A Generalized Bass Model for Product Growth in Networks

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Abstract

Many products and innovations become well-known and widely adopted through the social interactions of individuals in a population. The Bass diffusion model has been widely used to model the temporal evolution of adoption in such social systems. In the model, the likelihood of a new adoption is proportional to the number of previous adopters, implicitly assuming a global (or homogeneous) interaction among all individuals in the network. Such global interactions do not exist in many large social networks, however. Instead, individuals typically interact with a small part of the larger population. To quantify the growth rate (or equivalently the adoption timing) in networks with limited interactions, we study a stochastic adoption process where the likelihood that each individual adopts is proportional to the number of adopters among the small group of persons he/she interacts with (and not the entire population of adopters). When the underlying network of interactions is a random $k$-regular graph, we compute the sample path limit of the fraction of adopters. We show the limit coincides with the solution of a differential equation which can viewed as a generalization of the Bass diffusion model. When the degree $k$ is bounded, we show the adoption curve differs significantly from the one corresponds to the Bass diffusion model. In particular, the adoption grows more slowly than what the Bass model projects. In addition, the adoption curve is asymmetric, unlike that of the Bass diffusion model. Such asymmetry has important consequences for the estimation of market potential. Finally, we calculate the timing of early adoptions at finer scales, e.g., logarithmic in the population size.

1 Introduction

The diffusion of innovations and products via social interactions has long been observed in various social systems [Rogers (2003)]. In this process, a few pioneers adopt an innovation and influence those persons in contact with them. These people, in turn, adopt the innovation and influence their contacts, and the innovation spreads through the network as a result of these social interactions. The impact of social interactions on the spread of innovation has intensified with the rapid growth and popularity of online social interactions. Smartphone applications are a good example of a product whose popularity rests on the social interactions (and word-of-mouth communication) of the users.

Understanding the growth rate of the diffusion of a product/innovation in a population is imperative for both marketing and managerial decisions, such as inventory management and pricing. Bass first studied the timing of product adoption using a simple differential equation later known as the Bass diffusion model [Bass (1969)]. In this model, at any time, the growth rate is proportional

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to the fraction of the population who has adopted it so far. This implicitly relies on the assumption that the population is homogeneously mixing, and thus, a non-adopter can be influenced by all adopters. Such global interactions do not exist in many modern social networks, however. Although the size of an online social network may be massive, each person on that network is usually in contact with a small group of friends and he/she is influenced only by those persons. This raises the following question: How does product adoption evolve in networks with limited interactions? In this paper, we develop a machinery for characterizing product growth in a large population where the structure of the underlying network of interactions belongs to a large class of random graphs. When the underlying network of interactions is a $k$-regular random graph, we provide a generalization to the Bass model and contrast its adoption curve with the one corresponds to the Bass model.

The Bass diffusion model is often presented in the following differential form: $\frac{ds}{dt} \propto s(1-s)$, where $s(t)$ is the fraction of adopters at time $t$. We show that when the underlying network is a random $k$-regular graph, the adoption process grows at the following rate

$$\frac{ds}{dt} \propto \left[1 - (1-s)^{1/\bar{d}}\right](1-s) \quad (1)$$

The above differential equation implies, fixing the fraction of non-adopters $(1-s)$, the growth rate depends sub-linearly on the fraction of adopters (as opposed to linearly in the Bass model). This difference stems from the limited interactions in the network. However, as the degree $k$ grows, the factor $\left[1 - (1-s)^{1/\bar{d}}\right]$ converges to $s$. Thus, the Bass diffusion model can be seen as a special case of differential equation (1).

Comparing the adoption curve resulted from these two differential equations, we show: (i) the adoption grows more slowly than what the Bass model projects, therefore, using the Bass model will over-estimate the adoption growth. (ii) unlike the adoption curve corresponding to the Bass model, the true adoption curve is asymmetric. In particular, the adoption spreads faster in the second half (i.e., after reaching half the population) than the first half (see Figure 1 and Figure 2). Such asymmetry can result in misestimating the future demand based on observations early in the adoption process.

In order to establish the above result (and a few others), we study a natural stochastic adoption process which works as follows. Agents are nodes on a graph, and an edge between two nodes means these agents interact which each other. Initially, one random node adopts the product. Later, each node contacts a randomly selected neighbor at an independent Poisson process (with a given rate). If the contacting node is an adopter and the contacted neighbor is not, the latter adopts the product with a given probability. Like Bass (1969), we are mainly concerned with the timing of the adoption in the regime that a fraction of the population has already adopted. We denote this phase the major adoption regime, and we analyze the time it takes to increase the fraction of adopters by a constant (independent of the population size). This is in the same spirit as fluid limits in queueing theory; Whitt (2002); Chen and Yao (2001). In particular, we show that the sample paths of the scaled adoption process (i.e., number of adopters divided by the population size) almost surely converges to a deterministic

1 Note that this is a special case of the Bass model where the coefficient of innovation is zero.

2 Note here we do not need to scale time, because the contact rate grows proportionally with the number of adopters.
function. First, as a sanity check, we find the limit for the complete network (which corresponds to the homogenously mixing population) and confirm the limit of our adoption process coincides with the Bass model (see Theorem 2.1 and Remark 2.2). Next, and far more importantly, we establish the limit for random $k$-regular graphs (where $k$ is a constant independent of the population size) and show it equates with the solution of (1) (see Theorem 2.5 and Remark 2.6).

We note that for similar stochastic diffusion processes, a differential equation approximation (particularly Kurtz’s theorem (Kurtz (1970))) has been used to re-derive the Bass model when the underlying graph is assumed to be complete (e.g., Massoulie and Draief (2010)). However, such an approach cannot be directly applied to other network structures. In fact, analyzing the scaled sample path of the diffusion process for general graphs is prohibitively difficult. Recent work has used concepts from mean field theory to approximate the growth rate for a certain class of random graphs [Jackson and Rogers (2007); Shakkottai and Johari (2010); Dover et al. (2012)]. The basic idea of these models is to approximate the fraction of adopter neighbors of each agent by the fraction of adopters in the whole population. However, our analysis shows that when the degree is bounded, an adopter is more likely to be connected to adopters. Therefore, the fraction of his adopter neighbors will be higher than the fraction of adopters in the population. Accordingly, the aforementioned method of approximation tends to over-estimate the growth rate in random regular graphs, even though it does improve upon the Bass model. In order to exactly characterize the growth rate, we develop a new technique to incorporate the effect of network structure in the evolution of the adoption process for random regular graphs. In Section 4, we describe how to generalize our analysis to compute the limits for random graphs with more general degree distributions (under certain conditions for the distribution). We also explain how to modify our analysis to accommodate a more general Bass model with innovators and an SIR epidemic model. 

In addition to finding the limits in the major adoption regime, we find the limit of timing in the early adoption regime which refers to the phase when the number of adopters is logarithmic in the population size. In this regime, we show that the time needed to acquire a logarithmic number of adopters scales double logarithmically in the population size. We also show that compared to complete graphs, the adoption process grows more slowly in random $k$-regular graphs by a factor of $k^{-2}$ (see Theorem 2.8).

Besides marketing decisions, several managerial questions arise in the presence of product diffusion (sometimes called social learning or word-of-mouth effects), for example, how to manage demand when the supply is constrained [Ho et al. (2002); Kumar and Swaminathan (2003); Shen et al. (2011)], how to price optimally [Shen et al. (2014)], and how to facilitate diffusion for the adoption of green technologies [Alizamir et al. (2014); Diaz-Rainey and Tzavara (2012)]. The Bass model has been extensively used to study these problems, but in situations where each agent can only influence a limited number of others, it tends to misestimate the adoption growth. Accordingly, our proposed technique for exactly characterizing the product growth can prove useful in developing more accurate managerial insights for product diffusion in networks with limited interactions.

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3. When dealing with random graphs with general degree distribution, some of these methods approximate the fraction of adopter neighbors with a given degree $d$ by the fraction of adopters with degree $d$ in the whole population.

4. These terminologies are used in infectious diseases; S stands for susceptible, I for infectious and R for removed, i.e. immune or dead.

5. For pricing in presence of externalities or word-of-mouth effect in social networks, see also Campbell (2013); Ajourou et al. (2014); Ifrach et al. (2012); Candogan et al. (2012); Cohen and Harsha (2016).
1.1 Related Work

The adoption model we study in this paper has counterparts in many other areas, ranging from epidemiology to economics. It is a stochastic version of the SI (Susceptible Infected) model used in epidemiology [Kermack and McKendrick (1927); Durrett (2006)]. It is also closely linked to the gossip algorithms used in data aggregation and distributed computing in sensor and peer-to-peer networks [Shah (2008); Mosk-Aoyama and Shah (2008)], and to the learning models studied in social and economic networks [Jackson (2008)]. Our work complements the earlier studies of epidemic processes by focusing on timing in the major adoption regime (i.e., when a fraction of the population has already adopted). Several papers have shown the growth of epidemics is related to the spectral radius and expansion properties of the underlying graphs [Mosk-Aoyama and Shah (2008); Jackson (2008) (for more general epidemic models, see Draief et al. (2008); Ganesh et al. (2005); Banerjee et al. (2014)]. It is well known that because random graphs have large expansion factors [Kahale (1992); Gkantsidis et al. (2003)], epidemics spread fast on them. However, the functional form of the growth has not previously been calculated, nor has the time needed to grow the fraction of nodes in epidemics from a constant $\alpha$ to another constant $\gamma$ been analyzed.

As mentioned above, several papers use approximation methods to develop tractable frameworks to analyze the adoption/epidemic process in networks with a given degree distribution. Jackson and Rogers (2007) use a mean field approach to study an SIS (Susceptible Infected Susceptible) model and relate stochastic dominance properties of the degree distribution to the infection rate. Shakkottai and Johari (2010) employ a mean field approximation to model the temporal evolution of demand for stored content on the Internet. Using this demand model, they examine the delay performance of several content distribution mechanisms. Even though such a mean field approximation method provides a tractable framework, our analysis show that it tends to over-estimate the demand growth by neglecting the phenomenon that an adopter is more likely to be connected to adopters and such correlation evolves over time.

Several papers in the area of marketing are concerned with adoption processes and the flow of information in networks (see Dover et al. (2012) and references therein). Closest to our work are Dover et al. (2012) who study an adoption process similar to ours on a random graph with a given degree distribution. They use an approximation method similar to that of Shakkottai and Johari (2010) to show the adoption growth rate depends on the mean and variance of the degree distribution. They use this model to uncover the degree distribution based on the observed adoption data. Further, they show when the network degree is significantly skewed, the adoption curve is asymmetrical. This has important consequences for the estimation of market potential. Interestingly, our rigorous analysis also shows the adoption curve is asymmetric, even on random $k$-regular graphs.

From a technical perspective, our work brings the literature on processes on random graphs together with that on stochastic differential equations and fluid limits. To analyze the adoption process on random graphs, we couple the (continuous) adoption process with the (discrete) graph generation process based on a configuration model [Wormald (1999b)]. Abstracting from time, our adoption process spreads on random graphs in the same way as the exploration process defined in Molloy and Reed (1995). The latter process was introduced to find the size of the largest connected component in a random graph with given degree distributions. We use ideas similar to Wormald (1995) to approximate the evolution of the adoption process. When coupling with time, we build on these results [Wormald (1995); Molloy and Reed (1995)] for random graphs to compute the limit of timing of the adoption process.
2 Model and Main Results

We represent the social network by graph $G_n = (V, E)$, where $|V| = n$. Each node $v \in V$ represents an agent in the system; nodes $v$ and $u$ are neighbors if $(v, u) \in E$. At time 0, a randomly selected node adopts a new product $Z$. The new product spreads through the local contacts between the neighbors. In particular, each node $v \in V$, contacts a randomly selected neighbor at an independent Poisson process with rate $\beta$. Suppose node $v$ adopts $Z$ at time $t$; at any contact after $t$, if node $v$ contacts a neighbor $u$ that has not yet adopted $Z$, $u$ will adopt the product with probability $p$. Given the thinning property of the Poisson process, WLOG, we assume $p = 1$.

In this adoption process, the number of adopters can only increase over time. If the underlying graph is connected, after a finite time, all agents will adopt the new product. For any $1 \leq x \leq n$, let $T_n(x)$ denote the minimum time needed to have $x$ adopted individuals. Our goal is to analyze limits of $T_n(x)$ for different scales of $x$. In particular, we define two main regimes: an early adoption regime in which $x = O(\log n)$ and a major adoption regime where $x = \Theta(n)$.

We analyze the adoption process on two classes of graphs: complete graphs and random $k$-regular graphs where $k$ is a constant. The former class represents a network with global (or homogeneous) interactions, and the latter serves as a model of limited interactions among individuals.

In the next section, we focus on the major adoption regime and give almost sure results on how long it takes to grow the fraction of adopters from $\alpha$ to $\gamma$, where $0 < \alpha \leq \gamma < 1$.

2.1 Timing in Major Adoption Regime

In the major adoption regime, we assume a constant fraction of the population has already adopted the product, and we are concerned with the time needed to add $\Theta(n)$ more adopters. More precisely, for any $0 < \alpha \leq \gamma < 1$, let $\Delta_n(\alpha n, \gamma n)$ be $T_n(\gamma n) - T_n(\alpha n)$. In this subsection, we compute the limit of $\Delta_n(\alpha n, \gamma n)$. We start by analyzing the timing in major adoption when the underlying graph is a complete graph and show that:

**Theorem 2.1** (Major adoption in a complete graph). Suppose for all $n > 1$, the underlying graph $G_n$ is the complete graph. Then, for any $0 < \alpha \leq \gamma < 1$:

$$\Delta_n(\alpha n, \gamma n) \xrightarrow{\text{a.s.}} \theta(\gamma) - \theta(\alpha),$$

where $\theta(s) = \frac{1}{\beta} \log \frac{s}{1-s}$, for $0 < s < 1$.

First note that function $\theta(s)$ is centered such that $\theta(1/2) = 0$. Also, note that function $\theta(s)$ is strictly increasing, and, thus, it is an injective function. Its inverse is $s(t) = \frac{e^t}{1+e^t}$, logistic equation that is a special case of the Bass model.

**Remark 2.2.** Let $S_n(t)$ be the number of adopters at time $t$. Theorem 2.1 implies that $\frac{S_n(t)}{n} \xrightarrow{\text{a.s.}} s(t)$, where $s(t)$ is the solution of the following differential equation:

$$\frac{ds}{dt} = \beta s(1-s)$$

(3)
Thus, the limit of the scaled sample paths of our probabilistic adoption process coincides with the deterministic logistic function. Further, note that function \( \theta(s) \) has the following symmetry property: for any \( 0 < s < 1 \), \( \theta(s) = -\theta(1 - s) \). The time it takes to grow the fraction of the adopters from \( \alpha \) to \( 1/2 \) is the same as the time it takes to grow the fraction from \( 1/2 \) to \( 1 - \alpha \) where \( 0 < \alpha < 1/2 \). This symmetry results from having a complete graph (a homogenously mixing population) and is intuitively explained as follows: at any time, the subgraph including the adopters is a complete graph, and so is the subgraph consisting of nodes who have not yet adopted. Now, we can look at the process in a backward way; if node \( u \) is a non-adopter, and it contacts node \( v \) who is an adopter, then node \( v \) will abandon product \( Z \); the abandonment of the product will spread through the network in this way. Because the processes of adoption and discard spread in exactly the same way, the time needed to grow the set of non-adopters from \( 1 - s \) to \( 1/2 \) will be the same as the time required to grow the set of adopters from \( s \) to \( 1/2 \).

The limit result (3) can be proven directly by using stochastic differential equations and Kurtz’s theorem (for instance, see Massoulie and Draief (2010), Section 1.3.1). Here, we present an alternative proof that analyzes the random times between any two consecutive adoptions and directly establishes the time limit (2).

Proof. For any \( 1 \leq i \leq n - 1 \), let \( \tau_i \) be the time it takes to grow the number of adoptions from \( i \) to \( i + 1 \). First note that \( \Delta_n(\gamma n, an) = \sum_{i=an}^{\gamma n-1} \tau_i \). Further, note that conditioned on the set of adopted nodes, \( \tau_i \)’s are independent exponential random variables. Let \( \lambda_i \) be the rate of \( \tau_i \). For the complete graph, we compute the rate \( \lambda_i \) as follows: there are \( i \) adopter nodes who can contact non-adopters. When any adopter node \( v \) makes a contact, it contacts a neighbor who has not adopted yet with probability \( (n - i)/(n - 1) \). Thus, using the thinning property of the Poisson processes, we have:

\[
\lambda_i = \beta \frac{i(n - i)}{n - 1}.
\]

First, to prove the theorem, we make the following claim:

**Claim 2.3.** \( E[\Delta_n(\gamma n, an)] \to \theta(\gamma) - \theta(\alpha) \).

The claim is proven in Appendix [A]. Next, we establish the concentration bounds shown in the second claim, given as:

**Claim 2.4.** Suppose \( \epsilon \) is a fixed small positive number,

\[
P(\{|\Delta_n(\gamma n, an) - E[\Delta_n(\gamma n, an)]| \geq \epsilon\} \leq e^{-\delta n},
\]

where \( \delta \) is a small positive number given in Equation (27).

The second claim is proven in Appendix [A] as well. This implies that

\[
\sum_{n=1}^{\infty} P(|\Delta_n(\gamma n, an) - E[\Delta_n(\gamma n, an)]| \geq \epsilon) < \infty.
\]

Now, applying the Borel-Cantelli lemma, we have: \( \Delta_n(an, \gamma n) \overset{a.s.}{\to} E[\Delta_n(an, \gamma n)] \) which completes the proof.

□
Next, we analyze the adoption process on random $k$-regular graphs, where $k$ is a constant. To ensure all nodes eventually adopt, we limit the sample space of the graphs to only include connected ones.

**Theorem 2.5** (Major adoption in random $k$-regular graphs). Suppose for all $n > 1$, the underlying graph $G_n$ is sampled uniformly at random from the set of all connected $k$-regular graphs with $n$ nodes, where $k \geq 3$ is bounded. For any $0 < \alpha \leq \gamma < 1$, the following limit holds:

$$\Delta_n(\gamma n, \alpha n) \overset{a.s.}{\to} \tilde{\theta}(\gamma) - \tilde{\theta}(\alpha),$$

where $\tilde{\theta}(s) = k \beta \left( 1 - s \right)^{k-2} \left[ \log \left( 1 - s \right)^{2^{k-3}} - \log \left( 1 - 2^{1-\frac{3}{k}} \right) \right]$.  

**Remark 2.6.** Let $\tilde{S}_n(t)$ be the number of adopters at time $t$. Theorem 2.5 implies $\frac{\tilde{S}_n(t)}{n} \overset{a.s.}{\to} \tilde{s}(t)$, where $\tilde{s}(t)$ is the solution of the following differential equation:

$$\frac{d\tilde{s}}{dt} = \beta \left[ 1 - (1 - \tilde{s})^{1 - \frac{3}{k}} \right] (1 - \tilde{s}) \quad (7)$$

Figure 1 compares the solution of differential equations (3) and (7) for initial value $s(0) = 0.01$, and $k = 5$. As we can see, the adoption grows much more slowly on a random 5-regular graph than on a complete graph. The same can be observed in the left plot of Figure 2 which basically shows the inverse function. (Note: the left plot of Figure 2 shows the limit results of the time it takes to grow the fraction of adopters from $0.01$ to $s \in [0.01, 0.99]$ on the complete graph and the random 5-regular graph.) The high level intuition behind this observation is as follows: suppose we reach the time that $i$ nodes have already adopted, where $i = \Theta(n)$; the rate of contact of adopters is $\beta i$ regardless of the underlying graph. However, the probability that an adopter contacts a non-adopter is higher on a complete graph for two reasons. First, on a $k$-regular graph, the subgraph induced by the adopters is connected; therefore, each adopter has $k-1$ neighbors who are likely to be non-adopters. Second, those $k-1$ neighbors are not uniform samples among the remaining $n-2$ nodes. In fact, we show it is more likely that the neighbor of an adopter belongs to the set of adopters itself. This is a result of the connectivity properties of the subgraph induced by the adopters.

To further highlight the effect of connectivity among the adopters, let us compute the rate of $\tau_i$ on a random graph using a mean field approximation (in the same spirit of approximation as Jackson and Rogers (2007); Shakkottai and Johari (2010); Dover et al. (2012)). We denote this approximate rate as $\tilde{\lambda}_i^M$. As explained above, the rate of contact by adopters is $\beta_i v_i$; each adopter has at least one adopter neighbor with probability 1. For adopter node $v_i$, let $v'_i$ be the neighbor who adopted before $v_i$ and was the first adopter who contacted $v_i$. Clearly, if $v_i$ contacts node $v'_i$, this will not result in a new adoption. Now suppose node $v_i$ selects a random neighbor other than $v'_i$; this happens with probability $(k-1)/k$. In a mean field approximation, we assume the rest of the neighbors of $v_i$ are uniformly sampled among the other $n-2$ nodes. Thus, the probability node $v_i$ will contact a non-adopter is $\frac{n-2}{n-2}$. This implies

$$\tilde{\lambda}_i^M = \frac{\beta(k-1)}{k} \frac{i(n-1)}{n-2}. \quad (8)$$
Figure 1: Evolution of the fraction of adopters ($s(t)$); comparing a complete and a 5-regular random graph. Time is normalized such that at time 0 the fraction of adopters is 0.01.

The approximation rate of (8) has the same form as (4) and is only scaled by $(k - 1)/k$. The time limit resulting from this mean field approximation is plotted in Figure 2. As we can see, it significantly differs from the actual limit, and, in particular, it underestimates the adoption time.

Further, on the right plot of Figure 2, we observe that unlike the complete graph, the normalized process for the random regular graph (such that $\tilde{\theta}(1/2) = 0$) is not symmetric around $1/2$, and the time it takes to grow the process from $\alpha < 1/2$ to $1/2$ is larger than the time it take to grow it from $1/2$ to $1 - \alpha$. This is again related to the connectivity properties of random graphs. If we look at the backward process, we see the subgraph of non-adopters is not necessarily connected; thus, the backward process grows faster.

**Proof sketch of Theorem 2.5:**

Similar to the proof for the complete graph, we compute the rate of the exponential time between any two consecutive adoptions. Recall that we denote the time it takes to grow the number of adopters from $i$ to $i + 1$ as $\tau_i$ and its rate by $\lambda_i$. Unlike the complete graph, we cannot compute the rate $\lambda_i$ only based on the number of adopters: suppose node $v$ is an adopter, and it samples one of its $k$ neighbors to contact. Knowing only $i$, we cannot determine how many of $v$'s neighbors have not yet adopted. To overcome this problem, we first note that the random graph can be generated using an iterative pairing process called the configuration model \cite{Wormald1999}. A configuration model works as follows: we start with $n$ isolated nodes. Each node has $k$ unpaired clones (or half edges). At each step, a new edge is formed by pairing two randomly chosen clones; the process ends after $nk/2$ steps, when all the clones are paired.

Given this observation, we couple the graph generation and the adoption process in the following manner.: We assume the graph has not been realized before the adoption process. Thus, at time 0, we have $n$ isolated nodes, each with $k$ unpaired clones. Any time an adopter makes a contact, it chooses one of its clones uniformly at random. If the clone has already been paired, this means both ends of this edge have already adopted. In this case, neither the adoption process nor the
Figure 2: Left: The time it takes to grow the fraction of adopters from 0.01 to \( s \in [0.01, 0.99] \) (functions \( \theta(s) - \theta(0.01), \tilde{\theta}(s) - \tilde{\theta}(0.01) \), and \( k/(k-1)(\theta(s) - \theta(0.01)) \) for \( s \in [0.01, 0.99] \)). Right: The normalized timing functions in major adoption regime (functions \( \theta(s) \) and \( \tilde{\theta}(s) \) for \( s \in [0.01, 0.99] \)).

set of formed edges will grow. If the clone has not been paired, we perform a *new iteration* of the configuration model and form a new edge by sampling a clone at random among all unpaired ones. If the sampled clone belongs to a non-adopter node, then the adoption process grows by one; otherwise, the adoption set remains the same.

Abstracting away from the time, we first analyze the evolution of the number of adopted nodes and their unpaired clones in terms of the number of iterations (which are discrete time random processes). For the analysis, we use the differential equation method proposed by Wormald (1999a, 1995) to approximate discrete random processes using a deterministic function. The same approach has been used to find the size of the giant connected components in random graphs by Molloy and Reed (1995, 1998).

Next, we compute the exponential times between any two consecutive iterations, and based on the result, we compute \( \mathbb{E} [\Delta_n(n, \alpha_n)] \). At the end, similar to the proof of Theorem 2.1, we use some concentration bound and the Borel-Cantelli lemma to establish almost sure convergence.

The proof also deals with some technical subtleties; for example, it obtains a bound in a deterministic approximation stronger than the bound established in Wormald (1999a, 1995). It also confirms the concentration results hold when we limit the sample space to simple and connected graphs (rather than all possible pairings of the clones.).

The detailed proof of Theorem 2.5 is presented in Section 3. In Section 4, we explain how to generalize the above proof ideas to analyze the adoption process on a random graph with more general degree distributions. We also describe how to modify our analysis to more general Bass model with innovators and an SIR (Susceptible-Infected-Remove) epidemic model.

Finally, note that for \( k = 2 \), the only connected regular graph is a cycle of length \( n \). The following proposition asserts the different time scalings of the major adoption regimes for such graphs:
Proposition 2.7. For all $n > 1$, let the underlying graph be a cycle of length $n$. Then, for any $0 < \alpha \leq \gamma < 1$,

$$\frac{\Delta_n(\gamma n, \alpha n)}{n} \xrightarrow{a.s.} \frac{\gamma - \alpha}{\beta}.$$ 

Proof. For any $i \geq 1$, the set of adopters forms a path of length $i$. For any $1 < i < n$, there are only two nodes at the two ends of the path that can contact non-adopters. Suppose node $v$ is an end point, and it makes a contact. With probability $1/2$, it contacts a non-adopter neighbor. Thus, $\lambda_i = \beta$ for any $1 < i < n$, implying that $\tau_i$’s are i.i.d. By the strong law of large numbers, the above limit holds.

□

2.2 Timing in Early Adoption Regime

In a major adoption regime, the rate of contacts grows linearly with $n$; therefore, the adoption process spreads very quickly. Further, as Theorem 2.1 and 2.5 assert, the time to grow from fraction $\alpha$ to fraction $\gamma$ is constant. However, in the early adoption regime, the growth rate is much slower, as there are only a few adopters. In this section, we analyze the timing in this slower regime; more specifically, we find the limit of the time it takes to get $\Theta(\log n)$ adopters. We establish the limit for both the complete graphs and the random $k$-regular graphs. For both graphs, we establish that the time needed to have $\Theta(\log n)$ adopter scales as $\log\log n$. Further, we show the process grows faster on the complete graph (compared to the random $k$-regular graph).

Theorem 2.8 (Early adoption). For any constant $C > 0$ the following hold:

(a) If for all $n > 1$, graph $G_n$ is a complete graph, then:

$$\frac{T_n(C \log n)}{\log\log n} \xrightarrow{p} \frac{1}{\beta}.$$  \hspace{1cm} (9)

(b) If for all $n > 1$, graph $G_n$ is a uniformly random sample from the set of all connected $k$-regular graphs, where $k \geq 3$ is bounded, then:

$$\frac{T_n(C \log n)}{\log\log n} \xrightarrow{p} \frac{k}{\beta(k - 2)}.$$  \hspace{1cm} (10)

The proof of part (a) follows the same line of the proof of Theorem 2.1; note that the rate given by (4) holds for any $1 \leq i < n$. Using this rate, we first show that $\frac{E[T_n(C \log n)]}{\log\log n} \rightarrow \frac{1}{\beta}$, and then show $\frac{T_n(C \log n)}{\log\log n}$ converges to its mean (in probability) by proving its variance converges to zero. The details are given in Appendix B.

Proof sketch of part (b)

As in the previous proofs, we aim to compute $\lambda_i$, for $1 \leq i \leq C \log n$. First note that we can view the adoption process as the following: each edge $(v, u)$ makes contacts at an independent

\hspace{3cm} *Except for the special case of a single cycle.
Poisson rate $\beta/k$ from $v$ to $u$ and similarly from $u$ to $v$. Given $i$ adopters, the total number of contacts (along edges) that can result in a new adoption is the total number of edges between the set of adopters and non-adopters. Observe that in our coupled process (defined in proof sketch of Theorem 2.5), at each iteration, the sub-graph of the adopters formed so far is connected; thus, the total number of edges that can result in a new adoption is, at most, $(k-2)i+2$. To compute the exact number of these edges, we use the locally tree-like property of random $k$-regular graphs Dembo and Montanari (2010) which confirms that, with high probability, on the final realized graph (i.e., after the formation of all edges), the subgraph containing these $i$ nodes is a tree and does not contain a cycle. Thus, the remaining $(k-2)i+2$ edges are all between an adopter node and a non-adopter one. This implies that with high probability, $\lambda_i \approx \beta/k[(k-2)i]$ for $1 \leq i \leq C \log n$. Once we have the rates, the rest of the proof handles the convergence of random variable $T_n(C \log n)$ to its mean. The detailed proof is given in Appendix B.

The locally tree-like property of the random graph carries over to a subgraph of size $o(\sqrt{n})$; thus, we can use similar techniques to prove the following:

**Remark 2.9.** Similar limit results hold for $T_n(\sigma(n)) \log \sigma(n)$ for any $\sigma(n) = o(\sqrt{n})$.

### 3 Proof of Theorem 2.5

In this section we formally prove Theorem 2.5. For the sake of brevity, the proof of all technical lemmas of this section is deferred to Appendix C. As explained in the proof sketch, we first study the (edge formation) iteration process and analyze the evolution of the number of adopters in terms of the iterations. Similar to Molloy and Reed (1995, 1998), we call this the exploration process. In this process every node is associated with $k$ clones. For clone $c$ of node $v$, all other clones belonging to node $v$ are considered as $c$’s siblings. We start at iteration $j = 0$. At any iteration $j$ in the exploration process, there are three kinds of clones: ‘sleeping’ clones, ‘active’ clones, and ‘dead’ clones. At the beginning, all clones are sleeping. If all clones of a node are sleeping the node is said to be a sleeping node; if all its clones are dead, the node is considered dead; otherwise, it is considered active. Given this terminology, the exploration process works as follows.

**Exploration Process**

1. **Initialization**: Pick a node uniformly at random from the set of all sleeping nodes and set the status of all its clones to active.

2. Repeat the following two steps as long as there are active clones:
   (a). Sample a clone $c$ uniformly at random from the set of active clones and kill it.
   (b). Pair the clone $c$ with clone $c'$ that is chosen uniformly at random from the set of all remaining unpaired (active or sleeping) clones. Kill $c'$ and make all its siblings active.

The set of active clones at iteration $j$ is denoted by $A(j)$. The union of the set of sleeping and active clones is denoted by $L(j)$; they are called ‘living’ clones. Finally, we denote the number of sleeping nodes by $N(j)$.
3.1 Evolution of Exploration Process

In a second paper, Molloy and Reed (1998) used results by Wormald (1995) to track the evolution of the exploration process. We employ a similar technique, but do not directly use Wormald’s result. Instead, we use insights from the proof technique and tighten the probability of error needed to get almost sure convergence. When coupling with the adoption process, we introduce an additional variable which tracks the (random) re-scaled time in the adoption process.

At every iteration of the exploration process, the number of living clones reduces by two; i.e.,

\[ L(j + 1) = L(j) - 2. \]

Hence we have

\[ L(j) = nk - 2j. \]

At each iteration, the number of sleeping nodes, \( N(j) \), reduces by one, if in step 2(b) of the exploration process, the clone neighbor chosen \( (c') \) is a sleeping one. Otherwise, \( N(j) \) remains the same.

After initialization, all nodes are sleeping except the one we have awakened for the initiation (note that when coupling with the adoption process, this will be the first node to adopt the product). Therefore, at \( j = 0 \), we have \( A(0) = k \).

At every iteration, the evolution of the number of sleeping nodes and the number of active clones is as follows:

1. With probability \( \frac{kN(j)}{kn - 2j} \), we have

\[ N(j + 1) = N(j) - 1 \]
\[ A(j + 1) = A(j) + (k - 2). \]  

(11)  

(12)

2. With probability \( 1 - \frac{kN(j)}{kn - 2j} \), we have

\[ N(j + 1) = N(j) \]
\[ A(j + 1) = A(j) - 2. \]  

(13)  

(14)

Note that the above equations (for the evolution of sleeping nodes and active clones) only hold when the graph is connected. Later, in Lemma 3.7, we show a random \( k \)-regular graph is connected with probability \( 1 - \Theta(n^{-2}) \). We further show that our limit result holds when conditioning on being connected. For now, we assume the graph is connected and find the limits of the scaled random variables, \( N(j)/n \) and \( A(j)/n \), evolving according to (11) - (14).

At any iteration \( j \) in the exploration process, we have \( A(j) = L(j) - kN(j) = k[n - N(j)] - 2j \). So it suffices to characterize the evolution of only one of these parameters, e.g., \( N(j) \). Let \( H(j) \) denote the history of the exploration process until iteration \( j \). By the equations (11) - (14), we have

\[ E[N(j + 1) - N(j)|H(j)] = -\frac{kN(j)}{kn - 2j} = -\frac{kN(j)/n}{k - j/n}. \]  

(15)

From the above, using Wormald’s result (Theorem 1 in Wormald (1995)), it follows that for any \( 0 < j < (k - \epsilon_0)n/2 \), with high probability

\[ N(j) = nf(j/n) + o(n), \]  

(16)

uniformly over \( j \), where
\[ f(x) = \left(1 - \frac{2x}{k}\right)^{\frac{1}{2}}, \] (17)

which is the unique solution to the differential equation
\[ f'(x) = -\frac{k f(x)}{k - 2x}, \] (18)

with initial condition \( f(0) = 1 \). Here \( \epsilon_0 > 0 \) is a fixed constant.

The result in [Wormald 1995] is for a fairly general setting, but the bound given for the probability of convergence is not strong enough for us to prove a.s. convergence. Thus, in the following lemma, we specialize the result of Wormald (Theorem 1 in [Wormald 1995]) to our case so we can obtain a stronger bound on the probability of event (16).

**Lemma 3.1.** Fix a constant \( \epsilon_0 > 0 \). For any iteration \( 0 \leq j < (k/2 - \epsilon_0)n \), with probability \( 1 - o(n^{-3}) \),
\[ |N(j) - nf(j/n)| \leq \delta_1(n), \]
uniformly over \( j \), where the function \( f(x) \) is defined in (17) and \( \delta_1(n) = o(n) \).

Next we find an approximation for \( A(j) \): define \( g(x) = k(1 - f(x)) - 2x \). The following corollary is an immediate corollary of Lemma 3.1.

**Corollary 3.2.** With probability \( 1 - o(n^{-3}) \), for any \( 0 < j < (k - \epsilon_0)n/2 \), we have
\[ |A(j) - ng(j/n)| \leq \delta_2(n), \] (19)
uniformly over \( j \), for some \( \delta_2(n) = o(n) \).

We now find an approximation for the number of iterations needed to have \( an \) active or dead nodes. Note that when coupled with the adoption process, these are the adopter nodes. Let \( \delta(n) = \max \{\delta_1(n), \delta_2(n)\} \) for \( \delta_1(n) \) and \( \delta_2(n) \), as defined in Lemma 3.1 and Corollary 3.2. Let \( A \triangleq (A(j), 0 \leq j \leq (k - \epsilon_0)n/2) \) be the vector of the random number of active clones and let \( a \) be a particular realization of this random vector. Also, let \( S \triangleq \{a(j) - ng(j/n) \leq \delta(n)\} \). In the next auxiliary lemma, we show the number of iterations needed to have \( an \) active or dead nodes, denoted by \( J_a \), is close to \( f^{-1}(1 - \alpha) \).

**Lemma 3.3.** Let \( j_{\alpha} \triangleq f^{-1}(1 - \alpha) \) and \( c = |f'(\frac{k-\epsilon_0}{2})| \). If \( A \in S \), for any \( \alpha \)
\[ |J_a - n j_{\alpha}| \leq \frac{2}{c} \delta(n). \]

### 3.2 Coupling Exploration and Adoption Processes

We now couple the exploration and adoption processes. At any time, the set of active and dead nodes correspond to the set of adopters. At a random time, one of these nodes “times-out” and decides to use one of its outgoing edges (or one of its clones, say clone \( c \)) to contact a neighbor at the other end of this outgoing edge. Then, one of the following happens:
Case 1: Clone $c$ has already been paired with clone $c'$.

(a) Clones $c$ and $c'$ are dead clones.
(b) The node to which clone $c'$ belongs has already adopted.

Case 2: Clone $c$ has not been paired yet. It chooses clone $c'$ uniformly at random among all living clones.

(a) Clone $c$ is an active clone.
(b) If clone $c'$ is a sleeping clone, the node to which it belongs will adopt; if clone $c'$ is an active clone, the node to which it belongs has adopted before this contact.

This implies only contacts made through active clones will ensure the exploration process proceeds. Further, only these contacts may result in the growth of the adoption set. As mentioned, we can view the adoption process in the following way: each clone (or half edge) makes contact at an independent Poisson process at rate $\beta/k$. Therefore, at any iteration $j$, the time it takes to add one edge (go to iteration $(j+1)$) is an exponential random variable with rate $\frac{k}{\beta}A(j)$. We denote this random variable by $\tilde{\tau}(j)$. Using the notation defined in Section 2 and in the previous subsection, it follows that

$$\Delta_n(an, \gamma n) = \sum_{j=J_a}^{J_j} \tilde{\tau}(j).$$

**Remark 3.4.** Conditioned on \{A = a\}, the random variables $\tilde{\tau}(j)$ for $0 < j < (k - \epsilon_0)n/2$ are independent exponentially distributed random variables with mean $\frac{k}{\beta}A(j)$.

First, we compute $E[\Delta_n(an, \gamma n)|A = a \in S]$.

By Lemma 3.3, for $a \in S$, we have $\Delta \leq \Delta_n(an, \gamma n) \leq \bar{\Delta}$, where

$$\Delta \triangleq \sum_{n_{ja} - \frac{1}{2}\delta(n)}^{n_{ja} + \frac{1}{2}\delta(n)} \tilde{\tau}(j), \quad \text{and} \quad \bar{\Delta} \triangleq \sum_{n_{ja} - \frac{1}{2}\delta(n)}^{n_{ja} + \frac{1}{2}\delta(n)} \tilde{\tau}(j).$$

Next, we compute

$$E[\bar{\Delta}|A = a \in S] = \sum_{n_{ja} - \frac{1}{2}\delta(n)}^{n_{ja} + \frac{1}{2}\delta(n)} \frac{k}{\beta A(t)} \geq \frac{k}{\beta} \sum_{n_{ja} - \frac{1}{2}\delta(n)}^{n_{ja} + \frac{1}{2}\delta(n)} \frac{1}{ng(t/n) + \delta(n)}$$

$$= \frac{k}{\beta} \int_{J_a}^{J_j} \frac{1}{g(\alpha)} dx + o(1) = \tilde{\vartheta}(\gamma) - \tilde{\vartheta}(\alpha) + o(1),$$

where the inequality holds by Corollary 3.2. In a similar way, we can prove an upper bound for $E[\bar{\Delta}|A = a \in S]$. These bounds prove that

$$E[\bar{\Delta}|A = a \in S] \rightarrow \tilde{\vartheta}(\gamma) - \tilde{\vartheta}(\alpha). \quad (20)$$
Now, we are in a position to prove Theorem 2.5. Let \( E \doteq \overline{\Delta} - E[\overline{\Delta}] \). Fix \( \epsilon > 0 \). We start with

\[
P(|E| \geq \epsilon) \leq \sum_{a \in S} P(|E| \geq \epsilon | A = a)P(A = a) + P(A \notin S)
\]

(21)

By Corollary 3.2, the second term is \( o(n^{-3}) \). To bound the first term, we first notice that for any \( \epsilon_0n \leq j \leq kn/2 - \epsilon_0n \) and any \( p > 0 \), conditioned on \( a \in S \), we have:

\[
P\left( \tilde{\tau}(j) \geq \frac{kp \log n}{\beta^2n} | A = a \right) \leq n^{-p}, \tag{22}
\]

where \( g \doteq \frac{1}{2}n \min_{x \in \epsilon_0, k/2 - \epsilon_0} \delta(x) \), and we use the following remark:

**Remark 3.5.** If \( A \in S \), then \( A(j) \geq n \min_{x \in \epsilon_0, k/2 - \epsilon_0} \delta(x) + o(n) \geq \frac{1}{2}n \min_{x \in \epsilon_0, k/2 - \epsilon_0} \delta(x) \), for all \( \epsilon_0n \leq j \leq (k/2 - \epsilon_0)n \) and large enough \( n \).

Let \( B \) be the event that \( \{ \tilde{\tau}(j) \leq \frac{kp \log n}{\beta^2n} \} \) for all \( \epsilon_0n \leq j \leq kn/2 - \epsilon_0n \) and conditioned on \( a \in S \). By (22) and the union bound, we have \( P(B) \geq 1 - n^{-p} \), or equivalently, \( P(\overline{B}) \leq n^{-p} \). Going back to bounding the first term of (21), for any \( a \in S \) it follows that

\[
P(|E| \geq \epsilon | A = a) \leq P(|E| \geq \epsilon | A = a, B) + n^{-p}.
\]

Applying the Hoeffding bounding to the first term, we get

\[
P(|E| \geq \epsilon | A = a) \leq 2 \exp \left( -\frac{2n}{\log n} \frac{\epsilon^2 \beta^2 g^2}{k^2p^2} \right) + O(n^{-p}).
\]

Using (20), for a large enough \( n \), we have:

\[
P(\overline{\Delta} - [\tilde{\theta}(y) - \tilde{\theta}(a)]) \geq 2\epsilon | A = a) \leq 2 \exp \left( -\frac{2n}{\log n} \frac{\epsilon^2 \beta^2 g^2}{k^2p^2} \right) + O(n^{-p}).
\]

We can prove a similar bound for \( |\Delta - [\tilde{\theta}(y) - \tilde{\theta}(a)]| \). Since \( \Delta \leq \Delta_n(an, \gamma n) \leq \overline{\Delta} \), the same bound holds for \( |\Delta_n(an, \gamma n) - [\tilde{\theta}(y) - \tilde{\theta}(a)]| \). Let \( p = 4 \). So far we have proved that

\[
P(|\Delta_n(an, \gamma n) - [\tilde{\theta}(y) - \tilde{\theta}(a)]| \geq 2\epsilon) = O(n^{-3}). \tag{23}
\]

The last step of the proof is to show that when conditioning on the event that the graph obtained as a result of matching random clones is a simple and connected graph, the same order of error probability (i.e., \( O(n^{-3}) \)) holds. Let \( \mathcal{G} \) denote the graph eventually obtained after \( nk/2 \) iterations. Conditioned on being connected and simple, \( \mathcal{G} \) is a \( k \)-regular graph sampled uniformly among all connected simple \( k \)-regular graphs. It follows from inequality (23) that

\[
P\left( |\Delta_n(an, \gamma n) - [\tilde{\theta}(y) - \tilde{\theta}(a)]| \geq 2\epsilon \right) \cap \{ \mathcal{G} \text{ is connected} \cap \{ \mathcal{G} \text{ is simple} \} \} = O(n^{-3}). \tag{24}
\]

To prove that conditioned on \( \{ \mathcal{G} \text{ is connected} \cap \{ \mathcal{G} \text{ is simple} \} \} \), the error probability is \( O(n^{-3}) \), it suffices to show \( P(|\Delta_n(an, \gamma n) - [\tilde{\theta}(y) - \tilde{\theta}(a)]| = O(1) \). This follows from the next two lemmas.
Lemma 3.6. \( P(\mathcal{G} \text{ is simple}) = \Theta(1) \).

The above lemma is a well-known result (see for example Wormald (1999b), Bender and Canfield (1978)). It allows us to carry over properties which hold with high probability from the configuration model to the subset of simple random graphs. The next lemma shows a uniform sample among simple graphs is connected with probability \( 1 - O(n^{-2}) \):

Lemma 3.7. \( P(\{\mathcal{G} \text{ is not connected}\} \cap \{\mathcal{G} \text{ is simple}\}) = O(n^{-2}) \).

Putting (24) and Lemmas 3.6 and 3.7 together implies that for any graph \( G_n \) sampled uniformly at random from the set of all connected \( k \)-regular graphs with \( n \) nodes and a large enough \( n \),

\[
P \left( |\Delta_n(\alpha_n, \gamma_n) - [\tilde{\theta}(\gamma) - \tilde{\theta}^{\prime}(\alpha)]| \geq 2\epsilon \right) = O(n^{-3}) < n^{-2}.
\] (25)

Since \( \epsilon \) is arbitrary, and \( \sum_{n=1}^{\infty} n^{-2} < \infty \), the theorem (the limit (3)) follows by applying the Borrel-Cantelli lemma.

4 Discussions

The techniques developed here to analyze the adoption process for random \( k \)-regular graphs can be generalized to the following settings.

Random graphs with given degree distributions: We can analyze the adoption process defined in Section 2 for a more general class of random graphs with a given degree distribution. For these random graphs, we couple the adoption process and the configuration model. We first analyze the exploration process. Let \( D \) be the set of all degrees with a nonzero probability in the degree distribution. Let \( N_d(j) \) and \( A_d(j) \) to be the number of sleeping nodes of degree \( d \) and the number of active clones belonging to a node of degree \( d \). We can write equations similar to (11)-(14) for the evolution of the vectors \((N_d(j), d \in D)\) and \((A_d(j), d \in D)\). Again, we prove an approximation for \( 1/n (N_d(j), d \in D) \) using Wormald’s result Wormald (1995). We connect the exploration process to the adoption process in the same way as in Subsection 3.2.

For comparative purposes, see Figure 3. The figure shows simulation results comparing the process on three different random graphs with mean degree 5. The theoretical curve derived in this paper is included for reference and matches very well with the simulation results. Interestingly, when there is more heterogeneity in the degree distribution in the network, the process proceeds more or less at the same rate in the beginning, but slows down towards the end for those with higher disparity. Arguably, towards the end of the process, most of the higher degree nodes have already adopted, and the rate of spread is limited by the remaining lower degree nodes.

Adoption process with innovators: We extend our analysis to include “innovators”, the agents who adopt without being contacted by an adopter. In particular, suppose each non-adopter adopts at an independent Poisson process with rate \( \beta^{\prime} \). To include an innovator in the set of adopters, we modify our analysis in the following way. In the exploration process, at iteration \( j \), with probability \( \frac{\beta N(j)}{\beta N(j)+\beta A(j)k} \), a sleeping node wakes up and all of its \( k \) clones become active. Note this is the probability of a non-adopter becoming an innovator before one of the adopters makes a contact through one of its active half-edges. If this event does not occur (with probability \( 1 - \frac{\beta N(j)}{\beta (N(j)+A(j))k} \)), steps (a) and (b) are performed as described. All of the analysis for the evolution
of the exploration process and the coupling exploration and adoption process can be modified accordingly.

**SIR model on random graphs:** As mentioned in the introduction, the adoption process studied here is a special case of adoption processes used to describe the transmission of communicable diseases by individuals or the spread of computer viruses in a network, known as the SI (Susceptible-Infected) model. We can use the same ideas to analyze a more general model called SIR that works as follows. The process of infection is the same as that shown in the SI model. Each infected node is removed (they can be interpreted as either dead or immune) at a certain rate. A removed node cannot infect its neighbors. Suppose each infected node is removed at a independent Poisson process with rate $\beta' < \beta$. To extend our framework to this model, in the exploration model, we need to keep track of the nodes that are awake (or, equivalently, are infected) but have been removed as well.

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APPENDIX

A Missing proofs of Theorem 2.1

Proof of Claim 2.3. The proof of this claim is mainly algebraic and is given for the sake of completeness.

\[
\begin{align*}
\Delta_n(\gamma, \alpha) &= \frac{1}{\beta n} \left[ \int_0^\gamma \frac{1}{x} dx + \int_0^\gamma \frac{1}{1-x} dx + \mathcal{E}_n \right] \\
&= \frac{1}{\beta n} \left[ \log \frac{\gamma}{1-\gamma} - \log \frac{\alpha}{1-\alpha} \right] + \mathcal{E}'_n,
\end{align*}
\]

where \( \mathcal{E}_n \) and \( \mathcal{E}'_n \) represent the error terms. We are left to show that \( \mathcal{E}'_n \to 0 \). Note that \( \sum_{i=\alpha}^{\gamma - 1} i \) gives an upper-bound for the integral \( \int_0^\gamma \frac{1}{x} dx \). Further, \( \sum_{i=\alpha}^{\gamma - 1} i \) gives a lower-bound for it. Now the difference between these two sums is \( O(1/n) \). Similarly, we can show the error contribution of the second sum is also order \( O(1/n) \) which completes the proof.

Proof of Claim 2.4. In the following proof, to simplify the notation, we present \( \Delta_n(\gamma, \alpha) \) by \( \Delta_n \).

By the Chernoff's bound, for any \( s \geq 0 \):

\[
P(\Delta_n - E[\Delta_n] \geq \epsilon) \leq e^{-s \epsilon E[\epsilon(\Delta_n - E[\Delta_n])] + e^{-s \epsilon E[\Delta_n]} E[\epsilon \Delta_n]}
\]

Note that \( \Delta_n \) is sum of independent exponential random variables, thus we can compute \( E[\epsilon \Delta_n] \) as follows:

\[
E[\epsilon \Delta_n] = \prod_{i=\alpha}^{\gamma - 1} \left( 1 + \frac{s}{\lambda_i - s} \right).
\]

For any real number \( z \), we have \( (1 + z) \leq e^z \). Therefore,

\[
E[\epsilon \Delta_n] \leq e^{\sum_{i=\alpha}^{\gamma - 1} \frac{s}{\lambda_i - s}}
\]

Let \( \lambda^* \) be \( \min(\lambda_{\alpha n}, \lambda_{\gamma - 1}) \), and define \( s^* = \frac{m}{1 + 2E[\Delta_n]} \lambda^* \). Because for any \( \alpha n \leq i \leq \gamma n - 1 \), \( \lambda_i \geq \lambda^* \), it follows that:

\[
\frac{1}{\lambda_i - s^*} \leq \frac{1}{\lambda_i} \left( 1 + \frac{\epsilon}{2E[\Delta_n]} \right).
\]

Setting \( s \) to be \( s^* \) in the Chernoff’s bound, we have:

\[
P(\Delta_n - E[\Delta_n] \geq \epsilon) \leq e^{-\frac{\epsilon}{2}}
\]
Similarly, we can show that:

$$P\left(-\left(\Delta_n - E[\Delta_n]\right) \geq \varepsilon\right) \leq e^{-\frac{\varepsilon^2}{2}}.$$  

Define

$$\delta = \left(\frac{e^{\frac{\varepsilon^2}{2 E[\Delta_n]}}}{1 + \frac{\varepsilon^2}{2 E[\Delta_n]}}\right) \lambda^*/n. \tag{27}$$

Note that $\lambda^*/n$ is a constant bounded away from zero. More precisely,

$$\lambda^*/n = \min\left\{\frac{n - \alpha n}{n - 1}, \frac{(\gamma n - 1)(n - \gamma n + 1)}{n(n - 1)}\right\}.$$  

Thus the inequality (5) holds with the above $\delta$. \hfill \Box

\section*{B Proof of Theorem 2.8}

\textbf{Proof of part (a).} To prove this part, we show that $E[T_n(C \log n)] \rightarrow \frac{1}{\beta}$ and $\text{Var}(T_n(C \log n))$ is bounded. Thus the statement follows by applying Chebyshov’s inequality. Using (4), we have:

$$E[T_n(C \log n)] = \frac{1}{\beta} \sum_{i=1}^{C \log n} \frac{n-1}{i(n-i)} = \frac{1}{\beta} \log \log n + o(\log \log n).$$

The steps of the above calculation are similar to the ones presented in (26), thus we remove the details. Further, note that $T_n(C \log n)$ is the sum of independent exponential random variables, thus:

$$\text{Var}(T_n(C \log n)) = \sum_{i=1}^{C \log n} \frac{1}{\lambda_i^2} = \frac{1}{\beta^2} \sum_{i=1}^{C \log n} \left(\frac{n-1}{i(n-i)}\right)^2 \leq \frac{1}{\beta^2} \sum_{i=1}^{\infty} \left(\frac{n-1}{i(n-i)}\right)^2 \leq M,$$

for some constant $M$. This completes the proof. \hfill \Box

\textbf{Proof of part (b).} Similar to part (a), we show that $E[T_n(C \log n)] \rightarrow \frac{k}{\beta(k-2)}$ and $\text{Var}(T_n(C \log n))$ is bounded. Following the proof sketch, we use the known fact that, w.h.p., a random $k$-regular graph is locally tree like (for instance see Dembo and Montanari (2010)). For the sake of completeness, in the following lemma, we state this using the terminology for the exploration process described in Section 3.

\textbf{Lemma B.1.} For $j = O(\log n)$, w.h.p., the component of the configuration model revealed until $j$ iterations is a tree. \hfill \Box

\footnote{Note that the result in the literature is stronger than this statement, and it asserts that even after forming the whole graph, the subgraph formed by these nodes is a tree w.h.p.}
**Proof of Lemma 3.1.** For iteration $j \leq C \log n$ in the exploration process, the number of active clones satisfies $A(j) \leq kC \log n$. Thus the probability that there are no cycles in the multigraph formed so far by the configuration model is at least $(1 - \frac{kC \log n}{kC \log n})^{C \log n} = 1 - o(1)$. This implies that w.h.p., the multi-graph formed so far, is a tree.

Lemma 3.1 implies that in this early adoption regime, at each step of the exploration process, one sleeping node is awakened and using our coupling with the adoption process, this means one extra node adopts $Z$. Also, at any time step $j \leq C \log n$, the number of active clones is given by $A(j) = k + j(k - 2)$. This gives

$$E[T_n(C \log n)] = \frac{k}{\beta} \sum_{i=1}^{C \log n} \frac{1}{k + i(k - 2)} = \frac{k}{\beta k - 2} \log \log n + o(\log \log n).$$

Similar to part (a), the variance of $T_n(C \log n)$ can be calculated as:

$$\text{Var}(T_n(C \log n)) = \frac{k^2}{\beta^2} \sum_{i=1}^{C \log n} \left(\frac{1}{k + i(k - 2)}\right)^2 \leq \frac{k^2}{\beta^2} \sum_{i=1}^{\infty} \left(\frac{1}{k + i(k - 2)}\right)^2 \leq M,$$

for some constant $M$. Part (b) of Theorem 2.8 then follows by using the Chebyshev’s inequality.

**C Missing proofs of Section 3**

**Proof of Lemma 3.2.** The proof is a simple modification of Wormald’s original proof, where the modification is mainly in how we choose the various asymptotic functions involved in the proof. Let $F(x, y) = \frac{ky}{k - x}$ defined for $0 \leq x \leq k/2 - \epsilon_0$ and $0 \leq y \leq 1$. Then

$$\frac{\partial F}{\partial x} + \frac{\partial F}{\partial y} = \frac{2ky}{(k - 2x)^2} + \frac{k}{k - 2x} \leq \frac{k}{2\epsilon_0} + \frac{k}{2\epsilon_0} = \Phi.$$

So, $F$ is Lipschitz with Lipschitz constant $\Phi$. Also note that for any $0 < j < n$, we have $F(j/n, N(j)/n) = f'(j/n)$ (defined in (18)). Let $\lambda = \frac{n}{(\log n)^2}$ and $\delta = \frac{1}{\log n}$. We first show that:

**Claim C.1.**

$$P(|N(j + \lambda) - N(j) - \lambda F(j/n, N(j)/n)| \geq 4\delta \lambda) \leq 2e^{-\frac{j^2}{2}}. \tag{28}$$

**Proof of Claim C.1.** For each $0 \leq l \leq \lambda$, we have

$$E[N(j + l + 1) - N(j + l)|H(j + l)] = F(j + l)/n, N((j + l)/n)] \leq F(j/n, N(j)/n) + \Phi \lambda/n.$$

Thus there exists a function $\Delta(n) = \Phi \lambda/n$ such that conditional on $H(j)$, the sequence

$$Z(l) = N(j + l) - N(j) - lF(j/n, N(j)/n) - l\Delta(n)$$

for $0 \leq l \leq \lambda$ is a supermartingale w.r.t. the sigma fields generated by $H(j), H(j + 1), \ldots, H(j + \lambda)$. Further $Z(l)$, $0 \leq l \leq \lambda$ has bounded increment: $|Z(l + 1) - Z(l)| \leq |N(j + l + 1) - N(j + l)| +$
\(|F(j/n, N(j)/n)| + |\Delta(n)| \leq 3\). Thus using concentration results for supermartingales from Wormald (1999a) (Lemma 4.2), we have

\[
P(N(j + \lambda) - N(j) - \lambda F(j/n, N(j)/n) \geq \lambda \Delta(n) + 3\delta \lambda) \leq e^{-\frac{\delta \lambda}{2}}.
\]

(29)

The following two observations complete the proof: (i) \(\lambda \Delta(n) \leq \delta \lambda\) (ii) A similar inequality can be obtained for the lower tail of \(Z(\lambda)\).

\[\square\]

Next, for \(i = 0, 1, \ldots, (k/2 - \varepsilon_0)n/\lambda\), by induction we prove that:

**Claim C.2.** \(P(|N(i\lambda) - f(i\lambda/n)| \geq \varepsilon_i) \leq i e^{-\frac{\delta \lambda}{2}}\), where \(\varepsilon_i = 5\delta \lambda \left[\frac{(1 + \Delta(n)\varepsilon_i - 1)}{\lambda(n)}\right]\).

**Proof of Claim C.2.** The base case follows from Claim C.1 (inequality (28)), and the fact that \(|f(\lambda) - \lambda f'(0)| \leq \delta \lambda\). Assuming that the claim holds for \(1, 2, \ldots, i\), we now prove it for case \(i + 1\). We have

\[|N(i + 1)\lambda) - nf((i + 1)\lambda/n)| \leq |N(i\lambda) - nf(i\lambda/n)| + |N((i + 1)\lambda) - N(i\lambda) + nf(i\lambda/n) - nf((i + 1)\lambda/n)|.\]

By induction hypothesis, with probability \(1 - i e^{-\frac{\delta \lambda}{2}}\), we have \(|N(i\lambda) - nf(i\lambda/n)| \leq \varepsilon_i\). Further, we write:

\[|N((i + 1)\lambda) - N(i\lambda) + nf(i\lambda/n) - nf((i + 1)\lambda/n)| \leq |N((i + 1)\lambda) - N(i\lambda) - \lambda F(i\lambda/n, N(i\lambda)/n)| + |\lambda F(i\lambda/n, N(i\lambda)/n) + nf(i\lambda/n) - nf((i + 1)\lambda/n)|.\]

From (28), we have with probability \(1 - e^{-\frac{\delta \lambda}{2}}, |N((i + 1)\lambda) - N(i\lambda) - \lambda F(i\lambda/n, N(i\lambda)/n)| \leq 4\delta \lambda\). Also,

\[nf(i\lambda/n) - nf((i + 1)\lambda/n) = -\lambda f'(i\lambda/n) + O(\lambda^2/n) = -\lambda F(i\lambda/n, f(i\lambda/n)) + O(\lambda^2/n).\]

Hence,

\[|\lambda F(i\lambda/n, N(i\lambda)/n) + nf(i\lambda/n) - nf((i + 1)\lambda/n)| \leq |\lambda F(i\lambda/n, N(i\lambda)/n) - \lambda F(i\lambda/n, f(i\lambda/n))| + O(\lambda^2/n) \leq \Delta(n)\varepsilon_i + O(\lambda^2/n).\]

where in the inequality holds because \(F(x, y)\) is Lipschitz. Note that \(\lambda^2/n = o(\delta \lambda)\). Putting all these together, we have with probability at least \(1 - (i + 1)e^{-\frac{\delta \lambda}{2}}\),

\[|N((i + 1)\lambda) - nf((i + 1)\lambda/n)| \leq (1 + \Delta(n))\varepsilon_i + 5\delta \lambda = \varepsilon_{i+1}.
\]

This complete the induction and the proof. \[\square\]

To complete the proof of the Lemma, first note that \(i = O(n/\lambda)\), so \(\varepsilon_i = O(n\delta) = o(n)\). Now for any general \(j\), find \(i^*\) such that \(i^*\lambda\) is the nearest integer to \(j\) among all \(i\lambda\)'s, \(i = 0, 1, \ldots, (k/2 - \varepsilon_0)n/w\).

We have:

\[|N(j) - nf(j/n)| \leq |N(j) - N(i^*\lambda)| + |N(i^*\lambda) - nf(i^*\lambda/n)| + |nf(i^*\lambda/n) - f(j/n)| = |N(i^*\lambda) - nf(i^*\lambda/n)| + O(\lambda).\]

Noting that \(\frac{\lambda}{\lambda} e^{-\frac{\delta \lambda}{2}} = o(n^{-3})\) completes the proof. \[\square\]
Proof of Lemma 3.3. First note that for any $0 \leq x \leq \frac{k-\epsilon_0}{2}$, we have $f'(x) \leq -|f'(\frac{k-\epsilon_0}{2})| = -c$. Using the mean value theorem we have: $nf(j_{\alpha} + \frac{2}{c} |\delta(n)|/n) \leq nf(j_{\alpha} + 2\delta(n))$. From Lemma 3.1, we have $N(nj_{\alpha} + \frac{2}{c} |\delta(n)|) \leq nf(j_{\alpha} + \frac{2}{c} |\delta(n)|/n) + \delta(n) \leq nf(t_{\alpha}) - |\delta(n)| = n(1 - \alpha) - |\delta(n)|$. By definition, $N(T_{\alpha}) = n(1 - \alpha)$, and $N(\cdot)$ is decreasing in the number of iterations. Thus, $J_{\alpha} \leq nj_{\alpha} + \frac{2}{c} |\delta(n)|$. Using a similar argument, we can prove $J_{\alpha} \geq nj_{\alpha} - \frac{2}{c} |\delta(n)|$ and the proof is complete.

Proof of Lemma 3.7. Let $E$ be the event that the configuration model is not connected and let $E_s$ be the event that there exists a subgraph $H$ of size $s$ which is isolated in the configuration model. For any positive even integer $m$, the number of possible pairings of $m$ clones is $\frac{m!}{(\frac{m}{2})!^2}$. Using this fact we can bound the probability of $E_s$ by simply counting the number of pairings as follows.

$$\mathbb{P}(E_s) \leq \binom{n}{s} \frac{(\frac{nk}{2})^{s/2}}{(\frac{nk}{2})^{s/2}}.$$ 

The above bound is asymptotically largest when $s$ is a constant with respect to $n$. See Wormald (1999b) for similar proof techniques. In this case for any $\epsilon_1 > 0$, we can obtain:

$$\mathbb{P}(E) = O(n^{-s(k/2-1)+\epsilon_1}). \quad (30)$$

Since $k \geq 3$, when $G$ is simple, it cannot have an isolated component of size less than 4 nodes. The worst case in (30) is when $k = 3$ and $s = 4$ which gives the required bound. □