The Spread of Epidemics on Random Graphs:
A Modified Bass Model for Product Growth in Networks
(Working Paper)

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Abstract

Many products and innovations become widespread through the social interaction of indi-
viduals in a population. Predicting the growth rate of adoption of a product is crucial for demand
management and sales. Bass model has been widely used to model the temporal evulsion of the
adoption in such social systems. In such a model, the likelihood of a new adoption is linearly
related to the number of previous adopters, implicitly assuming a global interaction among
all individuals in the network. Such global interactions, however, do not exists in many large
social networks. In such networks each individual typically interacts with a small part of the
population.

To quantify the growth rate (or equivalently the adoption timing) in networks with limited
interactions, we study the evolution of a simple epidemic model on random $k$-regular graphs.
First, we show that our model is equivalent to the Bass model for complete graphs (i.e., when
interactions are global). Then we analyze the adoption timing for $k$-regular random graphs and
present the limit results for the time it takes for a fraction of the population to adopt. Further,
we provide the timing of early adoptions at finer scales, e.g., logarithmic in the population size.

1 Introduction

Since many decades ago, diffusion of ideas and innovations through social interactions has been
widely observed in various social systems [Rogers 2003]. It often happens that a few pioneers
adopt an innovation and they influence people in contact with them. Those in turn, adopt and
influence their contacts, and the innovation spreads through the network as a result of these social
interactions.

A powerful class of marketing techniques known as viral marketing mainly relies on the the
notion that ideas spread like viruses, and uses social networks to increase awareness about an
innovation. The emergence of online social networks in recent years has significantly contributed

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to the effectiveness of viral marketing. A recent study [Purcell et al. 2010] reports that 52% of people who read news online forward it to their contacts via social networks, email, or posts. Also, many websites such as Amazon and Facebook offer and encourage recommendation and/or referral services to users.

From a marketing and sales perspective, it is imperative to predict the temporal evolution of the sales of the product introduced/advertised through such social interactions. 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 linearly depends on the number of people who have adopted so far. This relies on the assumption that all agents are in contact with each other, and thus, a non-adopter can be influenced by all adopters. Such global interaction, however, do not exist in many modern social networks with billions of users. In online social networks, usually each person is in contact with a small group of friends and he/she is only influenced by these people. Thus the structure of the underlying network comes into play in product growth. More recent literature investigates the role of network structure on the diffusion process mainly through simulation and approximation [Goldenberg et al. 2001], [Barthelemy et al. 2004], [Peres 2013]. In this paper, we take a rigorous approach to study the network effects on the product adoption by analyzing a simple diffusion model in a large class of random graphs.

We use the same notion of innovation diffusion as the Bass model [Bass 1969], but include the limitation on social interactions. In particular, we assume that at any time the likelihood that a non-adopter adopts a product linearly depends on the number of its neighbors who have previously adopted. As an equivalent model, we use a simple contact process that works as follows: agents are nodes of a graph, and an edge between two nodes means that these agent are neighbors. Initially one random node adopts the product. Later, each node makes contact at random times and each time, with one neighbor selected uniformly at random. If the contacting node is an adopter and the contacted one is not, then the latter adopts the product with a given probability.

Similar to [Bass 1969], we are mainly concerned with timing in the regime that a fraction of the population have already adopted. We denote this phase by major adoption regime and we analyze the time it takes to increase the fraction of adopters by a constat (i.e., from $\alpha n$ adopters to $\gamma n$, where $n$ is the population size), and on the effect of network structure on the timing in major adoption regime.

We establish fluid limits for the sample paths of the resulting stochastic (adoption) process in certain networks. First, we find the limit for the complete network (see Theorem 2.1) and confirm that the fluid limit of our epidemic model coincides with the Bass model. Next and far more importantly, we establish the limit for random $k$-regular graphs (see Theorem 2.4) and show how it differs from the result of complete graphs in different aspects. We show that the innovation spreads more slowly in random graphs compared to complete graphs. Further, unlike the complete graph, in random regular graphs, the process spreads faster in the second half of the adoption process (i.e., after reaching $n/2$) compared to the first half. We also describe how to generalize our analysis to compute the timing limits for random graphs with a more general degree distribution (under certain condition on the distribution).

In addition, we find the limit of timing in the early adoption regime which refers to the phase that the first $\Theta(\log n)$ nodes adopt the product (see Theorem 2.6). In this regime, we also show that compared to complete graphs, the process grows more slowly in random $k$-regular graphs by a factor of $(k - 2)/k$.

The epidemic model that 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 studied 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 Mosk-Aoyama and Shah [2008], and to the learning models studied in social and economic networks Jackson [2008]. Our results complement the earlier studies of epidemic processes by focusing on the timing in the major adoption regime. It has been shown in several papers that the growth of epidemics is related to the expansion properties of the underlying graphs Mosk-Aoyama and Shah [2008], Jackson [2008]. Since random graphs have large expansion factors Kahale [1992], Gkantsidis et al. [2003], it is well known that epidemics spread fast in these graphs. However, the functional form of the growth has not been previously computed, and the time needed to grow the fraction of nodes in epidemics from a constant \( \alpha \) to another constant \( \gamma \) has not be analyzed.

Our work brings together the literature on analyzing processes on random graphs, and on stochastic differential equations and fluid limits. To analyze the epidemic process on random graphs, we couple the (continues) contact process with the (discrete) graph generation process based on configuration model Wormald [1999a]. Abstracting away from time, our epidemic process spreads on random graphs in the same way as the exploration process, defined in Molloy and Reed [1995], does. The latter was introduced to find the size of the largest connected component in random graph with given degree distributions. We use similar ideas as in Wormald [1995] to approximate the evolution of the epidemic process. When coupling with time and the contact process, we build upon these results for random graphs Wormald [1995], Molloy and Reed [1995] to compute the limit of timing in 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 adopted \( Z \) yet, then \( u \) will adopt the product with probability \( p \). Given the thinning property of the Poisson processes, WLOG, we assume that \( p = 1 \).

In this epidemic model, the number of adopted nodes can only increase over time. If the underlying graph is connected, after a finite time, all the nodes 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: early adoption regime in which \( x = o(n) \) and the major adoption regime where \( x = \Theta(n) \).

We analyze the contact 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 interactions, and the latter serves as a model of limited interactions among the individuals.

First, we focus on the major adoption regime and give almost sure results on how long it takes to grow the fraction of the adopters form \( \alpha \) to \( \gamma \), where \( 0 < \alpha \leq \gamma < 1 \).
2.1 Timing in Major Adoption Regime

In the major adoption regime, we assume that a constant fraction of the population have 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 $\Delta_n(\alpha, \gamma n)$ be $T_n(\gamma n) - T_n(\alpha n)$. In this subsection, we compute the limit of $\Delta_n(\alpha, \gamma n)$. 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 complete graphs). Suppose for all $n > 1$, the underlying graph $G_n$ is the complete graph. Then for any $0 < \alpha \leq \gamma < 1$:

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

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 $s(t) = \frac{e^{\beta t}}{1 + e^{\beta t}}$, which is the *logistic equation* that is a special case of the Bass model. This is the form of Bass model [Bass 1969] in which the innovation coefficient is 0, and the imitation coefficient is $1/\beta$. i.e., the product only spreads as a result imitating the behavior of the previous adopters.

Let $S_n(t)$ be the number of adopters at time $t$. The above almost sure result, implies that

$$\frac{S_n(t)}{n} \overset{a.s.}{\rightarrow} s(t).$$

Thus the limit of the scaled sample paths of our probabilistic contact process coincides with the deterministic logistic function. Further, note that function $\theta(s)$ has the following symmetry property: for any $0 < s < 1$, $\theta(s) = -\theta(1-s)$. Thus the time it takes to grow the fraction of the adopters form $\alpha$ to 1/2 is the same that time it takes to grow the fraction form 1/2 to $1 - \alpha$ where $0 < \alpha < 1/2$. This symmetry is the result of having a complete graph (also called perfect mixing) and can be intuitively seen as follow: at any time, the subgraph including the adopters is a complete graph, and so is the subgraph consisting of nodes who have not 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 the product $Z$, and abandoning of the product spreads in the network in this way. Because the process of adoption and discarding spread in exactly the same way, the time needed to grow the set of non-adopters from $1 - s$ to 1/2 would be the same as the time it takes to grow the set of adopters from $s$ to 1/2.

The limit result [2] can be proven directly by using stochastic differential equations and the 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 [1].

**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, with probability \( (n - i)/(n - 1) \) it contacts a neighbor who has not adopted yet. Thus using the thinning property of the Poisson processes, we have:

\[
\lambda_i = \beta \frac{i(n - i)}{n - 1}.
\] (3)

To prove the theorem, first in the following claim, we show that:

**Claim 2.2.** \( E[\Delta_n(\gamma n, an)] \to \theta(\gamma) - \theta(a) \).

The claim is proven in the appendix. Next, we establish the following concentration bounds:

**Claim 2.3.** Suppose \( \epsilon \) is a fixed small positive number, \( P(|\Delta_n(\gamma n, an) - E[\Delta_n(\gamma n, an)]| \geq \epsilon) \leq e^{-\delta n} \), (4)

where \( \delta \) is a small positive number given in (29).

The above claim is proved in the appendix as well, and it implies that

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

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

Next, we analyze the contact process in random \( k \)-regular graphs, where \( k \) is a constant. To ensure that all the nodes eventually adopt, we limit the sample space of the graphs to only include connected ones. We show that:

**Theorem 2.4 (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:

\[
\Delta_n(\gamma n, an) \overset{a.s.}{\rightarrow} \tilde{\theta}(\gamma) - \tilde{\theta}(\alpha),
\] (5)

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

The left plot of Figure 1 plots the limit results of the time it takes to grow the fraction of adopters from 0 to \( s \in [0.01, 0.09] \) for the complete graph and random 5-regular graph. We observe that, in random graphs the process grows more slowly compared to the complete 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 underlaying graph. However, the probability that an adopter contacts a non-adopter is higher in complete graph because of two reasons: (i) In a \( k \)-regular graph, the subgraph induced by the adopters is connected. Therefore, each adopter has effectively \( k - 1 \) neighbors who are likely to be non-adopters. (ii) Even those \( k - 1 \) neighbors are not uniform samples among the remaining \( n - 2 \) nodes. It is more likely that the neighbor of an adopter belongs to the set of adopter itself. This is a result of connectivity properties of the subgraph induced by adopters.
To further highlight the effect of connectivity among the adopters, let us compute the rate of \( \tau_i \) in a random graph using a mean field approximation. We denote this approximate rate by \( \tilde{\lambda}_i^M \). As explained above the rate of contact by adopters is \( \beta \); each adopter has at least one adopter neighbor with probability 1. For adopter node \( v \), let \( v' \) be the neighbor who had adopted before \( v \) and was the first adopter who contacted \( v \). Clearly if \( v \) contacts node \( v' \), it will not result in a new adoption. Now suppose node \( v \) selects a random neighbor other than \( v' \); this happens with probability \( \frac{k-1}{k} \). In a mean field approximation, we assume that the rest of neighbors of \( v \) are uniformly sampled among the other \( n-2 \) nodes. Thus with probability \( \frac{n-i}{n-2} \) node \( v \) will contact a non-adopter, and this implies that:

\[
\tilde{\lambda}_i^M = \frac{\beta(k-1)i(n-i)}{k} \frac{n-2}{n-2}.
\] (6)

Comparing to (5), this approximation rate has the same form and it is only scaled by \( \frac{k-1}{k} \). The time limit resulting from this mean filed approximation is also plotted in Figure 1. 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 (5), 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, here the subgraph of non-adopters is not necessarily connected, thus the backward process grows faster.

Figure 1: Left: 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 \( s \in [0.01,0.99] \)).
Proof sketch. Similar to the proof for the complete graph, we aim to compute the rate of the exponential time between any two consecutive adoption. Recall that we denote the time it takes to grow the number of adoptions from $i$ to $i + 1$ by $\tau_i$ 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 a to contact. Knowing only $i$, we cannot determine how many of $v$’s neighbor have not adopted yet. In order 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}. Configuration model works as follows: we start by $n$ isolated nodes. Each node has $k$ clones (or half edges), and at each step, a new edge is formed by pairing two randomly chosen clones; the process ends after $nk/2$ steps, where all the clones are paired.

Given this observation, we use the following idea: we couple the graph generation and the contact process: We assume that the graph has not been realized before the contact process. Thus at time $0$, we have $n$ isolated nodes each with $k$ unpaired clones. Anytime an adopter makes a contact, it chooses one of its clones uniformly at random. If the clone has already been paired, it means that both ends of this edge have already adopted. In this case, neither the adoption process grows nor the set of formed edges. On the other hand, if the clone has not been paired yet, then 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 of \cite{Wormald1999b,Wormald1995} to approximate the discrete random processes by a deterministic function. The same approach has been used to find the size of the giant connected components in random graphs \cite{MolloyReed1995,MolloyReed1998}.

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

The proof also deals with a few other technical subtleties such as obtaining a bound in (the deterministic) approximation that is stronger than that of \cite{Wormald1999b,Wormald1995} and confirming that the same concentration results hold when we limit the sample space to only include simple and connected graphs (rather than all possible pairings of the clones.).

The detailed proof is presented in Section 3. Further, in the Section 5, we explain how to generalize the above proof ideas to analyze the contact process on random graph with more general degree distributions and also how to analyze similar epidemic models such as SIS and SIR models. \footnote{These are the terminologies used in the infectious diseases; S stands for susceptible, I for infectious and R for removed, i.e. immune or dead}

Finally note that for $k = 2$, the only connected regular graph is a cycle of length $n$. The following asserts the different time scaling of the major adoption for such graphs:

**Proposition 2.5.** For all $n > 1$, let the underlying graph be a cycle of length $n$. Then for any...
\(0 < \alpha \leq \gamma < 1,\)
\[
\frac{\Delta_n(\gamma n, \alpha n)}{n} \xrightarrow{a.s.} \frac{\gamma - \alpha}{\beta}.
\]
(7)

**Proof.** For any \(i \geq 1\), the set of adopters form 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.

\[
\square
\]

### 2.2 Timing in Early Adoption Regime

In the major adoption regime, the rate of contacts grows linearly with \(n\), therefore, the adoption process spreads very fast: as Theorem 2.1 and 2.4 assert, the time to grow from a constant 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 and in particular, we find the limit of the time it takes to have \(\Theta(\log n)\) adopters. We establish the limit for both the complete graphs and random \(k\)-regular graphs. For both of these graphs, we show that the time needed to have \(\Theta(\log n)\) adopters scales as \(\log \log n\). Further, the process grows faster in the complete graph (compared to the random \(k\)-regular graph).

**Theorem 2.6 (Early adoption).** For any constant \(C > 0,\)

(a) If for all \(n > 1\), graph \(G_n\) is a complete graph, then:
\[
\frac{T_n(C \log n)}{\log \log n} \xrightarrow{p} \frac{1}{\beta}.
\]
(8)

(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:
\[
\frac{T_n(C \log n)}{\log \log n} \xrightarrow{p} \frac{k}{\beta(k - 2)}.
\]
(9)

The proof of part (a) follows the same line of the proof of Theorem 2.1; note that the rate given by (3) holds for any \(1 \leq i < n\). Using this rate, we first show that \(\frac{E[T_n(C \log n)]}{\log \log n} \xrightarrow{p} \frac{1}{\beta}\), and then show that \(\frac{T_n(C \log n)}{\log \log n}\) converges to its mean (in probability) by proving that its variance converges to zero. The details are given in the Section 4.

**Proof sketch of part (b).** Similar to the previous proofs, we aim to compute \(\lambda_i\), for \(1 \leq i \leq C \log n\). First note that we can view the contact process as the following process: each edge \((v, u)\) makes contacts at an independent 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 that the set of adopter and non-adopters. Observe that in our coupled process, 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 \((k - 1)i + 1\). To compute the number of these edges, we use the \textit{locally tree-like} property of the random \(k\)-regular graphs [Dembo and Montanari 2010] which confirms that, with high probability, in 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 \((k - 2)i + 1\) edges are all between an adopter node and a non-adopter one, and with high probability, \(\lambda_i = \beta/k[(k - 2)i + 1]\) for \(1 \leq i \leq C\log n\). Having 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 Section 4. □

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

**Remark 2.7.** Similar limit results hold for \(\frac{T_n(o(n))}{\log o(n)}\) for any \(o(n) = o(\sqrt{n})\).

### 3 Proof of Theorem 2.4

As explained in the proof sketch, we first study the iteration process and analyze the evolution of the number of adopters in terms of the iterations. Similar to Molloy and Reed [1995], we call this process the \text{exploration process}. In this process every node is associated with \(k\) clones. For clone \(c\) of node \(v\), all the 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 the clones are sleeping. If all clones of a node are sleeping then the node is said to be a sleeping node; if all of its clones are dead, then the node is considered dead, otherwise it is considered to be 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 among the set of all remaining unpaired clones. Kill \(c’\) and make all its siblings active.

The set of active cones at iteration \(j\) is denoted by \(A(j)\). Also, the union of the set of sleeping and active clones is denoted by \(L(j)\), and they are called ‘living’ clones. Further, we denote the number of sleeping nodes by \(N(j)\).

3.1 **Evolution of Exploration Process**

In their second paper Molloy and Reed [Molloy and Reed 1998] used results by Wormald [Wormald 1995] to track the evolution of the exploration process. We will use a similar technique, but will not
directly use Wormald’s result. Instead, we will use insights from the proof technique and tighten the probability of error needed to get almost sure (w.p. 1) convergence. Further, when coupling with the contact process, we introduce an additional variable which tracks the (random) re-scaled time in the epidemic process.

In every iteration of the exploration process, the number of living clones reduces by two, i.e., we have \( L(j + 1) = L(j) - 2 \). 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 the nodes are sleeping except the one we have awakened for the initiation (note that when coupling with the contact process, this node will be the first node that initially adopts the product). Therefore, at \( j = 0 \), we have \( A(0) = k \).

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

2. With probability \( 1 - \frac{kN(j)}{kn - 2j} \), we have
   \[
   N(j + 1) = N(j) \\
   A(j + 1) = A(j) - 2.
   \]

Note that the above equations (for the evolution of sleeping nodes and active clones) only hold when the graph is connected. Later, in Lemma 3.9, we show that a random \( k \)-regular graph is connected with probability \( 1 - \Theta(n^{-2}) \) and we further show that our limit result holds when conditioning on being connected. For now, we assume that the graph is connected, and find the limits of the scaled random variables \( N(j)/n \) and \( A(j)/n \) evolving according to (10)-(13).

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 (10) - (13), we have

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

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

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

\[
f(x) = \left(1 - \frac{2x}{k}\right)^{\frac{k}{2}},
\]
which is the unique solution to the differential equation

\[ f'(x) = -\frac{kf(x)}{k - 2x}, \tag{17} \]

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

The result in \cite{Wormald1995} is for a fairly general setting, but the bound it gives 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 \cite{Wormald1995}) to our case so that we can obtain a stronger bound on the probability of event (15).

**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 \cite{Wormald18} and \( \delta_1(n) = o(n) \).

**Proof.** 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 \( F(x, y) = \frac{ky}{k - 2x} \)

defined for \( 0 \leq x \leq k/2 - \epsilon_0 \) and \( 0 \leq y \leq 1 \). Then

\[
\left| \frac{\partial F}{\partial x} \right| + \left| \frac{\partial F}{\partial y} \right| = \frac{2ky}{(k - 2x)^2} + \frac{k}{k - 2x} \leq \frac{k}{2\epsilon_0^2} + \frac{k}{2\epsilon_0} \leq \Phi.
\]

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 \cite{Wormald18}). Let \( \lambda = \frac{n}{(\log n)^2} \) and \( \delta = \frac{1}{\log n} \). We first show that:

**Claim 3.2.**

\[
P(|N(j + \lambda) - N(j) - \lambda F(j/n, N(j)/n)| \geq 4\delta \lambda) \leq 2e^{-\frac{\delta^2}{2}}. \tag{18}
\]

**Proof.** 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 \cite{Wormald1999} (Lemma 4.2), we have

\[
P(N(j + \lambda) - N(j) - \lambda F(j/n, N(j)/n) \geq \lambda \Delta(n) + 3\delta \lambda) \leq e^{-\frac{\delta^2 \lambda}{2}}. \tag{19}
\]

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 \(i = 0, 1, ..., (k/2 - \epsilon_0)n/\lambda\), by induction we prove that:

**Claim 3.3.** \(P(|N(i\lambda) - f(i\lambda/n)| \geq \epsilon_i) \leq ie^{-\frac{\epsilon_i^2}{2}}\), where \(\epsilon_i = 5\Delta\lambda \left[ \frac{(1+\Delta(n))i-1}{\Delta(n)} \right] \).

**Proof.** The base case follows from Claim 3.2 (inequality (18)), and the fact that \(|f(\lambda) - \lambda f'(0)| \leq \delta\lambda\). Assuming that the claim holds for \(1, 2, ..., i\), we now prove it for \(i + 1\). 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 \(1 - ie^{-\frac{\epsilon_i^2}{2}}\), we have \(|N(i\lambda) - nf(i\lambda/n)| \leq \epsilon_i\). Further, we write:

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

From (18), we have with probability \(1 - e^{-\frac{\epsilon_i^2}{2}}\), \(|N((i + 1)\lambda) - N(i\lambda) - \lambda F(i\lambda/n, N(i\lambda)/n)| \leq 4\delta\lambda\). 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,

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

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 \(1 - (i + 1)e^{-\frac{\epsilon_i^2}{2}}\),

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

This complete the induction and the proof. \(\square\)

To complete the proof of the Lemma, first note that \(i = O(n/\lambda)\), so \(\epsilon_i = O(n\delta) = o(n)\). Now for any general \(j\), find \(\hat{i}\) such that \(\hat{i}\lambda\) is the nearest integer to \(j\) among all \(\lambda i\)'s, \(i = 0, 1, ..., (k/2 - \epsilon_0)n/\lambda\). We have:

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

Noting that \(\frac{n}{\lambda} e^{-\frac{\epsilon_i^2}{2}} = o(n^{-3})\) completes the proof. \(\square\)

Next we find approximation for \(A(j)\): Define \(g(x) \equiv k(1 - f(x)) - 2x\). The following is an immediate corollary of Lemma 3.1.
Corollary 3.4. With probability $1-o(n^{-3})$, for any $0 < j < (k - \epsilon_0)n/2$, we have

$$|A(j) - ng(j/n)| \leq \delta_2(n),$$

uniformly over $j$, for some $\delta_2(n) = o(n)$.

Next we find an approximation for the number of iterations needed to have an active or dead nodes. Note that when coupled with the epidemic process, these are the adopter nodes. Let $\delta(n) = \max \{\delta_1(n), \delta_2(n)\}$ for $\delta_1(n)$ and $\delta_2(n)$ defined in Lemma 3.1 and Corollary 3.4. Let $A \equiv (A(j), 0 \leq j \leq (k - \epsilon_0)n/2)$ be the vector of the random number of active clones and let $a$ be a particular realization of this random vector. Also, let $S \equiv \{a : |a(j) - ng(j/n)| \leq \delta(n)\}$. In the next auxiliary lemma, we show that the number of iterations needed to have an active or dead nodes, which we denote by $J_a$, is close to $f^{-1}(1 - \alpha)$.

Lemma 3.5. Let $J_a \equiv f^{-1}(1 - \alpha)$ and $c = |f^{' \left(\frac{k-\epsilon_0}{2}\right)}|$. If $A \in S$, then for any $\alpha$

$$|J_a - n j_a| \leq \frac{2}{c} \delta(n).$$

Proof. First note that for any $0 \leq x \leq \frac{k-\epsilon_0}{2}$, we have $f'(x) \leq -|f^{' \left(\frac{k-\epsilon_0}{2}\right)}| = -c$. Using the mean value theorem we have: $nf(j_a + \frac{2}{c}|\delta(n)|/n) \leq nf(j_a) + 2\delta(n)$. From Lemma 3.1, we have $N(n j_a + \frac{2}{c}|\delta(n)|) \leq n f(j_a + \frac{2}{c}|\delta(n)|/n) + \delta(n) \leq nf(j_a) - |\delta(n)| = n(1 - \alpha) - |\delta(n)|$. By definition, $N(T_a) = n(1 - \alpha)$, and $N(\cdot)$ is decreasing in the number if iterations. Thus, $J_a \leq n j_a + \frac{2}{c}|\delta(n)|$. Using a similar argument, we can prove $J_a \geq n j_a - \frac{2}{c}|\delta(n)|$ and the proof is complete.

3.2 Coupling Exploration and Epidemic Processes

After analyzing the exploration process, we now couple the exploration and epidemic 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 cases happen:

Case 1: Clone $c$ has already been paired to 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 then the node to which clone $c'$ belongs will adopt, otherwise, if clone $c'$ is an active clone then the node to which clone $c'$ belongs has adopted before this contact.
This implies that only contacts made through active clones will result in proceeding with the exploration process. Further, only these contacts may result in the growth of the adoption set size. As mentioned before, we can view the contact 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 $\frac{\beta}{k}A(j)$. We denote this random variable by $\tilde{\tau}(j)$. Using the notation defined in Section 2 and in the previous subsection, it follows that:

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

**Remark 3.6.** 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 3.5, for $a \in S$, we have $\Delta \leq \Delta_n(an, \gamma n) \leq \bar{\Delta}$, where:

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

We then compute

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

$$= \frac{k}{\beta} \int_{j_a}^{j} \frac{1}{g(x)} dx + o(1) = \bar{\theta}(y) - \bar{\theta}(\alpha) + o(1),$$

where the inequality holds by corollary 3.4. In a similar way, we can prove an upper bound for $E[\bar{\Delta}|A = a \in S]$. These bounds prove that:

$$E[\bar{\Delta}|A = a \in S] \rightarrow \bar{\theta}(y) - \bar{\theta}(\alpha).$$

Now, we are in the position to prove Theorem 2.4. Let $\bar{\Delta} \triangleq \Delta - E[\bar{\Delta}]$. Fix $\epsilon > 0$. We start with:

$$P(|\Delta| \geq \epsilon) \leq \sum_{a \in S} P(|\Delta| \geq \epsilon|A = a)P(A = a) + P(A \notin S) \tag{22}$$

From Corollary 3.4, the second term is $o(n^{-3})$. To bound the first term, we first notice that for any $\epsilon_0 n \leq j \leq (k - \epsilon_0)n/2$ and any $p > 0$, conditioned on $a \in S$, we have:

$$P\left(\tilde{\tau}(j) \geq \frac{kp \log n}{\beta^2 n} A = a \right) \leq n^{-p}, \tag{23}$$

where $\bar{g} \triangleq \frac{1}{\epsilon} \min_{x \in [\epsilon_0 k/2, \epsilon_0]} g(x)$, and we use the following remark:
Remark 3.7. If $A \in S$, then $A(j) \geq n \min_{x \in \{e_0, k/2 - e_0\}} \delta(x) + o(n) \geq \frac{1}{2} n \min_{x \in \{e_0, k/2 - e_0\}} \delta(x)$, for all $e_0 n \leq j \leq (k/2 - e_0)n$ and large enough $n$.

Let $B$ be the event that $\left\{ \tau(j) \leq \frac{k \log n}{p \omega} \right\}$ for all $e_0 n \leq j \leq kn/2 - e_0 n$ and conditioned on $a \in S$. By (23) and the union bound we have $P(B) \geq 1 - n^{1-p}$, or equivalently $P(\overline{B}) \leq n^{1-p}$. Going back to bounding the first term of (22), for any $a \in S$ it follows that:

$$P(|E| \geq \epsilon|A = a) \leq P(|E| \geq \epsilon|A = a, B) + n^{1-p}.$$

Applying the Hoeffding bounding to the first term, we get:

$$P(|E| \geq \epsilon|A = a) \leq 2 \exp \left( -\frac{2n \epsilon^2 \beta^2 g^2}{\log n} k^2 p^2 \right) + O(n^{1-p}).$$

Using (21), for $n$ large enough, we have:

$$P(|\Delta - [\tilde{\theta}(\gamma) - \tilde{\theta}(\alpha)]| \geq 2\epsilon|A = a) \leq 2 \exp \left( -\frac{2n \epsilon^2 \beta^2 g^2}{\log n} k^2 p^2 \right) + O(n^{1-p}).$$

We can prove a similar bound for $|\Delta - [\tilde{\theta}(\gamma) - \tilde{\theta}(\alpha)]|$. Since $\Delta \leq \Delta(n, \gamma n) \leq \Delta$, the same bound holds for $|\Delta(n, \gamma n) - [\tilde{\theta}(\gamma) - \tilde{\theta}(\alpha)]|$ as well. Let $p = 4$, so far we have proved that:

$$P(|\Delta(n, \gamma n) - [\tilde{\theta}(\gamma) - \tilde{\theta}(\alpha)]| \geq 2\epsilon) = O(n^{-3}). \quad (24)$$

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., $O(n^{-3})$) still holds. Let $G$ denote the graph eventually obtained after $nk/2$ iterations. Conditioned on being connected and simple, $G$ is a $k$-regular graph sampled uniformly among all connected simple $k$-regular graphs. It follows form inequality (24) that:

$$P\left( \left| \Delta(n, \gamma n) - [\tilde{\theta}(\gamma) - \tilde{\theta}(\alpha)] \right| \geq 2\epsilon \right) \cap \{G \text{ is connected} \} \cap \{G \text{ is simple} \} = O(n^{-3}). \quad (25)$$

To prove that conditioned on $\{G \text{ is connected} \} \cap \{G \text{ is simple} \}$, the error probability is $O(n^{-3})$, it suffices to show that $P\left( \{G \text{ is connected} \} \cap \{G \text{ is simple} \} \right) = O(1)$. This follows from the next two lemmas.

**Lemma 3.8.** $P(G \text{ is simple}) = \Theta(1)$.

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

**Lemma 3.9.** $P(G \text{ is not connected}) \cap \{G \text{ is simple} \} = O(n^{-2})$. 

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Proof. Let $E$ be the event that the configuration model is not connected and let $E_s$ be the event that there exists a subgraph $\mathcal{H}$ 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 $\binom{m}{m/2}^2$. Using this fact we can bound the probability of $E_s$ by simply counting the number of pairings as follows.

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

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

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

(26)

Since $k \geq 3$, when $G$ is simple, it cannot have an isolated component of size less than 4 nodes. The worst case in (26) is when $k = 3$ and $s = 4$ which gives the required bound.

Putting (25), and Lemmas 3.8, and 3.9 together imply that for any graph $G_n$ sampled uniformly at random from the set of all connected $k$-regular graphs with $n$ nodes, and $n$ large enough:

$$P\left(\left|\Delta_n(\alpha n, \gamma n) - \tilde{\theta}(\gamma) - \tilde{\theta}(\alpha)\right| \geq 2\epsilon\right) = O(n^{-3}) < n^{-2}.\quad (27)$$

Since $\epsilon$ is arbitrary, and $\sum_{n=1}^{\infty} n^{-2} < \infty$, the theorem (the limit (7)) follows by applying the Borrel-Cantelli lemma.

4 Proof of Theorem 2.6

Proof of part (a). To prove this part, we show that $\frac{\mathbb{E}[T_n(C\log n)]}{\log \log n} \rightarrow \frac{1}{\beta}$ and $\text{Var}(T_n(C\log n))$ is bounded. Thus the statement follows by applying Chebyshev’s inequality. Using (23), we have:

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

The steps of the above calculation are similar to the ones presented in (28), thus we remove the details. Further, note that $T_n(C\log n)$ is the sum of independent exponential random variables, thus:

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

for some constant $M$. This completes the proof.

Proof of part (b). Similar to part (a), we show that $\frac{\mathbb{E}[T_n(C\log n)]}{\log \log n} \rightarrow \frac{k}{\beta(k-2)}$ 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.
Lemma 4.1. For \( j = O(\log n) \), w.h.p., the component of the configuration model revealed until \( j \) iterations is a tree.

Proof. 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 \( \left(1 - \frac{kC \log n}{kn - C \log n}\right)^{C \log n} = 1 - o(1) \). This implies that w.h.p., the multi-graph formed so far, is a tree. □

Lemma 4.1 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

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

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 2.6 then follows by using the Chebyshev’s inequality. □

5 Discussions

The techniques that we developed here to analyze the contact process for the random \( k \)-regular graphs can be generalized to the following settings:

**Contact process on random graphs with given degree distributions:** We can analyze the contact process defined in Section 2 for a more general class of random graphs with a given degree distribution. For these random graphs, we similarly couple the contact process and the configuration model. We first analyze the exploration process: Let \( D \) be the set of all degree that have 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 (10)-(13) 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 the Wormald’s result [Wormald 1995]. Then we connect the exploration process to the contact process in the same way that is presented in Subsection 3.2.

For comparison, see Figure 2 which 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. The figure shows that it matches very well with the simulation results. Interestingly, when there is more inhomogeneity in the degree distribution in the network, we observe that the process proceeds more or less at the same rate in the beginning, but the ones with higher disparity

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3Note 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.
slow down towards the end. This is perhaps because towards the end of the process most of the higher degree nodes have already adopted and the rate of spread is limited by the lower degree nodes that are left.

![Graph](image.png)

**Figure 2:** Simulated time to grow the fraction of adopters from $0.01$ to $s \in [0.01, 0.99]$ (functions $\theta(s) - \theta(0.01)$ for 5-regular, 4-6 and 3-7 random graphs.)

**SIR model on random graphs:** As mentioned in the introduction, the contact process we studied here is a special case of epidemic processes used to describe the transmission of communicable disease through individuals or spread of computer viruses in a network. This is the SI (S stands for susceptible and I for infected). 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 the SI model. Each infected node gets removed (which can be interpreted as either dead or immune) at a certain rate. A removed node cannot infect its neighbors. Suppose the each infected node gets 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 has been removed as well.

**References**


A Missing proofs

Proof of Claim 2.2 The proof of this claim is mainly algebraic and is given for the sake of completeness.

\[
E[\Delta_n(yn, \beta n)] = \sum_{i=\alpha n}^{\gamma n-1} \frac{1}{\lambda_i} = \frac{n-1}{\beta n} \sum_{i=\alpha n}^{\gamma n-1} \left( \frac{1}{i} + \frac{1}{n-i} \right)
\]

\[
= \frac{n-1}{\beta n} \left[ \int_\gamma^1 \frac{1}{x} dx + \int_1^{\gamma-n} \frac{1}{1-x} dx + E_n \right]
\]

\[
= \frac{1}{\beta} \left[ \log \frac{\gamma}{1-\gamma} - \log \frac{\alpha}{1-\alpha} \right] + E'_n
\]

where \( E_n \) and \( E'_n \) represent the error terms. We are left to show that \( E'_n \to 0 \). Note that \( \sum_{i=\alpha n}^{\gamma n-1} \frac{1}{i} \) gives an upper-bound for the integral \( \int_\gamma^1 \frac{1}{x} dx \). Further, \( \sum_{i=\alpha n}^{\gamma n-1} \frac{1}{i-1} \) 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. \( \square \)

Proof of Claim 2.3 In the following proof, to simplify the notation, we present \( \Delta_n(yn, \beta n) \) by \( \Delta_n \). By the Chernoff’s bound, for any \( s \geq 0 \):

\[
P(\Delta_n - E[\Delta_n] \geq \epsilon) \leq e^{-\epsilon^2 E[\Delta_n]} = e^{-s(\epsilon + E[\Delta_n])} E[e^{s\Delta_n}].
\]

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

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

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

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

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

\[
\frac{1}{\lambda_i - s^*} \leq \frac{1}{\lambda_i} \left( 1 + \frac{e}{2E[\Delta_n]} \right).
\]
Setting $s$ to be $s^\ast$ in the Chernoff’s bound, we have:

$$P(\Delta_n - E[\Delta_n] \geq \varepsilon) \leq e^{-s^2 \varepsilon^2 / 2}$$

Similarly, we can show that:

$$P(-(\Delta_n - E[\Delta_n]) \geq \varepsilon) \leq e^{-s^2 \varepsilon^2 / 2}.$$

Define

$$\delta = \left( \frac{s^2 \varepsilon^2}{2E[\Delta_n]} + \frac{s^2 \varepsilon^2}{2E[\Delta_n]} \right) \lambda^\ast / n. \quad (29)$$

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

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

Thus the inequality (29) holds with the above $\delta$. \hfill \Box