $\pi_n$  is the uniform distribution on  $\Omega_n$ .)

If  $\Omega_n = G(\mathbf{k})$  for some graphical sequence  $\mathbf{k} = (k_1, \dots, k_n)$  then  $\log |\Omega_n| = O(M \log M)$ , where M is the sum of the entries of  $\mathbf{k}$ . This can be proved using the configuration model: see (6.4). So an FPAUS for  $G(\mathbf{k})$  must have running time bounded above by a polynomial in n and  $\log(1/\varepsilon)$ , since  $M \leq n^2$ .

Sampling and counting are closely related, and an algorithm for one problem can often be transformed into an algorithm for the other. While our focus is firmly on sampling, we will also need the following definition which describes a good approximate counting algorithm.

**Definition 2.4** Let  $(\Omega_n)_{n\in\mathcal{I}}$  be a sequence of finite sets indexed by a parameter n from some infinite index set  $\mathcal{I}$ , such that  $|\Omega_n| \to \infty$  as  $n \to \infty$ . A fully-polynomial randomised approximation scheme (FPRAS) for  $\Omega_n$  is an algorithm which accepts as input a parameter  $\varepsilon > 0$  and outputs an estimate X for  $|\Omega_n|$  such that

$$\Pr\left((1-\varepsilon)|\Omega_n| \le X \le (1+\varepsilon)|\Omega_n|\right) \ge \frac{3}{4},$$

with runtime polynomial in  $\log |\Omega_n|$  and  $\varepsilon^{-1}$ .

The probability in this definition can be easily increased from  $\frac{3}{4}$  to  $1 - \delta$ , for any fixed  $\delta \in (\frac{3}{4}, 1)$ , by obtaining  $O(\log \delta^{-1})$  estimates and taking the median [105, Lemma 2.1].

Before moving on, we say a little more about the connection between sampling and counting. Jerrum, Valiant and Vazirani [79] proved that for self-reducible problems, polynomial-time approximate counting is equivalent to polynomial-time almost-uniform sampling. Without going into too much detail, a problem is self-reducible if the solutions for a given instance can be generated recursively using a small number of smaller instances of the same problem. For example, consider the set  $\mathcal{M}(G)$  of all matchings (of any size) in a graph G. Remove the edges of G one-by-one (in lexicographical order, say) to form the sequence

$$G = G_m > G_{m-1} > \cdots > G_1 > G_0 = (V, \emptyset).$$

Then  $|\mathcal{M}(G_0)| = 1$  and hence  $|\mathcal{M}(G)| = \prod_{j=1}^m |\mathcal{M}(G_j)|/|\mathcal{M}(G_{j-1})|$ . The j'th ratio is the inverse of the probability that  $e_j \notin M$ , where M is a matching chosen uniformly at random from  $\mathcal{M}(G_j)$  and  $e_j$  is the unique edge in  $E(G_j) \setminus E(G_{j-1})$ . If we can sample almost-uniformly from the sets  $\mathcal{M}(G_j)$  to sufficient accuracy then estimates for these probabilities can be multiplied together to provide a good estimate for  $1/|\mathcal{M}(G)|$ . In this way, approximate counting can be reduced to almost-uniform sampling. See [74, Chapter 3] for full details.

For sampling graphs, the situation is a little more complicated. Erdős et al [41] showed that the problem of sampling graphs, or directed graphs, with given degrees can be made self-reducible by supplying as input a small set of forbidden edges, and sampling from the set of graphs (or bipartite graphs, or directed graphs) with

specified degrees which avoid the forbidden edges. Using the fact that directed graphs can be modelled as bipartite graphs which avoid a given perfect matching, the set of forbidden edges can be taken to be a star (for undirected graphs) or the the union of a star and a perfect matching. We remark that the exact counting problem (given a graphical sequence k, calculate |G(k)|) is not known to be #P-complete, and similarly for bipartite or directed variants.

## 2.4 Sampling graphs with given degrees: an overview

We assume that for all n in some infinite index set  $\mathcal{I}$ , we have a graphical degree sequence  $\mathbf{k}(n) = (k_1(n), \dots, k_n(n))$ . The length of  $\mathbf{k}(n)$  is n, and the elements of  $\mathbf{k}(n)$  might themselves be functions of n. Our sequence  $(\Omega_n)_{n\in\mathcal{I}}$  of sets (as discussed in the previous subsection) is given by taking  $\Omega_n = G(\mathbf{k}(n))$ . From now on, we simply write  $\mathbf{k} = (k_1, \dots, k_n)$  for the degree sequence, but we should remember that in fact we have a sequence of degree sequences, indexed by n.

The maximum entry in a degree sequence k is denoted  $k_{\max}$ . Let  $M = \sum_{j \in [n]} k_j$  be the sum of the degrees. Then m = M/2 the number of edges of any graph in G(k).

There are a few different methods for sampling graphs with given degrees (restricted to algorithms which can be rigorously analysed). We outline the main approaches here, and go into more detail in the subsequent sections.

- The configuration model was introduced by Bollobás [16] in 1980, as a convenient way to calculate the probability of events in random regular graphs. The model can be used as an algorithm for sampling uniformly at random from  $G(\mathbf{k})$ . However, the expected runtime is high unless the degrees are very small: specifically,  $k = O(\sqrt{\log n})$  in the regular case.
- McKay and Wormald's switchings-based algorithm [91] from 1990 performs (exactly) uniform sampling from  $G(\mathbf{k})$  in expected polynomial time, for a much wider range of degrees than the algorithm arising from the configuration model, namely  $k_{\text{max}} = O(M^{1/4})$ . Gao and Wormald [59] and Arman, Gao and Wormald [5] have extended and improved the McKay-Wormald algorithm, allowing it to apply to a wider range of degrees and making it more efficient. These algorithms are fast, but a little complicated and difficult to implement. See the end of Section 5.1.
- Another approach is to use a  $Markov\ chain$  with uniform stationary probability over a state space  $G'(\mathbf{k})$  which contains  $G(\mathbf{k})$ . If the Markov chain converges rapidly to its stationary distribution, and each step of the Markov chain can be implemented efficiently, then this gives an FPAUS for  $G'(\mathbf{k})$ . In 1990, Jerrum and Sinclair [76] described and analysed a Markov chain which samples from a set  $G'(\mathbf{k})$  of graphs with degree sequence close to  $\mathbf{k}$ . The Jerrum–Sinclair chain is efficient only when  $G(\mathbf{k})$  forms a sufficiently large fraction of  $G'(\mathbf{k})$ . When this condition on  $G(\mathbf{k})$  holds, rejection sampling can be used to restrict the output of the chain to  $G(\mathbf{k})$ . The requirement that  $|G(\mathbf{k})|/|G'(\mathbf{k})|$  is sufficiently large gives rise to a notion of stability of degree sequences. Another well-studied Markov chain, the  $switch\ chain$ , has state space  $G(\mathbf{k})$  and thus avoids

rejection sampling. Most proofs in this area use Sinclair's multicommodity flow method [104], and the resulting bounds, when polynomial, tend to be rather high-degree and are not believed to be tight.

• In 1999, Steger and Wormald [106] presented an algorithm for performing asymptotically uniform sampling for k-regular graphs. Their aim was to provide an algorithm which is both genuinely fast (runtime  $O(k^2n)$  when k is a small power of n) and easy to implement. While the idea for the algorithm is motivated by the bounded-degree graph process [101], the algorithm is presented as a modification of the configuration model. We also describe extensions and enhancements by Kim and Vu [82] and Bayati, Kim and Saberi [7]: in particular, Bayati et al. [7] used sequential importance sampling to provide an algorithm which is almost an FPAUS, when  $k_{\text{max}} = O(M^{\frac{1}{4}-\tau})$  for any constant  $\tau > 0$ .

The configuration model is described in Section 3, followed in Section 4 by the sequential algorithms beginning with the work of Steger and Wormald. Switchings-based algorithms are discussed in Section 5, and Markov chain (MCMC) algorithms are presented in Section 6.

# 3 The configuration model

The configuration model, introduced by Bollobás [16], is very useful in the analysis of random graphs with given degrees. It also arose in asymptotic enumeration work of Bender and Canfield [9], and was first explicitly used as an algorithm by Wormald [119].

Given a degree sequence k, and recalling that  $M = \sum_{j \in [n]} k_j$ , we take M objects, called *points*, grouped into n cells, where the j'th cell contains  $k_j$  points. Each point is labelled, and hence distinguishable. (You can think of the points corresponding to vertex j as being labelled by  $(j, 1), \ldots, (j, k_j)$ , say. But we will not refer to these labels explicitly.)

In the network theory literature (for example [50]), points are sometimes called *stubs*, or *half-edges*, without the concept of a cell (so that  $k_j$  half-edges emanate from vertex j).

A configuration, also called a pairing, is a partition of the M points into M/2 pairs. This is often described as a perfect matching of the M points. Given a configuration P, shrinking each cell to a vertex and replacing each pair by an edge gives a multigraph G(P) with degree sequence k. The multigraph is simple if it has no loops and no repeated edges, and in this case we also say that P is simple.

Figure 1 shows two configurations with the same degree sequence, namely  $\mathbf{k} = (3, 3, 1, 2, 2, 3, 2, 2)$  if cells are labelled clockwise from the top-left. The small black circles represent points, which are shown inside cells, and the lines between points represent pairs. The configuration on the left is not simple, as it will produce a loop on the vertex corresponding to the cell marked with "\*", and a repeated edge between the vertices corresponding to the two cells marked with "\*\*". The configuration on the right is simple.

Let  $\mathcal{P}(\mathbf{k})$  be the set of all configurations corresponding to the degree sequence  $\mathbf{k}$ . The term *configuration model* typically refers to the uniform probability model over

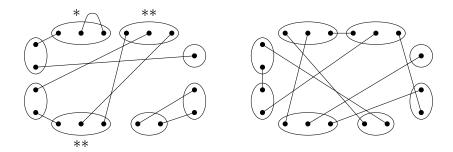


Figure 1: Two configurations with the same degree sequence

the set  $\mathcal{P}(\mathbf{k})$ . A uniformly random configuration from  $\mathcal{P}(\mathbf{k})$  can be chosen in O(M) time, as follows. Starting with all points unmatched, at each step take an arbitrary point p and pair it with a point chosen uniformly at random from the remaining unmatched points (excluding p). Once all points have been paired up, we have a configuration P and each configuration is equally likely.

The configuration model can be used as an algorithm for sampling uniformly from  $G(\mathbf{k})$ , by repeatedly sampling  $P \in \mathcal{P}(\mathbf{k})$  uniformly at random until G(P) is simple. This algorithm is displayed in Figure 2.

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Configuration model sampling algorithm Input: graphical sequence k Output: element of G(k)

repeat choose P \in \mathcal{P}(k) u.a.r. until G(P) is simple output G(P)
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Figure 2: The configuration model as a sampling algorithm

Observe that if G is a simple graph with degree sequence k then G corresponds to exactly  $\prod_{j \in [n]} k_j!$  configurations, as there are  $k_j!$  ways to assign points to the edges incident with vertex j, and these assignments can be made independently for each vertex  $j \in [n]$ . Hence every element of G(k) is equally likely to be produced as output of the above process.

This gives a Las Vegas sampling algorithm, with expected runtime which depends linearly on the probability that a random configuration is simple. Hence, the configuration model can be used for efficient sampling when the probability that a randomly chosen configuration is simple is bounded below by 1/p(n), for some polynomial p(n). In this case, the expected number of trials before a simple configuration is found is at most p(n), and the expected runtime is O(M p(n)).

A multigraph is simple if and only if it contains no 1-cycles (loops) and no 2-cycles (arising from repeated edges). If the maximum degree is not too large compared to the number of edges, then in a uniformly random element of  $\mathcal{P}(\mathbf{k})$ , the number

of 1-cycles and the number of 2-cycles are asymptotically independent Poisson random variables. In the k-regular case, Bender and Canfield [9] proved in 1978 that a uniformly random configuration is simple with probability  $(1 + o(1)) e^{-(k^2 - 1)/4}$ . Hence the configuration model for k-regular graphs gives an expected polynomial time algorithm as long as  $k = O(\sqrt{\log n})$ . A very precise estimate of Pr(simple), with many significant terms, was given by McKay and Wormald [92] in 1991 under the assumption that  $k_{\text{max}}^3 = o(M)$ . To prove the following result, we use the estimate (3.1) obtained by Janson [71] in 1999, which is valid for a wider range of degrees.

**Theorem 3.1** [71] Let  $R = R(\mathbf{k})$  be defined by  $R = \sum_{j \in [n]} k_j^2$ . The configuration model gives a uniform sampling algorithm for  $G(\mathbf{k})$ . If  $k_{\max}^2 = o(M)$  then the expected runtime of this algorithm is

$$\Theta(M \exp(R^2/(4M^2)))$$

when  $k_{\max}^2 = o(M)$ . So the expected runtime is polynomial if and only if  $R = \Theta(M\sqrt{\log n})$ . In particular, if  $k_{\max} = O(\sqrt{\log n})$  then the expected runtime is polynomial.

**Proof** (Sketch.) The output is distributed uniformly as each element of  $G(\mathbf{k})$  is simple, and hence corresponds to the same number of configurations in  $\mathcal{P}(\mathbf{k})$ . The expected number of trials required before a simple configuration is found is  $1/\Pr(\text{simple})$ , where  $\Pr(\text{simple})$  denotes the probability that a uniformly chosen configuration from  $\mathcal{P}(\mathbf{k})$  is simple. Janson [71] proved that if  $k_{\text{max}}^2 = o(M)$  then the probability that a random configuration is simple is

$$\Pr(\text{simple}) = \exp\left(-\frac{R^2}{4M^2} + \frac{1}{4}\right) + o(1).$$
 (3.1)

Hence the expected runtime of the algorithm is  $\Theta(M/\Pr(\text{simple}))$ , which is bounded above by a polynomial if and only if  $R = \Theta(M\sqrt{\log n})$ . The last statement of the theorem follows since  $R \leq k_{\max}M$ .

There are versions of the configuration model which can be used to sample bipartite graphs, directed graphs or hypergraphs with a given degree sequence. In all cases, the expected runtime is polynomial only for constant or very slowly-growing degrees.

# 4 Sequential algorithms and graph processes

The study of graph processes dates back to the very beginnings of the study of random graphs, in the work of Erdős and Rényi [47]. In a random graph process, edges are added to an empty graph one by one, chosen randomly from the set of all non-edges, sometimes with additional constraints. In 1979, Tinhofer [110] described such an algorithm for sampling from  $G(\mathbf{k})$  non-uniformly. The *a posteriori* output probability could be calculated and, in theory, this could be combined with a rejection step in order to achieve uniformly distributed output. However, the runtime of the resulting algorithm (with the rejection step) is not known.

Recall that G(n, k) denotes the set of all k-regular graphs on [n]. The bounded-degree graph process starts with the empty graph on n vertices (with no edges), and repeatedly chooses two distinct non-adjacent vertices with degree at most k-1, uniformly at random, and joins these two vertices by an edge. When no such pair of vertices remain, either we have a k-regular graph or the process has become stuck. (The name "bounded-degree graph process" does not mean that all the degrees are O(1). Rather, it means that we add edges sequentially but do not allow the degree of any vertex to exceed k, so we maintain this upper bound on all degrees.)

Ruciński and Wormald [101] proved that for any constant k, the process produces a k-regular graph with probability 1 - o(1). The output distribution is not uniform, and is not well understood. However, it is conjectured that the output of the bounded-degree graph process is contiguous with the uniform distribution over G(n, k): see Wormald [120, Conjecture 6.1]. (Two sequences of probability spaces are *contiguous* if any event with probability which tends to 1 in one sequence must also tend to 1 in the other.)

We now turn to sequential algorithms which produce asymptotically uniform output.

## 4.1 The regular case

Steger and Wormald [106] described an algorithm for sampling from G(n, k) using the following modification of the configuration model algorithm. Instead of choosing a configuration P uniformly at random, and then rejecting the resulting graph G(P) if it is not simple, we choose one pair at a time and only keep those pairs which do not lead to a loop or a repeated edge. Specifically, we start with kn points in n cells, each with k points. Let U be the set of unpaired points, which initially contains all kn points. A set of two points  $\{p, p'\} \subseteq U$  is suitable if p and p' belong to different cells, and no pair chosen so far contains points from the same two cells as p, p'. After repeatedly choosing pairs of suitable points, the algorithm may get stuck, or else reaches a full configuration P (with kn/2 pairs) and outputs the simple k-regular graph G(P). The algorithm is given in pseudocode in Figure 3.

Though the explanation above involves the configuration model, Steger and Wormald state that their algorithm arose from adapting the bounded-degree processes. In this setting, the Steger-Wormald algorithm corresponds to choosing the vertices u, v to add at the next step with a non-uniform probability. To be specific, if k'(x) denotes the current degree of vertex x in the graph formed by the edges chosen so far, then the Steger-Wormald algorithm chooses  $\{u, v\}$  as the next edge with probability proportional to (k - k'(u))(k - k'(v)).

The following theorem is a combination of Steger and Wormald's results [106, Theorems 2.1, 2.2 and 2.3].

**Theorem 4.1** [106] Let Pr(G) denote the probability that a given graph  $G \in G(n, k)$  is produced as output of the Steger-Wormald algorithm.

(i) If  $k = O(n^{1/28})$  then there exists a function f(n,k) = o(1) such that for every  $G \in G(n,k)$ ,

$$\left| \Pr(G) - |G(n,k)|^{-1} \right| < \frac{f(n,k)}{|G(n,k)|}.$$

```
Steger-Wormald Algorithm Input: n and k, with kn even Output: element of G(n,k)

repeat
let U be the set of all kn points
let P:=\emptyset
repeat
choose a set of two distinct points \{p,p'\}\subseteq U u.a.r.
if \{p,p'\} is suitable then add \{p,p'\} to P and delete \{p,p'\} from U until U contains no suitable pairs of points
until G(P) is k-regular output G(P)
```

Figure 3: The Steger-Wormald algorithm

(ii) If  $k = o((n/\log^3 n)^{1/11})$  then there exists a function f(n,k) = o(1) and a subset  $\mathcal{X}(n,k) \subseteq G(n,k)$  such that

$$Pr(G) = (1 + O(f(n,k))) |G(n,k)|^{-1}$$

for all  $G \in \mathcal{X}(n,k)$ , and  $|\mathcal{X}(n,k)| = (1 - f(n,k)) |G(n,k)|$ .

(iii) Under the same condition as (ii), the expected number of times that the outer loop of the algorithm is performed (that is, until G(P) is regular) is 1 + o(1), and hence the runtime of the algorithm is  $O(k^2n)$ .

In particular, when  $k = o((n/\log^3 n)^{1/11})$ , the output distribution of the Steger–Wormald algorithm is within o(1) of uniform in total variation distance.

Kim and Vu [82] gave a new analysis of the Steger-Wormald algorithm using a concentration result of Vu [115], increasing the upper bound on the degree and confirming a conjecture of Wormald [120].

**Theorem 4.2** [82] Let  $0 < \varepsilon < \frac{1}{3}$  be a constant. Then for any  $k \le n^{1/3-\varepsilon}$  and  $G \in G(n,k)$ , the probability  $\Pr(G)$  that G is output by the Steger-Wormald algorithm satisfies  $\Pr(G) = (1+o(1)) |G(n,k)|^{-1}$ .

#### 4.2 The irregular case, and an almost-FPAUS

The Steger-Wormald algorithm was generalised to irregular degree sequences in 2010 by Bayati, Kim and Saberi [7]. They stated their algorithm in terms of graphs, not configurations, and report failure (rather than restarting) if the procedure gets stuck. The pseudocode for this algorithm, which is called PROCEDURE A in [7], is given in Figure 4. Recall that  $m = M/2 = \frac{1}{2} \sum_{j \in [n]} k_j$ . We write  $\binom{[n]}{2}$  for the set of all unordered pairs of distinct vertices in [n].

This procedure is equivalent to the Steger-Wormald algorithm when k is regular, since then the factor  $1-k_ik_i/(4m)$  does not introduce any bias. For irregular degrees,

```
BAYATI, KIM AND SABERI: PROCEDURE A
            graphical sequence k
Input:
Output: element of G(\mathbf{k}), or fail
repeat
let E := \emptyset
                 (set of edges, initially empty)
let \hat{k} := k
                (current degree deficit)
let a := 1
repeat
   choose an unordered pair of distinct vertices \{i, j\} \in {[n] \choose 2} \setminus E with probability proportional to p_{ij} := \hat{k}_i \hat{k}_j \left(1 - \frac{k_i k_j}{4m}\right)
   let a := a \times p_{ii}
   add \{i,j\} to E and reduce each of k_i, k_j by 1
until no more edges can be added to E
if |E| = m then
   output G(P) and N = (m! a)^{-1}
else
   report fail and output N=0
```

Figure 4: Bayati, Kim and Saberi's asymptotically-uniform sampling algorithm

this factor is chosen for the following reason. If two vertices of high degree are joined by an edge, then this choice makes it more difficult for the process to complete successfully. In [7], the authors show that the bias from edge  $\{i,j\}$  is roughly  $\exp(k_ik_j/(4m))$ , and hence the probability  $1 - k_ik_j/(4m) \approx \exp(-k_ik_j/(4m))$  is designed to cancel out this bias.

Bayati, Kim and Saberi [7, Theorem 1 and Theorem 2] proved the following properties of PROCEDURE A.

**Theorem 4.3** [7] Let k be a graphical degree sequence and  $\tau > 0$  an arbitrary constant.

- (i) Suppose that  $k_{\text{max}} = O(m^{1/4-\tau})$ . Then PROCEDURE A terminates successfully with probability 1 o(1) in expected runtime  $O(k_{\text{max}} m)$ , and the probability  $\Pr(G)$  that any given  $G \in G(\mathbf{k})$  is output satisfies  $\Pr(G) = (1+o(1)) |G(\mathbf{k})|^{-1}$ .
- (ii) Now suppose that  $\mathbf{k} = (k, ..., k)$ , where  $k = O(n^{1/2-\tau})$ . Then PROCEDURE A has output distribution which is within distance o(1) from uniform in total variation distance.

Part (i) of this theorem extends the Kim–Vu result (Theorem 4.2) to the irregular case with essentially the same condition, since m=kn when k is k-regular. Similarly, part (ii) of Theorem 4.3 generalises Theorem 4.1(ii) to irregular degree sequences with much higher maximum degree.

When successful, PROCEDURE A outputs a graph and a nonnegative number N. The value of N is not needed for asymptotically-uniform sampling, but is used to give

a fully-polynomial randomised approximation scheme (FPRAS) for approximating  $|G(\mathbf{k})|$ , using a technique known as sequential importance sampling (SIS) which we outline below. Recall the definition of FPRAS from Definition 2.4.

Let  $\mathcal{N}(\mathbf{k})$  be the set obtained by taking all possible edge-labellings of graphs  $G(\mathbf{k})$ , labelling the edges  $e_1, \ldots, e_m$ . Then  $|\mathcal{N}(\mathbf{k})| = m! |G(\mathbf{k})|$ . We can slightly modify Procedure A so that it labels the edges in the order that they were chosen. This modified Procedure A produces  $H \in \mathcal{N}(\mathbf{k})$  with probability  $P_A(H)$ , denoted by a in Figure 4. The expected value of  $1/P_A(\cdot)$  for an element of  $\mathcal{N}(\mathbf{k})$  chosen according to the distribution  $P_A$ , is

$$\sum_{H \in \mathcal{N}(\mathbf{k})} \frac{1}{P_A(H)} P_A(H) = |\mathcal{N}(\mathbf{k})| = m! |G(\mathbf{k})|.$$

Therefore we can estimate  $|G(\mathbf{k})|$  by performing r trials of PROCEDURE A and taking the average of the resulting r values of  $(m! P_A(H_i))^{-1}$ . (Note that  $m! P_A(H)$  is precisely the value denoted N in Figure 4 when the edge-labelled graph H is output.)

Bayati et al. prove [7, Theorem 3] that taking  $r = O(\varepsilon^{-2})$  gives an FPRAS for estimating  $|G(\mathbf{k})|$ .

Finally, Bayati et al. [7] showed how to adapt the SIS approach to estimate  $P_A(G)$  for (non-edge-labelled)  $G \in G(\mathbf{k})$ . This leads to an algorithm which is almost an FPAUS for  $G(\mathbf{k})$ , when  $k_{\text{max}} = O(m^{1/4-\tau})$  for some  $\tau > 0$ . The algorithm satisfies every condition from the definition of FPAUS except for the runtime: in an FPAUS the runtime must be polynomial in n and  $\log(1/\varepsilon)$ , but the algorithm given in [7, Section 3] has runtime which is polynomial in n and  $1/\varepsilon$ . In a little more detail, the Bayati–Kim–Saberi algorithm proceeds as follows:

- Given a graphical degree sequence k and parameters  $\varepsilon, \delta \in (0, 1)$ , the FPRAS is used to obtain a sufficiently good estimate X for |G(k)| (with high probability), and a random graph  $G \in G(k)$  is obtained using PROCEDURE A.
- Next, we need an estimate  $P_G$  for the probability  $P_A(G)$  that PROCEDURE A outputs G. This probability is estimated as follows: repeatedly choose a random ordering of the edges of G, calculate the probability that these edges were chosen in this order during the execution of PROCEDURE A, and take the average of these probabilities (averaged over the different orders chosen).
- Finally, G is returned as output of the almost-FPAUS with probability given by  $\min\{\frac{1}{cXP_G}, 1\}$ , where c is a universal constant independent of k,  $\varepsilon$ ,  $\delta$ .

Bayati, Kim and Saberi [7, Remark 1] state their main results can be adapted to give analogous results for sampling bipartite graphs with given degrees, under the same assumptions on the maximum degree. Independently, Blanchet [13] used sequential importance sampling to give an FPRAS for counting bipartite graphs with given degrees, when the maximum degree in one part of the vertex bipartition is constant, while in the other part the maximum degree is  $o(M^{1/2})$  and the sum of the squares of the degrees is O(M). The arguments provided by Bayati et

al. [7] and Blanchet [13] utilise concentration inequalities and Lyapunov inequalities, respectively.

Sequential importance sampling was used by Chen, Diaconis, Holmes and Liu [21] and Blitzstein and Diaconis [14] to sample graphs and bipartite graphs with given degrees, but without fully rigorous analysis. Sequential importance sampling algorithms also appear in the physics literature, for example [29, 81], again without rigorous analysis.

While sequential importance sampling algorithms may perform well in practice in many cases, Bezáková et al. [12] showed that these algorithms are provably slow in some cases.

# 4.3 Other graph processes

The property of having maximum degree at most k can be rephrased as the property of having no copy of the star  $K_{1,k}$ . More generally, for a fixed graph H, the H-free process proceeds from an empty graph by repeatedly choosing a random edge and adding it to the graph if it does not form a copy of H. See for example [18, 97, 117]. In particular, the triangle-free process is very well studied and has connections with Ramsey Theory [15, 48, 99] (we do not attempt to be comprehensive here as there is a large literature on this topic). The main focus in this area is extremal, as analysis of these processes provides a lower bound on the maximum number of edges possible in an H-free graph. This often involves application of the differential equations method, see [121]. Some pseudorandom properties of the output have been proved for these processes, see for example [15, 99]. However, it is not clear how far the output distribution varies from uniform, and so these processes may not be suitable for almost-uniform sampling.

An exception is the work of Bayati, Montanari and Saberi [8], who adapted the methods of [7] to analyse a sequential algorithm for generating graphs with a given number of edges and girth greater than  $\ell$  (that is, no cycles of length at most  $\ell$ ), where  $\ell$  is a fixed positive integer. As in [7, 106], the next edge is chosen non-uniformly, such that the probability that an edge e is selected is (approximately) proportional to the number of successful completions of the subgraph  $G' \cup \{e\}$ , where G' denotes the current graph. Bayati et al. [8] prove that the output of their algorithm is asymptotically uniform after  $m = O(n^{1+1/(2\ell(\ell+3))})$  edges have been added. The expected runtime of the algorithm is  $O(n^2m)$ .

# 5 Switchings-based algorithms

In the sampling algorithm based on the configuration model (Figure 2), a configuration P is chosen from  $\mathcal{P}(\mathbf{k})$  uniformly at random, repeatedly, until the corresponding graph G(P) is simple. That is, if G(P) contains any "defect" (in this case, a loop or a repeated edge) then this choice is rejected and we choose again. In 1990, McKay and Wormald [91] introduced a uniform sampling algorithm for  $G(\mathbf{k})$  which begins by choosing a random element of  $\mathcal{P}(\mathbf{k})$  and rejecting it only if there are "too many" defects. Once a configuration has been found with "not too many" defects, operations called *switchings* are applied, one by one, to reduce the number of defects until a simple configuration is obtained. To maintain a uniform distribution, McKay

and Wormald introduce a carefully-chosen rejection probability at each step of the process.

We describe the McKay-Wormald algorithm in some detail, as this will set the scene for the significant improvements introduced by Gao and Wormald [59], to be discussed in Section 5.1. The structure of the McKay-Wormald algorithm is based on the *switching method*, introduced by McKay [89]. The switching method is used in asymptotic enumeration to obtain good approximations for the cardinality of large combinatorial sets, such as the set of all graphs with given degrees [92], when the maximum degree is not too large.

To make the phrase "not too many defects" precise, recall that a *loop* in a configuration is a pair between two points from the same cell. A *triple pair* in a configuration is a set of three distinct non-loop pairs between the same two cells, and a *double pair* is a set of two distinct non-loop pairs between the same two cells.

**Definition 5.1** Let  $M_2 = M_2(\mathbf{k}) = \sum_{j \in [n]} k_j(k_j - 1)$ . (Note that  $M_2$  counts the number of ways to choose an ordered pair of points from the same cell.) Define  $B_1 = M_2/M$  and  $B_2 = (M_2/M)^2$ . Say that a configuration  $P \in \mathcal{P}(\mathbf{k})$  is good if every cell contains at most one loop, there are no triple pairs, P contains at most  $B_1$  loops and at most  $B_2$  double pairs. Write  $\mathcal{P}^*(\mathbf{k})$  for the set of all good configurations in  $\mathcal{P}^*$ .

Combining McKay and Wormald [91, Lemma 2 and Lemma 3'] with [5, Lemma 8], we can prove that if  $k_{\text{max}}^4 = O(M)$  then there exists a constant  $c \in (0, 1)$  such that a uniformly-random element of  $\mathcal{P}(\mathbf{k})$  is good with probability at least c.

Next, let  $\mathcal{C}_{\ell,d}$  be the set of all good configurations with exactly  $\ell$  loops and d double pairs. These sets form a partition of  $\mathcal{P}^*(\mathbf{k})$ . McKay and Wormald defined two switching operations, which we will refer to as loop-switchings and double-switchings. A loop-switching is used to reduce the number of loops by one, and a double-switching is used to reduce the number of double pairs by one. These switchings are illustrated in Figure 5. For example, in the loop-switching, a loop is selected together with two other pairs, such that there are 5 distinct cells involved, and performing the switching does not result in any repeated pairs. The loop-switching transforms an element of  $\mathcal{C}_{\ell,d}$  to an element of  $\mathcal{C}_{\ell-1,d}$ . To describe a loop-switching we specify an ordered 6-tuple of points, and similarly a double-switching is specified using an ordered 8-tuple of points.

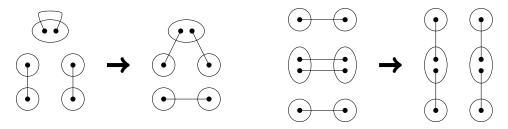


Figure 5: A loop-switching (left) and a double-switching (right)

It is possible to remove loops and double pairs using simpler switchings. In fact, McKay used simpler switching operations (as illustrated in Figure 10 below) in

a very early application [90] of the switching method for asymptotic enumeration. Subsequently, McKay and Wormald found that by using the slightly more complicated switchings shown in Figure 5, they could obtain an asymptotic formula with vanishing error for a wider range of degree sequences (with a weaker bound on the maximum degree, to be precise), compared with the result of [90]. The benefits obtained by using the slightly more complicated switchings also hold here in the algorithmic setting.

The first step of McKay and Wormald's algorithm is to repeatedly choose a uniformly random element of  $\mathcal{P}(k)$  until it is good. At this point, the configuration P is a uniformly random element of  $\mathcal{P}^*(k)$ . Next, if P contains a loop then a loop-switching is chosen uniformly at random from the set of all available options (that is, from all possible loop-switchings which could be applied to P). This switching is rejected with some probability, otherwise it is accepted and performed. The rejection probability is carefully chosen to ensure that if P has a uniform distribution over  $\mathcal{C}_{\ell-1,d}$ . If rejection occurs at any step then the entire algorithm restarts from the beginning.

When a configuration is reached with no loops, any double pairs are removed one by one using double-switchings, again with a rejection probability chosen to maintain uniformity. Finally, when the current configuration P belongs to  $C_{0,0}$  it is simple, and the algorithm outputs G(P) and terminates. The algorithm is given in pseudocode in Figure 6.

```
McKay-Wormald algorithm
Input:
          graphical sequence k
Output: element of G(\mathbf{k})
repeat
  choose P \in \mathcal{P}(\mathbf{k}) u.a.r.
until P is good
# remove loops
while P has at least one loop
  obtain P' from P by performing a loop-switching chosen u.a.r.
  calculate the rejection probability q_{loop}(P, P')
  restart with probability q_{loop}(P, P'); otherwise P := P'
# remove double pairs
while P has at least one double pair
  obtain P' from P by performing a double-switching chosen u.a.r.
  calculate the rejection probability q_{\text{double}}(P, P')
  restart with probability q_{\text{double}}(P, P'); otherwise P := P'
output G(P)
```

Figure 6: High-level description of the McKay-Wormald algorithm

To complete the specification of the McKay-Wormald algorithm, we must define the rejection probabilities  $q_{\text{loop}}$  and  $q_{\text{double}}$ . For  $P \in \mathcal{P}^*(\mathbf{k})$ , let f(P, X) denote the number of possible X-switchings  $P \mapsto P'$  which may be applied to P, for  $X \in$  {loop, double}. Similarly, let b(P',X) be the number of ways to produce P' using an X-switching  $P \mapsto P'$ , for all  $P' \in \mathcal{P}^*(\mathbf{k})$  and  $X \in \{\text{loop, double}\}$ . McKay and Wormald [91, Lemma 4] gave expressions  $\underline{m}(\ell,d,\text{loop})$  and  $\underline{m}(d,\text{double})$ , omitted here, such that for all  $P \in \mathcal{C}_{\ell,d}$ ,

$$f(P, \text{loop}) \le \overline{m}(\ell, \text{loop}) = 2\ell M^2, \qquad b(P, \text{loop}) \ge \underline{m}(\ell, d, \text{loop})$$
 (5.1)

and for all  $P \in \mathcal{C}_{0,d}$ ,

$$f(P, \text{double}) \le \overline{m}(d, \text{double}) = 4d M^2, \qquad b(P, \text{double}) \ge \underline{m}(d, \text{double}).$$
 (5.2)

Regarding the lower bounds  $\underline{m}(\cdot)$ , we will only need the fact that they are positive when  $k_{\max}^4 = O(M)$ , for all  $\ell \leq B_1$  and all  $d \leq B_2$ .

The upper bounds in (5.1) and (5.2) arise by counting the number of ways to choose a tuple of points (6 points for a loop-switching and 8 points for a double-switching) which satisfy some constraints of the switching and not others: typically the required pairs must be present, but we do not check that all cells involved in the switching are distinct, or that the switching does not introduce any new loops or repeated pairs. For the lower bounds, we require an upper bound on the number of bad choices of tuples, so that this may be subtracted. When the degrees get too high, the number of bad choices increases and there will be a lot of variation in this number, making the estimates less precise.

The rejection probabilities are defined by

$$q_{\text{loop}}(P, P') = 1 - \frac{f(P, \text{loop}) \underline{m}(\ell - 1, d, \text{loop})}{\overline{m}(\ell, \text{loop}) b(P', \text{loop})},$$

$$q_{\text{double}}(P, P') = 1 - \frac{f(P, \text{double}) \underline{m}(d - 1, \text{double})}{\overline{m}(d, \text{double}) b(P', \text{double})}$$
(5.3)

for all  $(P, P') \in \mathcal{C}_{\ell,d} \times \mathcal{C}_{\ell-1,d}$  which differ by a loop-switching, and all  $(P, P') \in \mathcal{C}_{0,d} \times \mathcal{C}_{0,d-1}$  which differ by a double-switching, respectively. These probabilities are well-defined if the lower bounds  $\underline{m}(\cdot)$  are positive.

**Lemma 5.2** [91, Theorem 2] If  $k_{\text{max}}^4 = O(M)$  then the output of the McKay-Wormald algorithm has uniform distribution over  $G(\mathbf{k})$ .

**Proof** As mentioned earlier, the condition  $k_{\max}^4 = O(M)$  implies that the lower bounds  $\underline{m}(\cdot)$  are positive, and hence the rejection probabilities are well-defined. The initial good configuration P is distributed uniformly over  $\mathcal{P}^*(\mathbf{k})$ . Hence, if the initial configuration belongs to  $\mathcal{C}_{\ell,d}$  then it has the uniform distribution over  $\mathcal{C}_{\ell,d}$ . We prove by induction that if a switching  $P \mapsto P'$  is accepted and P has the uniform distribution over some set  $\mathcal{C}_{\ell,d}$ , then P' has the uniform distribution over the codomain of that switching. (The codomain is  $\mathcal{C}_{\ell-1,d}$  if the switching is a loop-switching, while for a double-switching  $\ell=0$  and the codomain is  $\mathcal{C}_{0,d-1}$ .) For ease of notation we prove this for double-switchings, and note that the same argument holds for loops-switchings. For all  $P' \in \mathcal{C}_{0,d-1}$ , the probability that the proposed switching is not rejected and results in P' is given by

$$\Pr(P') = \sum_{\substack{P \in \mathcal{C}_{0,d} \\ P \mapsto P'}} \frac{\Pr(P)}{f(P, \text{double})} \left(1 - q_{\text{double}}(P, P')\right).$$

The sum is over all configurations  $P \in \mathcal{C}_{0,d}$  such that P' can be obtained from P using a double-switching, and the factor 1/f(P, double) is the probability that this particular double-switching is chosen to be applied to P. Substituting the value of the rejection probability from (5.3), and using the assumption that P is uniformly distributed over  $\mathcal{C}_{0,d}$ , we find that

$$\Pr(P') = \frac{\underline{m}(d-1, \text{double})}{|\mathcal{C}_{0,d}| \, \overline{m}(d, \text{double})} \sum_{\substack{P \in \mathcal{C}_{0,d} \\ P \mapsto P'}} \frac{1}{b(P', \text{double})}.$$

But the number of summands is precisely b(P', double), so the sum evaluates to 1 and we conclude that

$$\Pr(P') = \frac{\underline{m}(d-1, \text{double})}{|\mathcal{C}_{0,d}| \, \overline{m}(d, \text{double})}.$$

This depends only on d, and not on the particular configuration  $P' \in \mathcal{C}_{0,d-1}$ . Hence every element of  $\mathcal{C}_{0,d-1}$  is equally likely to be produced after the double-switching, proving that the uniform distribution is maintained after each accepted switching step. Thus, by induction, at the end of the algorithm P is a uniformly random element of  $\mathcal{C}_{0,0}$ . It follows that G(P) is a uniformly random element of  $G(\mathbf{k})$ , as claimed.

The previous result shows that the output of the McKay-Wormald algorithm is always correct. But what conditions on k are needed for the algorithm to be efficient? If the degrees become too large then it becomes unlikely that the randomly-chosen initial configuration is good, and there will be too much variation in the parameters f(P, X), b(P', X), leading to large rejection probabilities.

**Theorem 5.3** [91, Theorem 3] Suppose that  $\mathbf{k}$  is a graphical degree sequence with  $k_{\text{max}} = O(M^{1/4})$ . The McKay-Wormald algorithm for sampling from  $G(\mathbf{k})$  can be implemented so that it has expected runtime  $O(k_{\text{max}}^2 M^2) = O(k_{\text{max}}^4 n^2)$ . If  $\mathbf{k} = (k, k \dots, k)$  is regular then there is an implementation with expected runtime  $O(k^3 n)$ , under the assumption that  $k = O(n^{1/3})$ .

**Proof** (Sketch.) Recall that a randomly chosen element of  $\mathcal{P}(\mathbf{k})$  is good with probability at c when  $k_{\max}^4 = O(M)$ , for some constant  $c \in (0,1)$ . Hence it takes expected time O(M) to produce a uniformly-random element of  $\mathcal{P}^*(\mathbf{k})$ . McKay and Wormald prove that the probability that there is no restart during the loop-switchings and doubles-switchings is 1 - o(1) when  $k_{\max}^4 = o(M)$ , and is bounded below by a constant when  $k_{\max}^4 = \Theta(M)$ .

It remains to consider the cost of performing the switching operations. Suppose that at some point in the execution of the algorithm, the current configuration is P. To choose a potential switching of the appropriate type, we can select the points of a randomly chosen loop or double pair, in a random order, and then choose the points of two other pairs, in a random order. The number of ways to make this selection is exactly given by the relevant upper bound from (5.1) or (5.2), and the probability that the result P' of this switching is a valid configuration in the codomain (that is, only the chosen loop/double pair has been removed, and no additional defects have been introduced) is exactly  $f(P, X)/\overline{m}(x, X)$ , where  $(x, X) \in$ 

 $\{(\ell, \text{loop}), (d, \text{double})\}$ . This means that the value of f(P, X) does not need to be calculated.

However, we do need to calculate the value b(P',X) precisely for the proposed switching  $P \mapsto P'$ , in order to restart with the correct probability. This can be done by maintaining some information about numbers of small structures in the configuration, which is initialised before any switchings have been performed, and updated after each switching operation. The initialisation takes runtime  $O(k_{\text{max}}^2 M_2^2)$ , which dominates the expected time required for the updates from each switching. See [91, Theorem 3] for more details.

In the k-regular case a further efficiency is possible, but with a much more complicated implementation, as explained in the proof of [91, Theorem 4].

McKay and Wormald also explained how to modify their algorithm to sample bipartite graphs with given degrees, uniformly at random, see [91, Section 6]. The expected runtime of the uniform sampler for bipartite graphs with given degrees is  $O(k_{\max}^4 n^2)$  when  $k_{\max} = O(M^{1/4})$ , where (as usual)  $k_{\max}$  denotes the maximum degree.

## 5.1 Improvements and extensions

Starting from the McKay–Wormald algorithm, Gao and Wormald [59] introduced several new ideas which culminated in an algorithm for uniformly sampling k-regular graphs, which they called REG. The expected runtime of the Gao–Wormald algorithm is  $O(k^3n)$  when  $k = o(\sqrt{n})$ . This is a significant increase in the allowable range of k compared with the McKay–Wormald algorithm.

In order to handle degrees beyond  $O(n^{1/3})$ , Gao and Wormald must deal with triple pairs, as well as loops and double pairs. So the set of good configurations is redefined to allow "not too many" triple pairs (but still ruling out any pairs of multiplicity four or higher) and a new switching phase is performed to remove triple pairs one by one. However, it turns out that triple pairs are easily handled. In fact, the first two phases of the algorithms (removing loops and removing triples, respectively) proceed as in the McKay–Wormald algorithm. As the double pairs are the most numerous "defect", new ideas are required in phase 3, where double pairs must be removed.

The innovations introduced by Gao and Wormald in [59] are designed to reduce the probability of a rejection during a double-switching step. These ideas are described in a very general setting in [59], for ease of applications to other problems. Here, we given an overview of these ideas in the context of the double-switching, performed on configurations which have no loops, no triple pairs and at most  $B_2$  double pairs, where  $B_2 = \lfloor (1+\gamma)(k-1)^2/4 \rfloor$  for some sufficiently small constant  $\gamma > 0$ .

Since we now discuss only double-switchings, we drop "double" from our notation. Write  $\mathcal{C}_d$  for the set of good configurations with no loops, no triple pairs and exactly d double pairs. Observe from (5.3) that the probability that a proposed switching  $P \mapsto P'$  is not rejected is a product of a factor  $f(P)/\overline{m}(d)$  which depends only on  $P \in \mathcal{C}_d$ , and a factor  $\underline{m}(d-1)/b(P')$  which depends only on  $P' \in \mathcal{C}_{d-1}$ . Gao and Wormald aim to reduce both the probability of forward rejection, or f-rejection

(which depends only on P), and the probability of backwards rejection, or b-rejection, which depends only on P'.

To reduce the likelihood of an f-rejection, Gao and Wormald allow some double-switchings which would be rejected in the McKay-Wormald algorithm. The aim is to bring the values of f(P) closer to the upper bound  $\overline{m}(d)$ . Specifically, a double-switching which introduces exactly one new double pair is allowed, as illustrated in Figure 7. The original double-switching, shown on the right of Figure 5, is known as a type I, class A switching, while switching in Figure 7 is a type I, class B switching.

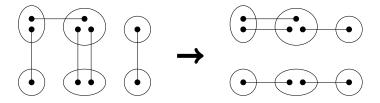


Figure 7: A type I, class B double-switching  $\mathcal{C}_d \to \mathcal{C}_d$ 

Next, Gao and Wormald observed that some configurations in  $\mathcal{C}_{d-1}$  are less likely to be produced by a (type I) double-switching than others. These configurations bring down the lower bound  $\underline{m}(d-1)$  and hence increase the b-rejection probability for every element of  $\mathcal{C}_{d-1}$ . For this reason, Gao and Wormald introduced another new switching, called a *type II* switching, which actually increases the number of double pairs by one, as shown in Figure 8. All type II switchings have class B.

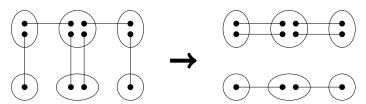


Figure 8: A type II, class B double-switching  $\mathcal{C}_d \to \mathcal{C}_{d+1}$ 

To perform a switching step, from current configuration  $P \in \mathcal{C}_d$ , first the type  $\tau \in \{I, II\}$  of switching is chosen, according to a probability distribution  $\rho$  (with a small restart probability if no type is chosen). Next, a type  $\tau$  switching  $P \mapsto P'$  is proposed, chosen randomly from all  $f_{\tau}(P)$  type  $\tau$  switchings available in P. The f-rejection probability is  $1 - f_{\tau}(P)/\overline{m}_{\tau}(d)$ , where  $\overline{m}_{\tau}(d)$  is an upper bound on  $f_{\tau}(P)$  over all  $P \in \mathcal{C}_d$ . Let  $d' \in \{0, \ldots, B_2\}$  be the unique index such that  $P' \in \mathcal{C}_{d'}$ . The class  $\alpha \in \{A, B\}$  of the proposed switching  $P \mapsto P'$  can now be observed, and the b-rejection probability is  $1 - b_{\alpha}(P')/\underline{m}_{\alpha}(d')$ , where  $\underline{m}_{\alpha}(d')$  is a lower bound on  $b_{\alpha}(P')$  over all  $P' \in \mathcal{C}_{d'}$ . If there is no f-rejection or b-rejection then the proposed switching is accepted and P' becomes the current configuration. As soon as an element  $P \in \mathcal{C}_0$  is reached, the algorithm stops with output G(P). Here we see that the f-rejection probability depends on P and the chosen type, while the b-rejection probability depends on the outcome P' and the class  $\alpha$  of the proposed switching from P.

Rather than maintaining a uniform distribution after each switching, as in the

McKay-Wormald algorithm, the goal in the Gao-Wormald algorithm is to ensure that the expected number of visits to each configuration  $P \in \mathcal{C}_d$ , over the course of (the doubles-reducing phase of) the algorithm, depends only on d and is independent of P. In particular, this guarantees that each element of  $\mathcal{C}_0$  is equally likely, and hence the output of the algorithm is a uniformly random element of G(n, k).

In [59, Lemma 6 and Lemma 8], Gao and Wormald gave expressions for  $\overline{m}_{\tau}(d)$ ,  $\underline{m}_{\alpha}(d)$  and showed how to choose values for  $\rho_{\tau}(d)$  satisfying a certain system of linear equations. By [59, Lemma 5], when the parameters  $\rho_{\tau}(d)$  satisfy this system of equations then the last element visited by the algorithm is distributed uniformly at random from  $C_0$ , assuming that no rejection occurs. Furthermore, the solution can be chosen to satisfy  $\rho_I(d) = 1 - \varepsilon > 0$  for all  $1 \le d \le B_2$ , where  $\varepsilon = O(k^2/n^2)$ . Since  $k = o(n^{1/2})$  this means that almost every step is a "standard" double-switching (type I, class A) switching.

Having set these parameter values, the algorithm is completely specified. It remains to show that the probability of rejection during the course of the algorithm is o(1), which requires careful analysis. The runtime analysis is very similar to Theorem 5.3, resulting in the following.

**Theorem 5.4** If  $1 \le k = o(\sqrt{n})$  then the Gao-Wormald algorithm REG is a uniform sampler from G(n, k), and can be implemented with expected runtime  $O(k^3n)$ .

Recent work of Armand, Gao and Wormald [5] which gives an even more efficient uniform sampler for the same range of k is discussed in Section 5.1.3.

A k-factor is a k-regular spanning subgraph of a given graph. Gao and Greenhill [55] used the Gao-Wormald framework to give algorithms for sampling k-factors of a given graph  $H_n$  with n vertices, under various conditions on k and the maximum degree  $\Delta$  of the complement  $\overline{H}_n$  of  $H_n$ . The edges of the complement of  $H_n$  can be thought of as "forbidden edges", and we want to sample k-regular graphs with no forbidden edges.

**Theorem 5.5** [55, Theorem 1.1 and 1.2] Let  $H_n$  be a graph on n vertices such that  $\overline{H}_n$  has maximum degree  $\Delta$ .

- There is an algorithm which produces a uniformly random k-factor of  $H_n$ , and has expected runtime  $O((k + \Delta)^3 n)$  if  $(k + \Delta)k\Delta = o(n)$ .
- Now suppose that  $H_n$  is  $(n \Delta 1)$ -regular. There is an algorithm which generates a uniformly random k-factor of  $H_n$  and has expected runtime

$$O\bigl((k+\Delta)^4(n+\Delta)^3+(k+\Delta)^8\,k^2\Delta^2/n+(k+\Delta)^{10}\,k^2\Delta^3/n^2\bigr)$$
 if  $k^2+\Delta^2=o(n)$ .

In [55], the algorithms described in Theorem 5.5 are called Factoreasy and Factoreuniform, respectively. Previously the only algorithm for this problem was a rejection algorithm of Gao [54] which has expected linear runtime when k = O(1) and  $\overline{H}_n$  has at most a linear number of edges (but the maximum degree of  $\overline{H}_n$  can be linear).

**5.1.1** Asymptotically-uniform algorithms based on switchings In [59, Theorem 3], Gao and Wormald described an algorithm REG\* which performs asymptotically-uniform sampling from G(n,k) in expected runtime O(kn). This algorithm is obtained from REG by never performing any rejection steps and never performing any class B switchings. (So only loop-switchings, triple-switchings and type I, class A double-switchings will be used.) This is more efficient as computation of the brejection probabilities is the most costly part of the algorithm. The output of REG\* is within total variation distance o(1) of uniform when  $k = o(\sqrt{n})$ . Indeed, Gao and Wormald remark that the McKay-Wormald algorithm can be modified in the same way, giving an asymptotically-uniform sampling algorithm with expected runtime O(M) whenever  $k_{\text{max}} = O(M^{1/4})$ .

A similar performance was obtained by Zhao [122] using a slightly different approach, involving the use of a Markov chain to make local modifications starting from G(P), where P is a uniformly random element of  $\mathcal{P}(\mathbf{k})$ .

Recently, Janson [72] introduced and analysed the following switching-based algorithm for asymptotically-uniform sampling from  $G(\mathbf{k})$ . Say that a pair in a configuration is bad if it is a loop or part of a double pair. (Recall that, as we have defined it here, "double pair" does not mean that the multiplicity of the corresponding edge is exactly two: only that the multiplicity is at least two.)

```
Janson algorithm Input: graphical sequence k Output: element of G(k), denoted \widehat{G} choose P \in \mathcal{P}(k) u.a.r. repeat choose and orient a bad pair pp' in P u.a.r. choose and orient a distinct pair qq', u.a.r. delete pairs pp', qq' from P, and replace with pairs pq, p'q' until G(P) is simple output \widehat{G} = G(P)
```

Figure 9: Janson algorithm, corresponding to the switched configuration model

Starting from a uniformly random configuration  $P \in \mathcal{P}(\mathbf{k})$ , if G(P) is simple then we output G(P). Otherwise, choose a pair uniformly at random from the set of all bad pairs in P. Next, choose a pair uniformly at random from the set of all other pairs in P. Update P by removing these two pairs and replacing them by two other pairs using the same four points, chosen uniformly at random. (In the pseudocode, this is done by randomly ordering the points in each chosen pair.) This gives a new configuration in  $\mathcal{P}(\mathbf{k})$ . At each step, the switching removes the chosen bad pair, and may cause other pairs to stop being bad or to become bad. Repeatedly apply the switching step until G(P) is simple, and let  $\hat{G} = G(P)$  denote the output graph. This algorithm is shown in Figure 9. Janson calls the resulting probability space the switched configuration model. This is a non-uniform probability space over  $G(\mathbf{k})$ .

The switchings used in this process are illustrated in Figure 10. They were used

by McKay [90] in a very early application of the switching method, and are simpler than the switchings in Figure 5. Note however that Janson does not insist that the cells involved in the switching are all distinct, or that the new pairs pq, p'q' do not increase the multiplicity of an edge. So Figure 10 should be interpreted differently to Figure 5: in Figure 5, it is implied that all illustrated cells are distinct and that all new pairs lead to edges with multiplicity 1.

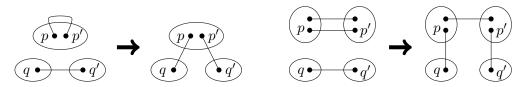


Figure 10: Possible switchings in Janson's algorithm, with chosen points labelled

Janson proved the following result [72, Theorem 2.1]. Recall the definition of  $R = R(\mathbf{k})$  from Theorem 3.1.

**Theorem 5.6** [72] Suppose that k is a graphical degree sequence which satisfies

$$k_{\text{max}} = o(n^{1/2}), \qquad M = \Theta(n), \qquad R = O(n)$$
 (5.4)

and let  $\widehat{G}$  denote the output of the switched configuration model for the degree sequence k. Then the distribution of  $\widehat{G}$  is within total variation distance o(1) of uniform. With high probability, the runtime is O(M) as only O(1) switching steps are required.

Janson remarks that the bad pair may also be chosen deterministically according to some rule, such as lexicographically. This would lead to a slightly different distribution on the output graph, but the conclusion of Theorem 5.6 would still hold.

Furthermore, Janson [72, Corollary 2.2 and Corollary 2.3] proved that under the same conditions (5.4), statements about convergence in probability and convergence in distribution which are true for  $\hat{G}$  are also true for uniformly-random elements of  $G(\mathbf{k})$ .

**5.1.2 Graphs with power-law degree distributions** Heavy-tailed distributions are often observed in real-world networks [24, 96], but are difficult to sample as they are far from regular and their maximum degree is too high for the sampling algorithms we have seen so far. In [60], Gao and Wormald showed how to adapt their approach to degree sequences which satisfy the following definition.

**Definition 5.7** [60, Definition 1] The degree sequence k is power-law distribution-bounded with parameter  $\gamma > 1$  if the minimum entry in k is at least 1, and there is a constant C > 0 independent of n such that the number of entries of K which are at least i is at most  $Cni^{1-\gamma}$  for all  $i \geq 1$ .

Other definitions of power-law degree sequences can be found in the literature, but some only allow maximum degree  $O(n^{1/\gamma})$ , which is  $o(n^{1/2})$  when  $\gamma \in (2,3)$ .

Definition 5.7 is more realistic as it allows higher degrees, as observed in real-world networks. Gao and Wormald [60, equation (4)] noted that if k is power-law distribution-bounded with parameter  $\gamma$  then

$$k_{\text{max}} = O(n^{1/(\gamma - 1)}), \qquad M = \Theta(n), \qquad M_2 = O(n^{2/(\gamma - 1)}),$$
 (5.5)

where  $M_2 = M_2(\mathbf{k})$  is given in Definition 5.1.

The most relevant range of  $\gamma$  for real-world networks is  $\gamma \in (2,3)$ . As observed by Gao and Wormald [60], when  $\gamma > 3$  it is easy to sample uniformly from  $G(\mathbf{k})$ . We provide a brief proof here.

**Lemma 5.8** [60] Suppose that  $\mathbf{k}$  is a power-law distribution-bounded degree sequence with  $\gamma > 3$ . Then the configuration model (Figure 2) gives a polynomial-time uniform sampler for  $G(\mathbf{k})$  with expected runtime O(M).

**Proof** It follows from (5.5) that 
$$k_{\max}^2 = o(M)$$
 and  $R = \sum_{j \in [n]} k_j^2 = M_2 + M = \Theta(M)$ . The proof is completed by applying Theorem 3.1.

While uniform sampling is easy when  $\gamma > 3$ , it is a very challenging problem when  $\gamma \in (2,3)$ . To cope with the very high maximum degree when  $\gamma < 3$ , Gao and Wormald utilised 6 different types of switching (all of the same class). First, they focussed on removing "heavy" edges or loops, where an edge is heavy if both its endvertices have high degree. They also introduced a new kind of rejection, called pre-b-rejection, which is used to equalise the number of ways to choose some additional pairs which are needed to perform some of the switchings. They described a uniform sampler PLD, and an asymptotically-uniform sampling algorithm called PLD\*, obtaining the following result [60, Theorem 2, Theorem 3] when the parameter  $\gamma$  is a little less than 3. These are the first rigorously-analysed algorithms which can efficiently sample graphs with a realistic power-law degree distribution for some values of  $\gamma$  below 3.

**Theorem 5.9** [60] Suppose that k is a power-law distribution-bounded degree sequence with parameter  $\gamma$  such that

$$\gamma > \frac{21 + \sqrt{61}}{10} \approx 2.881.$$

The algorithm PLD is a uniform sampler for  $G(\mathbf{k})$  with expected runtime  $O(n^{4.081})$ . The algorithm PLD\* performs asymptotically-uniform sampling from  $G(\mathbf{k})$  with expected runtime O(n).

In their analysis, Gao and Wormald used a new parameter,  $J(\mathbf{k})$ , which they introduced in the context of asymptotic enumeration in [58]. We have seen that a switching argument breaks down when the number of bad choices for a given switching operation becomes too large. This often involves counting paths of length two from a given vertex. In previous work, the bound  $k_{\text{max}}^2$  was often used for this quantity. (Of course  $k_{\text{max}}(k_{\text{max}}-1)$  is more precise but gives the same asymptotics.)

Instead, Gao and Wormald use the upper bound  $J(\mathbf{k})$ , defined as follows. First, let  $\sigma$  be a permutation of [n] such that  $k_{\sigma(1)} \geq k_{\sigma(2)} \geq \cdots \geq k_{\sigma(n)}$ . Then, define

$$J(\mathbf{k}) = \sum_{j=1}^{k_{\text{max}}} k_{\sigma(j)}, \tag{5.6}$$

noting that  $k_{\text{max}} = k_{\sigma(1)}$ . So  $J(\mathbf{k})$  is the sum of the  $k_{\text{max}}$  largest entries of  $\mathbf{k}$ , and hence forms an upper bound on the number of 2-paths from an arbitrary vertex.

If  $\mathbf{k}$  is regular then  $J(\mathbf{k}) = k_{\text{max}}^2$ , but when  $\mathbf{k}$  is far from regular,  $J(\mathbf{k})$  can be significantly smaller than  $k_{\text{max}}^2$ . In particular, if  $\mathbf{k}$  is a power-law distribution-bounded degree sequence with parameter  $\gamma$  then  $k_{\text{max}}^2 = n^{2/(\gamma - 1)}$ , while

$$J(\mathbf{k}) = O(n^{(2\gamma - 3)/(\gamma - 1)^2}) = o(n^{2/(\gamma - 1)}).$$

This bound on  $J(\mathbf{k})$  is proved in [57, Lemma 5], and more briefly in [60, equation (54)].

The parameter  $J(\mathbf{k})$  has proved very powerful when working with heavy-tailed degree distributions. As well as its use in asymptotic enumeration [58] and uniform sampling [60], it has also been used in the analysis [57] of the number of triangles and the clustering coefficient in a uniformly random element of  $G(\mathbf{k})$ , for heavy-tailed degree sequences  $\mathbf{k}$ . We will encounter  $J(\mathbf{k})$  again in Section 6.5.

**5.1.3** Incremental relaxation Very recently, Arman, Gao and Wormald [5] introduced a new approach, called *incremental relaxation*, which allows a more efficient implementation of the b-rejection step. In incremental relaxation, the b-rejection is performed iteratively over several steps, each with its own sub-rejection probability, such that the sub-rejection probabilities are much easier to calculate than the overall probability of b-rejection. Using this idea, Arman et al. obtain improvements on the runtime of the algorithms in [59, 60, 91], and give an algorithm for uniformly sampling bipartite graphs with given degrees when the maximum degree is  $O(M^{1/4})$ . We collect their results together below.

**Theorem 5.10** [5, Theorems 1–4] Let  $\mathbf{k}$  be a graphical degree sequence. There are algorithms, called INC-GEN, INC-REG, and INC-POWERLAW, respectively, which perform uniform sampling from  $G(\mathbf{k})$  under the following assumptions on  $\mathbf{k}$ , with the stated expected runtime:

- If  $k_{\text{max}}^4 = O(M)$  then the expected runtime of the algorithm INC-GEN is O(M).
- If  $k_{\text{max}} = (k, k, ..., k)$  is regular and  $k = o(n^{1/2})$  then the expected runtime of the algorithm INC-REG is  $O(kn + k^4)$ .
- If k is a power-law distribution-bounded degree sequence with parameter  $\gamma > \frac{21+\sqrt{61}}{10} \approx 2.881$  then the algorithm INC-POWERLAW has expected runtime O(n).

Now let  $\mathbf{k} = (\mathbf{s}, \mathbf{t})$  be a bipartite degree sequence with  $k_{\text{max}} = \max\{\max s_j, \max t_i\}$ . If  $k_{\text{max}}$  satisfies  $k_{\text{max}}^4 = O(M)$ , then there is an algorithm, called INC-BIPARTITE, which has expected runtime O(M) and produces a uniformly-random bipartite graph with degree sequence  $\mathbf{s}$  on one side of the bipartition and  $\mathbf{t}$  on the other.

Observe that incremental relaxation leads to greatly improved runtimes, for example from  $O(k_{\text{max}}^2 M^2)$  to O(M) for uniform sampling from  $G(\mathbf{k})$  when  $k_{\text{max}} = O(M^{1/4})$ , and from  $O(n^{4.081})$  to O(n) for power-law distribution-bounded degree sequences with  $\gamma > 2.882$ .

At the time of writing, C code for INC-GEN and INC-REG is available from Wormald's website<sup>2</sup>.

# 6 Markov chain algorithms

In this section we review sampling algorithms which use the *Markov chain Monte Carlo* (MCMC) approach. Here an ergodic Markov chain is defined with the desired stationary distribution: in our setting, the stationary distribution should be *uniform* over  $G(\mathbf{k})$ , or perhaps over a superset of  $G(\mathbf{k})$ . We refer to such algorithms as "Markov chain algorithms".

Rather than work steadily towards a particular goal, such as the sequential algorithms described in Section 4 or the McKay-Wormald algorithm discussed in Section 5, the Markov chains we consider in this section perform a random walk on  $G(\mathbf{k})$ , usually by making small random perturbations at each step. For example, the *switch chain* chooses two random edges, deletes them and replaces them with two other edges, while maintaining the degree sequence. See Figure 11. We will return to the switch chain in Section 6.4.



Figure 11: Transitions of the switch chain

A Markov chain needs a starting state: that is, we must be able to initially construct a single instance of  $G(\mathbf{k})$ . For graphs, bipartite graphs and directed graphs, if the degree sequence is graphical then a realization of that degree sequence can easily be constructed. This is done using the Havel–Hakimi algorithm [67, 68] for graphs, Ryser's algorithm [102] for bipartite graphs and an adaptation of the Havel–Hakimi algorithm for directed graphs [43]. We remark that the situation for hypergraphs is more complicated, as the existence problem ("Does a given degree sequence have a realization?") is NP-complete for 3-uniform hypergraphs [30].

In theoretical computer science, any polynomial runtime is seen as efficient. In practice, of course, an algorithm with a high-degree polynomial runtime may be too slow to use. All algorithms discussed in previous sections run until some natural stopping time is reached: that is, by looking at the current state we can tell whether or not the algorithm may successfully halt. In MCMC sampling, however, the user must specify the number of transitions T that the Markov chain will perform before producing any output. Typically T is defined to be the best-known upper bound on

 $<sup>^2</sup>$ https://users.monash.edu.au/ $\sim$ nwormald

the mixing time  $\tau(\varepsilon)$ , for a suitable tolerance  $\varepsilon$  (see Definition 6.1). For this reason, loose upper bounds on the mixing time have a significant impact on the runtime.

Most Markov chain approaches to sampling from  $G(\mathbf{k})$  have been analysed using the multicommodity flow method of Sinclair [104], which we describe in Section 6.3. Unfortunately, it is often very difficult to obtain tight bounds on the rate of mixing time of a Markov chain using the multicommodity flow method. In any case, it is an interesting theoretical challenge to try to characterise families of degree sequences  $\mathbf{k}$  for which natural Markov chains on  $G(\mathbf{k})$  have polynomial mixing time.

We now introduce some necessary Markov chain background. For more information see for example [74, 84].

#### 6.1 Markov chain background

A time-homogenous Markov chain  $\mathcal{M}$  on a finite state space  $\Omega$  is a stochastic process  $X_0, X_1, \ldots$  such that  $X_t \in \Omega$  for all  $t \in \mathbb{N}$ , and

$$\Pr(X_{t+1} = y \mid X_0 = x_0, \dots, X_t = x_t) = \Pr(X_{t+1} = y \mid X_t = x_t)$$

for all  $t \in \mathbb{N}$  and  $x_0, \ldots, x_t, y \in \Omega$ . These probabilities are stored in an  $|\Omega| \times |\Omega|$  matrix P, called the *transition matrix* P of  $\mathcal{M}$ . (This notation clashes with our earlier use of P for configurations, but we will not mention configurations in this section so this should not cause confusion.) So the (x, y) entry of P, denoted P(x, y), is defined by

$$P(x,y) = \Pr(X_{t+1} = y \mid X_t = x)$$

for all  $x, y \in \Omega$  and all t > 0.

A Markov chain is *irreducible* if there is a sequence of transitions which transforms x to y, for any  $x, y \in \Omega$ , and it is *aperiodic* if  $\gcd\{t \mid P^t(x, x) > 0\} = 1$  for all  $x \in \Omega$ . If a Markov chain is irreducible and aperiodic then we say it is *ergodic*. The classical theory of Markov chains says that if  $\mathcal{M}$  is ergodic then it has a unique stationary distribution which is the limiting distribution of the chain.

We say that the Markov chain  $\mathcal{M}$  is time-reversible (often just called reversible) with respect to the distribution  $\pi$  on  $\Omega$  if the detailed balance equations hold:

$$\pi(x)P(x,y) = \pi(y)P(y,x)$$

for all  $x, y \in \Omega$ . If a Markov chain  $\mathcal{M}$  is ergodic and is time-reversible with respect to a distribution  $\pi$ , then  $\pi$  is the (unique) stationary distribution of  $\mathcal{M}$ . (See for example [84, Proposition 1.19].) In particular, if P is symmetric then the stationary distribution is uniform. The detailed balance equations are often used to guide the design of the transition matrix of a Markov chain, so that it has the desired stationary distribution.

Now assume that  $\mathcal{M}$  is ergodic with stationary distribution  $\pi$ . For  $x \in \Omega$  let  $P_x^t$  denote the distribution of  $X_t$ , conditioned on the event  $X_0 = x$ . Recall the definition of total variation distance (Definition 2.2). For any initial state  $x \in \Omega$ , the distance  $d_{TV}(P_x^t, \pi)$  is a geometrically-decreasing function of t (see for example [84, Theorem 4.9]). This leads to the following definition.

**Definition 6.1** Let  $\varepsilon > 0$  be a constant. The *mixing time* of the Markov chain is the function

$$\tau(\varepsilon) = \max_{x \in \Omega} \min\{t \in \mathbf{N} \mid d_{TV}(P_x^t, \pi) < \varepsilon\}.$$

Here  $\varepsilon$  is a user-defined tolerance, which specifies how much variation from the stationary distribution is acceptable. The mixing time captures the earliest time t at which  $P_x^t$  is guaranteed to be  $\varepsilon$ -close to the stationary distribution, regardless of the starting state. Then  $P_x^t$  remains  $\varepsilon$ -close to the stationary distribution for all times  $t \geq \tau(\varepsilon)$  and for every initial state  $x \in \Omega$ .

As usual, we are really interested in sampling from a set  $\Omega_n$ , parameterised by n, where  $|\Omega_n| \to \infty$ , and we want to know how the runtime of the algorithm behaves as  $n \to \infty$ . The tolerance  $\varepsilon = \varepsilon_n$  may also depend on n. We say that the Markov chain is rapidly mixing if the mixing time is bounded above by a polynomial in  $\log |\Omega_n|$  and  $\log(\varepsilon^{-1})$ . Normally it is prohibitively difficult to find  $\tau(\varepsilon)$  exactly, so we aim to find an upper bound T which is polynomial in  $\log |\Omega_n|$  and  $\log(\varepsilon^{-1})$ . Then the Markov chain can be used as an FPAUS for sampling from  $\Omega_n$ , in the sense of Definition 2.3, as follows: starting from a convenient initial state, run the Markov chain for T steps and output the state  $X_T$ . See for example Figure 13.

We defer introduction of the multicommodity flow method until Section 6.3.

#### 6.2 The Jerrum-Sinclair chain

The first Markov chain algorithm for sampling from  $G(\mathbf{k})$  was given by Jerrum and Sinclair [76] in 1990. They used Tutte's construction [111] to reduce the problem to that of sampling perfect and near-perfect matchings from an auxiliary graph  $\Gamma(\mathbf{k})$ , then applied their Markov chain from [75] to solve this problem. This resulted in a Markov chain which has uniform stationary distribution over the expanded state space  $G'(\mathbf{k}) = \bigcup_{\mathbf{k}'} G(\mathbf{k}')$ , where the union is taken over the set of all graphical sequences  $\mathbf{k}' = (k'_1, \ldots, k'_n)$  such that  $k'_j \leq k_j$  for all  $j \in [n]$  and  $\sum_{j \in [n]} |k_j - k'_j| \leq 2$ .

The chain performs three types of transitions, which when mapped back to  $G'(\mathbf{k})$  are as follows: deletion of a random edge, if the current state belongs to  $G(\mathbf{k})$ ; insertion of an edge between the two distinct vertices with degree deficit one; or insertion of a random edge  $\{i, j\}$  together with the deletion of a randomly-chosen neighbouring edge  $\{j, \ell\}$ . (We will not specify the transition probabilities precisely here.) See Figure 12, where dashed lines represent non-edges. The third type of transition is called a hinge-flip by Amanatidis and Kleer [3], following [25].

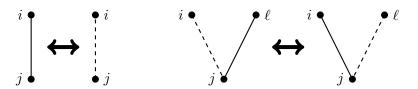


Figure 12: Transitions of the Jerrum–Sinclair chain: insertion/deletion (left) and hinge-flip (right)

We can use the Jerrum-Sinclair chain to repeatedly sample from  $G'(\mathbf{k})$  until

an element of  $G(\mathbf{k})$  is obtained. For this to be efficient, the expected number of iterations required must be bounded above by a polynomial.

**Definition 6.2** A class of degree sequences is called *P-stable* if there exists a polynomial q(n) such that  $|G'(\mathbf{k})|/|G(\mathbf{k})| \leq q(n)$  for every degree sequence  $\mathbf{k} = (k_1, \dots, k_n)$  in the class.

Jerrum and Sinclair proved the following result [76, Theorem 2.4], but did not give an explicit (polynomial) bound on the mixing time of their chain.

**Theorem 6.3** [76] There is an FPAUS for  $G(\mathbf{k})$  for any degree sequence  $\mathbf{k}$  which belongs to some P-stable class.

Various classes of degree sequences are known to be P-stable, including the class of all regular sequences, and all sequences with  $k_{\text{max}}$  sufficiently small. We discuss P-stability further in Section 6.5.

**6.2.1 A complete solution for the bipartite case** The Jerrum–Sinclair chain for sampling perfect matchings from a given graph [75] is slow when the ratio of the number of perfect matchings to the number of near-perfect matchings is exponentially small. In 2004, Jerrum, Sinclair and Vigoda [78] described and analysed an ingenious algorithm, based on simulated annealing, which overcame this problem for bipartite graphs. Their algorithm gives an FPAUS (and hence an FPRAS) for approximately-uniformly sampling (or approximately counting) perfect matchings from a given bipartite graph. An important idea in [78] is to use a non-uniform stationary distribution over the set of all perfect and near-perfect matchings, so that the stationary probability of the set of perfect matchings is at least  $1/(4n^2+1)$ ; that is, at most polynomially small. This is achieved by assigning weights to each "hole pattern" (for a near-perfect matching, this is the pair of vertices with deficit one, and for a perfect matching this is the empty set), as well as edge weights. Estimating good values for the weights is achieved iteratively, using simulated annealing.

As a corollary, using Tutte's construction [111], Jerrum, Sinclair and Vigoda obtained an FPAUS for sampling bipartite graphs with given degrees [78, Corollary 8.1]. In fact their result is more general: given an arbitrary bipartite subgraph H, they obtain an FPAUS for sampling subgraphs of H with a given degree sequence.

**Theorem 6.4** [78, Corollary 8.1] Given an arbitrary bipartite graph H, there is an FPAUS for the set of labelled subgraphs of H with a specified degree sequence, and there is an FPRAS for computing the number of these subgraphs.

Bezáková, Bhatnagar and Vigoda [11] gave a more direct implementation of the algorithm from [78], which avoids Tutte's construction. This allows them to obtain faster runtime bounds compared with [78]. It follows from the proof of [11, Theorem 1] that their FPAUS is valid for any bipartite degree sequence, and has running time

$$O((n_1n_2)^2M^3k_{\text{max}}\log^4(n_1n_2/\varepsilon)),$$

where  $n_1$  and  $n_2$  are the number of nodes in each part of the bipartition, and, as usual,  $k_{\text{max}}$  is the maximum degree and M is the sum of the degrees.

## 6.3 The multicommodity flow method

There are a few methods for bounding the mixing times of Markov chains. Before proceeding further we describe the multicommodity flow method, which has been used to analyse most MCMC algorithms for sampling graphs. For information on other methods for bounding the mixing times of Markov chains, see for example [36, 74, 84, 95].

Let  $\mathcal{M}$  be a time-reversible ergodic Markov chain and let  $N = |\Omega|$  be the cardinality of the state space. Then the eigenvalues of the transition matrix are real and satisfy

$$1 = \lambda_0 > \lambda_1 \ge \cdots \ge \lambda_{N-1} > -1.$$

The mixing time of the Markov chain is controlled by  $\lambda_{\max} = \max\{\lambda_1, |\lambda_{N-1}|\}$ . Denote the smallest stationary probability by  $\pi^* = \min\{\pi(x) \mid x \in \Omega\}$ . Then

$$\tau(\varepsilon) \le (1 - \lambda_{\max})^{-1} \log\left(\frac{1}{\varepsilon \pi^*}\right),$$
 (6.1)

see for example [104, Proposition 1]).

If  $\lambda_{\text{max}} = |\lambda_{N-1}|$  then in particular,  $\lambda_{N-1}$  must be negative, in which case  $1 - |\lambda_{N-1}| = 1 + \lambda_{N-1}$ . For many chains we can apply a result of Diaconis and Saloff-Coste [32, p.702] (see also [64]) to establish an upper bound on  $(1 + \lambda_{N-1})^{-1}$ . In particular, if there is a positive probability of a null transition at any state then the following special case of that result may be useful:

$$(1 + \lambda_{N-1})^{-1} \le \frac{1}{2} \max_{x \in \Omega} P(x, x)^{-1}.$$
(6.2)

Another option is to work with the *lazy* version of the Markov chain  $\mathcal{M}$ , by replacing the transition matrix P by (I+P)/2. This ensures that all eigenvalues are nonnegative and hence  $\lambda_{\max} = \lambda_1$ . We say that a Markov chain  $\mathcal{M}$  is *lazy* if  $P(x,x) \geq \frac{1}{2}$  for all  $x \in \Omega$ .

Sinclair's multicommodity flow method [104] provides an upper bound on  $(1 - \lambda_1)^{-1}$ . It is a generalisation of the canonical path method that Jerrum and Sinclair introduced in [75].

Given a Markov chain  $\mathcal{M}$  with uniform stationary distribution on a state space  $\Omega$ , let  $\mathcal{G}(\mathcal{M})$  be the underlying graph, where there is an edge from x to y if and only if P(x,y) > 0. We assume that  $\mathcal{M}$  is ergodic and time-reversible with respect to the distribution  $\pi$ . Let  $\mathcal{P}_{xy}$  be the set of all simple directed paths from x to y in  $\mathcal{G}(\mathcal{M})$ , and define  $\mathcal{P} = \bigcup_{x,y} \mathcal{P}_{xy}$ . A flow is a function  $f: \mathcal{P} \to [0, \infty)$  such that for all  $x, y \in \Omega$  with  $x \neq y$ ,

$$\sum_{p \in \mathcal{P}_{xy}} f(p) = \pi(x)\pi(y).$$

(In the canonical path method, there is only one flow-carrying path from between any two pairs of states.)

If the flow can be defined so that no transition of the chain is overloaded, then the state space does not contain any "bottlenecks" and the Markov chain will be rapidly mixing. To make this precise, the total flow through a transition e = xy is  $f(e) = \sum_{p \ni e} f(p)$ , and the load of e is defined by  $\rho(e) = f(e)/Q(e)$ , where

 $Q(e) = \pi(x)P(x,y)$  is the capacity of the transition e = xy. (By time-reversibility, Q is well-defined.) Finally, the maximum load of the flow is  $\rho(f) = \max_e \rho(e)$ , while  $\ell(f)$  denotes the length of the longest path p with f(p) > 0. Sinclair [104, Corollary 6'] proved that for any time-reversible Marvov chain any any flow f,

$$(1 - \lambda_1)^{-1} \le \rho(f) \ell(f).$$
 (6.3)

The next result specialises the multicommodity flow method to ergodic, timereversible Markov chains with the uniform stationary distribution over a set  $\Omega$ . It is obtained from (6.1) and (6.3), and allows two options for managing the smallest eigenvalue  $\lambda_{N-1}$ .

**Theorem 6.5** Let  $\mathcal{M}$  be an ergodic time-reversible Markov chain with uniform stationary distribution over  $\Omega$ . Define B to be 0, if it is known that  $\lambda_{\max} = \lambda_1$  (for example if  $\mathcal{M}$  is lazy). Otherwise, let B be an upper bound on  $(1 + \lambda_{N-1})^{-1}$ . Then the mixing time of the Markov chain  $\mathcal{M}$  satisfies

$$\tau(\varepsilon) \le \max\{\rho(f)\ell(f), B\} (\log |\Omega| + \log(\varepsilon^{-1})).$$

When the multicommodity flow method is applied to the problem of sampling graphs from  $G(\mathbf{k})$ , the start and end states are graphs G, G' with degree sequence  $\mathbf{k}$ . Usually the definition of the flow is guided by the symmetric difference  $H = G \triangle G'$  of G and G', and each step of a flow-bearing path is designed to make the symmetric difference smaller.

#### 6.4 The switch chain

The switch chain (also called swap chain [93] and Diaconis chain [11]) is the simplest Markov chain with uniform distribution over  $G(\mathbf{k})$ . A transition of the switch chain deletes two edges and inserts two edges, while maintaining the degree sequence and without introducing any repeated edges. This is illustrated in Figure 11, at the start of Section 6. This chain was introduced by Diaconis and Gangolli [31] in 1995 in order to sample contingency tables (matrices of nonnegative integers) with given row and column sums. The transitions can be easily adapted to bipartite graphs or directed graphs. The switch chain is ergodic for graphs, and for bipartite graphs, with given degrees.

In 1999, Kannan, Tetali and Vempala [80] considered the switch chain for sampling bipartite graphs with given degrees. They used the auxiliary graph  $\Gamma(\mathbf{k})$  obtained from Tutte's construction (modified to bipartite graphs) in order to define a multicommodity flow, and gave details only for the case of regular degrees. Unfortunately, there is a bug in their argument (specifically, in the proof of [80, Theorem 4.1]) which seems to be fatal.<sup>3</sup>

<sup>&</sup>lt;sup>3</sup>The symmetric difference of two perfect matchings in  $\Gamma(\mathbf{k})$  consists of the union of disjoint cycles. However, when mapped back to the symmetric difference of the two corresponding bipartite graphs, an alternating cycle in  $\Gamma(\mathbf{k})$  may correspond to an alternating walk, which could have linearly many repeated vertices (vertices which are visited more than once on the walk). The argument of [80] does not take this into account.

```
The switch chain Input: \quad \text{graphical sequence } \boldsymbol{k} \text{ and positive integer } T = T(\boldsymbol{k}) Output: \quad \text{element of } G(\boldsymbol{k}) let G be an arbitrary initial state for t = 0, \ldots, T-1 do choose two non-adjacent distinct edges \{a,b\}, \{c,d\} u.a.r. choose a perfect matching M of \{a,b,c,d\} u.a.r. if M \cap E(G) = \emptyset then delete the edges \{a,b\}, \{c,d\} and add the edges of M output G_T
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Figure 13: The switch chain for sampling from  $G(\mathbf{k})$ 

One implementation of the switch chain for  $G(\mathbf{k})$  is given in Figure 13. Cooper, Dyer and Greenhill [26] analysed the mixing time of the lazy version of this chain, restricted to regular degree sequences. (That is, they replaced the transition matrix P arising from the above procedure by (I+P)/2, which is equivalent to inserting the instruction "With probability  $\frac{1}{2}$ , do nothing" just inside the for-loop.) However, this is unnecessary, as the transition procedure given in Figure 13 guarantees that  $(1 + \lambda_{\text{max}})^{-1} \leq \frac{3}{2}$ , by (6.2). Hence we can take  $B = \frac{3}{2}$  in Theorem 6.5. Using a multicommodity flow argument, Cooper et al. established a polynomial bound on the mixing time for any regular degree sequence [26, 27].

**Theorem 6.6** [26, 27] For any  $k = k(n) \ge 3$ , the switch chain on G(n, k) has mixing time

$$\tau(\varepsilon) \leq k^{23} \, n^8 \, \big( k n \log(kn) + \log(\varepsilon^{-1}) \big).$$

**Proof** (Sketch.) Cooper et al. defined a multicommodity flow for the switch chain on G(n,k) and proved that maximum load  $\rho(f)$  is bounded above by a polynomial in n and k. (A brief outline of the argument is given below.) The length of any flow-carrying path is at most kn/2. Next,

$$|G(\mathbf{k})| \le \frac{M!}{2^{M/2} (M/2)! \prod_{j \in [n]} k_j!} \le \exp(\frac{1}{2} M \log M),$$
 (6.4)

where the first inequality follows from the configuration model. Applying Theorem 6.5 completes the proof.

Greenhill [63] used a similar argument to show that the switch chain for k-in, k-out (regular) directed graphs is rapidly mixing for any k with  $1 \le k = k(n) \le n-1$  and all  $n \ge 4$ .

We now give some more details on the design and analysis of the multicommodity flow for the switch chain. The flow between two graphs G, G' is defined with respect to the symmetric difference  $H = G \triangle G'$ . Note that the symmetric difference H need not be regular, even if G, G' are both regular. Greenhill and Sfragara [65] observed

that the multicommodity flow defined in [26] for regular degrees can also be used for irregular degrees. In fact, almost all parts of the analysis of the multicommodity flow also extends immediately to irregular degree sequences. For this reason, the description below is presented in the general setting of  $G(\mathbf{k})$ .

Starting from the symmetric difference  $H = G \triangle G'$ , Cooper et al. described how to decompose this symmetric difference into a sequence of smaller, edge-disjoint structures they called 1-circuits and 2-circuits. They identified several different ways to do this, parameterised by a set  $\Psi(G, G')$ . For each  $\psi \in \Psi(G, G')$ , the (canonical) path from G to G' indexed by  $\psi$  is denoted  $\gamma_{\psi}(G, G')$ . This path is created by "processing" each of the 1-circuits and 2-circuits, in a specified order. Processing a circuit changes the status of its edges from agreeing with G to agreeing with G', and adds some transitions to the path  $\gamma_{\psi}(G, G')$ . Finally, the flow from G to G' divided equally among these  $|\Psi(G, G')|$  paths.

Once the multicommodity flow is defined, it remains to prove that no transition is too heavily loaded. Suppose that e = (Z, Z') is a transition of the chain which is used on the path  $\gamma_{\psi}(G, G')$ . A common approach is to define an encoding L of a state Z, which records information about the symmetric difference  $H = G \triangle G'$  to help us recover G and G' from the transition (Z, Z') and the encoding L. This approach will work if the set of possible encodings for Z is at most polynomially larger than  $|G(\mathbf{k})|$ , and there are at most polynomially-many options for (G, G') once Z, Z', L are all specified. In [26], encodings are defined by

$$L + Z = G + G'$$

where G, G' and Z are identified with their  $n \times n$  adjacency matrices. Then L is an  $n \times n$  symmetric matrix with row sums given by k, and with almost all entries equal to 0 or 1. In fact, due to the careful way that 1-circuits and 2-circuits are processed, L has at most 4 entries equal to -1 or 2, and all other entries are 0 or 1. Hence L may also be thought of as a graph with most edges labelled 1, and at most four defect edges which may be labelled -1 or 2. The sum of all edge labels at vertex j must equal the degree  $k_j$  of j, for all  $j \in [n]$ . (There are some other constraints about the structure of the defect edges, stated in [26, Lemma 2].)

Given an encoding L, by removing the defect edges we obtain a graph with degree sequence which is very close to  $\mathbf{k}$ . This gives a connection between the ratio  $|\mathcal{L}(Z)|/|G(\mathbf{k})|$  and the ratio  $|G'(\mathbf{k})|/|G(\mathbf{k})|$  from the definition of P-stability (6.2). This connection is explored further in Section 6.5. In the regular case, we have the following bound.

**Lemma 6.7** [26, Lemma 4] For any  $Z \in G(n,k)$ , let  $\mathcal{L}(Z)$  denote the set of encodings L such that every entry of L + Z belongs to  $\{0,1,2\}$ . Then  $|\mathcal{L}(Z)| \leq 2k^6n^6|G(n,k)|$ .

**Proof** (Sketch.) This was proved by extending the switch operation to encodings, and showing that at most three switches suffice to transform an encoding into an element of G(n,k). The factor  $2k^6n^6$  is an upper bound on the number of encodings which can be transformed into an arbitrary element of G(n,k).

In fact, Greenhill and Sfragara observed that [26, Lemma 4] (restated as Lemma 6.7 above) was the *only* part of the argument from [26] which relied on the regularity

assumption for its proof. For this reason, they called it the "critical lemma". The proof of the lemma is essentially a switching argument, used to find the relative sizes of two sets. For irregular degrees, it was no longer possible to prove that a suitable switch could always be found in any encoding.

Greenhill and Sfragara bypassed this problem by using a more powerful switching operation to prove the critical lemma. Rather than use a switch, which swaps edges for non-edges around an alternating 4-cycle, they used a operation involving an alternating 6-cycle (deleting 3 edges and inserting 3 edges at a time), illustrated in Figure 14. This operation gave them sufficient flexibility to prove the critical lemma when  $k_{\text{max}}$  is not too large.



Figure 14: Switching edges around a 6-cycle

**Theorem 6.8** [65, Theorem 1.1] Let  $\mathbf{k}$  be a graphical degree sequence. If all entries of  $\mathbf{k}$  are positive and  $3 \le k_{\text{max}} \le \frac{1}{3}\sqrt{M}$  then the mixing time of the switch chain on  $G(\mathbf{k})$  satisfies

$$\tau(\varepsilon) \le k_{\max}^{14} M^9 \left(\frac{1}{2} M \log M + \log(\varepsilon)\right).$$

In Section 6.5 we will discuss connections between the stability of degree sequences and rapid mixing of the switch chain. First we discuss some results regarding the switch chain for bipartite graphs, directed graphs and hypergraphs, and some related topics.

**6.4.1 Bipartite graphs and directed graphs** We have seen in Theorem 6.4 that the algorithm of Jerrum, Sinclair and Vigoda [78] gives an FPAUS for sampling bipartite graphs with any given bipartite degree sequence. However, there is still interest in studying the switch chain for bipartite graphs, as it is a very natural and simple process.

A 1-regular bipartite graph is a permutation. Diaconis and Shahshahani [34] studied the Markov chain with state space  $S_n$ , the set of all permutations of [n], and transitions defined as follows: with probability 1/n do nothing, and otherwise choose a transposition (ij) uniformly at random (where  $i, j \in [n]$  are distinct), and multiply the current permutation by (ij) on the left, say. This random transposition chain is very closely related to the switch chain for a 1-regular bipartite degree sequence (the set of allowed transitions is identical, though the probability of each transition differs between the two chains). Diaconis and Shahshahani gave a very complete analysis of the random transposition chain in [34], calculating the eigenvalues and proving that the chain exhibits the "cutoff phenomenon", see [84, Chapter 18]. That is, the total variation distance to stationarity drops very quickly from 1 - o(1) to

o(1) when the chain has taken  $\frac{1}{2}n\log n + \Theta(n)$  steps (this is cutoff at  $\frac{1}{2}n\log n$  with window of order n).

Other than [34], the first analysis of the switch chain for sampling bipartite graphs with given degrees was the work of Kannan et al. [80], discussed earlier.

The multicommodity flow arguments from [26, 65] can be simplified when restricted to bipartite graphs, as the symmetric difference of two bipartite graphs with the same degree sequence can be decomposed into edge-disjoint alternating cycles, and these are relatively easy to handle. The resulting bounds on the mixing time of the switch chain for bipartite graphs with given degrees were recently presented in [37, Appendix A]. These show that the switch chain is rapidly mixing for any regular bipartite degree sequence, and for arbitrary bipartite degree sequences when the maximum degree is not too large compared to the number of edges. As usual, the mixing time bounds are very high-degree polynomials.

A bipartite degree sequence is *half-regular* if all degrees on one side of the bipartition are regular. Miklos, Erdős and Soukup [93] proved that the switch Markov chain is rapidly mixing for half-regular bipartite degree sequences. Their proof also used the multicommodity flow method, but the flow is defined differently to the Cooper–Dyer–Greenhill flow described above.

For some directed degree sequences, the switch chain fails to connect the state space, as it cannot reverse the orientation of a directed 3-cycle. Rao et al. [100] observed that by the Markov chain which performs switch moves and (occasionally) reverse directed 3-cycles, is ergodic for any directed degree sequence. They noted that for many degree sequences, this additional move did not seem to be needed in order to connect the state space. This was confirmed by the work of Berger and Müller-Hannemann [10] and LaMar [83], who characterised degree sequences for which the switch chain is irreducible.

Greenhill and Sfragara [65, Theorem 1.2] adapted their argument to directed graphs, proving a similar result to Theorem 6.8. As well as an upper bound on the maximum degree, [65, Theorem 1.2] also assumes that the switch chain connects the state space. Their argument built on Greenhill's analysis [63] of the switch chain for directed graphs, replacing the proof of the "critical lemma" from [63] by one which did not require regularity.

6.4.2 The augmented switch chain and the Curveball chain Erdős et al. [41] considered the switch chain augmented by an additional transition, namely switching the edges around an alternating 6-cycle as shown in Figure 14. They called this transition a triple swap. We will refer to this chain as the augmented switch chain. Building on the analysis from [93], Erdős et al. [41, Theorem 10] proved that the augmented switch chain for half-regular bipartite degree sequences remains rapidly mixing in the presence of set of forbidden edges given by the union of a perfect matching and a star. They also described an algorithm (similar to the Havel–Hakimi algorithm) for constructing a single realization [41, Theorem 9], to be used as the initial state. Since directed graphs can be modelled as bipartite graphs with a forbidden perfect matching, their algorithm also gives an FPAUS for directed graphs with specified in-degrees and out-degrees, where (say) the sequence of indegrees is regular. This explains the addition of the triple swap transitions, without which the chain might not be irreducible for some directed degree sequences. By

avoiding a star, the problem becomes *self-reducible* [79], which leads to an FPRAS for approximating the number of bipartite graphs with given half-regular degree sequence and some forbidden edges. As mentioned earlier, the algorithm of Jerrum, Sinclair and Vigoda [78, Corollary 8.1] can also be applied to this problem.

Erdős et al. [42] gave new conditions on bipartite and directed degree sequences which guarantee rapid mixing of the augmented switch chain. In particular, suppose that a bipartite degree sequence has degrees  $\mathbf{s} = (s_1, \ldots, s_a)$  in one part and degrees  $\mathbf{t} = (t_1, \ldots, t_b)$  in the other, where a + b = n. Let  $s_{\text{max}}, s_{\text{min}}, t_{\text{max}}, t_{\text{min}}$  be the maximum and minimum degrees on each side. If all degrees are positive and

$$(s_{\text{max}} - s_{\text{min}} - 1)(t_{\text{max}} - t_{\text{min}} - 1) \le \max\{s_{\text{min}}(a - t_{\text{max}}), t_{\text{min}}(b - s_{\text{max}})\}$$

then the augmented switch chain on the set of bipartite graphs with bipartite degree sequence (s,t) is rapidly mixing [42, Theorem 3]. They applied this result to the analysis of the bipartite Erdős–Rényi model  $\mathcal{G}(a,b,p)$ , with a vertices in one side of the bipartition, b vertices on the other and each possible edge between the two parts is included with probability p. Erdős et al. [42, Corollary 13] proved that if p is not too close to 0 or 1 then the augmented switch chain is rapidly mixing for the degree sequence arising from  $\mathcal{G}(a,b,p)$ , with high probability as  $n \to \infty$ , where n = a + b. They also proved analogous results for directed degree sequences [42, Theorem 4, Corollary 14]. To prove their results, they adjusted the multicommodity argument from [41, 93] and gave new proofs of the "critical lemma" for that argument.

The Curveball chain, introduced by Verhelst [114], is another Markov chain for sampling bipartite graphs with given degrees, which chooses two vertices on one side of the bipartition and randomises their neighbourhoods, without disturbing the degrees or set of common neighbours of the chosen vertices. Carstens and Kleer [20] showed that the Curveball chain is rapidly mixing whenever the switch chain is rapidly mixing.

- **6.4.3** New classes from old Erdős, Miklós and Toroczkai [45] described a novel way to expand the class of degree sequences (and bipartite degree sequences, and directed degree sequences) for which the switch chain is known to be rapidly mixing. Their approach utilised canonical degree sequence decompositions, introduced by Tyshkevich [112], and extended this concept to bipartite and directed degree sequences. Using the decomposition theorem from [44], if the switch chain (or augmented switch chain) is rapidly mixing on each component of this decomposition, then it is rapidly mixing on the original degree sequence.
- **6.4.4 Improved bounds using functional inequalities** Functional inequalities can be used to give tight bounds on the convergence of Markov chains. Suppose that  $\mathcal{M}$  is a Markov chain with state space  $\Omega$ , transition matrix P and stationary distribution  $\pi$ . The *Dirichlet form* associated to  $\mathcal{M}$  is defined by

$$\mathcal{E}_{P,\pi}(f,f) = \frac{1}{2} \sum_{x,y \in \Omega} (f(x) - f(y))^2 \pi(x) P(x,y)$$

for any  $f: \Omega \to \mathbf{R}$ . This is a weighted measure of how much f varies over pairs of states which differ by a single transition. The *variance* of f with respect to  $\pi$ ,

defined by

$$\operatorname{Var}_{\pi}(f) = \frac{1}{2} \sum_{x,y \in \Omega} (f(x) - f(y))^2 \pi(x) \pi(y),$$

captures the global variation of f over  $\Omega$ . These functions can be used to bound the second-largest eigenvalue  $\lambda_1$  of  $\mathcal{M}$  as follows:

$$1 - \lambda_1 = \min_{f} \frac{\mathcal{E}_{P,\pi}(f, f)}{\operatorname{Var}_{\pi}(f)},$$

where the minimum is taken over all non-constant functions  $f: \Omega \to \mathbf{R}$ . See for example [84, Lemma 13.12 and Remark 13.13]. The Markov chain satisfies a *Poincaré inequality* with constant  $\alpha$  if  $\operatorname{Var}_{\pi}(f) \leq \alpha \mathcal{E}_{P,\pi}(f,f)$  for any  $f: \Omega \to \mathbf{R}$ . The log-Sobolev inequality has a similar (but more complicated) definition and can also be used to bound the mixing time [33].

Very recently, Tikhomirov and Youssef [109] proved<sup>4</sup> a sharp Poincaré inequality, and established a log-Sobolev inequality, for the switch chain for regular bipartite graphs. Using their Poincaré inequality, Tikhomirov and Youssef proved [109, Corollary 1.2] that when  $3 \le k \le n^c$  for some universal constant c, the mixing time of the switch chain on k-regular bipartite graphs satisfies

$$\tau(\varepsilon) \le Ckn(kn\log kn + \log(2\varepsilon^{-1}))$$

for some universal constant C>0 (constants c,C not explicitly stated). This is a huge improvement on any previously-known bound. Tikhomirov and Youssef also state the following mixing time bound, obtained using their log-Sobolev inequality when  $k\geq 3$  is a fixed constant:

$$\tau(\varepsilon) \le C_k n \log n \left( \log n + \log \left( \frac{1}{2\varepsilon^2} \right) \right).$$

Here  $C_k > 0$  is an expression which depends only on k.

The proof in [109] is long and technical, and will likely be difficult to generalise. But it is exciting to see such a low-degree polynomial bound on the mixing time of the switch chain for this non-trivial class of bipartite degree sequences.

**6.4.5** Hypergraphs A hypergraph is uniform if every edge contains the same number of vertices. The incidence matrix of a hypergraph can be viewed as the adjacency matrix of a bipartite graph, with one part of the bipartition representing the vertices of the hypergraph and the other part representing the edges. Conversely, a bipartite graph gives rise to a simple hypergraph, by reversing this construction, if all vertices on the "edge" side of the bipartition have distinct neighbourhoods. This is needed to avoid creating a repeated edge. In the case of uniform hypergraphs, if the resulting hypergraph is simple then it arises from precisely m! distinct bipartite graphs, where m is the number of edges of the hypergraph.

Hence, any algorithm for sampling bipartite graphs with a given half-regular degree sequence can be transformed into an algorithm for sampling uniform hypergraphs with given degrees, using rejection sampling. This is explored by Dyer et al.

<sup>&</sup>lt;sup>4</sup>Subject to refereeing.

in [37]. Note that a configuration model may be defined for hypergraphs, though it is equivalent to the corresponding bipartite configuration model. The configuration model only gives polynomial-time uniform sampling when the maximum degree multiplied by the edge size is  $O(\log n)$ , see [37, Lemma 2.3].

Chodrow [22] introduced a Markov chain which works directly on uniform hypergraphs. A transition involves choosing two edges e, f and deleting them, then inserting two edges e', f' chosen randomly so that the degree sequence is unchanged and  $e' \cap f' = e \cap f$ . This transitions of this chain are analogous to the transitions of the Curveball chain [20] for sampling bipartite graphs. Chodrow proved that this chain is ergodic, but did not analyse the mixing time. It is an open problem to determine classes of degree sequences and edge sizes for which this chain is rapidly mixing.

### 6.5 Stability of degree sequences

Informally, a class of degree sequences is *stable* if  $|G(\mathbf{k})|$  varies smoothly as  $\mathbf{k}$  ranges over the class [77]. Work on the connection between the stability of degree sequences and mixing rates of Markov chains for sampling from  $G(\mathbf{k})$  began with Jerrum and Sinclair's definition of P-stability [76], stated in Definition 6.2 above. A slightly different version of P-stability was studied by Jerrum, Sinclair and McKay [77]. Let  $\|\mathbf{x}\|_1 = \sum_{j \in [n]} |x_j|$  denote the 1-norm of the vector  $\mathbf{x} = (x_1, \ldots, x_n)$ , and define the set  $U(\mathbf{k})$  of all degree sequences  $\tilde{\mathbf{k}}$  such that

$$\|\tilde{k}\|_1 = \|k\|_1$$
 and  $\|\tilde{k} - k\|_1 = 2$ .

Jerrum, Sinclair and McKay said that a class of degree sequences is P-stable if there exists a polynomial q(n) such that

$$\left| \bigcup_{\tilde{\boldsymbol{k}} \in U(\boldsymbol{k})} G(\tilde{\boldsymbol{k}}) \right| \leq q(n) |G(\boldsymbol{k})|$$

for all k in the class. If this holds then k is also P-stable in the original sense (Definition 6.2). Let  $k_{\min}$  denote the smallest entry of k. Jerrum et al. [77, Theorem 8.1, Theorem 8.3] gave two sufficient conditions for a degree sequence to belong to a P-stable class.

**Theorem 6.9** [77] Recall that  $M = M(\mathbf{k})$  is the sum of entries in the degree sequence  $\mathbf{k}$ .

(i) The class of graphical degree sequences  $\mathbf{k} = (k_1, \dots, k_n)$  which satisfy

$$(k_{\text{max}} - k_{\text{min}} + 1)^2 \le 4k_{\text{min}} (n - k_{\text{max}} - 1)$$

is P-stable.

(ii) The class of graphical degree sequences  $\mathbf{k} = (k_1, \dots, k_n)$  which satisfy

$$(M - k_{\min} n)(k_{\max} n - M)$$
  
  $\leq (k_{\max} - k_{\min})((M - k_{\min} n)(n - k_{\max} - 1) + k_{\min}(k_{\max} n - M))$ 

is P-stable.

Jerrum et al. [77] listed several examples of classes of degree sequences which satisfy one of these sufficient conditions and hence are P-stable, including

- all regular sequences;
- all graphical sequences with  $k_{\min} \ge 1$  and  $k_{\max} \le 2\sqrt{n} 2$ ;
- all graphical sequences with  $k_{\min} \ge n/9$  and  $k_{\max} \le 5n/9 1$ .

Using (5.5) and recalling Definition 5.7, we see that the sufficient condition from Theorem 6.9(i) does not cover heavy-tailed distributions such as the power-law distribution-bounded degree sequences with  $\gamma \in (2,3)$ . The condition from Theorem 6.9(ii) may hold in some cases but fails whenever  $M > 2k_{\min} n$ . The first and third examples show that a P-stable class does not have to be sparse.

It is possible to define classes of degree sequences which are not P-stable but for which the switch chain is rapidly mixing. Jerrum, Sinclair and McKay [77] illustrated this using the degree sequence

$$\mathbf{k} = \mathbf{k}(n) = (2n - 1, 2n - 2, \dots, n + 1, n, n, n - 1, \dots, 2, 1)$$

on 2n vertices. There is a unique realisation of this degree sequence, so  $|G(\mathbf{k})| = 1$  and the switch chain is trivially rapidly mixing on  $G(\mathbf{k})$ . However,  $|G(\mathbf{k}')|$  is exponential in n, where

$$\mathbf{k}' = \mathbf{k}'(n) = (2n - 2, 2n - 2, \dots, n + 1, n, n, n - 1, \dots, 2, 2)$$

is obtained from k by decreasing the largest degree by 1 and increasing the smallest degree by 1. Hence the class  $\{k(n) \mid n \geq 2\}$  is not P-stable. Erdős et al. [40] described more general classes of degree sequences with these properties. So P-stability is not a necessary condition for the switch chain to be efficient. Rather, the standard proof techniques tend to break down when the class of degree sequences is not P-stable.

**6.5.1 Strong stability** Amanatidis and Kleer [3, 4] defined a new notion of stability, called *strong stability*, which is possibly stronger than P-stability. Recall that  $G'(\mathbf{k})$  denotes the state space of the Jerrum-Sinclair chain. Say that graphs G, H are at JS-distance r if H can be obtained from G using at most r transitions of the Jerrum-Sinclair chain. Next, let  $d_{JS}(\mathbf{k})$  denote the maximum, over all  $G \in G'(\mathbf{k})$ , of the minimum distance from G to an element of  $G(\mathbf{k})$ . Then every element of the augmented state space  $G'(\mathbf{k})$  can be transformed into an element of  $G(\mathbf{k})$  in at most  $d_{JS}(\mathbf{k})$  transitions of the Jerrum-Sinclair chain.

**Definition 6.10** A class of graphical degree sequences is *strongly stable* if there is a constant  $\ell$  such that  $d_{JS}(\mathbf{k}) \leq \ell$  for all degree sequences  $\mathbf{k}$  in the class.

Amanatidis and Kleer proved [3, Proposition 3] that every strongly stable family is P-stable. It is not known whether the converse is also true. The main result of [3] is the following.

**Theorem 6.11** [4, Proposition 2.3 and Theorem 2.4] The switch chain is rapidly mixing for all degree sequences from a strongly stable family.

The proof of Theorem 6.11 rests on the observation that it is much easier to define a good multicommodity flow for the Jerrum–Sinclair chain than for the switch chain. Next, Amanatidis and Kleer prove that when k is strongly stable, a good flow for the Jerrum–Sinclair chain can be transformed into a good flow for the switch chain.

Amanatidis and Kleer gave analogous results for bipartite degree sequences [3, Theorem 17]. Their framework provided a unified proof of many rapid mixing results for the switch chain for graphs, and bipartite graphs, with given degrees. The authors of [3] remark that their "unification of the existing results [...] is qualitative rather than quantitative, in the sense that our simpler, indirect approach provides weaker polynomial bounds for the mixing time."

**6.5.2** Rapid mixing for P-stable degree classes Erdős et al. [39] defined a new multicommodity flow for the switch chain. The symmetric difference is decomposed into primitive alternating circuits, such that no vertices is visited more than twice on a primitive circuit, and if a vertex is visited twice then the two occurrences are at an odd distance from each other around the circuit. Then the primitive alternating circuits are processed in a carefully-chosen order. An encoding is defined (and is called an "auxiliary matrix") such that it is at most three switches away from (the adjacency matrix of) an element of the set  $G'(\mathbf{k})$ . By definition, P-stability guarantees that  $|G'(\mathbf{k})| \leq q(n) |G(\mathbf{k})|$  for some polynomial q(n). Furthermore, there are a polynomial number of ways to choose each of the (at most 3) switches. Hence, when  $\mathbf{k}$  is P-stable, we conclude that the number of encodings is at most polynomially larger than  $|G(\mathbf{k})|$ . This proves the "critical lemma" for this flow, and establishes the following.

**Theorem 6.12** [39, Theorem 1.3] The switch Markov chain is rapidly mixing on all degree sequences contained in a P-stable class.

Erdős et al. adapted their analysis to bipartite degree sequences and directed degree sequences [39], proving the analogue of Theorem 6.12 in those settings. Hence their result extends Theorem 6.11 from strongly stable to P-stable degree classes, and includes directed degree sequences. bipartite degree sequences and directed degree sequences.

Applying Theorem 6.9(ii) and Theorem 6.12 to the degree sequence of  $\mathcal{G}(n,p)$  leads to the following result.

**Corollary 6.13** [39, Corollary 8.6] When  $n \ge 100$ , the degree sequence of the binomial random graph  $\mathcal{G}(n,p)$  satisfies the condition of Theorem 6.9(ii) with probability at least 1-3/n, so long as  $p, 1-p \ge \frac{5\log n}{n-1}$ . Hence the switch chain is rapidly mixing on  $\mathcal{G}(n,p)$  with probability at least 1-3/n.

Indeed, applying Theorem 6.3 we can also conclude that if the conditions of Corollary 6.13 hold then with probability at least 1-3/n, the Jerrum–Sinclair chain gives an FPAUS for sampling from G(n, p).

**6.5.3** A new notion of stability Recently, Gao and Greenhill [56] introduced a new notion<sup>5</sup> of stability for classes of degree sequences.

<sup>&</sup>lt;sup>5</sup>Called "k-stability" in [56], but here we reserve k for degrees.

**Definition 6.14** Given a positive integer b and nonnegative real number  $\alpha$ , a graphical degree sequence k is said to be  $(b,\alpha)$ -stable if  $|G(k')| \leq M(k)^{\alpha} |G(k)|$  for every graphical degree sequence k' with  $||k'-k||_1 \leq b$ . Let  $\mathcal{D}_{b,\alpha}$  be the set of all degree sequences that are  $(b,\alpha)$ -stable. A family  $\mathcal{D}$  of degree sequences is b-stable if there exists a constant  $\alpha > 0$  such that  $\mathcal{D} \subseteq \mathcal{D}_{b,\alpha}$ .

Gao and Greenhill proved [56, Proposition 6.2] that 2-stability is equivalent to P-stability. The relationship between strong stability and 2-stability is not known.

Recall that by removing all defect edges, an encoding gives rise to a graph with degree sequence not too far from k. Gao and Greenhill observe that all degree sequences k' which correspond to encodings arising from the multicommodity flow of [26, 65] satisfy  $||k'-k||_1 \leq 8$ . Next, assuming  $(8,\alpha)$ -stability they found an upper bound on the number of encodings compatible with a given graph  $Z \in G(k)$ : this proves the "critical lemma" and leads to the following result.

**Theorem 6.15** [56, Theorem 2.1] If the graphical degree sequence  $\mathbf{k}$  is  $(8, \alpha)$ -stable for some  $\alpha > 0$  then the switch chain on  $G(\mathbf{k})$  is rapidly mixing, and

$$\tau(\varepsilon) \le 12 k_{max}^{14} n^6 M^{3+\alpha} \left(\frac{1}{2} M \log M + \log \varepsilon^{-1}\right).$$

Gao and Greenhill provided a sufficient condition for a degree sequence to be 8-stable, and a slightly weaker condition which guarantees P-stability and strong stability. These conditions involve the parameter  $J(\mathbf{k})$  defined in (5.6), and have been designed to work well for heavy-tailed degree sequences.

### **Theorem 6.16** [56, Theorem 2.2]

- (i) Let  $\mathbf{k}$  be a graphical degree sequence. If  $M > 2J(\mathbf{k}) + 18k_{\text{max}} + 56$  then  $\mathbf{k}$  is (8,8)-stable.
- (ii) Suppose that  $\mathcal{D}$  is a family of degree sequences which that  $M > 2J(\mathbf{k}) + 6k_{\max} + 2$  for all  $\mathbf{k} \in \mathcal{D}$ . Then  $\mathcal{D}$  is both P-stable and strongly stable.

The proof of Theorem 6.16(i) uses the switching method. Then Theorem 6.16(ii) follows using the fact, proved in [56, Lemma 4.1], that if every graphical degree sequence  $\mathbf{k}'$  with  $\|\mathbf{k}' - \mathbf{k}\|_1 \le 6$  is  $(2, \alpha)$ -stable then  $\mathbf{k}$  is  $(8, 4\alpha)$ -stable.

Finally, Gao and Greenhill prove that various families of heavy-tailed degree sequences satisfy the condition of Theorem 6.16(i), and hence are 8-stable, strongly stable and P-stable. In particular [56, Theorem 5.3], the family of power-law distribution-bounded sequences with parameter  $\gamma > 2$  is P-stable.

Gao and Greenhill gave analogous definitions and results for directed degree sequences [56, Section 7].

### 6.6 Restricted graph classes

We briefly describe some related work on using rapidly mixing Markov chains to sample from restricted classes of graphs with given degrees.

**6.6.1** Joint degree matrices In some applications, it is desirable to be able to specify not just the degrees of a graph, but also the number of edges between vertices with given degrees. This can help to capture network properties such as assortativity, which is the tendency for vertices with similar degrees to be adjacent. A joint degree matrix [2, 98] stores the number of edges  $J_{ij}$  with one endvertex of degree i and the other of degree i, for all relevant i, j. A sequential importance sampling approach for sampling graphs with a specified joint degree matrix was given in the physics literature by Bassler et al. [6], without full analysis.

The switch chain can be adapted to sample from the set of all graphs with a given degree sequence and given joint degree matrix, by rejecting any transition which would change any entry in the joint degree matrix. Stanton and Pinar [107] gave empirical evidence that suggests that the switch chain mixes rapidly on graphs with a prescribed joint degree matrix, but there are few rigorous results. Erdős, Miklós and Toroczkai [44] proved that the switch chain is rapidly mixing on the set of all balanced realizations of a given joint degree matrix. Here a realization is balanced if for all vertices v with degree i, the number of neighbours w of v with degree i is within 1 of the value  $J_{ij}/n_i$ , where  $n_i$  is the number of vertices with degree i. Their proof involved a new Markov chain decomposition theorem [44, Theorem 4.3], similar to that of Martin and Randall [87].

Amanatidis and Kleer [3] showed that the switch chain is rapidly mixing on the set of all realizations of any joint degree matrix with just two degree classes. Their analysis is quite technical, and moving beyond two degree classes seems to be a challenging problem.

**6.6.2 Connected graphs** The switch chain may disconnect a connected graph, which can be undesirable in some applications such as communications networks. One possibility is to simply reject any proposed switch which would disconnect the graph. Gkantsidis et al. [62] investigated the performance of this restricted switch chain empirically, but without rigorous analysis. Note that the set of connected graphs with given degree sequence was shown to be connected under switches by Taylor [108] in 1981.

Mahlmann and Schindelhauer [86] proposed an alternative operation, called the k-Flipper. Here a switch is performed if the edges of the switch are at distance at most k apart in the graph. In the 1-Flipper, or *flip chain*, the switch operation takes a path of length 3 and exchanges its endvertices, as shown in Figure 15. Clearly this operation, known as a *flip*, cannot disconnect a connected graph.

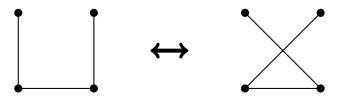


Figure 15: Transitions of the flip chain

The flip chain is rapidly mixing on the set of all connected k-regular graphs, for any k. This was investigated by Feder et al. [49], with full analysis and improved

mixing time bound given by Cooper et al. [28]. These proofs involve a comparison argument, where a sequence of flips is used to simulate a single switch. If a switch disconnects or connects components, then a clever "chaining" argument from [49] is used to stay within the space of connected graphs.

The flip operation can be used to re-randomise a given connected network (such as a communications network) without any risk of disconnecting the network. Expander graphs are fixed graphs which enjoy some pseudorandom properties, such as logarithmic diameter and high connectivity [70]. Allen-Zhu et al. [1, Theorem 4.2] proved that when  $k \geq c \log n$  for some positive constant c, performing  $O(k^2n^2\log n)$  randomly-chosen flips produces an expander with high probability, starting from any k-regular graph. They also applied their methods to the switch chain, showing that O(kn) randomly-chosen switches suffice to produce an expander, with high probability. Hence in situations where the output does not need to be close to uniform, but where pseudorandomness is enough, the runtime of the algorithm can be much shorter.

## 7 Conclusion

We have discussed rigorously-analysed algorithms for sampling graphs with a given degree sequence, uniformly or approximately uniformly. Some algorithms are inefficient when the maximum degree becomes too high. For other approaches, the boundary between tractable and intractable degree sequences is not clear. Mapping out this frontier is an interesting open problem. Are there families of degree sequences for which the switch chain is provably slow? Connections with stability of degree sequences have also been discussed. As well as their theoretical interest, there are connections between the stability of degree sequences and network privacy, as investigated by Salas and Torra [103].

A challenging open problem is to find an FPRAS for counting graphs with given (arbitrary) degree sequences. The corresponding problem for bipartite graphs with solved by Jerrum, Sinclair and Vigoda [78].

There are many related sampling algorithms which are just outside the scope of this survey. One example is the use of Boltzmann samplers [35] to sample from other restricted graph classes, including planar graphs [53]. As well as providing algorithms, this approach can be used to investigate typical properties of random graphs generated in this way, see for example [88].

To close, we mention some algorithms where the degree sequence itself is a random variable. Some fuzziness in the degree sequence can be useful in some applications, perhaps to account for inaccuracies in the data, or to avoid overfitting. The excellent book by Van der Hofstad [113] is a very good reference for further reading on these topics.

• In the network theory literature, often  $k_1, \ldots, k_n$  are i.i.d. random variables drawn from some fixed distribution. If the resulting sum is odd then  $k_n$  is increased by 1. More generally, a degree sequence k can be drawn at random from a given distribution, and then a graph from G(k) can be sampled uniformly, or approximately uniformly, using one of the methods discussed in this survey.

- Inhomogeneous random graphs are similar to the binomial random graph  $\mathcal{G}(n,p)$  except that different edges have different probabilities. For a sequence  $\mathbf{w} \in \mathbf{R}^n$  of positive vertex weights and a function  $f: \mathbf{R}^2 \to [0,1]$ , the edge  $\{i,j\}$  is included in the graph with probability  $f(w_i, w_j)$ , independently for each edge. An example is the generalised random graph model [19] with  $f(w_i, w_j) = \frac{w_i w_j}{M(\mathbf{w}) + w_i w_j}$ , where  $M(\mathbf{w}) = \sum_{\ell \in [n]} w_\ell$  is the sum of the weights. The Chung-Lu algorithm [23] uses  $f(w_i, w_j) = w_i w_j / M(\mathbf{w})$ , under the assumption that the maximum entry of  $\mathbf{w}$  is  $o(M(\mathbf{w})^{1/2})$ . The output of the Chung-Lu algorithm is a random graph with expected degree sequence  $\mathbf{w}$ .
- Another algorithm which produces a graph with degree sequence close to some target sequence is the erased configuration model [19]. First sample a uniformly random configuration, and in the corresponding graph, delete any loops and delete all but one copy of each multiple edge. Call the resulting graph  $\hat{G}$ . If  $k_{\text{max}} = o(M^{1/2})$  and R = O(M) then, arguing as in the proof of Theorem 3.1, with high probability only a very small number of edges were deleted, and hence the degree sequence of  $\hat{G}$  is likely to be very close to k. Other variations of the configuration model are described in [113, Section 7.8], including models which are tailored to encourage other network properties, such as clustering.

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