Algorithms Using Local Graph Features to Predict Epipemics

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Abstract

We study a simple model of epidemics where an infected node transmits the infection to its neighbors independently with probability \( p \). This is also known as the independent cascade or Susceptible-Infected-Recovered (SIR) model with fixed recovery time. The size of an outbreak in this model is closely related to that of the giant connected component in “edge percolation”, where each edge of the graph is kept independently with probability \( p \), studied for a large class of networks including configuration model [Molloy et al. 2011] and preferential attachment [Bollobás and Riordan 2003, Riordan 2005]. Even though these models capture the effects of degree inhomogeneity and the role of super-spreaders in the spread of an epidemic, they only consider graphs that are locally tree like i.e. have a few or no short cycles. Some generalizations of the configuration model were suggested to capture local communities, known as household models [Ball et al. 2009], or hierarchical configuration model [van der Hofstad et al. 2015].

Here, we ask a different question: what information is needed for general networks to predict the size of an outbreak? Is it possible to make predictions by accessing the distribution of small subgraphs (or motifs)? We answer the question in the affirmative for large-set expanders with local weak limits (also known as Benjamini-Schramm limits). In particular, we show that there is an algorithm which gives a \((1 - \epsilon)\) approximation of the probability and the final size of an outbreak by accessing a constant-size neighborhood of a constant number of nodes chosen uniformly at random. We also present corollaries of the theorem for the preferential attachment model, and study generalizations with household (or motif) structure. The latter was only known for the configuration model.

Keywords: Infection process, local weak convergence, contact-tracing, configuration model, preferential attachment, expanders, local features.

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1 Introduction

One of the central tasks of epidemiology is to predict the likelihood or the size of a nascent or future epidemic from observed data. In the simplest model, the Susceptible-Infected-Recovered (SIR) model with homogeneous mixing, it is assumed that all individuals have the same probability of infecting one another, and the predictions rely on a single parameter, the basic reproduction number. At the same time, it is known for decades, going back at least to the study of the AIDS epidemics [Gupta et al. 1989], that the underlying network of contacts and their structure play an important role in the spread of the infection.

From a mathematical point of view, the effect of network structure on the spread of an epidemic has been analyzed for many random network models, including Erdős-Renyi graphs [Neal 2003], configuration models [Decreusefond et al. 2012b, Janson et al. 2014], and preferential attachment models [Pastor-Satorras and Vespignani 2001, Berger et al. 2005]. These models offer important insights about the spread of the infection and especially the devastating effects of high degree nodes.

One may be tempted to use the above network models to predict the likelihood and size of an epidemic from observed data by first estimating the parameters of the model, and then using the resulting network to make predictions about the epidemic. But this approach faces several challenges. First of all, it is not even clear which class of models to use: configuration models, preferential attachment models, inhomogeneous random graphs [Bollobás et al. 2007] or variants of those allowing for community structure? And even if we could agree on a class of models, it is unclear how predictions may change under network misspecifications by the slightest amount.

In the setting of dense graphs, the question of network misspecification and robustness can be addressed using the notions of quasi-random graphs and graph limits. In particular, for dense, exchangeable networks, the Aldous-Hoover Theorem [Aldous 1981, Hoover 1979] determines the class of models to be considered, the estimation of the underlying (graphon) model can be framed as a well defined non-parametric estimation problem [Wolfe and Olhede 2013], and the theory of graph limits [Borgs et al. 2008; 2012] allows one to analyze deviations from these models in terms of the so-called cut-metric. However, this is not a feasible approach for bounded degree networks, because there is no single natural random model for graphs with bounded average degree.

Therefore, instead of formulating the problem as a network estimation problem, we take a different approach: we propose an algorithm, which predicts parameters like the threshold and the size of an epidemic by probing and observing local neighborhoods of random nodes,
and show that those predictions are asymptotically consistent if (a) the network converges in the weak local sense, and (b) is sufficiently connected or more precisely, a large-set expander. These assumptions are true for many of the random networks mentioned above. At the same time the predictions are robust in the sense that they are made without ever explicitly assuming or estimating an underlying random network model.

In what follows, we will describe the the key notions and definitions and set the stage for our two main theorems and algorithm.

Epidemic model and percolation: We consider a simple model where an infected node transmits the infection to its neighbors independently with probability \( p \). This is known as independent cascade [Kempe et al. 2003] and turns out to be equivalent to the Susceptible-Infected-Recovered (SIR) model with fixed recovery time [Kiss et al. 2017]. In the latter model, infected nodes stay infected for a fixed time (say one unit of time) and while infected, transmit the disease to neighbors with rate \( \lambda \). Thus, an infected vertex has an opportunity to infect any of its neighbors independently with probability \( p = \frac{\lambda}{\lambda+1} \).

The size of an outbreak in this model is closely related to that of the giant connected component in “edge percolation”, where each edge of the graph is kept independently with probability \( p \), studied for a large class of random network models including the configuration model [Molloy et al. 2011] and preferential attachment models [Bollobás and Riordan 2003, Riordan 2005]. Phrased in terms of the consequences for the spread of an epidemic, one of the main implications of the above line of work is that with high probability, an infection either dies out quickly (after reaching a constant number of nodes) or it spreads to a linear fraction of vertices. Our first theorem substantially generalizes these results using the notion of weak local limit for graphs, as defined below.

Local weak limit: Roughly speaking, a sequence of (possibly random) graphs \( \{G_n\}_{n \in \mathbb{N}} \) is said to have a \textit{local weak limit in probability}, if the distributions of the neighborhoods of randomly sampled vertices converge in probability. The limit is then a probability measure \( \mu \) on the space \( \mathcal{G}_* \) of rooted, locally finite, connected graphs (more precisely, on equivalence classes under graph isomorphisms which map roots into roots). We will use \((G, o)\) for a graph \( G \) with root \( o \) in \( \mathcal{G}_* \), where \( G \) should be considered unlabeled, except for the label \( o \) for the root.

Consider now a sequence of graphs \( \{G_n\}_{n \in \mathbb{N}} \) with graph limit \((G, o)\) distributed according to some \( \mu \). We will study the percolated graph \( G(p) \), the subgraph obtained from \( G \) by independently keeping each edge with probability \( p \), and the component of the root in \((G(p), o)\), to be denoted by \( C(o) \). As we will see, the probability \( \zeta(p) \) of \( C(o) \) being infinite,
\[ \zeta(p) = \mu\left(\mathbb{P}_{G(p)}(|C(o)| = \infty)\right) \], turns out to the limit of the probability that an infection starting from a random vertex in \( G_n \) leads to an infection – under some technical conditions. One of them will be what we refer to as smoothness of \( \mu \) at \( p \), defined as the continuity of \( \zeta(p) \) at \( p \).

The second one will be an expansion property for \( G_n \).

**Large-set edge expansion:** Given a graph \( G = (V, E) \) and a constant \( \epsilon < 1/2 \), define

\[
\phi(G, \epsilon) = \min_{A \subseteq V : |V| \leq |A| \leq |V|/2} \frac{e(A, V - A)}{|A|}
\]

where \( e(A, V - A) \) is the number of edges joining \( A \) to its complement. Call a graph \( G \) an \((\alpha, \epsilon, \bar{d})\) large-set (edge) expander if the average degree of \( G \) is at most \( \bar{d} \) and \( \phi(G, \epsilon) \geq \alpha \). A sequence of possibly random graphs \( \{G_n\}_{n \in \mathbb{N}} \) is called a large-set (edge) expander sequence with bounded average degree, if there exists \( \bar{d} \) and \( \alpha > 0 \) such that for any \( \epsilon \in (0, 1/2) \) the probability that \( G_n \) is an \((\alpha, \epsilon, \bar{d})\) large-set (edge) expander goes to 1 as \( n \to \infty \).

**Outbreaks and their asymptotics.** Let \( \mathcal{N}(G) \) be the random variable giving the number of nodes that eventually get infected if one uniformly random vertex in \( G \) was infected initially. Note that there are two sources of randomness for \( \mathcal{N}(G) \): the randomness of the infection process and the choice of a random seed. The next theorem shows that under certain assumptions, with high probability, either the infection dies out after infecting a constant number number of vertices or it reaches a linear fraction of vertices. More precisely, \( \frac{\mathcal{N}(G)}{n} \) converges to a distribution on \([0, 1]\) with one atom at zero and possibly a second atom in \((0, 1]\).

**Theorem 1.1.** Let \( \{G_n\}_{n \in \mathbb{N}} \) be a sequence of (possibly random) large-set expanders with bounded average degree that converges in probability in the local weak sense to \((G, o) \in G_*\) with distribution \( \mu \). Let \( p \in [0, 1] \), and assume that \( \mu \) is smooth at \( p \). Then

1. The final infection size \( \mathcal{N} \) in an SIR model with constant recovery time is either linear in \( n \) or of order \( O(1) \). Formally, if \( \omega(n) \) is any function such that \( \lim_{n \to \infty} \omega(n) = \infty \) and \( \lim_{n \to \infty} \omega(n)/n = 0 \), then \( \mathbb{P}\left(\omega(n) \leq \mathcal{N} \leq \frac{n}{\omega(n)}\right) \to 0 \), where \( \mathbb{P} \) denotes probabilities with respect to the infection process and the randomness of \( G_n \).

2. The random variable \( \mathcal{N}/n \) converges weakly in probability to the two-atom random variable \( \chi_p = \begin{cases} \zeta(p) & \text{with probability } \zeta(p), \\ 0 & \text{with probability } 1 - \zeta(p). \end{cases} \)

A few explanations are in order. First of all, the necessary conditions of the theorem are
relatively weak. In Section 3, we show that the popular network models including preferential attachment and configuration models satisfy them, even after incorporating additional community (or motif) structures. In particular the above theorem characterizes the size and probability of outbreaks for configuration model [Janson et al. 2014], preferential attachment (see Corollary 1.4), configuration model with community structure [Trapman 2007, Ball et al. 2010, van der Hofstad et al. 2015] and preferential attachment with communities (see Corollary 1.10). As far as we know, the results on preferential attachment (with or without communities) was not known in the literature.

More importantly, the graph sequences considered in the theorem do not have to be ‘perfectly’ drawn from a random model for the result to hold. In fact, given an arbitrary random graph model with smooth limit (a property which holds for most random graph models, except possibly at the threshold), they can be ‘quasi-random’ in the sense that the they are (random or) deterministic graphs with the same local limit. As long as the sequence is a large-set expander, the size and probability of an infection on the sequence will be the same as for the random model.

Finally, it is worth noting that some notion of connectivity is necessary for the above theorem to hold. This can be seen by comparing $d$-regular random graphs on $n$ nodes to the union of two disjoint $d$-regular random graphs on $n/2$ nodes that are connected with one edge as described in Remark 2.6.

Next, we will state the algorithmic implications.

**Algorithm for estimating the probability and size of outbreak.** Suppose that we do not have access to the underlying contact network $G$. Instead, we have access to a black-box algorithm that takes a constant $k = O(1)$ as an input and runs the SIR process starting from a uniformly random node. Then the algorithm returns whether $k$ other nodes get infected eventually. So, for each query we get a $0-1$ answer, 1 when starting an infection from the chosen vertex has reached $k$ other nodes, and 0 otherwise (see Algorithm 1).

Let $\tilde{N}(k, q)$ be the average of answers for $q$ independent queries to Algorithm 1 with $k$ as an input. We prove that for any $\epsilon > 0$, there exist constants $k_\epsilon$ and $q_\epsilon$ independent of $n$ such that $\tilde{N}(k_\epsilon, q_\epsilon)$ gives an $(1 - \epsilon)$-approximation of both the probability of an outbreak and the relative size of an outbreak.

**Theorem 1.2.** Let $\{G_n\}_{n \in \mathbb{N}}$ and $\zeta(p)$ satisfy the conditions in Theorem 1.1. Then for any given $\epsilon > 0$ there exist integers $k_\epsilon, q_\epsilon$, such that the average output of $q_\epsilon$ independent runs of Algorithm 1 with $k_\epsilon$ as an input is a $(1 - \epsilon)$-approximation of the probability and the size of an outbreak in an SIR model with constant recovery time. Formally, there exists an $n_\epsilon > 0$,
ALGORITHM 1: Local infection algorithm
A constant $k > 0$ and the contact network $G$.
Draw a uniformly random node $v$.
Find $B_k(v)$, the set of the nodes of distance at most $k$ from $v$.
Run SIR process in $B_k(v)$ starting from $v$:

- Initialize susceptible nodes $S = B_k(v) - \{v\}$, infected nodes $I = \{v\}$, and removed nodes $R = \emptyset$.
- while $I \neq \emptyset$ do
  - Let $u$ be the next node in $I$.
  - Remove infected neighbors of $u$ in $S$ and add them to $I$.
  - Remove $u$ from $I$ and add it to $R$.
- end
- if $|R| \geq k$ then
  - Return 1.
- else
  - Return 0.
- end

such that for all $n \geq n_\epsilon$

$$\mathbb{P}(|\tilde{N}(k_\epsilon, q_\epsilon) - \zeta(p)| \geq \epsilon) \leq \epsilon.$$ 

Here $\mathbb{P}$ denotes the probabilities first over the randomness of $G_n$ and then the infection process and the sampled vertices contributing to $\tilde{N}(k_\epsilon, q_\epsilon)$.

Note that while Theorem 1.2 requires that the graph sequence converges, we do not need to use the properties of or even know the limit graph. We can determine the size and the probability of an epidemics only by sampling the local neighborhoods of a constant number of nodes.

In the next section, Section 1.1, we show that our main theorems are applicable to many known random graph models. In addition, in Section 1.2, we introduce a new class of random graph model with community structure, generalizing several older models, and apply our result to the new set of models.

1.1 Application: Classical Random Graph Models

In the following section, we consider examples of graphs for which we can apply the results of Theorems 1.1 and 1.2. We show the following models converge in a local weak sense and $\zeta(p)$ on their limit is continuous for every $p \in [0, 1]$. 1. The preferential attachment model. 2. The configuration model.
1.1.1 Preferential Attachment Models

Preferential attachment models describe a dynamic population where each new individual contacts the older individuals proportional to their degree. More precisely, the model has a parameter \( m \in \mathbb{N} \), and is defined as follows. Starting from a connected graph \( G_0 \) on at least \( m \) vertices, a random graph \( G_t \) is defined inductively: given \( G_{t-1} \) and its degree sequence \( d_i(t-1) \), we form a new graph by adding one more vertex, \( v_t \), and connect it to \( m \) distinct vertices \( w_1, \ldots, w_m \in V(G_{t-1}) \) by first choosing \( w_1, \ldots, w_m \in V(G_{t-1}) \) i.i.d with distribution \( \mathbb{P}(w_s = i) = \frac{d_i(t-1)}{2|E(G_{t-1})|}, s = 1, \ldots, m \), and then conditioning on all vertices being distinct (thus avoiding multiple edges). We denote the resulting random graph sequence by \( (PA_{m,n})_{n \geq 2m+1} \), and following [Berger et al. 2014], we call the version of preferential attachment we defined above the conditional model, while the model where the conditioning step is left off will be called the independent model.

The next lemma, which is a consequence of previous work on the preferential attachment graphs, will allow us to apply Theorems 1.1-1.2 to \( PA_{m,n} \).

**Lemma 1.3.** Let \( m \geq 2 \), and for a positive integer \( n \geq 2m + 1 \) let \( PA_{m,n} \) be the conditional preferential attachment graph defined above. Then the following holds. 1. There exists a distribution \( \mu \) on \( G_* \) such that the sequence \( \{PA_{m,n}\}_{n \geq 2m+1} \) converges in the local weak sense to \( (G,o) \) distributed as \( \mu \). Also, for all \( p \in [0,1] \) the percolation function \( \zeta(p) = \mu\left(\mathbb{P}_{G[p]}(C(o) = \infty)\right) \) is continuous.

2. Then there exists some \( \alpha > 0 \) independent from \( n \) such that for all \( \epsilon \in (0,1/2) \), with probability tending to 1, \( \{PA_{m,n}\}_{n \geq 2m+1} \) is an \( (\alpha, \epsilon, 2m) \) large-set expander.

The local weak convergence of preferential attachment models is well-established in [Berger et al. 2014], where they showed the limit is a Pólya-point process. Moreover, the continuity of the survival probability and the positive expansion of \( PA_{m,n} \) was shown in [Alimohammadi et al. 2021]. As a consequence of the above lemma the size and the probability of an outbreak is local under the preferential attachment model.

**Corollary 1.4.** Let \( m \geq 2 \), and let \( \{G_n\}_{n \geq 2m+1} = \{PA_{m,n}\}_{n \geq 2m+1} \) be the conditional preferential attachment graph defined above. Then the conclusions of Theorems 1.1 and 1.2 hold for all \( p \in [0,1] \).

**Proof.** As a direct consequence of Lemma 1.3 we can apply Theorems 1.1 and 1.2. \( \square \)
1.1.2 Configuration Model

The common way to construct a random graph given a degree sequence is the configuration model, introduced by [Bollobás 2001]. Let \( d_n = (d_1, \ldots, d_n) \) be a graphical degree sequence, i.e., there exists at least one simple graph with this degree sequence. Then to construct the configuration model \( CM(d_n) \), consider \( d_i \) half-edges for the vertex \( i \). The half-edges are then matched uniformly, in general resulting in a multi-graph with self-loops and multiple edges.

The uniform configuration model is defined as the random graph model whose samples are uniformly random among all simple graphs with degree sequence \( d_n \). We denote such a sample by \( CM^*(d_n) \). To generate a sample from the uniform model, one often first generates a sample from the so-called configuration model. It is well known that if the degree sequence is graphical, conditioning \( CM(d_n) \) to be a simple graph, gives a sample from the uniform model \( CM^*(d_n) \). See Chapter 7.5 in [van der Hofstad 2016] for the definition and properties of the uniform model and its relationship to the configuration model.

In order to apply our results to the configuration model, we first need to describe the conditions for the existence of the local weak limits. To formulate it, let \( D_n \) be the degree of a uniform random node in the degree sequence \( d_n \). Recall the definition of the empirical distribution \( F_n \) of the sequence \( d_n \),

\[
F_n(x) = \frac{1}{n} \sum_{j \in [n]} 1_{d_j \leq x}.
\]

**Condition 1.5.** Let \( d_n = (d_1, \ldots, d_n) \) be a graphical degree sequence. Then there exists a random variable \( D \) such that

(i) \( P(D \geq 3) = 1 \), and as \( n \to \infty \), \( D_n \overset{d}{\to} D \), and \( \mathbb{E}[D_n] \to \mathbb{E}[D] < \infty \).

(ii) The empirical distribution \( F_n \) satisfies, \( [1 - F_n](x) \leq c_F x^{-\tau - 1} \), for some \( c_F > 0 \) and \( \tau \in (2,3) \).

**Theorem 1.6.** Let \( \{G_n\}_{n \in \mathbb{N}} = \{CM^*(d_n)\}_{n \in \mathbb{N}} \), where \( \{d_n\}_{n \in \mathbb{N}} \) is a graphical degree sequence satisfying Condition 1.5. Then the conclusions of Theorems 1.1 and 1.2 hold for all \( p \in [0,1] \).

**Proof.** The expansion of \( CM^*(d_n) \) was shown in Lemma 12 in [Abdullah et al. 2012] under the Condition 1.5 (i). Also, the local weak convergence of \( CM^*(d_n) \) to a uni-modular branching processes was established under the Condition 1.5 (i)-(ii) in Theorem 4.5 in [van der Hofstad 2020]. Since the limit is a branching process the continuity of survival
probability is already known (see e.g., [Broman and Meester 2008] for a more general result). Hence, all the conditions needed for Theorems 1.1 and 1.2 hold for \( \{CM^*(d_n)\}_{n \in \mathbb{N}} \).

### 1.2 Application: Motif-Based Graph Models

One of the important characteristics of real-world networks is that they contain many short cycles [Scott 1988]. However, in most random graph models including the configuration model and preferential attachment model, the opposite is true: the neighborhood of a typical node looks like a tree.

One approach for addressing this problem is to incorporate the community structure directly, for example by replacing the nodes with dense graphs. For example, Trapman [Trapman 2007] replaces each vertex of degree \( k \) in \( G_n \) by a complete graph of size \( k \) with some fixed probability. The complete graphs represent households, where each individual interact with all others in their household, and has exactly one contact outside of the household. A more general model by Ball et. al. [Ball et al. 2009] extends the configuration model by allowing for drawing households independently from a family of graphs.

We extend this framework. Our model has two ingredients: a network of external connections (which at the current level of generality can be arbitrary), and a distribution on small graphs (motifs), describing internal connections of a group of people (see Fig. 1).

![Figure 1: A motif-based graph with 1) an internal level representing connections (solid edges) between individuals in one motif (colored areas), and 2) an external level representing connections (dashed edges) between motifs.](image)

Let us first define the notion of a motif, which is a pair \( M = (F, (d^\text{ext}_v)_{v \in V(F)}) \) contains (i) a simple graph \( F \), giving the internal connection of the nodes in the motif, and (ii) a collection of external degrees, \( (d^\text{ext}_v)_{v \in V(F)} \), one for each vertex in \( F \). For a motif \( M \), let \( d(M) = \sum_{v \in F} d^\text{ext}_v \) be the total external degree of the motif \( M \), and \( v(M) = |F| \) be number of vertices in the motif.

Now, to define a motif-based graph, specify a collection of probability distributions \( \mathcal{M}_d \) over motifs \( M \) with \( d(M) = d \), one for each \( d \). Then, given such a collection, plus an arbitrary
external graph $G^{ext}$ on $n$ vertices, replace all vertices of degree $d$ in $G^{ext}$ independently at random by a motif drawn from $M_d$, resulting in a larger graph $G$ containing precisely $n$ motifs.

**Condition 1.7.** (i) (Internal regularity) Let $M$ be the space of all motifs. Then there exists a constant $S_{\text{max}} < \infty$ such that $\sup_{M \in M} v(M) \leq S_{\text{max}}$.

(ii) (External regularity) There exists a probability distribution $\mu^{ext}$ on $G_*$ such that the sequence of (possibly random) external graphs $\{G^{ext}_n\}_{n \in \mathbb{N}}$ with a bounded average degree converges in the local weak sense to $(G^{ext}, o) \in G_*$ with distribution $\mu^{ext}$.

The combination of internal and external regularities is sufficient for local weak convergence.

**Lemma 1.8.** Let $\{G_n\}_{n \in \mathbb{N}}$ be a sequence of motif-based graphs satisfying the Condition (i) and (ii). Then there exists a probability distribution $\mu$ on $G_*$ such that $\{G_n\}_{n \in \mathbb{N}}$ converges in the local weak sense to $(G, o)$ drawn from distribution $\mu$.

**Corollary 1.9.** Let $\{G_n\}_{n \in \mathbb{N}}$ be a sequence of motif-based graphs satisfying the Condition (i) and (ii). If the external graph is a large set expander, then the conclusions of Theorems 1.1 and 1.2 hold for all $p \in [0, 1]$ for which $\zeta(p)$ is continuous.

On the way of proving this corollary, we prove a general result that might be of independent interest: large-set edge expansion along with the existence of local weak limit implies large-set vertex expansion (see Lemma 3.2). Finally, we consider special cases of the motif-based model where the external graph has the same limit as one of the models discussed in Section 1.1.

**Corollary 1.10** (Motif-Based Preferential Attachment). Let $m \geq 2$, and let $\{G_n\}_{n \geq 2m+1}$ be a sequence of motif-based graphs such that $G^{ext}_n = PA_{m,n}$. If the motif-distribution satisfies Condition (i), then the conclusions of Theorems 1.1 and 1.2 hold for all $p \in [0, 1]$.

**Corollary 1.11** (Motif-Based Configuration Model). Let $\{G_n\}_{n \in \mathbb{N}}$ be a sequence of motif-based graphs such that $G^{ext}_n = CM^*(d_n)$ for a graphical degree sequence $\{d_n\}_{n \in \mathbb{N}}$ satisfying Condition 1.5. If the motif distribution satisfies Condition (i), then the conclusions of Theorems 1.1 and 1.2 hold for all $p \in [0, 1]$.

Percolation on general household model with external configuration model was studied by Hofstad et. al. [van der Hofstad et al. 2015]. In particular, they proved that if the expected
size of household size and the average degree is finite, then the size of the giant after percolation converges in probability. They also compared the spread of an epidemics on motif-based configuration model with real-world networks empirically [Stegehuis et al. 2016]. In Section 2, we will give a different proof for the result in [van der Hofstad et al. 2015] by showing the large-set expansion and the smoothness of the limit motif-based configuration models. Our proof also applies to motif-based preferential attachment model along with other motif-based models, as stated in Corollary 1.9.

1.3 Other Related Work

Epidemics on networks. The study of epidemics on networks has got much attention in different communities. The work of [Newman et al. 2001] led to heuristics differential equations describing the evolution of SIR process on configuration models [Volz 2008, Volz and Meyers 2009]. Later works by [Decreusefond et al. 2012a, Janson et al. 2014] made the heuristics rigorous for the configuration model. In some special cases, the SIR process has been studied on trees [Sharkey et al. 2015] and grids [N’zi et al. 2019]. See the book [Kiss et al. 2017] for the results in theoretical biology and physics. The discrete version of the Markovian SIR process that we consider, is also referred to as the Reed-Frost model (see e.g., [Picard and Lefevre 1990]).

Also related to our work is the result of Ball et. al. [Ball et al. 2009] who study epidemics on networks in which the motifs are complete graphs and derive the expected size of the outbreak under the general SIR model [Ball et al. 2010].

Percolation. The study of percolation on expanders has recently received much attention in the probability community. In [Alon et al. 2004], it was shown that on bounded degree expanders, there exists at most one linear size component (giant). If in addition, one assumes a weak local limit, one obtains locality of the threshold for the appearance of a giant [Benjamini et al. 2011, Sarkar 2018], in the sense that it can be inferred from the limit. This result was generalized to Cayley graphs [Martineau and Tassion 2017].

The relative size of the giant, which is an important technical ingredients has only been studied recently. Earlier work studied the size on random trees [Bertoin and Bravo 2015], and hypercubes [van der Hofstad and Nachmias 2017], as well as the locality of the size of the giant on expanders for the case of bounded regular degree with high girth [Krivelevich et al. 2020]. In this case, the relative size of the giant is given by the survival probability of a percolated branching process. Here, our main input is the work of [Alimohammadi et al.}
where they proved convergence of the relative size of the giant for expanders with local weak limits, and applied their result to preferential attachment models.

Network Modeling and Estimation The question of network misspecification and robustness has been studied in dense graphs using the notion of quasi-random graphs and graph limits. For dense, exchangeable networks, the Aldous-Hoover Theorem [Aldous 1981, Hoover 1979] determines the class of models to be considered: it is the class of dense, inhomogeneous random graphs or graphon models, see [Orbanz and Roy 2014] for a modern treatment of this relationship. Misspecifications, or closeness to a random model can then be formulated as closeness in the cut-metric, with (not necessarily random) models which asymptotically “look” like an inhomogeneous random graph being precisely those which converge to the same graphon [Borgs et al. 2008; 2012]. In this context, estimation becomes a non-parametric estimation problem which has been well studied, see [Wolfe and Olhede 2013] where this problem was first formally formulated as a graphon estimation problem (note, however, that the basic idea is much older, and goes back to at least [Bickel and Chen 2009]). There are generalizations of this approach for sparse networks with divergent average degree, see [Borgs and Chayes 2017] for an overview, but there is no one natural random model for graphs with bounded average degree.

2 Proof of the Locality of Infection Processes

The first observation needed for proving Theorem 1.2 is that infection processes with fixed recovery times can be coupled to unoriented percolation. Section 2.1 is on this coupling. It will prove that when the relative size of the giant after percolation is concentrated, then the infection is also “local” in the sense that it can be read off from its local weak limit. In Section 2.2, we shift our focus to percolation, and the use of some recent results to show that first the size of the giant in large-set expanders converges to its limit, and second the size of the connected component of a random node can be bounded by a constant with high probability. Building upon the coupling and the results on percolation, we prove Theorems 1.1 in Section 2.3 and Theorem 1.2 in Section 2.4.

2.1 Coupling Infection Processes to Percolation

Suppose more than one node can be infected initially and let \( v_1, \ldots, v_k \) be the set of initially infected nodes. Also, let \( \mathcal{N}(v_i) \) be the set of nodes getting the infection eventually from node
Lemma 2.1. Given any graph $G$ of size $n$ and $k \leq n$, let $v_1, \ldots, v_k$ be the initial set of infected nodes in an SIR process with parameter $p$. Then for any $n' < n$, 
\[ \mathbb{P}\left( \sum_{i=1}^{k} \mathcal{N}(v_i) = n' \right) = \mathbb{P}_{G(p)}\left( | \cup C(v_i) | = n' \right). \]

Proof. To express an instance of SIR process, for each edge $(u, w) \in E(G)$ draw $t_{u,w}$ from $\exp(\frac{p}{1-p})$. The random variable $t_{u,w}$ can be viewed as the contact time of $u$ and $w$ after either of $u$ or $w$ gets infected first. If $t_{u,w} > 1$, then the contact time happens after the recovery of the endpoint, so in this case, let $t_{u,w} = \infty$. Moreover, for the convention, if an edge $(u, w)$ does not exist let $t_{u,w} = \infty$. Note that each edge in $G$ is set to $\infty$ independently with probability $1-p$. So, the set of edges with a finite value can be coupled to the set of edges that are retained in $G(p)$. So, it remains to show random variables $t_{u,v}$ specify a unique SIR process.

To describe the SIR process using the random variables $t_{u,v}$, let $t_v$ be the time that the node $v$ gets infected. Hence, for the initial infected nodes $t_{v_1} = \cdots = t_{v_k} = 0$. Start from time $t = 0$. For any time $t$, let $I_t$ be the set of infected nodes that their recovery times have not passed yet. Recall that the recovery time of the node $v$ is $t_v + 1$ by the definition of the SIR process. Also, let $N_S(I_t)$ be the set of susceptible neighbors of $I_t$ (the neighbors that are not infected yet). For each node $u \in N_S(I_t)$, let $t_u = \min_{v \in I_t} (t_v + t_{v,u})$, where the minimum is over all nodes $f u$ in $I_t$. Since all the non-neighbors have the contact time of $\infty$, they will affect $t_u$.  

Now, by the choice of contact times, if $t_u$ is finite, then it is infected before the time $t_u$. Let $u \in N_S(I_t)$ be the node with minimum infection time, i.e., $u = \arg\min_{u \in N_S(I_t)} t_u$. If $t_u < \infty$, add $u$ to the set of infected nodes $I_{t'}$, for all $t_u \leq t' < t_u + 1$. In addition, increase the time $t$ to $t_u$ and repeat the above process until we get to a time that the set of infected nodes are empty.

In the above procedure, we use each $t_{u,v}$ only for updating from at most one side. This is because either $v$ gets infected before $u$ or $u$ before $v$. So, a node is infected in the SIR process if and only if it is reachable by one of $v_1, v_2, \cdots, v_k$ in the $G(p)$.
2.2 Size of the Giant in Percolation

With the coupling of the infection process and the percolation in hand, the next step is the concentration of the giant component. It was shown in [Alimohammadi et al. 2021] that the relative size of the largest component for percolation on large-set expanders satisfying conditions in Theorem 1.1 converges in probability to $\zeta(p)$.

This is not enough to prove our main theorems. In fact, we need to bound the size of the connected component of a random node which is not in the largest component. In fact, concentration of the size of the giant is enough to prove the locality of infection processes. For that purpose, we give the following definition.

Definition 2.2 (Graphs with converging giant). Let $p \in [0, 1]$, and let $\mu$ be a probability distribution on $G_\ast$. A sequence $\{G_n\}_{n \in \mathbb{N}}$ of (possibly random) graphs with the local weak limit $(G, o) \sim \mu$ is called a sequence of graphs with a converging giant component if

$$\frac{|C_1|}{n} \xrightarrow{p} \zeta(p),$$

where $\zeta(p) = \mu(\mathbb{P}_{G(p)}(|C(o)| = \infty))$.

By a result of van der Hofstad [van der Hofstad 2021], it is easy to see that if a random node in graphs with converging giant is outside the largest component then its component size is $O_{k,p}(1)$.

Proposition 2.3. Let $\{G_n\}_{n \in \mathbb{N}}$ be a sequence of graphs with a converging giant. Then for a uniform random node $v$, if $\zeta(p) > 0$,

$$\lim_{k \to \infty} \lim_{n \to \infty} \mathbb{P}\left(v \notin C_1, \text{ and } |C(v)| \geq k\right) = 0,$$

and if $\zeta(p) = 0$, then $C(v) = O_{k,p}(1)$. Further, for two uniform random nodes $u$ and $v$,

$$\lim_{k \to \infty} \lim_{n \to \infty} \frac{1}{n^2} \mathbb{E}(|C(v)|, |C(u)| \geq k, C(v) \neq C(u)) = 0.$$

(2.1)

Proof of Proposition 2.3. By the sufficiency condition in Theorem 2.2 of [van der Hofstad 2021], for any graph sequence with a converging giant we know,

$$\lim_{k \to \infty} \lim_{n \to \infty} \frac{1}{n^2} \mathbb{E}(|C(v)|, |C(u)| \geq k, C(v) \neq C(u)) = 0.$$

Then it remains to show $C(v) = O_{k,p}(1)$ for $v \notin C_1$. The case that $\zeta(p) = 0$ directly
follows from (2.1). In the case that \( \zeta(p) > 0 \), choose \( 0 < \delta < \zeta(p) \). Then by the condition of converging giant for large enough \( n \) with high probability \( |C_1| \geq \delta n \). Therefore, with probability larger than \( \delta \) a random node lies in \( C_1 \) and

\[
\lim_{k \to \infty} \lim_{n \to \infty} \frac{1}{n^2} \mathbb{E}(|C(v)|, |C(u)| \geq k, C(v) \neq C(u)) \geq \lim_{k \to \infty} \lim_{n \to \infty} \delta \mathbb{P}(|C(v)| \geq k, v \not\in C_1),
\]

where in the right hand side the probability is over a uniform random node, and the left hand side goes to zero by (2.1).

Combining this with Theorem 1.1 in [Alimohammadi et al. 2021] we immediately get the following corollary.

**Corollary 2.4.** Let \( \mu, \{G_n\}_{n \in \mathbb{N}}, \) and \( \zeta \) obey the assumptions of in Theorem 1.1. Let \( C_i \) be the \( i \)th largest component of \( G_n(p) \). If \( \zeta \) is smooth with respect to \( p \), then

\[
\frac{|C_1|}{n} \xrightarrow{p} \zeta(p),
\]

with \( \xrightarrow{p} \) denoting convergence in probability with respect to both \( \mu \) and percolation. Further, if \( v \) is chosen uniformly at random then

\[
\lim_{k \to \infty} \lim_{n \to \infty} \mathbb{P}(v \not\in C_1, \text{ and } |C(v)| \geq k) = 0,
\]

and if \( \zeta(p) = 0 \), then \( |C(v)| = O_{k,p}(1) \).

In the following sections, we will lift the assumptions of the large-set expansion and the smoothness of \( \mu \) in Theorems 1.1 and 1.2 by assuming that the graph sequence have a converging giant.

### 2.3 Size of the Outbreak is Two-Atom

We will show that Theorem 1.1 holds when the sequence of graphs have a converging giant.

**Lemma 2.5** *(Generalization of Theorem 1.1)*. Let \( \{G_n\}_{n \in \mathbb{N}} \) be a sequence with a converging giant with the limit distributed as \( \mu \) on \( \mathcal{G}^* \). Then

1. If \( \omega(n) \) is such that \( \lim_{n \to \infty} \omega(n) = \infty \) and \( \lim_{n \to \infty} \omega(n)/n = 0 \), then \( \mathbb{P}(\omega(n) \leq \mathcal{N} \leq \frac{n}{\omega(n)}) \to 0 \), where \( \mathbb{P} \) denotes probabilities with respect to the infection process and the randomness of \( G_n \).

2. Let \( \chi_p \) be the random variable that is equal to \( \zeta(p) \) with probability \( \zeta(p) \) and equal to 0 with probability \( 1 - \zeta(p) \). Then \( \mathcal{N}/n \) converges weakly in probability to \( \chi_p \).
Proof. Recall that by Lemma 2.1, \( \mathcal{N} \) is equal to the size of the connected component of a uniform random node,

\[
\mathbb{P}\left( \frac{n}{\omega(n)} \geq \mathcal{N} \geq \omega(n) \right) = \mathbb{P}_{G_n(p), \mathcal{P}_n} \left( \frac{n}{\omega(n)} \geq |C(v)| \geq \omega(n) \right),
\]

where the second probability is both over percolation and choosing a random node.

First, assume \( \zeta(p) = 0 \). Then by Proposition 2.3,

\[
\lim_{k \to \infty} \lim_{n \to \infty} \mathbb{P}_{G(n)}(|C(v)| \geq k) = 0.
\] (2.2)

Then for any increasing function \( \omega(n) \) with \( \lim_{n \to \infty} \omega(n) = \infty \), \( \mathbb{P}(|C(v)| \geq \omega(n)) \to 0 \). To see this, fix some \( \epsilon > 0 \) and \( n \), and let \( k = \omega(n) \). Then by (2.2), there exists an \( n_0 > 0 \) such that for all \( n' \geq \max(n_0, n) \), we have \( \mathbb{P}_{G(n')}(|C(v)| \geq \omega(n)) \leq \epsilon \). Then since \( \omega \) is increasing, for \( n' \geq \max(N, n) \)

\[
\mathbb{P}_{G(n')}(|C(v)| \geq \omega(n')) \leq \mathbb{P}_{G(n')}(|C(v)| \geq \omega(n)) \leq \epsilon,
\]

which proves the claim in the case that \( \zeta(p) = 0 \). Now, since the graph sequence have a converging giant if \( \zeta(p) > 0 \), then there exists \( \epsilon > 0 \) such that for large enough \( n \), \( |C_1| \geq \epsilon n \). Therefore, if \( v \in C_1 \) then for large enough \( n \), \( |C(v)| \geq \frac{n}{\omega(n)} \). Then again by Proposition 2.3 and similar to above argument it is easy to see that

\[
\mathbb{P}_{G_n(p), \mathcal{P}_n}(v \notin C_1 \text{ and } |C(v)| \geq \omega(n)) \to 0.
\]

This proves part 1.

So, it remains to prove part 2. Again by Lemma 2.1,

\[
\lim_{k \to \infty} \lim_{n \to \infty} \mathbb{P}(|\mathcal{N} \geq k) = \lim_{k \to \infty} \lim_{n \to \infty} \mathbb{P}_{G_n(p), \mathcal{P}_n}(|C(v)| \geq k).
\]

Then consider two cases. First, assume \( \zeta(p) = 0 \). Fix some \( \epsilon > 0 \). Proposition 2.3, implies that there exists \( K_0 \) and \( N_0 \) such that for all \( k \geq K_0 \) and \( n \geq N_0 \)

\[
\mathbb{P}(\mathcal{N} \geq k) \leq \epsilon.
\]
Given $\epsilon' > 0$, let $n \geq \max(N_0, ke^{-1})$, then we have

$$\mathbb{P}(\frac{N}{n} \geq \epsilon') \leq \mathbb{P}(\frac{N}{n} \geq \frac{k}{n}) \leq \epsilon,$$

which proves Part 2 in the first case.

Now, assume $\zeta(p) > 0$. For a fixed $\epsilon \in (0, \zeta(p)/2)$, by Lemma 2.1,

$$\mathbb{P}(\frac{N}{n} \geq \epsilon) = \mathbb{P}_{G_n(p), P_n}\left(\frac{|C(v)|}{n} \geq \epsilon \right).$$  \hspace{1cm} (2.3)

Moreover, by Proposition 2.3, if a random node has a linear sized component then it is in the largest component with high probability, i.e., for any $\epsilon' > 0$,

$$\mathbb{P}_{G_n(p)}\left(\mathbb{P}_{P_n}\left(\frac{|C(v)|}{n} \geq \epsilon \right) - \mathbb{P}_{P_n}(v \in C_1, and \frac{|C(v)|}{n} \geq \epsilon) \right) \to 0. \hspace{1cm} (2.4)$$

It is obvious that,

$$\mathbb{P}_{G_n(p), P_n}\left(v \in C_1, and \frac{|C(v)|}{n} \geq \epsilon \right) = \mathbb{P}_{G_n(p), P_n}\left(\frac{|C_1|}{n} \geq \epsilon \right). \hspace{1cm} (2.5)$$

Therefore by the converging giant and (2.3), (2.4), and (2.5)

$$\mathbb{P}(\frac{N}{n} \geq \epsilon) \to \zeta(p). \hspace{1cm} (2.6)$$

Similarly, be the coupling in Lemma 2.1,

$$\mathbb{P}\left(\zeta(p) - \epsilon \geq \frac{N}{n} \leq \epsilon \right) = \mathbb{P}_{G_n(p), P_n}\left(\zeta(p) - \epsilon \geq \frac{|C(v)|}{n} \geq \epsilon \right).$$

Now, again, $\mathbb{P}_{P_n}(\zeta(p) - \epsilon \geq \frac{|C(v)|}{n} \geq \epsilon)$ converges in probability to the case that the random node $v$ is in $C_1$ and the same inequalities for $|C(v)|$ hold. However, by the converging giant condition we know that the probability that $\frac{|C_1|}{n} \leq \zeta(p) - \epsilon$ goes to zero. Therefore,

$$\mathbb{P}\left(\zeta(p) - \epsilon \geq \frac{N}{n} \geq \epsilon \right) \to 0. \hspace{1cm} (2.7)$$

To finish the proof of part 2, let $f : [0, 1] \to \mathbb{R}^+$ be any given continuous function bounded by $B > 0$. Since it is continuous, for any $\epsilon' > 0$ there exists $\delta$ such that $|f(x) - f(\zeta(p))| \leq \epsilon'$ for any $x \in (\zeta(p) - \delta, \zeta(p) + \delta)$, and also $|f(x) - f(0)| \leq \epsilon'$ for any $x \in [0, \delta)$. Then to find the expectation of $f$, let $A_\delta$ be the event that $\frac{N}{n} \leq \delta$, let $A_{\zeta(p)}$ be the event that $|\frac{N}{n} - \zeta(p)| \leq \delta$,
and let $A'$ be the event that none of $A_{\zeta(p)}$ and $A_{\delta}$ happen. Then

$$\mathbb{E}[f\left(\frac{N}{n}\right)] = \mathbb{E}[f\left(\frac{N}{n}\right) | A_{\delta}] \mathbb{P}(A_{\delta}) + \mathbb{E}[f\left(\frac{N}{n}\right) | A_{\zeta(p)}] \mathbb{P}(A_{\zeta(p)}) + \mathbb{E}[f\left(\frac{N}{n}\right) | A'] \mathbb{P}(A').$$

Similarly, we can write $\mathbb{E}[f(\chi_{p})]$. Therefore,

$$|\mathbb{E}\left[f\left(\frac{N}{n}\right)\right] - \mathbb{E}[f(\chi_{p})]| \leq |\mathbb{E}\left[f\left(\frac{N}{n}\right) | A_{\delta}\right] \mathbb{P}(A_{\delta}) - f(0)(1 - \zeta(p))|$$

$$+ |\mathbb{E}\left[f\left(\frac{N}{n}\right) | A_{\zeta(p)}\right] \mathbb{P}(A_{\zeta(p)}) - \zeta(p)f(\zeta(p))| + |\mathbb{E}\left[f\left(\frac{N}{n}\right) | A'\right] \mathbb{P}(A')|$$

$$\leq |f(0)(\mathbb{P}(A_{\delta}) - (1 - \zeta(p)))| + |f(\zeta(p))(\mathbb{P}(A_{\zeta(p)}) - \zeta(p))| + \epsilon| + B\mathbb{P}(A').$$

Now, the convergence of $\mathbb{P}(A_{\delta})$ to $1 - \zeta(p)$ proved in (2.6) and $\mathbb{P}(A_{\zeta(p)})$ to $\zeta(p)$ given in (2.7) implies the convergence of $\mathbb{P}(A')$ to 0 and finishes the proof.

**Proof of Theorem 1.1.** The proof is a direct implication of Lemma 2.5 and Corollary 2.4. □

**Remark 2.6.** The local weak convergence of the graph sequence $\{G_{n}\}_{n \in \mathbb{N}}$ alone is not sufficient to read off the relative size of the outbreak from its limit. We can see this by comparing two graph sequences. For the first one, consider a graph sequence $\{H_{n}\}_{n \in \mathbb{N}}$ made by connecting two $d$-regular random graph components of size $\left\lfloor \frac{n}{2} \right\rfloor$ with one edge. For the second sequence, consider $\{G_{n}\}_{n \in \mathbb{N}}$, where $G_{n}$ is a $d$-regular random graph of size $n$. The local weak limit of both $\{H_{n}\}_{n \in \mathbb{N}}$ and $\{G_{n}\}_{n \in \mathbb{N}}$ is a $d$-regular tree.

However, in $H_{n}$ with probability at least $1 - p$ the edge between the two $d$-regular component is removed, and the relative size of infection will be roughly $\frac{\zeta(p)}{2}$. While there is also a chance that the two giant component becomes connected and result in a giant of the relative size $\zeta(p)$. So, in this case the size of an outbreak will have 3 atoms instead.

### 2.4 Analysis of Algorithm 1

Similar to the previous section, we will show that Algorithm 1 works whenever the graph sequence has a converging giant. Again, we use the coupling in Lemma 2.1 so we can focus only on the connected components after edge percolation. Then in graphs with a converging giant we know that, if a random node is not in the largest component, then the size of its component is $O_{k, p}(1)$. So, if after the percolation or equivalently the infection process, the size of the connected component of the starting point is larger than $k$, then with high
probability it lies in the giant component. Following that, a simple Chernoff bound gives
the desired result.

**Lemma 2.7** (Generalization of Theorem 1.2). Let \( \{G_n\}_{n \in \mathbb{N}} \) be a graph sequence with a
converging giant with the limit distributed as \( \mu \) on \( \mathcal{G}_* \). Then for any given \( \epsilon > 0 \) there exist
integers \( k_\epsilon, q_\epsilon, N_\epsilon \), such that for all \( n \geq N_\epsilon \)
\[
\mathbb{P}(|\tilde{N}(k_\epsilon, q_\epsilon) - \zeta(p)| \geq \epsilon) \leq \epsilon.
\]
Here \( \mathbb{P} \) denotes probabilities first over the randomness of \( G_n \) and then the infection process
and the sampled vertices contributing to \( \tilde{N}(k_\epsilon, q_\epsilon) \).

*Proof.* Fix some \( \epsilon \). First consider the case that \( \zeta(p) > 0 \). By the assumption of converging
giant, there exist \( k_\epsilon \) and \( N_\epsilon \) such that for \( n \geq N_\epsilon \),
\[
|C_{\epsilon}(\frac{|C_{\epsilon}|}{n} - \zeta(p))| \leq \frac{\epsilon}{3}.
\]
Then by Proposition 2.3
\[
\mathbb{P}(|C(v)| \geq k_\epsilon, \text{ and } v \not\in C_1) \leq \frac{\epsilon}{3}.
\]
(2.8)

We need to make sure that when we sample \( q \) nodes, their \( k \) neighborhoods are disjoint
with high probability. So, running the SIR process in each neighborhood is independent.
Let \( v_1, \ldots, v_q \) be the sampled initial nodes, and \( X_1, \ldots, X_q \in \{0, 1\} \) be the outputs of the
Algorithm 1. Let \( A_q \) be the event that the neighborhoods of \( v_1, \ldots, v_q \) are disjoint. We claim
that for large enough \( n \)
\[
\mathbb{P}(A_q) \geq 1 - q^2 \frac{\log n}{n} - \frac{\epsilon}{3}.
\]
(2.9)

Then given \( A_q \), infection process in \( B_k(v_1), \ldots, B_k(v_q) \) are independent as well since the
random variable drawn for edges are disjoint. Therefore,
\[
\mathbb{P}(X_1, \ldots, X_q | A_q) = \prod_{i=1}^{q} \mathbb{P}(X_i | A_q),
\]
and we will be able to use Chernoff bound to give concentration bounds. Before that, we
prove (2.9).

Now, to prove (2.9), define \( V_{r, \Delta} \) as the set of set of nodes such that the maximum degree
in their \( r \) neighborhood is at most \( \Delta \). Since the limiting graph \( (G, o) \) is locally finite, for all
\( \epsilon > 0 \), there exists \( \Delta < \infty \) and \( N'_\epsilon < \infty \) such that for \( n \geq N'_\epsilon \), with probability \( 1 - \frac{\epsilon}{4} \) we have
\[
|\frac{|V_{r, \Delta}|}{n}| \geq 1 - \frac{\epsilon}{4}.
\]
Let \( E_\epsilon \) be the event that \( |\frac{|V_{r, \Delta}|}{n}| \geq 1 - \frac{\epsilon}{4} \), that \( \phi(G_n, \epsilon) \geq \alpha \), and that
\( G_n \) has average degree at most \( \bar{d} \). Increasing \( N_\epsilon \) if needed, we have that for \( n \geq N_\epsilon \), \( E_\epsilon \) has
probability at least $1 - \epsilon/3$. Given $E_\epsilon$, then by a union bound

$$\mathbb{P}(A_q \text{ does not happen}) \leq \mathbb{P}(A_q \text{ does not happen} \mid E_\epsilon) + \mathbb{P}(E_\epsilon) \leq q^2 \frac{\Delta k}{n} + \frac{\epsilon}{3}.$$ 

Since $q$ and $\Delta$ are independent from $n$, by choosing $n$ large enough we get (2.9).

To finish the proof, recall that $\tilde{N}(k, q) = \sum_{i=1}^{q-1} X_i$. Also, since $\zeta(p) > 0$, for large enough $n$ we know $|C_1| \geq k$. With this and the definition of converging giant

$$\zeta(p) - \epsilon \leq \frac{|C_1|}{n} \leq \mathbb{P}(X_i = 1).$$

Then combining the last equation with (2.8),

$$\zeta(p) - \epsilon \leq \mathbb{P}(X_i = 1) \leq \frac{|C_1|}{n} + \epsilon \leq \zeta(p) + 2\epsilon.$$

Therefore, $|\mathbb{E}[X_i] - \zeta(p)| \leq 2\epsilon$. Moreover,

$$\mathbb{P}(A_q) \mathbb{E}(X_i \mid A_q) \leq \mathbb{E}(X_i) \leq \mathbb{P}(A_q) \mathbb{E}(X_i \mid A_q) + (1 - P(A_q)).$$

Hence by (2.9), $|\mathbb{E}[X_i \mid A_q] - \zeta(p)| \leq 3\epsilon$. As a result, by Chernoff bound,

$$\mathbb{P}(|\tilde{N}(k, q) - \zeta(p)| \geq t + 3\epsilon \mid A_q) \leq e^{-qt^2}.$$ 

Now we can get a concentration bound without conditioning on $A_q$,

$$\mathbb{P}(|\tilde{N}(k, q) - \zeta(p)| \geq t + 3\epsilon) \leq \mathbb{P}(|\tilde{N}(k, q) - \zeta(p)| \geq t + 3\epsilon \mid A_q) + 1 - \mathbb{P}(A_q)$$

$$\leq e^{-qt^2} + q^2 \frac{\log n}{n} + \frac{\epsilon}{3},$$

which gives the desired result in the case that $\zeta(p) > 0$.

The case $\zeta(p) = 0$ is similar, except that we can choose $k_\epsilon$ such that $\mathbb{P}(|C(v)| \geq k_\epsilon) \leq \frac{\epsilon}{3}.$

Proof of Theorem 1.2. The proof follows from Corollary 2.4 and Lemma 2.7.

Remark 2.8. In the proof above, one can lift the assumption that the initial infected node is chosen uniformly at random. In fact, as long as each nodes is chosen with probability $O(1/n)$ then the relative size of an outbreak will still converge to $\zeta(p)$, since the size of the largest
component in \( G(p) \) converges to \( \zeta(p) \) and the Chernoff bounds in the proof above follows similarly and the relative size of the largest component still.

However, the probability of an outbreak might change. When the initial infection happens proportional to some local feature of nodes such as the degree, we can first draw uniform random samples, calculate their local features (degrees), and then do rejection sampling to get the probability of an infection when one infects by choosing vertices according to the local feature (degree). When the local feature is degree and the degrees have a finite second moment, then by applying Theorem 2.23 [van der Hofstad 2020] we can see the local limit of the above rejection sampling procedure exists and gives the right probability of an outbreak. It is an interesting question to characterize other local features that starting the infection with respect to them keeps the probability of an outbreak a local property, i.e., it can be derived from the rejection sampling modification of Algorithm 1.

3 Proofs of Applications to Motif-Based Graph Models

This section is on the proof of applications to motif-based models. For that purpose, we need to check 1) local weak convergence, 2) large-set expansion of the sequence, and 3) continuity of the survival probability in the limit. We go over the proofs of these properties in the same order. Then in Section 3.4, we show Theorems 1.1 and 1.2 hold for the motif-based configuration model and the preferential attachment models.

3.1 Locality of Motif-Based graphs

We start by proving the locality stated in Lemma 1.8. Let us first state the precise definition of local weak convergence. For this purpose, we define a function \( f : \mathcal{G}_* \to \mathbb{R} \) to be \( k \)-local if \( f(G, o) \) depends only on the \( k \)-neighborhood of \( o \) in \( G \). Given a sequence of (possibly) random graphs \( \{G_n\}_{n \in \mathbb{N}} \), and a (non-random) probability \( \mu \) on \( \mathcal{G}_* \), we say \( G_n \) converges in probability in the local weak sense to \( \mu \) if for \( k < \infty \), and any bounded \( k \)-local function \( f : \mathcal{G}_* \to \mathbb{R} \),

\[
\mathbb{E}_{P_n}[f] \xrightarrow{P} \mathbb{E}[f], \quad (3.1)
\]

where \( P_n \) is the uniform distribution over random vertices in \( G_n \) and \( \mathbb{E}_{P_n}[f] \) is a shorthand for \( \mathbb{E}_{v_n \sim P_n}[f(G_n, v_n)] \).

\footnote{Alternatively, local weak convergence can be defined by introducing a metric on \( \mathcal{G}_* \) and then using continuous functions and weak convergence with respect to this metric [Aldous and Steele 2004, Benjamini and Schramm 2001]; hence the name local weak convergence. The equivalence of the two is...}
To prove Lemma 1.8 and hence local weak convergence of a general class of motif-based models, we will use the second moment method to prove (3.1). The key idea is to map functions on the motif-based graphs to the ones on the external graphs by averaging over all vertices in a motif and then use the local weak convergence of the external graphs. But before, we need a technical result, which shows the expected size of a motif converges in probability.

**Proposition 3.1.** Let \( \{G_n\}_{n \in \mathbb{N}} \) be a motif-based graph sequence satisfying Conditions (i) and (ii). Let \( E_n \) denote the probability distribution of a uniform random motif among all \( n \) motifs of \( G_n \), then there exist \( \bar{v} < \infty \),

\[
E_n[v(M)] \xrightarrow{P} \bar{v}.
\]

Here \( \xrightarrow{P} \) denotes convergence in probability with respect to the possible randomness of the degree distribution of the external graph, as well as the randomness from assigning motifs iid at random according to \( M_d \).

**Proof.** Let \( \bar{v} \) be the expectation of \( E_n[v(M)] \) conditioned on \( G_{ext}^n \). We can write this expectation as

\[
\bar{v} = \frac{1}{n} \sum_{i=1}^{n} v_{d_i},
\]

where \( d_i \) is the degree of vertex \( i \) in \( G_{ext}^n \), and \( v_d = E_{M_d}[v(M)] \). On the other hand, the expectation of the square of \( E_n[v(M)] \) conditioned on \( G_{ext}^n \) is equal to

\[
\frac{1}{n^2} \sum_{i \neq j}^{n} v_{d_i}v_{d_j} + \frac{1}{n^2} \sum_{i}^{n} E_{M_d}[v^2(M)] \leq \bar{v}^2 + \frac{S_{\text{max}}^2}{n}.
\]

Thus, by the second moment method

\[
P(|E_n[v(M)] - \bar{v}| \geq \epsilon) \leq \frac{S_{\text{max}}^2}{n\epsilon^2}
\]

where the probability is over the random motif assignments. Combined with the fact that \( \bar{v} \) converges in probability by the assumed weak local convergence of \( G_{ext}^n \), this proves the proposition.

**Proof of Lemma 1.8.** To prove the local weak limit of the motif-based graph, we need to proven, e.g., in Section 2 of [van der Hofstad 2020]).
define the probability distribution of the limiting graph $\mu$, which we want to construct using $\mu^{ext}$. For any graph $H$, with the abuse of notation we use $\mathcal{M}(H)$ as the graph constructed by replacing each vertex $v$ in $H$ with a motif drawn from the distribution $\mathcal{M}_{d_v}$ (here, $d_v$ is the degree of $v$).

We need to make sure the neighborhood of a uniform random node in $G_n$ converges to the neighborhood of the graph $(G, o) \sim \mu$. For that purpose, we need to re-weight nodes in the external network based on their motif sizes. So, let $\bar{\mu}^{ext}$ be the weighted probability measure on the external graphs, i.e., we draw $(G_{ext}, o)$ proportional to $\mathbb{E}_{\mathcal{M}_{d_o}}[v(M)]\mu^{ext}(G^{ext}, o)$, where $d_o$ is the degree of the root $o$. Let $\mu$ be the probability measure that replaces each node $v$ of $(G_{ext}, o) \sim \bar{\mu}^{ext}$ with a motif drawn from $\mathcal{M}_{d_v}$, and then chooses a uniform random node $o'$ from $M_o$ (the motif of the external root) to be the new root of the graph.

Fix an integer $k > 0$ and a $k$-local bounded function $f$ on $G$. Let $n' = \sum_{i=1}^n v(M_i)$ be the number of nodes in the motif-based graph $G_n$, and let $\mathcal{P}_{n'}$ denote the distribution of a uniform random node among the $n'$ nodes in the motif graph $G_n$. For the proof of local weak convergence, we need to show that

$$
\mathbb{E}_{\mathcal{P}_{n'}}[f(G_n)] \overset{p}{\to} \mu(f(G, o)),
$$

(3.2)

where, with a slight abuse of notation, we used $\mathbb{E}_{\mathcal{P}_{n'}}[f(G_n)]$ for $\mathbb{E}_{v \sim \mathcal{P}_{n'}}[f(G_n, v)]$.

We will use the second moment method to prove (3.2). Given an external graph $G_{ext}^n$, we use $\mathbb{E}_{\mathcal{M}(G_{ext}^n)}$ for expectations with respect to a random graph $G_n$ drawn from $\mathcal{M}(G_{ext}^n)$. For the first moment we need to show,

$$
\mathbb{E}_{\mathcal{M}(G_{ext}^n)}[\mathbb{E}_{\mathcal{P}_{n'}}[f(G_n)]] \overset{p}{\to} \mathbb{E}_{\mathcal{M}(G^{ext})}[\mu(f(G, o))],
$$

where the convergence in probability is over all possible randomness of $G_{ext}^n$. Note that

$$
\mathbb{E}_{\mathcal{M}(G_{ext}^n)}[\mathbb{E}_{\mathcal{P}_{\sum_{i \in [n]} v(M_j)}}[f(G_n)]] = \frac{1}{n} \sum_{i \in [n]} \mathbb{E}_{\mathcal{M}(G_{ext}^n)}[\frac{n}{\sum_{i \in [n]} v(M_j)} \sum_{v \in M_i} f(G_n, v)].
$$

By Proposition 3.1, $\frac{n}{\sum_{i \in [n]} v(M_j)}$ converges in probability to $\frac{1}{v}$. So, if we define

$$
\bar{f}(G_{ext}^n, i) = \mathbb{E}_{\mathcal{M}(G_{ext}^n)}[\frac{1}{v} \sum_{v \in M_i} f(G_n, v)],
$$

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then
\[
\mathbb{E}_{M(G^\text{ext})}[\mathbb{E}_{\Sigma_{i \in [n]} v(M_j)}[f(G_n)] - \frac{1}{n} \sum_{i \in [n]} \tilde{f}(G^\text{ext}_n, i)] = \frac{1}{n} \mathbb{E}_{M(G_n)}\left(\left(\frac{n}{\sum_{j \in [n]} v(M_j)} - \frac{1}{\bar{v}}\right)\left(\sum_{v \in M_i} f(G^\text{ext}_n, v)\right)\right).
\]

Fix some \( \epsilon > 0 \), and let \( B \) be the bound on \( f \). Then by Proposition 3.1,
\[
\mathbb{P}\left(|\frac{n}{\sum_{j \in [n]} v(M_j)} - \frac{1}{\bar{v}}| \geq \frac{\epsilon}{B}\right) \to 0.
\]
Therefore,
\[
\mathbb{P}\left(\left|\frac{1}{n} \mathbb{E}_{M(G_n)}\left(\left|\frac{n}{\sum_{j \in [n]} v(M_j)} - \frac{1}{\bar{v}}\right|\left(\sum_{v \in M_i} f(G_n, v) \geq \epsilon\right)\right)\right| \to 0.,
\]
and as a result,
\[
\mathbb{P}\left(\left|\mathbb{E}_{M(G_n)}[\mathbb{E}_{\Sigma_{j \in [n]} v(M_j)}[f(G_n)] - \frac{1}{n} \sum_{i \in [n]} \tilde{f}(G^\text{ext}_n, i)] \geq \epsilon\right| \to 0.
\]

So, to prove the first moment it is enough to show,
\[
\mathbb{E}_{P_n} \tilde{f}(G^\text{ext}_n) \xrightarrow{p} \mathbb{E}_{M(G^\text{ext})}[\mu\left(f(G, o)\right)]. \tag{3.3}
\]
Note that \( \tilde{f} \) is bounded because
\[
\tilde{f}(G^\text{ext}_n, i) = \mathbb{E}_{M(G_n)}[\frac{1}{\bar{v}} \sum_{v \in M_i} f(G_n, v)] \leq \frac{BS_{\text{max}}}{\bar{v}}.
\]
Furthermore, if \( j \) has distance \( k \) from \( i \), then any node in \( M_i \subset G_n \) has distance at least \( k \) from any node in \( M_j \subset G_n \), showing that \( \tilde{f}(G^\text{ext}_n, i) \) depends only on the \( k \)-neighborhood of \( i \) in \( G^\text{ext}_n \). Thus \( \tilde{f} \) is a \( k \)-local, bounded function, and local weak convergence of the external graphs implies that
\[
\mathbb{E}_{P_n} \tilde{f}(G^\text{ext}_n) \xrightarrow{p} \mu^\text{ext}\left(\tilde{f}(G^\text{ext}, o)\right) = \mu^\text{ext}\left(\mathbb{E}_{M(G^\text{ext})}[\frac{1}{\bar{v}} \sum_{v \in M_o} f(G, v)]\right),
\]
which implies (3.3).
For the second moment, we first note that with high probability two uniform random motifs in $G_n^{\text{ext}}$ have disjoint $k$-neighborhoods. In fact, if $\text{dist}_{G_n^{\text{ext}}}(i, j)$ is the distance of motifs $i$ and $j$ in $G_n^{\text{ext}}$, then by the local weak convergence of $G_n^{\text{ext}}$, Corollary 2.19 in [van der Hofstad 2020] implies that $\text{dist}_{G_n^{\text{ext}}}(i, j) \xrightarrow{P} \infty$. Next, we show the second moment argument follows from the large distances of motifs. We can write,

$$
\mathbb{E}_{M(G_n^{\text{ext}})}[(\sum_{v \in V(G_n)} f(G_n, v))^2] = \mathbb{E}_{M(G_n^{\text{ext}})}[(\sum_{i,j \in [n]} (\sum_{v \in M_i} f(G_n, v))(\sum_{u \in M_j} f(G_n, u))].
$$

Then if we divide the outer sum into two cases based on whether the distance of $M_i$ and $M_j$ is larger or smaller than $k$, we can use the fact when it is larger than $k$, the expectation over the choice of motifs factors, giving

$$
\mathbb{E}_{M(G_n^{\text{ext}})}[(\sum_{v \in V(G_n)} f(G_n, v))^2] = \sum_{i,j \in [n], \text{dist}_{G_n^{\text{ext}}}(i,j) > k} \mathbb{E}_{M(G_n^{\text{ext}})}[(\sum_{v \in M_i} f(G_n, v))(\sum_{u \in M_j} f(G_n, u))].
$$

Here we used that the distance of two nodes in $G_n$ is at least the distance of their corresponding motifs in the external graph. Then we choose $n$ large enough such that for random motifs (proportional to their sizes) their distance is less than $k$ with probability at most $\epsilon$,

$$
\sum_{i,j \in [n], \text{dist}_{G_n^{\text{ext}}}(i,j) \leq k} \mathbb{E}_{M(G_n^{\text{ext}})}[(\sum_{v \in M_i} f(G_n, v))(\sum_{u \in M_j} f(G_n, u))] \leq \epsilon n^2 S_{\max}^2 B^2,
$$

where $B$ is the bound on $f$. Therefore, since $\epsilon$ was arbitrary

$$
\mathbb{E}_{M(G_n^{\text{ext}})}[(\frac{1}{n} \sum_{v \in V(G_n)} f(G_n, v))^2] \xrightarrow{P} \mathbb{E}_{M(G_n^{\text{ext}})}[\frac{1}{n} \sum_{v \in V(G_n)} f(G_n, v)]^2,
$$

where the convergence in probability is over the randomness of the external graph $G_n^{\text{ext}}$. 

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On the other hand,
\[
\mathbb{E}_{\mathcal{M}(\mathcal{G}^{\text{ext}}_n)}\left[ \frac{1}{(\sum_{i \in [n]} v(M_i))^2} \left( \sum_{v \in V(G_n)} f(G_n, v) \right)^2 \right]
= \frac{1}{n^2} \sum_{i \in [n]} \mathbb{E}_{\mathcal{M}(\mathcal{G}^{\text{ext}}_n)}\left[ \frac{n^2}{(\sum_{i \in [n]} v(M_i))^2} \left( \sum_{v \in M_i} f(G_n, v) \right)^2 \right].
\]

Again, using Proposition 3.1,
\[
\mathbb{E}_{\mathcal{M}(\mathcal{G}^{\text{ext}}_n)}\left[ \frac{1}{(\sum_{i \in [n]} v(M_i))^2} \left( \sum_{v \in V(G_n)} f(G_n, v) \right)^2 \right] \xrightarrow{p} \mathbb{E}_{\mathcal{M}(\mathcal{G}^{\text{ext}}_n)}\left[ \frac{1}{n} \sum_{v \in V(G_n)} f(G_n, v) \right]^2,
\]
and
\[
\mathbb{E}_{\mathcal{M}(\mathcal{G}^{\text{ext}}_n)}\left[ \left( \frac{1}{n} \sum_{v \in V(G_n)} f(G_n, v) \right)^2 \right] \xrightarrow{p} \mathbb{E}_{\mathcal{M}(\mathcal{G}^{\text{ext}}_n)}\left[ \frac{1}{(\sum_{i \in [n]} v(M_i))^2} \left( \sum_{v \in V(G_n)} f(G_n, v) \right)^2 \right],
\]

which gives the convergence of the second moment, i.e.,
\[
\mathbb{E}_{\mathcal{M}(\mathcal{G}^{\text{ext}}_n)}\left[ \frac{1}{(\sum_{i \in [n]} v(M_i))^2} \left( \sum_{v \in V(G_n)} f(G_n, v) \right)^2 \right] \xrightarrow{p} \mathbb{E}_{\mathcal{M}(\mathcal{G}^{\text{ext}}_n)}\left[ \frac{1}{(\sum_{i \in [n]} v(M_i))^2} \left( \sum_{v \in V(G_n)} f(G_n, v) \right)^2 \right].
\]

As a result,
\[
\frac{\text{Var}_{\mathcal{M}(\mathcal{G}^{\text{ext}}_n)} \left( \mathbb{E}_{\mathcal{P}_{\sum_{i \in [n]} v(M_i)}} [f] \right)}{\mathbb{E}_{\mathcal{M}(\mathcal{G}^{\text{ext}}_n)} \left( \mathbb{E}_{\mathcal{P}_{\sum_{i \in [n]} v(M_i)}} [f] \right)^2} \xrightarrow{p} 0.
\]

Then by Chebyshev’s inequality,
\[
\frac{\mathbb{E}_{\mathcal{P}_{\sum_{i \in [n]} v(M_i)}} [f]}{\mathbb{E}_{\mathcal{M}(\mathcal{G}^{\text{ext}}_n)} \left( \mathbb{E}_{\mathcal{P}_{\sum_{i \in [n]} v(M_i)}} [f] \right)} \xrightarrow{p} 1. \tag{3.4}
\]

So by the convergence of the first moment (3.3), we get the desired result in (3.2).

3.2 Expansion of Motif-Based Graphs

Next we show that motif based graphs inherit large-set expansion from their external graph structure if the motif sizes are bounded. Edge percolation on motifs can be viewed as an analog of vertex percolation on the external graph. So, in order to prove edge-expansion
of motif-based graphs, we first prove that large-set edge expansion of the external graph \( \{ G_n^{\text{ext}} \}_{n \in \mathbb{N}} \) implies large-set vertex expansion.

For that purpose, we first define large-set vertex expansion similar to the definition of large-set edge expansion. Given a graph \( G = (V, E) \) and a set \( A \subset V \), let \( \partial_{\text{out}} \) be the set of vertices in \( V - A \) that have at least one neighbor in \( A \), and let \( \delta_{\text{out}}(A) = |\partial_{\text{out}}| \). For \( \epsilon < 1/2 \), we then define
\[
\phi_{\text{out}}(G, \epsilon) = \min_{A \subseteq V, |V| \leq |A| \leq |V|/2} \frac{\delta_{\text{out}}(A)}{|A|}. \tag{3.5}
\]
Call a graph \( G \) an \((\alpha, \epsilon, \bar{d})\) large-set vertex expander if the average degree of \( G \) is at most \( \bar{d} \) and \( \phi_{\text{out}}(G, \epsilon) \geq \alpha \). A sequence of possibly random graphs \( \{ G_n \}_{n \in \mathbb{N}} \) is called a large-set vertex expander sequence with bounded average degree, if there exists \( \bar{d} < \infty \) and \( \alpha > 0 \) such that for any \( \epsilon \in (0, 1/2) \) the probability that \( G_n \) is an \((\alpha, \epsilon, \bar{d})\) large-set vertex expander goes to 1 as \( n \to \infty \).

In the following, we prove that large-set edge expansion together with local weak convergence is enough to imply large-set vertex expansion. Note that this is straightforward when the maximum degree is bounded. Here, the main observation is that graphs with local weak limits have a tight local neighborhood, in the sense that the degree of nodes in the neighborhood of a random edge is bounded with high probability.

**Lemma 3.2.** Let \( \mu \) be a probability distribution on \( G_* \), and let \( \{ G_n \}_{n \in \mathbb{N}} \) be a sequence of \((\alpha, d)\) large-set edge expanders with the local weak limit \((G, \circ) \sim \mu \). Then \( \{ G_n \}_{n \in \mathbb{N}} \) is a large-set vertex expander as well.

**Proof.** Assume to the contrary that there exists some \( \epsilon > 0 \) such that there exists an infinite subsequence \( \{ \tilde{G}_{n'} \} \) with \( \phi(\tilde{G}_{n'}, \epsilon) \geq \alpha \) but \( \phi_{\text{out}}(\tilde{G}_{n'}, \epsilon) = o(1) \). Then for any \( \delta > 0 \) and large enough \( n \) we have \( \phi_{\text{out}}(\tilde{G}_{n'}, \epsilon) < \delta \). Let \( A_n \subset V(G_n) \) be a set with bad vertex expansion, i.e., \( \epsilon n \leq |A_n| \leq n/2 \) and \( \delta_{\text{out}}(A_n) \leq \delta |A_n| \). On the other hand, by the edge expansion of \( A_n \), the number of edges coming out of \( A_{\text{out}} = \partial_{\text{out}}(A_n) \) is at least \( \alpha |A_n| \). So, the average number of edges coming out of a node from \( A_{\text{out}} \) is at least \( \alpha/\delta \). Therefore, if we choose a uniform random edge from the edges coming out of \( A_{\text{out}} \) with probability at least 1/2 its endpoint has degree larger than \( \alpha/(2\delta) \). To see this, let \( d_1 \geq d_2 \geq \cdots \geq d_{m'} \) be the number of edges coming out of each vertex in \( A_{\text{out}} \), and let \( \bar{d} = \frac{\sum_{m'=1}^{m'} d_i}{m} \) be the average of them. Also, let \( s \) be the index that \( d_1 \geq \cdots \geq d_s \geq \frac{\bar{d}}{2} \geq d_{s+1} \geq \cdots \geq d_{m'} \). Now if we choose a random edge it will be incident to one of the vertices of degree larger than \( \bar{d}/2 \) with probability \( \frac{d_1 + \cdots + d_s}{d_1 + \cdots + d_{m'}} \).

So to prove our claim, we need to show that \( d_1 + \cdots + d_s \geq d_{s+1} + \cdots + d_{m'} \). Assume, to the
contrary that this is not true. Then we have

\[ m' \bar{d} = \sum_{i=1}^{m'} d_i \leq 2(d_{s+1} + \cdots + d_{m'}) \leq (m' - s) \bar{d}, \]

which is a contradiction. Note that since \( \delta \) was arbitrary, we can make \( \alpha/2\delta \) as large as we want. We will see this will result in a contradiction.

To see this, pick a uniform random edge from \( G_n \). With probability at least \( \alpha |A_n| / \bar{d} n \geq \alpha \epsilon \bar{d} \), it will be in the boundary of \( A_{out} \). Hence, with probability at least \( \alpha \epsilon / 2\bar{d} \) the degree of the endpoint of the edge is at least \( \alpha \bar{d} / 2 \). On the other hand, by Theorem 2.23 in [van der Hofstad 2020], since the average degree is bounded and hence the degree of a random node in \( G_n \) is uniformly integrable, the probability that the neighborhood of a uniformly random edge \( e \) is isomorphic to a finite graph \( H \in \mathcal{G}_s \) converges in probability to \( \mu[H] \). Since the local neighborhoods in \( \mathcal{G}_s \) are finite, we conclude that exists \( \Delta \) such that for \( n \) large enough, with probability at least \( 1 - \alpha \epsilon / 4\bar{d} \), the degree of the neighbors of a random edge in \( G_n \) is at most \( \Delta \). If we choose \( \delta \) in such a way that \( \Delta < \alpha \bar{d} / 2 \), we get a contradiction.

Next we prove that large-set edge-expansion of motif-based graphs follows form large-set vertex expansion of the external graphs.

**Proposition 3.3.** Let \( \{G_n\}_{n \in \mathbb{N}} \) be a sequence of motif-based graphs satisfying Conditions (i) and (ii). Assume the external sequence \( \{G^e_n\}_{n \in \mathbb{N}} \) is a large-set expander with bounded average degree. Then \( \{G_n\}_{n \in \mathbb{N}} \) is a large-set expander with bounded average degree as well.

**Proof.** We first show the large-set edge-expansion of \( \{G_n\}_{n \in \mathbb{N}} \) and then we bound the average degree. Fix some \( \epsilon \in (0, 1/2) \) and a set \( S \subset V(G_n) \) with \( |S| \geq \epsilon n \). Since there are \( n \) motifs in \( G_n \) each of size at most \( S_{\text{max}} \), \( |S| \geq \frac{\epsilon}{S_{\text{max}}} |V(G_n)| \). Note that some motifs are divided between \( S \) and \( V(G_n) - S \), and some motifs are either completely in \( S \) or \( V(G_n) - S \). Let \( M(S) \) be the set of motifs that are completely in \( S \), i.e., for each motif \( M \in M(S) \) we have \( V(M) \subset S \). Also, let \( \tilde{M}(S) \) be the set of motifs that have at least one vertex in \( S \), so \( M(S) \subseteq \tilde{M}(S) \).

Since the size of each motif is at most \( S_{\text{max}} \), we have \( |\tilde{M}(S)| \geq \frac{|S|}{S_{\text{max}}} \geq \frac{\epsilon}{S_{\text{max}}} n \). Now, consider two cases. First, assume that the number of motifs divided between \( S \) and \( V(G_n) - S \) (motifs in \( \tilde{M}(S) - M(S) \)) is at least \( \frac{|S|}{2S_{\text{max}}} (\geq \frac{\epsilon}{2S_{\text{max}}} n) \). Since, each motif is a connected graph, there are at least \( \frac{|S|}{2S_{\text{max}}} \) edges between \( S \) and \( V(G_n) - S \). Therefore, the edge expansion of \( S \) in \( G_n \) is at least \( \frac{1}{2S_{\text{max}}} \).
In the second case, $|\tilde{M}(S) - M(S)| \leq \frac{|S|}{2S_{\text{max}}}$ and as a result, $|M(S)| \geq \frac{|S|}{2S_{\text{max}}}$. Here, we use large-set vertex expansion of external graphs. By Lemma 3.2, there exists some $\alpha > 0$ independent of $\epsilon$ such that with high probability $\phi_{\text{out}}(G_n^\text{ext}, \frac{\epsilon}{2S_{\text{max}}}) \geq \alpha$. Note that all motifs in $\partial_{\text{out}}(M(S))$ are either divided between $S$ and $V(G_n) - S$ or they are completely in $V(G_n) - S$ but connected to a motif in $M(S)$. In both cases, each of the motifs contribute at least one edge to $e(S, V(G_n) - S)$. Therefore the edge expansion of $S$ in $G_n$ is whp at least $\alpha$. As a result, the sequence $\{G_n\}_{n \in \mathbb{N}}$ is a large-set edge expander.

Now it remains to bound the average degree. For the graph $H$, let $d_{\text{avg}}(H)$ be the average degree. Let $\{M_i = (F_i, d_i)\}_{i=1}^n$ be the motifs of $G_n$. Then we can compute the average degree by summing up the internal and external edges,

$$d_{\text{avg}}(G_n) = \frac{\sum_{i=1}^n v(M_i)d_{\text{avg}}(F_i)}{\sum_{i=1}^n v(M_i)} + \frac{nd_{\text{avg}}(G_n^\text{ext})}{\sum_{i=1}^n v(M_i)} \leq S_{\text{max}}^2 + \bar{d} \left( \frac{\sum_{i=1}^n v(M_i)}{n} \right) \quad (\text{Condition (i)}),$$

where $\bar{d}$ is the average degree of the external graph. Since each motif has size at least 1 the average degree is upper bounded by $S_{\text{max}}^2 + \bar{d}$. \hfill \qed

As a direct implication of large-set expansion and local weak limit of motif-based graphs we get Corollary 1.9.

**Proof 1.9.** By Proposition 3.3 the sequence $\{G_n\}_{n \in \mathbb{N}}$ is a large-set edge expander, and by Lemma 1.8 the sequence has a local weak limit. Therefore, we can apply Theorems 1.1 and 1.2 to motif-based graph with a smooth limit. \hfill \qed

### 3.3 Continuity of Survival Probability

Finally, we need to prove the smoothness of the local weak limit for the motif-based preferential attachment and configuration model. The limit of the preferential attachment and configuration model without motifs are in a subclass of multi-type branching processes, called threshold regular branching processes, for which the continuity of the survival probability was proven in Lemma 6.2. in [Alimohammadi et al. 2021]. We extend the results of [Alimohammadi et al. 2021] to motif-based graphs where the external sequence $\{G_n^\text{ext}\}_{n \in \mathbb{N}}$ is a threshold regular branching processes.

At high level, in the multi-type branching processes considered in [Alimohammadi et al. 2021], each vertex has a label in the continuum interval $[0, 1]$, and the distribution of the
number and types of children of a node \( v \) conditioned on its label is independent of the tree above \( v \). The condition of threshold regularity then requires that for \( \zeta(p) > 0 \), the multi-type branching process conditioned on the label of the root \( (X_0 \in [0,1]) \) survives with a probability that is bounded away from zero uniformly in \( X_0 \). See the precise definition in Section 6.1. of [Alimohammadi et al. 2021]. Next, we give an overview of their proof to extend their result.

The proof starts with the observation that \( \zeta(p) \) is the point-wise limit of a sequence of functions \( \tilde{\zeta}_k(p) \), defined as the probability of the event \( A_k \) that after percolation, the component of the root extends to at least distance \( k \) from the root. Continuity of \( \zeta \) is then established by finding a uniform upper bound on \( \frac{d}{dp}\tilde{\zeta}_k(p) \). This in turn is achieved with the help of Russo’s formula [Russo 1981]. To state it, define an edge \( e \) to be pivotal if exactly one of \( G(p) \cup \{e\} \) and \( G(p) - \{e\} \) is in \( A_k \). The Margulis–Russo formula [Russo 1981] then says that

\[
\frac{d}{dp}\tilde{\zeta}_k(p) = \sum_{e \in [m]} \mathbb{P}_p(e \text{ is pivotal}).
\] (3.6)

If \( e \) is pivotal, and \( e \) is an edge in \( G(p) \), the edge is called a \( k \)-bridge. Since edges appear with probability \( p \), the right hand side is \( 1/p \) times the expected number of \( k \)-bridges in \( G(p) \). Thus our goal is to find a uniform bound on the number of \( k \)-bridges, which can be reduced to bounding the number of \( \infty \)-bridges, defined as edges such that their removal turns the infinite component of the root into a finite component.

In [Alimohammadi et al. 2021], the upper bound on the number of \( k \)-bridges is established by using threshold regularity to prove the probability that an edge is an \( \infty \)-bridge decays as the distance from the root increases. But unfortunately, threshold regularity does not necessarily hold when we add motifs to the tree. However, we are still able to extend their proof, by bounding the number of \( k \)-bridges in the motif-based graphs, which is at most the number of \( k \)-bridges in the external graph multiplied by the maximum household size. The complete proof appears in Appendix A.

**Lemma 3.4.** Let \( \{G_n\}_{n \in \mathbb{N}} \) be a sequence of motif-based graphs with the limit \( \mu \in \mathcal{G}_e \) satisfying the Condition (i) and (ii). Also, assume that \( \mu_{\text{ext}} \), the limit of the external graph, is threshold regular (Definition 6.2 in [Alimohammadi et al. 2021]). Then \( \zeta(p) = \mu(\mathbb{P}_{G(p)}((C,o) = \infty) \) is continuous for all \( p > p_\text{c}(\mu_{\text{ext}}) \), where \( p_\text{c}(\mu_{\text{ext}}) \) is the percolation threshold for the limit of the external graph.
3.4 Proofs of the Motif-Based Configuration Model and Preferential Attachment

Finally, we prove Corollaries 1.10 and 1.11, by noting that continuity of the survival probability in the limit is already implied by Lemma 3.4 for motif-based preferential attachment and motif-based configuration models.

**Proof of Corollary 1.10.** Motif-based preferential attachment graphs, are large-set expanders by the expansion of preferential attachment models shown in Lemma 1.3 and Proposition 3.3. Their local weak limit (which exists by Lemma 1.8) has a continuous survival probability by Lemma 3.4 above and the fact that the external graph has a smooth survival probability at $p_c(\mu^{ext}) = 0$ by Corollary 6.8 in [Alimohammadi et al. 2021]. The continuity of the motif-based graph at $p = 0$ follows from the fact that $\zeta(p) \leq \zeta^{ext}(p)$, because by percolating edges in a motif the corresponding super node in the external graph will be removed when the motif becomes disconnected. This event happens with a positive probability because the size of the motifs are bounded by some constant $S_{\text{max}}$. Therefore since $\zeta^{ext}(p) \to 0$ as $p \to 0$, we get that $\zeta(p) \to 0$ for $p \to 0$ as well.

As a result Theorems 1.1 and 1.2 applies to motif-based preferential attachment graphs.

**Proof of Corollary 1.11.** Similar to the motif-based preferential attachment model, the expansion follows from the expansion of the external graph proved in Lemma 12 in [Abdullah et al. 2012] and Proposition 3.3. The continuity follows from Lemma 3.4 and noting that the limit of the external graphs is a two-stage branching process(by Theorem 4.5 in [van der Hofstad 2020]) and hence has a continuous survival probability ( see e.g., [Broman and Meester 2008]).

We only need to check the continuity at or below $p_c^{ext}$, the percolation threshold for the external graph. Similar to the argument in Corollary 1.10 $\zeta(p) \leq \zeta^{ext}(p)$. Therefore, $\zeta(p) = 0$ for all $p < p_c^{ext}$. Moreover, since $\zeta^{ext}(p) \to 0$ as $p \to p_c^{ext}$ for the configuration model (see e.g., [Broman and Meester 2008]), then $\zeta(p) \to 0$ for $p \to p_c^{ext}$ as well. As a result, all the conditions needed for Theorems 1.1 and 1.2 hold and their result is applicable to motif-based configuration models.
4 Future Work

A natural next step is to prove that our results hold for the general SIR model, where the recovery time is drawn from a distribution. Intuitively, Algorithm 1 is related to the probability of an outbreak starting from a uniform random node. For a general SIR model this is not the case and one can define a backward infection process (analogous to the forward process described in Algorithm 1) to compute the relative size of an outbreak. The backward process at each step, finds which of the undiscovered neighbors could have transmitted the disease to the original node. Note that if a node is infected in an outbreak, then its backward infection must be large and hence it will reach \( k \) other nodes. So, the possible next step would be to characterize graphs such that the backward and forward processes describe the size and probability of an outbreak for a generalized SIR model.

Further, we conjecture that the assumption on continuity of \( \zeta(p) \) in all of our results can be lifted, i.e., the local weak limit of a sequence of large-set expanders has a continuous survival probability.

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A Proof of Lemma 3.4

To give the formal proof, first recall the definition of threshold regular trees from [Alimohammadi et al. 2021]. Using their terminology, types of vertices in a multi-type branching process $G$ are labelled by a label $x \in [0,1]$. The distribution on the types and the number of children of a vertex of type $x$ only depends on $x$ and can be as general as desired. Let $\mu_x$ be the distribution over trees generated starting from a vertex of type $x$, and let $G_x$ be a graph drawn from $\mu_x$. Then define $\zeta_x(p) = \mu_x(|C(x)| = \infty \text{ in } G_x(p))$.

The threshold regular condition (Definition 6.1. in [Alimohammadi et al. 2021]) says that if $\zeta(p - \epsilon) > 0$ for some $\epsilon > 0$, then there exists $\delta$ such that $\zeta_x(p) \geq \delta$ for all $x \in S$. Then similar to the derivation of (3.6) we get

$$p\zeta_x(p) = \mathbb{E}_{G_x(p)}[b_{p,k}(x)],$$

(A.1)

where $b_{p,k}(x)$ is the number of $k$-bridges in $G_x(p)$. Now, we are ready to prove the lemma.

For the motif-based graph $G$, define $E^{ext}(G)$ as the set of external edges in $G$. Let $e \in E^{ext}(G)$ be an external $k$-bridge in $G$. Since $G^{ext}$ is a tree, then there exists a $k' < k$ such that $e$ is a $k'$-bridge for $G^{ext}$. Further, we can find a lower bound on $k'$ by Condition (i). By this condition, each motif can add at most $S_{\max}$ to the distance of the root $o$ from the boundary. Therefore a $k$-bridge in $G$ is an external $k'$-bridge in $G^{ext}$, where $k' \geq k/S_{\max}$.

Then because the number of $k'$-bridges is decreasing in $k'$,

$$\mathbb{E}_{G_x(p)}[b^{ext}_{p,k}(x)] \leq \mathbb{E}_{G^{ext}_x(p)}[b_{p,k/S_{\max}}(x)].$$

By applying Lemma C.2. in [Alimohammadi et al. 2021] there exists $L$ such that for all $p \geq p_c(\mu^{ext}) + \epsilon$ and all $x \in S$ and all $k \geq 0$

$$\mathbb{E}_{G_x(p)}[b^{ext}_{p,k}(x)] \leq \mathbb{E}_{G^{ext}_x(p)}[b_{p,k/S_{\max}}(x)] \leq L,$$

which bounds the number of external $k$-bridges in $G_x(p)$.

Now, to bound the number of internal $k$-bridges, note that each internal bridge $e$ can be mapped to the an external $k$-bridge which connects the motif containing $e$ to its ancestor motif. Further by Condition (i) there are at most $(S_{\max})^2$ internal edges mapped to the same
external bridge. Therefore,

\[
\mathbb{E}_{G_x(p)}[b^{int}_{p,k}(x)] \leq \left( \frac{S_{\text{max}}}{2} \right) \mathbb{E}_{G_x(p)}[b^{\text{ext}}_{p,k}(x)] \leq S_{\text{max}}^2 L. \tag{A.2}
\]

As a result, the total number of \( k \)-bridges is at most \((S_{\text{max}}^2 + 1)L\).

To finish the proof, as in the proof of Lemma 6.2. in [Alimohammadi et al. 2021], we can write,

\[
0 \leq \tilde{\zeta}_k(p') - \tilde{\zeta}_k(p) = \mu \left( \int_{p}^{p'} \frac{1}{p''} \mathbb{E}_{G(p)}[b_{p'',k}] dp'' \right) \leq \frac{1}{\epsilon} \mu \left( \int_{p}^{p'} \mathbb{E}_{G(p)}[b_{p'',k}] dp'' \right) \\
\leq \frac{S_{\text{max}}^2 L}{\epsilon} |p' - p|,
\]

where the last inequality follows by (A.2). Since the bound on \( \tilde{\zeta}_k(p') - \tilde{\zeta}_k(p) \) is uniform in \( k \), we conclude that \( \zeta(p) \) is Lipschitz continuous and hence continuous \( p \geq p_c(\mu^{\text{ext}}) + \epsilon \). Since \( \epsilon > 0 \) was arbitrary, this gives continuity above \( p_c(\mu^{\text{ext}}) \). \( \square \)