SIR EPIDEMIC ON RANDOM REGULAR GRAPHS

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Contents

2. Notation

(1) $G_n = ([n], E)$ is a graph on n vertices and m edges.
(2) $X_i(t) :=$ indicator that i is infected at time t. $X(t)$ denotes the vector $(X_i(t))_{i\in[n]}$
(3) $R_i(t) :=$ indicator that i is removed at time t. $R(t)$ denotes the vector $(R_i(t))_{i\in[n]}$
(4) λ is the infection rate, recovery rate is 1, Removed individuals become susceptible at rate α, i.e.,

$$S \xrightarrow{\lambda} I \xrightarrow{1} R$$

3. Preliminaries

Lemma 3.1. *Let $\xi_1, \xi_2, \dots \xi_n$ be iid Exp(λ) random variables. Then*

$$\mathbb{E}\max\{\xi_1, \dots \xi_n\} \geq \frac{1}{\lambda}\log n.$$

We include the simple proof for completeness.

Proof. We show the proof for $\lambda = 1$. The general case follows from the fact that $\lambda\xi_i \sim Exp(1)$. Let X_n be the random variable representing the maximum of $\xi_1, \dots \xi_n$. Then $\mathbb{P}(X_n \leq x) = P(\xi_i \leq x)^n = (1 - e^{-x})^n$. Thus $\mathbb{E}[X_n] = \int_0^\infty 1 - (1 - e^{-x})^n$

Now let $I_n = \mathbb{E}[X^{(n)}] = \int_0^\infty 1 - (1 - e^{-x})^n$. Notice that we can calculate the differences of $I_n - I_{n-1}$ then use a telescoping sum to calculate I_n.

$I_n - I_{n-1} = \int_0^\infty [1 - (1 - e^{-x})^n] - [1 - (1 - e^{-x})^{n-1}]\, dx = \int_0^\infty (1 - e^{-x})^{n-1} e^{-x}\, dx$. Using u-sub with $u = 1 - e^{-x}$, we get that $I_n - I_{n-1} = -\int_1^0 u^{n-1}\, du = \frac{1}{n}$.

Thus $I_n = I_0 + (E_1 - E_0) + \cdots + (E_n - E_{n-1}) = 0 + \frac{1}{1} + \frac{1}{2} + \cdots + \frac{1}{n} \geq \int_1^n \frac{1}{x} dx = \log n$. □

Lemma 3.2. *Consider a branching process whose offspring distribution has mean $\mu > 1$ and finite second moment. Let z_n be the number of offsprings in the n-th generation. There exists positive constants $\varepsilon > 0$ and $c > 0$ such that $\mathbb{P}(z_n > \varepsilon\mu^n) > \frac{c}{2}$ for all n sufficiently large.*

Proof. Let $W_n = \frac{z_n}{\mu^n}$. It's a standard result (see for instance [Dur07, Theorem 2.1.6]), there exists a nonnegative random variable W that is not identically 0 such that

$$\lim_{n\to\infty} \frac{z_n}{\mu^n} = \lim_{n\to\infty} W_n = W$$

almost surely. Thus, with positive constants c, ε such that

$$\mathbb{P}(W > \varepsilon) > c.$$

Define $X_n = \mathbf{1}_{(z_n/\mu^n \geq \varepsilon)}$ and define $\mathrm{X} = \mathbf{1}_{(W>\varepsilon)}$. Notice that $\liminf X_n \geq X$ almost surely. Thus, applying Fatou's lemma, we get that $\mathbb{E}[\liminf X_n] \leq \liminf \mathbb{E}[X_n]$. Thus, we get $\mathbb{E}[X] \leq \mathbb{E}[\liminf X_n] \leq \liminf \mathbb{E}[X_n]$. By definition, this means that there exists an n_0 sufficiently large such that $\forall n > n_0$, $\mathbb{P}(z_n/\mu^n \geq \varepsilon) \geq \frac{c}{2}$, as desired. □

4. SIR on d-regular trees

A d-regular tree is a tree in which every vertex has degree d.

Theorem 4.1. *[Number of infected vertices in regular trees] Consider the SIR on the d-regular tree T_d with the root infected initially where d is a constant.*

1. *(Subcritical) If $\lambda < \frac{1}{d-2}$, then the expected number of ever-infected vertices is finite.*
2. *(Critical) If $\lambda = \frac{1}{d-2}$, then a.s. the number of ever-infected vertices is finite.*
3. *(Super-critical) If $\lambda > \frac{1}{d-2}$, then with positive probability, there are infinitely many infected vertices.*

Proof. Let X be the number of children that a vertex v infects. Let t be the time until cure of v. We have that $\mathbb{E}[X] = (d-1) \cdot \mathbb{P}(\text{Child is infected before v recovers} = (d-1)\mathbb{P}(Exp(\lambda) < Exp(1))$. Thus, we get $\mathbb{E}[X] = (d-1) \cdot \frac{\lambda}{\lambda+1}$. Solving this for $\mathbb{E}[X] = 1$, we get $\lambda = \frac{1}{d-2}$.

We associate the SIR process on T_d with the following Galton-Watson tree where the offspring distribution is the law of X. This tree contains all ever-infected vertices of T_d. The proof now follows from standard results about survival of Galton-Watson trees (see for instance [Dur07, Section 2.1]). □

Moving from the number of infected vertices to the survival time, we use Lemmas 4.3 and 4.4.

Lemma 4.2. *Let G be a subset of G'. Say we run an SIR process on G and G', with the set of initially infected vertices being $V_0 \subset V_G \subset V_{G'}$. Denote X_G and $X_{G'}$ as the set of ever infected vertices of the SIR process G and G'. Then*

$$|X_G| \preceq |X_{G'}|.$$

Proof. When running the SIR process, for each vertex $v \in V(G')$, a recovery clock $t_v \sim \text{Exp}(1)$ is sampled, and for each edge $e \in E(G')$, a infection clock $t_e \sim \text{Exp}(\lambda)$ is sampled. Then whenever a vertex v is infected, for each of its edges e_{vh} that connects v to some vertex h, if $t_{e_{vh}} \leq t_v$ then the infection is sent to h. However, infection is not sent if h has already been infected.

Consider the coupling of the SIR process on G and G', where for all $v \in V(G)$ and $e \in E(G)$, we use the same clock sample t_v, t_e.

Then, in this coupling, $X_G \subset X_{G'}$ because a vertex v on G is infected at time t if

(1) v is also infected on G' at time t or,
(2) v is already infected on G' at some time in the past (and may have recovered).

□

Lemma 4.3. *Consider the SIR on any graph G with any initial condition. Let X_G be the set of vertices ever infected. Let τ be the survival time. Let $D = max_{v\in V} d_v$ be the maximum degree of all vertices in the graph. Then*

$$\mathbb{E}[\tau | X(G)] \geq \frac{1}{1+\lambda D} \log |X_G|. \tag{1}$$

In particular, we have

$$\mathbb{E}\tau \geq \frac{1}{1+\lambda D} \mathbb{E} \log |X_G|. \tag{2}$$

Moreover, on the event that $|X_G| = \infty$, we have $\tau = \infty$ a.s.

Proof. We want to lower bound the survival time in terms of the number of ever infected vertices, $|X_G|$. The idea is the following: since the survival time must include all the recovery of all ever infected vertices, say $\xi_1, \ldots, \xi_{X_G} \sim Exp(1)$ independently. In other words,

$$\tau \geq \max\{\xi_1, ...\xi_{|X_G|}\}.$$

In particular, if $|X_G| = \infty$, then $\tau = \infty$ a.s. In the case that $|X_G|$ is finite, we still have

$$\mathbb{E}[\tau] \geq \mathbb{E}[max\{\xi_1, ...\xi_{|X_G|}\}] = \mathbb{E}[\mathbb{E}[max\{\xi_1, ...\xi_{|X_G|}\}|X_G]].$$

If conditioning on X_G, the $\xi_1, ...\xi_{|X_G|}$ were still independent, then by Lemma 3.1, we see that $\mathbb{E}[max\{\xi_1 ...\xi_{X_G}\}] \gg \mathbb{E}\log(X_G)$, giving (2). The challenge here is that this is not the case. We provide a rigorous treatment as follows.

In this proof, we sample the clocks in two parts:

(1) For each vertex v, we will sample the order of recovery at v and infection clocks from v to its neighbors;
(2) Then we sample the minimum time that an infection or recovery occurs.

More precisely, for each vertex $v \in V$, we have d_v outgoing infection wait times, one to each of its neighbors $v_1, \ldots, v_{d_v}$. For the first step, we only sample the ordering of these $d_v + 1$ wait times (for example, the recovery clock appears in the first place with probability $\frac{1}{1+d_v\lambda}$ and conditioned on that, the infection clock from v to v_1 happens at the second place with probability $\frac{1}{d_v}$). That is, we don't sample the time they occur but just the order at which

these waiting times occur. The result is that $\forall v$, we have sampled a permutation $a_{v,i} \in S_{d_v+1}$ with $i = 0, 1, \dots d_v$, where the 0 represents the recovery time, and for $1 \leq j \leq d_v$, j represents the infection clock for the j-th neighbor.

Using this collection of permutations $(a_{v,i})_{v \in V}$, we construct a directed graph G' with the same vertices as G as follows. For every vertex $v \in G$, its corresponding vertex $v' \in G'$ has an outgoing edge from v' to $u' \in G'$ if:

(1) (v, u) is an edge in G and,
(2) In the permutation $a_{v,i}$ has j before 0, where j corresponds to u in G (u is the j-th neighbor of v in G).

These directed edges represent the infections that go through. Observe that $w \in X_G$ if and only if there exists a path from X_0 to w in G'. Therefore, if we let $\mathcal{O}$ be the sigma-algebra generated by the orderings at all vertices in V, we have $\sigma(X_G) \subset \mathcal{O}$.

Conditioned on $\mathcal{O}$, we now sample the first wait time that occurs for each v, that is $\eta_v = \min\{\text{Exp}(1), \text{Exp}(\lambda_1), \dots, \text{Exp}(\lambda_{d_v})\} = \text{Exp}(\lambda d_v + 1)$, independently for each $v \in V$. By property of exponentials, the $(\eta_v)_v$ is independent of $\mathcal{O}$. In particular, the $(\eta_v)_v$ are independent of X_G. Observe that by memoryless of the exponential distributions, $\tau \geq \max\{\eta_i, ..., \eta_i, ...\eta_{|X_G|}\}$ where each η_i is the wait time of the first action taken of the i-th vertex in X_G. Taking the expected value of both sides, we get

$$\mathbb{E}[\tau|\mathcal{O}] \geq \mathbb{E}[max\{\eta_1, ...\eta_{|X_G|}\}|\mathcal{O}] = \mathbb{E}[\max\{\eta_1 ...\eta_{X_G}\}] \geq \frac{1}{\lambda D + 1} \log(X_G).$$

Since $\sigma(X_G) \subset \mathcal{O}$, by tower property, we obtain (1) and complete the proof of the lemma. □

In this lemma, we show that the survival time is bounded above by the number of ever infected vertices.

Lemma 4.4. *Consider the SIR on any graph G with any initial condition. Let X_G be the set of vertices ever infected. Let τ be the survival time. We have*

(1) $\mathbb{E}[\tau] \leq |V(G)|$,
(2) $\mathbb{E}[\tau] \leq (D+1)\mathbb{E}|X_G|$,

where $D = max_{v \in V} d_v$. In particular, on the event that $|X_G| < \infty$, we have $\tau < \infty$ a.s.

Proof of Lemma 4.4. Let $\xi_1, \xi_2, \dots$ be iid Exp(1) random variables that to be used for the recovery time of the i-th infected vertex ($i = 1, 2, \dots$), if any. We observe that only $\xi_1, \dots, \xi_{X_G}$ are actually used. Almost surely, $\tau \leq \sum_{i=1}^{|X_G|} \xi_i$ since all events involving the i-th infected vertex (i.e., recovery and infection from this vertex) occur during time ξ_i.

Since $X_G \leq |V(G)|$, we have $\tau \leq \sum_{i=1}^{X_G} \xi_i \leq \sum_{i=1}^{|V(G)|} \xi_i$. Taking the expected value of both sides, we get $\mathbb{E}[\tau] \leq |V_G|$ as claimed in the first part of the lemma.

In order to get a bound in terms of X_G, the difficulty is that once we condition on X_G, the distribution of ξ_i changes. Thus we use the same trick as before in Lemma 4.3, where we first condition on the order of actions at each vertex. Once we do so, we get that each ξ_i becomes conditioned on the fact that some of the infections come before it.

Let $\mathcal{O}$ be the sigma-algebra generated by the orderings at all vertices in V as before. Consider the i-th infected vertex v, assume WLOG that under $\mathcal{O}$, vertices $v_1, \dots, v_k$ are infected (in that order), and then v recovers, and then the infection clocks at $v_{k+1}, \dots, v_{d_v}$ ring, also in that order, for some $k \in \{0, \dots, d_v\}$. Let θ_1 be the time it takes for v to infect v_1, then conditioned on $\mathcal{O}$, θ_1 is distributed as $\text{Exp}(1 + d_v\lambda)$. Conditioned on $\mathcal{O}$ and θ_1, let θ_2 be the time it takes from θ_1 until v infects v_2. By memoryless, θ_2 is distributed as

$\mathrm{Exp}(1+(d_v-1)\lambda)$. Similarly, we get θ_3, θ_k. Conditioned on $\mathcal{O}, \theta_1, \dots, \theta_k$, the time θ_0 that it takes from $\theta_1 + \cdots + \theta_k$ until v recovers is an independent $\mathrm{Exp}(1+(d_v-k)\lambda)$. Thus,

$$\begin{aligned}\mathbb{E}(\xi_v|\mathcal{O}) &= \mathbb{E}(\theta_1 + \cdots + \theta_k + \theta_0|\mathcal{O}) \\ &= \mathbb{E}(\mathbb{E}(\theta_1 + \cdots + \theta_k + \theta_0|\mathcal{O}, \theta_1, \dots, \theta_k)|\mathcal{O}) \\ &= \mathbb{E}(\theta_1 + \cdots + \theta_k|\mathcal{O}) + \mathbb{E}(\theta_0|\mathcal{O}, \theta_1, \dots, \theta_k)|\mathcal{O}) \\ &= \mathbb{E}(\theta_1 + \cdots + \theta_k|\mathcal{O}) + \frac{1}{1+(d_v-k)\lambda}.\end{aligned}$$

The final equality comes from the memoryless property, and that $\theta_0|\mathcal{O}$ is a minimum of exponential variables. Repeating this, we get

$$\mathbb{E}(\xi_v|\mathcal{O}) = \sum_{i=0}^{k} \frac{1}{1+(d_v-i)\lambda} \leq \sum_{i=0}^{d_v} \frac{1}{1+i\lambda} \leq \sum_{i=0}^{D} \frac{1}{1+i\lambda} \leq D+1.$$

Thus

$$\mathbb{E}[\tau|\mathcal{O}] \leq \sum_{i=1}^{|X_G|} \mathbb{E}[\xi_i|\mathcal{O}] = |X_G|\mathbb{E}[\xi_i|\mathcal{O}] \leq |X_G|(D+1) = (D+1)|X_G|$$

since X_G becomes a constant once you condition on $\mathcal{O}$. Taking the expected value of both sides, we get $\mathbb{E}[\tau] \leq (D+1)\mathbb{E}[|X_G|]$ as desired. □

Combining Lemmas 4.3 and 4.4, we have the following corollary of Theorem 4.1 about the survival time of the SIR on regular trees.

Corollary 4.5. *[Survival time in regular trees] Consider the SIR on the d-regular tree T_d with the root infected initially where d is a constant.*

1. *(Subcritical) If $\lambda < \frac{1}{d-2}$, then the expected survival time of the SIR process is finite.*
2. *(Critical) If $\lambda = \frac{1}{d-2}$, then a.s. the survival time is finite.*
3. *(Super-critical) If $\lambda > \frac{1}{d-2}$, then with positive probability, the survival time is infinite.*

5. Truncated trees

Theorem 5.1. *Let d be a positive constant. Let τ be the survival time of the SIR on the truncated d-regular tree $T_{d,L}$ of depth L.*

1. *(Subcritical) If $\lambda < \frac{1}{d-2}$, then $\mathbb{E}\tau_L = \Theta(1)$ dependent of L.*
2. *(Super-critical) If $\lambda > \frac{1}{d-2}$, then $\mathbb{E}\tau_L = \Theta_{\lambda,d}(L)$ where the asymptotic is with respect to $L \to \infty$.*

Here the implicit constants only depend on c and d.

The subcritical part follows directly from the corresponding part in Corollary 4.5 as the survival time in the truncated tree is bounded from above by that on the infinite tree. The rest of this section is devoted to the proof of the latter part.

5.1. **Proof of Theorem 5.1 (2): the lower bound.** Note that running the SIR on $T_{d,L}$ is the same as running the SIR on T_d and then project to $T_{d,L}$ because the infection cannot go upwards. By Lemma 3.2 applied to the branching process of the infections defined in the proof of Theorem 4.1, there exist constants ε, c, μ depending only on λ, d such that the set of ever infected vertices $X_{T_{d,L}}$ satisfies

$$\mathbb{P}(|X_{T_{d,L}}| > \varepsilon\mu^L) \geq c.$$

Call this the event A. By Lemma 4.3, we have

$$\mathbf{1}_A \mathbb{E}(\tau | X_{T_{d,L}}) = \mathbb{E}(\tau \mathbf{1}_A | X_{T_{d,L}}) \gg \mathbf{1}_A \log |X_{T_{d,L}}| \gg \mathbf{1}_A L.$$

Thus,

$$\mathbb{E}\tau \geq \mathbb{E}\mathbf{1}_A \mathbb{E}(\tau | X_{T_{d,L}}) \gg \mathbb{P}(A) L \gg L.$$

5.2. **Proof of Theorem 5.1 (2): the upper bound.** The upper bound follows from the following lemmas. In the first lemma, we show that the survival time is bounded by a maximum of $(d-1)^{L-1}$ Gamma random variables where we recall that the sum of L independent random variables with $\text{Exp}(\lambda)$ distribution is $\text{Gamma}(L, \lambda)$.

Lemma 5.2. *Let $G_i \sim Gamma(L, \lambda)$ be independent. Let $Y = max\{G_1, G_2, \dots G_{(d-1)^{L-1}}\}$. Then the time it takes for all ever-infected vertices in T_L to be infected is stochastically dominated by Y.*

In the next lemma, we show that the maximum of $(d-1)^{L-1}$ Gamma random variables has order L.

Lemma 5.3. *Let Y be as in Lemma 5.2. Then $\mathbb{E}Y = \Theta(L)$.*

We note that τ is bounded by the time it takes for all ever-infected vertices in T_L to be infected (denoted by $\tilde{\tau}$), and the time that it takes for all of the infected vertices to recover, which is at most $\frac{1}{\lambda} \log(d^L) = \Theta(L)$ in expectation by Lemma 3.1. By Lemmas 5.2 and 5.3, $\mathbb{E}\tilde{\tau} = \Theta(L)$, proving the desired upper bound in Theorem 5.1. In the rest of this section, we prove these lemmas.

Proof of Lemma 5.2. For each edge (u, v) on T_L with u being the parent, let $t_{u,v}$ be an $\text{Exp}(\lambda)$ clock that represents the time it takes from when u is infected to when it sends the first infection to v (which may not be effective if u recovers before sending the infection).

The time that it takes for every vertex in T_L to receive an infection (whether it is effective or not) is bounded by

$$\max_{v=1:(d-1)^L} \sum_{i=0}^{L-1} t_{v_i, v_{i+1}} \tag{3}$$

where the sum runs over all leaves v of T_L and where $(v_0 = \rho, v_1, \dots, v_{L-1}, v)$ is the path from ρ to v.

Note that for each leaf v, the sum $\sum_{i=0}^{L-1} t_{v_i, v_{i+1}}$ is distributed according $\text{Gamma}(L, \lambda)$. However, these sums are not independent because the paths to different leaves share common edges. So, it is left to show that the expression (3) is dominated by Y, which means we can replace the overlapping terms in (3) by independent copies. This follows from a simple observation: if $X_0, \dots, X_k$ are iid random variables independent from $(Y_i)_{i=1}^k$, then

$$\max\{X_0 + Y_1, \dots, X_0 + Y_k\} \preceq \max\{X_1 + Y_1, \dots, X_k + Y_k\}. \tag{4}$$

Indeed, we first sample the (Y_i) and assume that $Y_i = \max\{Y_1, \dots, Y_k\}$. Conditioned on this event,

$$\max\{X_0 + Y_1, \dots, X_0 + Y_k\} = X_0 + Y_i \stackrel{d}{=} X_i + Y_i \leq \max\{X_1 + Y_1, \dots, X_k + Y_k\}.$$

□

Proof of Lemma 5.3. To lower bound $\mathbb{E}[Y]$, we simply notice that $Y \succeq G_i$, so $\mathbb{E}[Y] \geq \mathbb{E}[G_i] = \frac{L}{\lambda}$. For $\lambda G_i \sim \text{Gamma}(L, 1)$, we can assume for this proof that $\lambda = 1$. Let $n = (d-1)^{L-1}$. For the upper bound, we first bound the tail event that $G_i \gg L$. Let k be a large constant depending on d to be chosen. We will show that

$$\mathbb{P}(G_i \geq k(L-1), \forall i = 1, \dots n) \leq \frac{1}{n^{20}}. \tag{5}$$

Assuming (5), let $\mathcal{A}$ be the event that $Y \geq kL$. Then $\mathbb{E}[Y] = \mathbb{E}[Y\mathbf{1}_{\mathcal{A}}] + \mathbb{E}[Y\mathbf{1}_{\mathcal{A}^c}]$. From the inequality above, we have that $\mathbb{P}(\mathcal{A}) \leq \frac{1}{n^{20}}$.

Clearly, $\mathbb{E}[Y\mathbf{1}_{\mathcal{A}^c}] \leq kL$. We can upperbound $\mathbb{E}[Y\mathbf{1}_{\mathcal{A}}]$ using the Cauchy Schwartz inequality:

$$\mathbb{E}[Y\mathbf{1}_{\mathcal{A}}] \leq \mathbb{E}[Y^2]^{\frac{1}{2}}\mathbb{E}[\mathbf{1}_{\mathcal{A}}^2]^{\frac{1}{2}} = \mathbb{E}[Y^2]^{\frac{1}{2}}\mathbb{E}[\mathbf{1}_{\mathcal{A}}]^{\frac{1}{2}} = \mathbb{E}[Y^2]^{\frac{1}{2}}\mathbb{P}(\mathcal{A})^{\frac{1}{2}}$$

We can obtain an upperbound on $\mathbb{E}[Y^2]$ by examining an upper bound on the variance. Clearly, Y $\preceq Y'$, where $Y' = G_1 + \cdots + G_n$. Thus $\mathbb{E}[Y^2] \leq \mathbb{E}[Y'^2]$ since Y and Y' are nonnegative. We have

$$\mathbf{Var}[Y'] = n \cdot \mathbf{Var}[G_i] = n \cdot \frac{L}{\lambda^2}$$

since the G_i are independent. Also,

$$\mathbb{E}[Y] \leq \mathbb{E}[Y'] = n \cdot \mathbb{E}[G_i] = n \cdot \frac{L}{\lambda}.$$

Thus $\mathbb{E}[Y'^2] = \mathbf{Var}[Y'] + [\mathbb{E}Y']^2 \ll n^2L^2$.

Substituting this back into $\mathbb{E}[Y^2]^{\frac{1}{2}}\mathbb{P}(\mathcal{A})^{\frac{1}{2}}$, we get that

$$\mathbb{E}[Y\mathbf{1}_{\mathcal{A}}] \leq \mathbb{E}[Y^2]^{\frac{1}{2}}\mathbb{P}(\mathcal{A})^{\frac{1}{2}} \ll (n^2L^2)^{\frac{1}{2}}\frac{1}{n^{10}} = L\frac{1}{n^9} \leq L.$$

Thus, we get

$$\mathbb{E}[Y] = \theta(L)$$

as desired.

It's left to prove (5). The pdf of a gamma variable $\text{Gamma}(L, 1)$ is

$$f(x) = \frac{x^{L-1}e^{-x}}{\text{Gamma}(L)} = \frac{x^{L-1}e^{-x}}{(L-1)!}.$$

We have

$$\begin{aligned}
\mathbb{P}(G_i \geq kL) &= \frac{1}{(L-1)!}\int_{kL}^{\infty} x^{L-1}e^{-x}dx \\
&= \frac{1}{(L-1)!}\left(\left[-x^{L-1}e^{-x}\right]_{kL}^{\infty} + (L-1)\int_{kL}^{\infty} x^{L-2}e^{-x}\,dx\right) \\
&\qquad \text{by integration by parts} \\
&= \frac{1}{(L-1)!}(kL)^{L-1}e^{-kL} + \frac{1}{(L-2)!}\int_{kL}^{\infty} x^{L-2}e^{-x}\,dx.
\end{aligned}$$

Note that the last term is the same as the original integration, except with $L-1$ instead of L. Applying integration of parts multiple times, we get

$$\begin{aligned}\mathbb{P}(G_i \geq kL) &= \sum_{j=1}^{L-1} \frac{1}{j!}(kL)^j e^{-kL} + \int_{kL}^{\infty} e^{-x}\,dx \\ &\leq k^L e^{-kL} \sum_{j=0}^{\infty} \frac{L^j}{j!} + e^{-kL} \\ &= k^L e^{-kL+L} + e^{-kL} \leq n^{-21}\end{aligned}$$

for sufficiently large constant k compared to d, where we recall that $n = (d-1)^{L-1}$. By the union bound over i, we get (5) and complete the proof of the Theorem. □

6. SIR on d-regular graphs $G_{n,d}$

Theorem 6.1 (Subcritical)**.** *Let $G_{n,d}$ denote a d-regular graph. Suppose $\lambda < \frac{1}{d-2}$.*
If $|X_0| = k$ is finite, then $\mathbb{E}|X_G|$ and $\mathbb{E}[\tau]$, for the graph $G_{n,d}$, is $\Theta(1)$.

Theorem 6.2. *(Super-critical) Consider the SIR process on the d-regular random graph $G_{n,d}$ with $d \geq 3$, beginning with a random vertex v infected. Assume that $\lambda > \frac{1}{d-2}$. Let τ be the survival time of the infection. Then*

$$\mathbb{E}[\tau] = \Theta(\log n).$$

6.1. **Subcritical phase on random regular graphs.** In this section, we prove Theorem 6.1. To this end, we will use a coupling between SIR on $G_{n,d}$ and that on $\mathbb{T}_d$. In this section we refer to these graphs as G and $\mathbb{T}$.

6.1.1. *Coupling with the regular tree.* We follow Lalley-Su [LS17] but adapt their construction to fit the SIR process. The goal is to run the SIR process on $\mathbb{T}$, and use that to construct a graph G that will follow the law of a random d-regular graph $G_{n,d}$.

We let $\phi : V_{\mathbb{T}} \to [n] \cup \{\text{red}\} \cup \{\text{no-color}\}$ represent the assignment of labels to vertices of $\mathbb{T}$ where red and no-color are just dummy labels (representing vertices that are infected on the tree but do not correspond to a vertex in a graph, and vertices on the tree that never get infected, respectively). The labeling function will determine both the projection from $\mathbb{T}$ to G and the edge structure of G. Let $\tilde{\xi}_t$ represent the set of infected vertices at time t on the tree starting with the root $\tilde{\rho}$ infected. Let ξ_t represent the corresponding process on G, starting with the vertex $\rho = \phi(\tilde{\rho})$ infected.

We often let $\tilde{v}$ represent a vertex in the tree which has the label $v \in [n]$, a vertex in G such that $\phi(\tilde{v}) = v$. At t = 0, only the label $\phi(\tilde{\rho}) = \rho$ is assigned.

In the SIR process, a vertex x "attempts" an infection at rate $d\lambda$. At every infection attempt, one of the d neighbors is chosen with uniform probability $\frac{1}{d}$ and the infection goes to that neighbor. Note that it could be possible that an infection attempt fails to take effect, because the neighbor has already been infected before (and may have recovered or not). It is a property of exponential random variables that this is the same process as running d independent Exp(λ) clocks.

To project $\tilde{\xi}_t$ onto the graph G, the idea is that we will partition the set $\tilde{\xi}_t = \tilde{\xi}_{t,\mathbf{Blue}} \cup \tilde{\xi}_{t,\mathbf{Red}}$, and let the projection

$$\phi(\tilde{\xi}_{t,\mathbf{Blue}}) = \xi_t$$

define the SIR process on the graph while $\phi(\tilde{\xi}_{t,\mathbf{Red}}) = \{\text{red}\}$. Here is how the colors are assigned: at time 0, $\tilde{\rho}$ is blue and the rest does not get any colors yet. At time t, assume that an event happens on $\mathbb{T}$, the graph structure, label function, and ξ_t is updated as detailed below.

- If the event at time t is a recovery of a vertex $\tilde{x}$. If $\tilde{x}$ is blue, then the vertex $\phi(x)$ recovers. Otherwise, nothing happens on the graph.
- If the event at time t is an infection attempt from a red vertex $\tilde{x}$ to another vertex, say $\tilde{v}$. Then nothing happens on the graph. On the tree, $\tilde{v}$ is colored red and we assign $\phi(\tilde{v}) = \text{red}$.
- If the event at time t is an infection attempt from a blue vertex $\tilde{x}$ with $\phi(\tilde{x}) = x$. At this time, some neighbors of $\tilde{x}$ might be labeled, namely $\tilde{y}_1, \dots \tilde{y}_l$ with $\phi(\tilde{y}_i) = y_i$ for $i = 1, \dots, l$. Denote the rest of neighbors by $\tilde{z}_1, \dots \tilde{z}_{d-l}$. At the same time t, the vertex $\phi(\tilde{x}) = x$ in G has some of its neighbors already determined, including $y_1, \dots y_l$, the corresponding labels for labeled neighbors of $\tilde{x}$. However, x may have other neighbors determined, and we call these $y_{l+1}, \dots, y_{l+k}$, where $l + k \leq d$.

  Now, consider a blue vertex $\tilde{x}$ is attempting an infection at time t. Then we have 3 scenarios:

  (1) No label is added in $\mathbb{T}$, and no edge is added in G.
  With probability $\frac{l}{d}$, the infection is sent to one of the its neighbor that has already been labelled. This can be the parent of $\tilde{x}$, or one of its children that it has already infected. In this case, ϕ is not augmented. On the graph G, there is already a determined edge between x and y.

  (2) No edge is added in G.
  With probabilitiy $\frac{k}{d}$, one of the vertices in the tree $\tilde{z}_1, \dots, \tilde{z}_{d-l}$ is chosen randomly, call it $\tilde{w}$. Then one of the labels $y_{l+1}, \dots, y_{l+k}$ is chosen uniformly at random, say w. The vertex w serves as $\tilde{w}$'s label $\phi(\tilde{w})$, i.e. ϕ is augmented so that $\phi(\tilde{w}) = w$ and $\tilde{w}$ is colored red.

  (3) Add an edge to G and label a neighbor in $\mathbb{T}$.
  With probability $1 - \frac{l}{d} - \frac{k}{d}$, the infection is sent to one of the unlabled neighbors $\tilde{z}_1, \dots \tilde{z}_{d-l}$. In this case, an unused half-edge (x, i) incident to x is chosen randomly. Another half-edge (w, j) is uniformly chosen among all remaining unused half-edges. (x, i) and (w, j) are matched to create an edge in G. One of $\tilde{z}_1, \dots \tilde{z}_{d-l}$, say $\tilde{w}$ is randomly selected. If the vertex $w \in G$ has already been assigned to another vertex $\tilde{z}$ that is blue (i.e. $\phi(\tilde{z}) = w$), then $\tilde{w}$ is colored red and $\phi(\tilde{w}) = \text{red}$. Otherwise, $\tilde{w}$ is colored blue and $\phi(\tilde{w}) = w$.

Consider an illustrating example for each of the 3 above cases in Figure 1. At t = 3.54, $\tilde{1}$ infects one of its children in the tree. On the graph, vertex 1 randomly pairs its outgoing half-edge with a half-edge that belongs to 2, which has already been infected and labelled at $t = 2.03$. Thus, this infection attempt results in case 3, where the new edge is established in G, but the child of $\tilde{1}$ will be colored red.

Then at $t = 5.72$, $\tilde{2}$ attempts to infect one of its neighbors. Two of its neighbors, ρ and $\tilde{3}$ have already been infected and labeled. One of its neighbors, call it $\tilde{1}$ corresponds to the edge established between 1 and 2 in G.

If ρ or $\tilde{3}$ is chosen for the infection attempt, this infection attempt would result in case 1, where no infection is sent. If instead $\tilde{1}$ is chosen, then the infection attempt would result in case 2 since the edge already exists in the graph. Thus for the infection at $t = 5.72$, we have

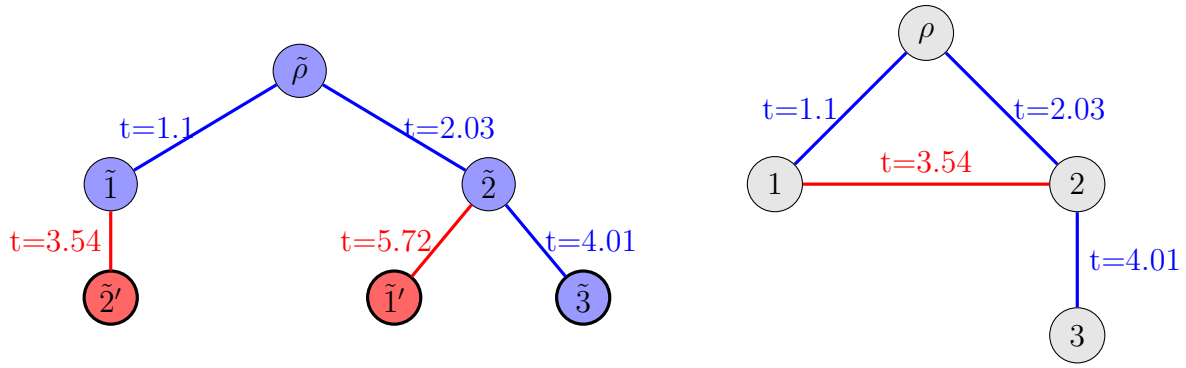

FIGURE 1. Example of a labeling scheme on the tree (left) and the corresponding graph (right).

$l = 2, k = 1$, i.e. there are 2 neighbors established in the tree for $\tilde{2}$, but 3 edges established in the graph for 2.

Note that for every vertex $v \in G$ that is ever infected, there is exactly one corresponding blue vertex $\tilde{v}$ on the tree such that $\phi(\tilde{v}) = v$, i.e. ϕ is injective on the blue vertices. The one-to-one mapping of $\xi = \phi(\tilde{\xi}_{Blue})$ ensures that the projected contact process has the appropriate recovery and infection rates.

At the end of the labeling process (when the blue infection on the tree dies out), we just continue the normal generation of G — randomly matching the rest of the unmatched half edges uniformly. For the remaining vertices $\tilde{v}$ in $\mathbb{T}$ (that do not get infected at all) will get no color and $\phi(\tilde{v}) =$ no-color.

Lemma 6.3. *Conditioned on the resulting graph G being simple, the pair $(G, (\xi_t)_{0\le t\le T})$ will have the same joint distribution as for the SIR process on a random regular graph.*

Proof. The graph G is uniform over $G(n, d)$ because when two unmatched half-edges are paired, the second half-edge is chosen uniformly from the unmatched pool.

The process $(\xi_t)_{0\le t\le T}$ has the same distriubtion as the SIR process on G since the following requirements are met. Conditioned on the final configuration of G, the target vertex for each infection attempt is uniformly selected at random from one of its d neighbors. Additionally, for a vertex $y \in G$ that has been infected, it will never be re-infected. Suppose a blue $\tilde{x}$ infects an unlabeled child $\tilde{z}$ in the tree. Then, say a half edge of $y \in G$ is chosen to match with the outgoing half edge of $x \in G$. If y has not already been an assigned label, it has been unexplored and uninfected up to this point. If y has been assigned as a label to a vertex $\tilde{y} \in T$, then we reach the case where an infection in the tree has already been infected in the graph. However, in this case $\tilde{y}$ will be colored red from the rules above. Thus the infection is not spread on $\tilde{\xi}_{t,\mathbf{Blue}}$ and since $\phi(\tilde{\xi}_{t,\mathbf{Blue}}) = \xi_t$ the infection also does not spread on G. Thus, ξ_t is an SIR contact process on G. □

6.1.2. *Bounding the number of ever-infected vertices on $G_{n,d}$.* In this lemma, we upper bound the number of vertices ever infected in $G_{n,d}$ by that of $\mathbb{T}_d$.

Lemma 6.4. *Denote X_0 as the set of vertices in $G_{n,d}$ that are initially infected. Let X_G be the set of vertices ever infected by an SIR process ξ_t on $G_{n,d}$ which begins with the set X_0 infected. Let $X_{\mathbb{T}}$ denote the set of vertices ever infected by an SIR process on $\mathbb{T}_d$ with the root initially infected.*

If $|X_0| = k$ is finite, then $|X_G| \preceq |X_{\mathbb{T}_1}| + \cdots + |X_{\mathbb{T}_k}|$ where $X_{\mathbb{T}_i}$ are iid copies of $X_{\mathbb{T}}$.

Proof. We start by proving this is true for $k = 1$. We consider the coupling of SIR on $G_{n,d}$ and SIR on $\mathbb{T}_d$ detailed above.The SIR process on the tree corresponds to $\tilde{\xi}_t = \tilde{\xi}_{t,\mathbf{Blue}} \cup \tilde{\xi}_{t,\mathbf{Red}}$. However, the SIR process on $G_{n,d}$ corresponds to $\xi_t = \phi(\tilde{\xi}_{t,\mathbf{Blue}})$. Thus, in this coupling, $|\xi_t| \leq |\tilde{\xi}_t|$. The infection on $\mathbb{T}$ always has more infected vertices than on G. Note also that $|X_G| \leq n$, but $|X_{\mathbb{T}}|$ can grow much larger than n. Since the process on G is dominated ($\forall t, \xi_t \preceq \tilde{\xi}_t$), the set of vertices ever infected will be ordered $|X_G| \preceq |X_{\mathbb{T}}|$.

Now consider the infection ξ with k vertices initially infected $|X_0| = k$. Let the portion of the infection starting from each of the k vertices, be called $\xi_i, 0 \leq i \leq k$, each of which starts from a vertex $v_i \in X_0$. Then $\xi = \cup_{i=1}^k \xi_i$, so $|X_G| \leq \sum_{i=1}^k |X_i|$ where X_i is the number of vertices ever infected by ξ_i.

Now, note that each of the ξ_i is dominated by the process which starts from v_i and does not have any other vertices initially infected, since additional infections can only limit the infection path starting from v_i. Thus, ξ_i is dominated by the infection on the graph starting at v_i, which as we showed earlier is dominated by the coupling above. We get $|X_i| \preceq |X_{\mathbb{T}}|$ and $|X_G| \preceq |X_{\mathbb{T}_1}| + \cdots + |X_{\mathbb{T}_k}|$ as desired. □

6.1.3. *Proof of Theorem 6.1.* By Theorem 4.1 (1), the SIR process on $\mathbb{T}_d$ has $\mathbb{E}X_{\mathbb{T}} < \infty$. By Lemma 6.4, we have that $\mathbb{E}|X_G| \leq \mathbb{E}|X_{\mathbb{T}_1}| + \cdots + \mathbb{E}|X_{\mathbb{T}_k}|$, where $X_{\mathbb{T}_i}$ are iid copies of $X_{\mathbb{T}}$. Thus, $\mathbb{E}X_G$ is $O(1)$. Then by Lemma 4.4, $\mathbb{E}[\tau] \leq (d+1)|X_G|$, so $\mathbb{E}[\tau]$ is $O(1)$ as desired.

6.2. **Proof of Theorem 6.2 for the supercritical case.**

6.2.1. *Lower bound.* Here we will use [BNNS21, Lemma 4.5], which asserts the following on the configuration model with given degree distribution.

Lemma 6.5. *For any degree distribution ν with finite exponential moment $\mathbb{E}e^{cD} < \infty$ for some $c > 0$ where $D \sim \nu$, there exists a constant γ such that with high probability, for all v in the graph $G \sim G_{conf}(n, \nu)$, the neighborhood $N(v, \gamma \log n)$ contains at most one cycle.*

This lemma was similar to [LS10, Lemma 2.1]. We apply this lemma to ν being the point mass at d. To pass the result to random d-regular graphs, we recall the fact that it is contiguous with respect to $G_{\text{conf}}(n, \nu)$.

Lemma 6.6 ([Jan09, vdH17])**.** *Suppose that $\mathbb{E}D^2 < \infty$ where $D \sim \nu$. Then, uniformly in n, we have*

$$\mathbb{P}_{G \sim \mathcal{G}_{conf}(n,\mu)}(G \text{ is simple}) \in (0, 1).$$

In particular, for any subset A_n of graphs with n vertices,

$$\mathbb{P}_{G \sim \mathcal{G}_{conf}(n,\mu)}(G \in A_n) \to 0 \quad \text{implies} \quad \mathbb{P}_{G \sim \mathcal{G}(n,\mu)}(G \in A_n) \to 0.$$

Using these lemma, there exists a constant γ such that with high probability, for all $v \in G_{n,d}$, the neighborhood $N(v, \gamma \log n)$ has at most one cycle. Let $\mathcal{N}$ be the collection of vertices in $N(v, \gamma \log n)$ that is connected to v by a unique path in the neighborhood. Observe that $\mathcal{N}$ is a tree of depth $\gamma \log n$ rooted at v which has d_v children and all other vertices have $d - 1$ children. Here $d_v = d - 2$ if there is one cycle and $d_v = d$ if there is no cycle. Let X_G be the set of ever-infected vertices of the SIR on $G_{n,d}$. By Lemma 4.2, X_G contains $X_{\mathcal{N}}$ which is the set of ever-infected vertices of the SIR on $\mathcal{N}$ only.

Starting with v infected in G, there is a positive constant probability $p = \frac{d_v \lambda}{1 + d_v \lambda} \geq \frac{(d-2)\lambda}{1+(d-2)\lambda}$ such that one of the d_v children is infected. Conditioning on this event, we call one of the

infected children v_1. The descendants of v_1 are now a $d-$regular tree (since there were only branches removed for the original v) that runs for $\gamma \log n - 1$ levels. We denote this tree $\mathbb{T}_{v_1}$, and note $\mathbb{T}_{v_1} \subset \mathcal{N}$. Let $X_{\mathbb{T}_{v_1}}$ be the set of ever-infected vertices of the SIR on $\mathbb{T}_{v_1}$. By 3.2, there exist positive constants c, ε such that with probability at least c,

$$|X_{\mathbb{T}_{v_1}}| \geq c((d-2)\lambda)^{\gamma \log n - 1} \geq c^{\gamma \log n} \geq n^{\varepsilon}.$$

Therefore, on an event of probability $\Theta(1)$, we have $|X_{\mathbb{T}_{v_1}}| \geq n^{\varepsilon}$ and hence, $\mathbb{E}|X_{\mathbb{T}_{v_1}}| \gg n^{\varepsilon}$. By Lemma 4.2, $\mathbb{E}|X_G| \geq \mathbb{E}|X_{\mathcal{N}}| \geq \mathbb{E}|X_G| \gg n^{\varepsilon}$.

By Lemma 4.3, we have that $\mathbb{E}[\tau] \gg_{d,\lambda} (\mathbb{E}[\log |X_G|]) \gg \log n$ as desired.

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