Analysis of the survival time of the SIS and SIRS process on stars and cliques

Tobias Friedrich* Andreas Göbel* Nicolas Klodt*
Martin S. Krejca† Marcus Pappik*

* Hasso Plattner Institute, University of Potsdam, Potsdam, Germany  
{tobias.friedrich, andreas.goebel, nicolas.klodt, marcus.pappik}@hpi.de
† Sorbonne University, CNRS, LIP6, Paris, France 
martin.krejca@lip6.fr

Abstract

We study two continuous-time Markov chains modeling the spread of infections on graphs, namely the SIS and the SIRS model. In the SIS model, vertices are either susceptible or infected; each infected vertex becomes susceptible at rate 1 and infects each of its neighbors independently at rate $\lambda$. In the SIRS model, vertices are either susceptible, infected, or recovered; each infected vertex becomes recovered at rate 1 and infects each of its susceptible neighbors independently at rate $\lambda$; each recovered vertex becomes susceptible at a rate $\varsigma$, which we assume to be independent of the size of the graph. The survival time of the SIS process, i.e., the time until no vertex of the host graph is infected, is fairly well understood for a variety of graph classes. Stars are an important graph class for the SIS model, as the survival time of SIS on stars has been used to show that the process survives on real-world graphs for a long time. For the SIRS model, however, to the best of our knowledge, there are no rigorous results, even for simple graphs such as stars.

We analyze the survival time of the SIS and the SIRS process on stars and cliques. We determine three threshold values for $\lambda$ such that when $\lambda < \lambda_c$, the expected survival time of the process is at most logarithmic, when $\lambda < \lambda_p$, it is at most polynomial, and when $\lambda > \lambda_s$, it is at least super-polynomial in the number of vertices. Our results show that the survival time of the two processes behaves fundamentally different on stars, while it behaves fairly similar on cliques. Our analyses bound the drift of potential functions with globally stable equilibrium points. On the SIRS process, our two-state potential functions are inspired by Lyapunov functions used in mean-field theory.

1 Introduction

Stochastic processes have been used to model a variety of spreading phenomena on networks, such as infections [PCM+15], mutations [Mor58], influence [KKT03], rumors [KSS+00], etc. One such process, studied extensively both empirically [KR08] and theoretically [Lig99], is the SIS model, which considers the spread of an infection on a given graph $G = (V,E)$. The SIS model is
Figure 1: State transitions in the SIS model (left) and the SIRS model (right), with associated transition rates. The letters represent the states of being susceptible (S), infected (I), or recovered (R). Arrows with solid lines indicate that the transition is driven by one Poisson clock with the respective rate per vertex. The arrows with dashed lines between the susceptible and infected states indicate that there is one clock per edge. In the latter case, a susceptible vertex is infected if it has an infected neighbor and the clock that corresponds to their shared edge triggers.

A continuous-time Markov chain where each vertex $v \in V$ is either susceptible or infected. Each infected vertex becomes susceptible at rate 1 and infects each of its neighbors independently at an infection rate $\lambda$ (see Figure 1, left). Since the infection can only spread while at least one vertex is infected, the single absorbing state of the SIS model is the one in which all the vertices of the graph are susceptible. This prompts the question of what the survival time\(^1\) of the process is, i.e., how long it takes until the SIS process reaches its absorbing state.

It is fairly well understood that the survival time of the SIS model exhibits a threshold behavior in terms of its infection rate $\lambda$ on various graphs. On infinite graphs, early results consider the survival time of the SIS model on $\mathbb{Z}^d$ [Har74] and on infinite $d$-regular trees [Lig96; Pem92; Sta96], while recent breakthroughs characterize the survival time on Galton–Watson trees [BNN+21; HD20; NNS22]. On finite structures, the results of Nam, Nguyen, and Sly [NNS22] consider Erdős–Rényi graphs, while the SIS model has also been studied on scale-free graphs [BBC+05; BCG+10]. These results rely on the survival time of the SIS process on simple subgraphs such as stars. Furthermore, Ganesh, Massoulié, and Towsley [GMT05] connect the survival time with the spectral radius and the isoperimetric constant of the host graph, which immediately translates to a variety of simple graphs.

It is less clear what happens if we assume a process where recently healed vertices are immune to re-infection for some time, as is the case for many real-world infections. This augmentation leads to the SIRS model, another continuous-time Markov chain where, in this case, each $v \in V$ is either susceptible, infected, or recovered. Each infected vertex becomes recovered at rate 1 and infects each of its susceptible neighbors independently at an infection rate $\lambda$, while each recovered vertex becomes susceptible at a deimmunization rate $\varrho$ (see Figure 1, right). In the SIRS model, we define the survival time to be the first point in time where there is no infected vertex. The latter is not necessarily the absorbing state, however, one can show that from any such state the process reaches its absorbing state rapidly.

Due to its relevance, there is a vast amount of literature on the survival time of the SIRS model. However, to the best of our knowledge, the results are restricted to be either empirical [KA01;\(^1\) Sometimes also referred to as the extinction time.]
Table 1: Survival time thresholds of SIS and SIRS contact processes on stars and cliques. In the SIRS model, we assume a constant deimmunization rate $\varphi$. With an infection rate $\lambda < \lambda_\ell$, the expected survival time is at most logarithmic in the number of vertices, with $\lambda > \lambda_p$, it is at most polynomial, and with $\lambda > \lambda_s$, the expected survival time is super-polynomial. The $n$ represents the number of vertices in the graph. An $\epsilon$ stands for an arbitrary small constant greater than 0. The thresholds that are not shown in this work are given by Ganesh, Massoulié, and Towsley [GMT05] or follow directly from their results.

| graph | SIS | SIRS |
|-------|-----|------|
|       | $\lambda_\ell$ | $\lambda_p$ | $\lambda_s$ | $\lambda_\ell$ | $\lambda_p$ | $\lambda_s$ |
| star  | $\Theta(n^{-1/2})$ | $\Theta(n^{-1/2+\epsilon})$ | $\Theta(n^{-1/2})$ | none | $\Theta(n^{-1/2})$ |
| clique | $\frac{1}{n-1}$ | $\frac{1}{n-n^{-1\epsilon}}$ | $\frac{1}{n-1} (5.6)$ | $\frac{1}{n-n^{-1\epsilon}}$ | $\frac{1}{n-1} (5.6)$ | $\frac{1}{n} (4.10)$ |

WCA+17, consist of mean-field analysis of the model [BP10], or consider deterministic variants of the model [Sai19]. Although the similarities of the SIRS model with its SIS counterpart suggest that understanding the behavior of SIRS on simple structures could be used to yield results on real-world graph models, this fundamental first step has not been done yet. The absence of rigorous results of the SIRS model even on simple graphs could perhaps be attributed to the fact that the design of potential functions, often used in the analyses of stopping times for stochastic processes, is far more complex when the processes involve more than two states.

Our Contributions We study the survival time of the SIS and the SIRS model on two families of host graphs, namely cliques and stars. Our results show that the survival time behaves similarly on cliques, while it differs significantly on stars. We consider three threshold values for the infection rate of both processes: the logarithmic extinction threshold $\lambda_\ell$, where for $\lambda < \lambda_\ell$, the expected survival time is at most logarithmic in the number of vertices of the host graph; the polynomial extinction threshold $\lambda_p$, where for $\lambda < \lambda_p$, it is at most polynomial; and the super-polynomial survival threshold $\lambda_s$, where for $\lambda > \lambda_s$, the expected survival time is super-polynomial. In our analysis we assume the deimmunization rate $\varphi$ to be constant. To the best of our knowledge, our results include the first rigorous analysis of the survival time of the SIRS model. A summary of our results appears in Table 1.

For the SIRS model on the star with $n \in \mathbb{N}_{>0}$ leaves, we show that the expected survival time is always bounded from above by a function polynomial in $n$ and exponential in the deimmunization rate $\varphi$, regardless of the infection rate $\lambda$ (Theorem 3.4). Thus, no super-polynomial survival threshold exists, similar to the deterministic variant of the process considered by Saif [Sai19]. This is in stark contrast to how the SIS model behaves on stars, where the super-polynomial survival threshold is at $n^{-1/2}$ (see Table 1). In order to see why the behavior is so different for the two models, note that, on a star, leaves can only be infected if the center is infected. In the SIS model, above the super-polynomial survival threshold, while the center is susceptible, not too many leaves heal such that, once the center is infected again, more leaves are infected than were healed.

A vast amount of non-rigorous results exist for the SIS model as well.
In the SIRS model, once the center is healed, it is immune to a reinfection for some time. If \( \varphi \) is independent of \( n \), the expected time until the center becomes susceptible is long enough for sufficiently many infected leaves to recover (and become immune) such that the infection almost surely does not survive for a super-polynomial time.

To explain our focus on stars as host graphs for the two processes under study, let us briefly discuss the arguments used to obtain the long survival time of the SIS model on scale-free graphs [BBC+05] and Galton–Watson trees [BNN+21]. In order to show that the SIS model has super-polynomial survival time on such graphs when \( \lambda \sim \Omega(n^{-1/2+\varepsilon}) \), it is first shown that the infection reaches, with high probability, a vertex \( v \) of high degree (e.g., \( \lambda^{-\Theta(1)} \) for scale-free graphs). Since the infection of the SIS process survives super-polynomially long on a star, it also survives for this long in the neighborhood of \( v \). This serves as a lower bound of the survival time of the infection on the entire graph. Therefore, our results suggest that if a proof of a super-polynomial survival time of the SIRS process on complex graphs exists, it cannot rely exclusively on a star as substructure on that the infection should survive long.

For the clique with \( n \) vertices, we show that, for a value \( \varepsilon \in R_{>0} \) independent of \( n \), the super-polynomial survival threshold is at most \((1 + \varepsilon)/n \) (Theorem 4.10), which is roughly the same value as in the SIS model, that is, the effect of deimmunization seems to be negligible. This showcases that while the two models behave completely different on a star, this difference is not solely due to the addition of the deimmunization rate but also due to the topology of the underlying graph, as the processes seem to have a similar behavior on the clique.

Our proof for the clique relies on a real-valued potential that we assign to the infection process. We prove that once this potential is low, which translates to the process being in a state with a constant fraction of infected vertices, the potential does not increase by much with high probability, translating to the number of infected individuals staying high. Our potential is an extension of the Lyapunov function utilized in the mean-field analysis of the SIRS model on the clique [KW02]. In other words, we transform the insights of mean-field theory into a probabilistic proof of the survival time. We believe this approach to be applicable to other settings analyzed by mean-field theory and, therefore, of independent interest.

Finally, we apply our technique for the analysis of the SIRS model on the \( n \)-clique to the SIS model (in a simplified way), and we derive tighter bounds for the extinction and survival thresholds. We prove, for any value \( \varepsilon \in (0, 1/2) \) independent of \( n \), that the super-polynomial survival threshold is at most \( 1/(n - n^{1/2+\varepsilon}) \) (Theorem 5.4), which improves the previous bound by a lower-order term [GMT05]. We complement this bound by showing that for any \( \alpha \leq n^{1/2} \), the SIS model with \( \lambda = 1/(n - \alpha) \) has an expected survival time polynomial in \( n \) (Theorem 5.6). Together, these bounds show to what degree the infection process needs to infect, in expectation, slightly more than one vertex per unit-time interval in order to become epidemic. We note that our lower bound corrects a minor mistake in the analysis by Ganesh, Massoulić, and Towsley [GMT05].

---

3 The authors claim that, for any value \( \alpha \in R_{>0} \), the infection has a super-polynomial survival time if \( \lambda > 1/(n - n^\alpha) \), which contradicts our result that the process has a polynomial survival time for \( \lambda = 1/(n - n^{-1/2}) \). This is a result of the authors incorrectly applying one of their theorems [GMT05, Corollary 4.1], which requires that \( \lambda(n - n^\alpha) > 1 \) uniformly in \( n \), which is only the case, for all \( \varepsilon \in R_{>0} \) independent of \( n \), if \( \bar{\lambda} > (1 + \varepsilon)/(n - n^\alpha) \). Note that if \( \alpha < 1/2 \), this last expression is greater than our bound.
In the remainder of the introduction (Sections 1.1 to 1.3), we give a more detailed overview of our proofs, and in Section 1.4, we discuss further implications of our results as well as future work.

### 1.1 The SIRS Model on the Star

Our main result for the star is the following theorem, which shows that the expected survival time is bounded from above by an expression independent of the infection rate.

**Theorem 3.4.** Let $G$ be a star with $n \in \mathbb{N}_{>0}$ leaves, and let $C$ be a contact process in the SIRS model on $G$ with infection rate $\lambda$ and with deimmunization rate $\varrho$. Let $T$ be the survival time of $C$. Then $E[T] \in O(n^{4\varrho} \ln(n))$.

If $\varrho \in O(1)$ with respect to asymptotics in $n$, there exists no super-polynomial survival threshold, as the expected survival time is at most polynomial in $n$. If $\varrho \in \omega(1)$, then this result does not tell whether a super-polynomial survival threshold exists or not.

The analysis mainly relies on the method of investigating independent phases in which the center is not infected, bounding the probability of the infection process dying out during that time, as is common [BBC+05; BCG+10]. A phase lasts at most until all leaves’ healing clocks triggered at least once, which occurs in expectation after a time of about $\ln(n)$. Thus, if the center just healed, it needs to become susceptible more quickly than that bound, as otherwise all leaves are healed. Since the triggers of the deimmunization clock follow an exponential distribution with rate $\varrho$, the probability that the center does not become susceptible in this time interval is about $e^{-\varrho \ln n}$, resulting in a probability of about $n^{-\varrho}$ that the infection dies out. Since these phases are independent, the infection processes survives, in expectation, about $n^{\varrho}$ of these trials, each lasting about $\ln(n)$ time in expectation.

Note that the deimmunization rate and the state recovered are important for this argument to hold. Without this additional state, that is, in the SIS model, it is quite likely that the center becomes quickly reinfected before all leaves heal, which leads to the super-polynomial survival threshold of $n^{-1/2}$ in this setting [GMT05].

### 1.2 The SIRS Model on the Clique

In contrast to the star, there exists a super-polynomial survival threshold on the clique if the deimmunization rate is independent of $n$, as our following main result shows.

**Theorem 4.10.** Let $G$ be a clique of size $n \in \mathbb{N}_{>0}$, and let $C$ be a contact process in the SIRS model on $G$ with infection rate $\lambda = \frac{c}{n}$ for a constant $c \in \mathbb{R}_{>1}$ and with constant deimmunization rate $\varrho$. Further, let $C$ start with exactly one infected vertex and no recovered vertices, and let $T$ be the survival time of $C$. Then for sufficiently large $n$, we have $E[T] = 2^{\Omega(n)}$.

The threshold is close to that of the SIS model on the clique, which is around $1/(n - n^{1/2})$ (Theorem 5.4). We note that although these two thresholds are only apart by a constant factor, our result in Theorem 4.10 shows an exponential expected survival time, not only a super-polynomial one. Thus, the actual super-polynomial survival threshold of the SIRS model is likely slightly
lower than what we state. Note that it cannot be much lower though, as our lower bound for the SIS model on the clique (Theorem 5.6) directly translates into the same lower bound for the SIRS model.

We prove Theorem 4.10 by carefully tracking the number of infected, susceptible, and thus also recovered vertices over time. The main reason that the survival time of the process is exponential is that with decent probability, the infection process gets close to a state where changing any of these three values is equally likely. We call this state the equilibrium. The equilibrium is an attractive state, that is, it has a neighborhood in which it is likely that the process gets closer to the equilibrium than moving away from it, which results in an exponential survival time. Theorem 4.10 then follows by showing that the probability of getting into the attractive neighborhood of the equilibrium has a chance that is larger than an inverse exponential function.

In order to formalize the attractive region around the equilibrium, we define a potential function $F$ that maps the current number of infected, susceptible, and recovered vertices to a real value. The minimum of $F$ is the equilibrium, and the potential of the SIRS process decreases in expectation, if there is a constant fraction of infected vertices in the attractive neighborhood of the equilibrium. Thus, $F$ is a strict supermartingale in this regime, and we apply a concentration bound by Oliveto and Witt [OW11] (Theorem 2.2) for strict supermartingales, known as negative-drift theorem, based on an intricate theorem by Hajek [Haj82]. The negative-drift theorem results in the lower exponential bound of the survival time.

Our definition of $F$ is based on a Lyapunov function $f$ used by Korobeinikov and Wake [KW02] in order to derive results on the global stability of the SIRS model via mean-field theory. Their function $f$ is already well suited for our purposes but is minimal for all values such that the number of susceptible vertices is equal to that of the equilibrium (regardless of the other values). In order to define a potential that has a unique minimum and thus yields a strict supermartingale, we appropriately augment $f$.

For showing that the infection processes ends up in a state such that $F$ is a strict supermartingale, we utilize an easier potential function that results in a submartingale. Applying the optional-stopping theorem to this potential function yields a sufficient probability bound.

We note that the key features to our proof method are, as is often the case with hitting-times of stochastic processes, the potential functions. However, the more involved potential function $F$ is based on an established Lyapunov function used in a mean-field theoretic approach for the same setting. As Lyapunov functions have been identified for a variety of processes, we believe that our approach could be used for rigorous analyses of the absorption time of such processes.

### 1.3 The SIS Model on the Clique

For the SIS model on the clique, we present two results that, jointly, provide a tighter super-polynomial survival threshold than the one previously known. The first result provides an upper bound on the threshold.

> **Theorem 5.4.** Let $G$ be a clique with $n \in \mathbb{N}_{>0}$ vertices, and let $C$ be a contact process in the SIS model on $G$ with infection rate $\lambda = \frac{1}{n-\alpha}$, for some $\alpha \in \mathbb{N}_{<n/2}$, that starts with at least one infected
vertex. Further, let there be a constant \( \varepsilon \in (0, 1/2) \) such that \( \alpha \geq n^{1/2+\varepsilon} \). Let \( T \) be the survival time of \( C \). Then

\[
E[T] \in \Omega(1.5^{n/\varepsilon}).
\]

The second result provides a lower bound that almost matches the upper one.

\begin{tcolorbox}
\textbf{Theorem 5.6.} Let \( G \) be a clique with \( n \in \mathbb{N}_{>0} \) vertices and let \( C \) be a contact process in the SIS model on \( G \) with infection rate \( \lambda = \frac{1}{n-\alpha} \) for some \( \alpha \in \mathbb{N}_{>0} \) with \( \alpha \leq n^{1/2} \) that starts with at least one infected vertex. Let \( T \) be the survival time of \( C \). Then

\[
E[T] \in O(n^2 \ln(n)).
\]

The previously best known upper and lower bound were, respectively, for any \( \varepsilon \in \mathbb{R}_{>0} \) independent of \( n \) and for any \( \alpha \in \mathbb{R}_{>0} \), \( (1+\varepsilon)/(n-n^\varepsilon) \) as well as \( 1/(n-1) \) [GMT05].

Our analysis for both results is similar to our analysis for the SIRS model on the clique in the sense that we consider again the equilibrium state, where the probability to decrease the number of infected vertices is equal to increasing it. We denote the number of infected vertices in the equilibrium by \( \alpha \). For both bounds, we utilize that the number of infected vertices, once above \( \alpha \), returns in expectation to \( \alpha \) in a time of at most about \( n \ln(n) \), which we prove by reducing the infection process in that regime to one on a smaller clique, for which the expected survival time is known. This leaves us with considering the regime when the number of infected vertices is close to and below \( \alpha \).

For both results, the infection process is similar to a biased gambler’s ruin process. For the upper bound, we split the process into independent phases each of which starts as soon as the process reaches \( \alpha/2 - 1 \) infected vertices. For each of the phases, we derive a probability bound of the infection dying out before reaching to a state with \( \alpha/2 \) infected vertices. For the lower bound, we consider the probability that the infection process dies out before reaching \( \alpha \). Since we derived beforehand that the process returns to \( \alpha \) quickly, once it is above it, we apply again a restart argument, which yields the result.

\subsection*{1.4 Discussion and Outlook}

Although inspired by mean-field theory, our analysis is fundamentally different. Mean-field theory shows the existence of an equilibrium that is globally stable, i.e. that there exists a state of the process, given in terms of number of infected vertices (together with the number of recovered vertices, if we consider the SIRS model) such that the whole process drifts towards that state. For example, for the SIS model on the clique, with \( \lambda = (n - \alpha)^{-1} \), this equilibrium is where the process has \( \alpha \) infected vertices. However, solely knowing that such an equilibrium exists does not suffice for determining the survival time of the process. In our previous example, \( \alpha = 1 \) yields a logarithmic extinction time, \( \alpha \in O(n^{1/2}) \) yields a polynomial extinction time, while \( \alpha \in \Omega(n^{1/2+\varepsilon}) \) yields a super-polynomial survival time. In order to obtain our results, we perform a refined analysis, determining the strength of the stochastic drift for each possible location of the equilibrium point.
This analysis becomes significantly more challenging when the equilibrium point is determined by more than one degree of freedom, which is the case for the SIRS model.

Assuming a constant deimmunization rate, our results show that the super-polynomial survival threshold of the SIRS model is fundamentally different from that of the SIS model on a star but not on a clique. Since the SIRS model does not have a super-polynomial survival threshold on the star in this regime but on the clique, our results highlight the importance of the topology of the network in the SIRS model. We note that real-world networks seem to be well-captured by random graph models with an underlying geometry [BBD+20], and graphs with an underlying geometry have been shown to contain large cliques [BFK18] (of size $\sqrt{n}$). Although promising, it is unclear whether cliques can be used as basic structures for the analysis of the SIRS model on such real-world network models. This is for two reasons: (a) it is not proven whether, starting with an arbitrary infected vertex, the infection reaches the vertices of the clique; (b) we do not know how the additional vertices and edges that do not belong in the clique affect the survival time. To see point (b), note that it is not obvious whether the survival time of the SIRS model increases when adding vertices and edges on the host graph, in contrast to the SIS model.

Our results for the super-polynomial survival threshold for the SIS model are already very close but still not matching. The exact location of the threshold (or whether such a threshold can be derived at all) remains an open problem. A further interesting question is how the survival time of the infection process scales with the infection rate once it is below the super-polynomial survival threshold. Ganesh, Massoulié, and Towsley [GMT05] provide a large parameter regime for which the expected survival time is at most logarithmic in the number of vertices. Our bound on the expected survival time (for larger infection rates still below the super-polynomial survival threshold) is only polynomial in the number of vertices. Future research can look more closely into this regime of the infection rate and try to see whether the expected survival time is still logarithmic for some infection rates and when the transition to super-logarithmic time occurs.

\section{Preliminaries}

We study contact processes on graphs in the SIS model and the SIRS model. Both are continuous-time Markov chains on a graph in which the vertices change between different states, following events triggered by Poisson processes. We analyze how these processes behave asymptotically in the number of vertices $n$ of the graph. Especially, when we use big-O notation or refer to variables as constants, this is with respect to $n$. If not stated otherwise, all variables we consider may depend on $n$. Whenever we talk about Poisson processes, we refer to one-dimensional Poisson point processes that output a random subset of the non-negative real numbers.

We first define our infection models and some related terms that we use throughout the paper. We then state the probabilistic tools we use in the proofs.

\subsection{Infection Processes}

Let $G = (V, E)$ be a graph with vertex set $V$ and edge set $E$. Further, let $\lambda, \gamma \in \mathbb{R}_{>0}$. In the SIRS model, for each edge $e \in E$, we define a Poisson process $M_e$ with parameter $\lambda$, and for each vertex
\(v \in V\), we define the two Poisson processes \(N_v\) with parameter 1 and \(O_v\) with parameter \(\varrho\). We refer to these processes as clocks, and when an event occurs in one of them, we say that the relevant clock triggers. We use \(Z\) to denote the set of all of these clocks, that is, \(Z = (\bigcup_{e \in E} \{M_e\}) \cup (\bigcup_{v \in V} \{N_v, O_v\})\). Let \(P\) denote the stochastic process in which all of the clocks in \(Z\) evolve simultaneously and independently, starting at time 0. Note that almost surely there is no time point at which two clocks trigger at once. There are almost surely a countably infinite number of trigger times in \(P\), which we index by the increasing sequence \(\{\tau_i\}_{i \in \mathbb{N}_{>0}}\), where \(\tau_0 = 0\).

A contact process \(C = (C_t)_{t \in \mathbb{R}_{\geq 0}}\) in the SIRS model has an underlying graph \(G = (V, E)\), an infection rate \(\lambda\), a deimmunization rate \(\varrho\), and an initial partition of \(V\) into susceptible, infected, and recovered vertices with the respective sets \(S'_0, I'_0\), and \(R'_0\). At every time \(t \in \mathbb{R}_{\geq 0}\), the state \(C_t\) is a partition of \(V\) into \(S'_t, I'_t\), and \(R'_t\). The state only changes at times in \(P\). Let \(i \in \mathbb{N}_{>0}\). We consider the following state transitions in \(\gamma_i\).

- If for some \(e = \{u,v\} \in E\) we have \(\gamma_i \in M_e, u \in I'_{y_{i-1}}, \text{and} v \in S'_{y_{i-1}}\), then \(S'_{y_i} = S'_{y_{i-1}} \setminus \{v\}\), \(I'_{y_i} = I'_{y_{i-1}} \cup \{v\}\), and \(R'_{y_i} = R'_{y_{i-1}}\). We say that \(v\) gets infected at time point \(y_i\) by \(u\).

- If for some \(v \in V\) we have \(\gamma_i \in N_v\) and \(v \in I'_{y_{i-1}}\), then \(S'_{y_i} = S'_{y_{i-1}}, I'_{y_i} = I'_{y_{i-1}} \setminus \{v\}\) and \(R'_{y_i} = R'_{y_{i-1}} \cup \{v\}\). We say that \(v\) recovers at time point \(y_i\).

- If for some \(v \in V\) we have \(\gamma_i \in O_v\) and \(v \in R'_{y_{i-1}}\), then \(S'_{y_i} = S'_{y_{i-1}} \cup \{v\}\), \(I'_{y_i} = I'_{y_{i-1}}\), and \(R'_{y_i} = R'_{y_{i-1}} \setminus \{v\}\). We say that \(v\) gets susceptible at time point \(y_i\).

If none of the above three cases occurs, the state of \(C\) at \(y_i\) is the same as the state of \(C\) at \(y_{i-1}\). Note that at all times between \(y_{i-1}\) and \(y_i\), \(C\) retains the same state as in \(y_{i-1}\).

In our proofs, we only consider the time points in \(P\) at which the state changes. To this end, let \(P' = \{y_0\} \cup \{y_i \mid i \in \mathbb{N}_{>0} \wedge C_{y_i} \neq C_{y_{i-1}}\}\). We index the times in \(P'\) by the increasing sequence \(\{\tau_i\}_{i \in \mathbb{N}}\). For all \(i \in \mathbb{N}\), we call \(\tau_i\) the \(i\)-th step of the process.

Contact processes in the SIS model are very similar to those in the SIRS model, with the difference that they have no deimmunization rate. That is, for an SIS process, we assume that the sets \(O_v\) and \(R'_v\) remain empty at all times and vertices that recover are added to \(S'_v\) instead of \(R'_v\).

In both models, the state in which \(S'_v = V\) is an absorbing state. As this state is the only absorbing state, it is reached almost surely at some point. In this article, we analyze how long it takes for the process to reach this state. We say that the infection dies out or goes extinct at the first (random) time \(T\) with \(I'_T = \emptyset\). We call \(T\) the survival time of the contact process. Observe that at \(T\), in the SIS model, the absorbing state is reached, while in the SIRS model, some of the vertices in \(V\) might be in \(R'_T\).

The graphs \(G\) we consider are cliques and stars. We give thresholds for the infection rate \(\lambda\) above or below which the survival time scales in a specific way with respect to \(n\).

- We call a threshold \(\lambda_l\) a logarithmic extinction threshold if for all \(\lambda \leq \lambda_l\) holds \(E[T] \in O(\ln(n))\).

- We call a threshold \(\lambda_p\) a polynomial extinction threshold if there exists a constant \(c \in \mathbb{R}\) such that for all \(\lambda \leq \lambda_p\) holds \(E[T] \in O(n^c)\).
• We call a threshold $\lambda_s$ a **super-polynomial survival threshold** if there exists a constant $c \in \mathbb{R}$ such that for all $\lambda \geq \lambda_s$ holds $E[T] \in \Omega(2^{\alpha \lambda})$.

We only keep track of the number of vertices in each of the sets. To this end, we define for all $t \in \mathbb{R}_{\geq 0}$ the random variables $S_t = |S'_t|$, $I_t = |I'_t|$, and $R_t = |R'_t|$. These random variables change depending on the Poisson clocks in $P$. We say that an event happens at a rate of $r$ if the set of Poisson clocks that cause this event when they trigger has a sum of rates $r$.

We use stochastic domination to transfer results from one random variable to another. We say that a random variable $(X_t)_{t \in \mathbb{R}}$ dominates another random variable $(Y_t)_{t \in \mathbb{R}}$ if there exists a coupling $(X'_t, Y'_t)_{t \in \mathbb{R}}$ in a way such that for all $t \geq 0$ we have $X'_t \geq Y'_t$.

### 2.2 Probabilistic Tools

We use general concepts from probability theory (see for example [Fel68; MU05]). In addition, we use the following theorems.

We use the optional-stopping theorem for submartingales to bound the probability of reaching a specific state.

**Theorem 2.1 (Optional stopping [MU05, page 298])**. Let $(X_t)_{t \in \mathbb{N}}$ be a submartingale and $T$ a stopping time, both with respect to a filtration $(\mathcal{F}_t)_{t \in \mathbb{N}}$. Assume that the following two conditions hold:

1. $E[T] < \infty$;
2. There is a $c \in \mathbb{R}$ such that for all $t \in \mathbb{N}$ we have $E[|X_{t+1} - X_t| \mid \mathcal{F}_t] \cdot 1 \{t < T\} \leq c \cdot 1 \{t < T\}$.

Then $E[X_T] \geq E[X_0]$.

We use the following theorem in order to show a super-polynomial survival time for a contact process. We state it in a fashion that better suits our purposes.

**Theorem 2.2 (Negative drift [OW11, Theorem 4] [OW12])**. Let $(X_t)_{t \in \mathbb{N}}$ be a random process over $\mathbb{R}$, adapted to a filtration $(\mathcal{F}_t)_{t \in \mathbb{N}}$. Let there be an interval $[a, b] \subseteq \mathbb{R}$, two constants $\delta, \varepsilon \in \mathbb{R}_{\geq 0}$ and, possibly depending on $l = b - a$, a function $r(l)$ satisfying $1 \leq r(l) = o(l/\log(l))$. Let $T = \inf \{t \geq 0 \mid X_t \geq b\}$. Suppose that for all $t \in \mathbb{N}$ the following two conditions hold:

1. $E[X_{t+1} - X_t \mid \mathcal{F}_t] \cdot 1 \{a < X_t < b\} \leq -\varepsilon \cdot 1 \{a < X_t < b\}$,
2. For all $j \in \mathbb{R}_{\geq 0}$ we have $\Pr[|X_{t+1} - X_t| \geq j \mid \mathcal{F}_t] \cdot 1 \{t < T\} \leq \frac{r(l)}{(1 + \delta) r(l)} \cdot 1 \{t < T\}$.

Then there exists a constant $c \in \mathbb{R}_{\geq 0}$ such that

$$\Pr[T \leq 2^{c l / r(l)} \mid \mathcal{F}_0] \cdot 1 \{X_0 \leq a\} = 2^{\Omega(l / r(l))} \cdot 1 \{X_0 \leq a\}.$$

We derive polynomial upper bounds for the survival time via the following theorem.
Theorem 2.3 (Additive drift [KK19, Theorem 4], [HY01]). Let \((X_t)_{t \in \mathbb{N}}\) be a random process over \(\mathbb{R}\), adapted to a filtration \((\mathcal{F}_t)_{t \in \mathbb{N}}\). Further, let \(T = \inf\{t \mid X_t \leq 0\}\), and let \(\delta \in \mathbb{R}_{>0}\). Suppose that for all \(t \in \mathbb{N}\) the following two conditions hold:

1. \(X_t \cdot 1\{t \leq T\} \geq 0\),
2. \(E[X_t - X_{t+1} \mid \mathcal{F}_t] \cdot 1\{t < T\} \geq \delta \cdot 1\{t < T\}\).

Then \(E[T \mid \mathcal{F}_0] \leq X_0/\delta\).

The following theorem bounds the expected value of the maximum of \(n\) exponentially distributed random variables.

Theorem 2.4 ([MU05, page 33]). Let \(n \in \mathbb{N}_{>0}\), and let \(\{X_i\}_{i \in [n]}\) be independent random variables that are each exponentially distributed with parameter \(\lambda \in \mathbb{R}_{>0}\). Let \(m = \max_{i \in [n]} X_i\), and let \(H_n\) be the \(n\)-th harmonic number. Then

\[
E[m] = \frac{H_n}{\lambda} < \frac{1 + \ln(n + 1)}{\lambda}.
\]

We use the following version of Wald’s equation, which does not require the addends to be independent.

Theorem 2.5 (Generalized Wald’s equation [DK22, Theorem 5]). Let \(c, c' \in \mathbb{R}\), and let \((X_t)_{t \in \mathbb{N}}\) be a random process over \(\mathbb{R}_{\geq c}\) such that \(\sum_{i \in [S]} X_i\) is integrable. Furthermore, let \((\mathcal{F}_t)_{t \in \mathbb{N}}\) be a filtration, and let \(S\) be a stopping time with respect to \(\mathcal{F}\). If for all \(i \in \mathbb{N}\) we have \(E[X_{i+1} \mid \mathcal{F}_i] \leq c'\), then

\[
E\left[\sum_{i \in [S]} X_i \mid \mathcal{F}_0\right] = E\left[\sum_{i \in [S]} E[X_i \mid \mathcal{F}_{i-1}] \mid \mathcal{F}_0\right].
\]

Some of the processes that we analyze are very similar to the well-known gambler’s ruin problem, as they increase and decrease by one with certain probabilities until they reach a limit in either direction. We consider the following version of the gambler’s ruin problem.

Theorem 2.6 (Gambler’s ruin [Fel68, page 345]). Let \(n \in \mathbb{N}_{>0}\), and let \(\{X_i\}_{i \in [n]}\) be independent random variables that are each exponentially distributed with parameter \(\lambda \in \mathbb{R}_{>0}\). Let \(m = \max_{i \in [n]} X_i\), and let \(H_n\) be the \(n\)-th harmonic number. Then

1. \(\Pr[P_T = l] = \frac{1-(p/q)^{n+P_0}}{1-(p/q)^{n+T}}\),
2. \(\Pr[P_T = u] = \frac{1-(q/p)^{P_0-l}}{1-(q/p)^{u-T}}\).
3 SIRS Star

In this section, we show that in the SIRS model on stars, the expected survival time is upper bounded by a polynomial in the number of vertices that is independent of the infection rate. To this end, we bound the number of times that the center becomes infected and the time in between two infections of the center. We use the fact that while the center is not infected, no leaf gets infected. Hence, if all of the leaves heal before the center becomes susceptible after it recovered, the infection dies out.

We first bound the expected time that it takes for all of the leaves to become healthy.

Lemma 3.1. Let $G$ be a star with $n \in \mathbb{N}_{>0}$ leaves and let $C$ be a contact process in the SIRS model on $G$ with infection rate $\lambda$ and with deimmunization rate $\varphi$. Let $T$ be the time that it takes for all healing clocks of the leaves to trigger at least once. Then $E[T] \leq \ln(n) + 2$.

Proof. The star has $n$ leaves, which all have a Poisson clock that heals them at a rate of 1. For each of the clocks, the time until the first trigger happens is exponentially distributed with parameter 1. Hence, $T$ is calculated as the maximum of the $n$ exponential distributions of the independent clocks. By Theorem 2.4, $E[T] \leq \ln(n + 1) + 1 \leq \ln(n) + 2$.

We now use the previous lemma to bound the time it takes from one infection of the center until it gets infected again or until the infection dies out.

Lemma 3.2. Let $G$ be a star with $n \in \mathbb{N}_{>0}$ leaves and let $C$ be a contact process in the SIRS model on $G$ with infection rate $\lambda$ and with deimmunization rate $\varphi$. Let $T_0$ be a time at which the infection has not died out yet. Further, let $T \in \mathbb{R}_{\geq 0}$ be the first time after $T_0$ at which either the center gets infected after being healthy or the infection dies out. Then $E[T - T_0] \leq \ln(n) + 3$.

Proof. If the center starts infected, in order for either the center to get infected again after being healthy or the infection to die out, the center has to recover first. Let $T' \in \mathbb{R}$ be the first time after $T_0$ at which the center recovers. As all vertices recover at a rate of 1, $T' - T_0$ is exponentially distributed with a parameter of 1.

Between $T'$ and $T$, no leaf gets infected as the center is not infected and all edges are incident to the center. Hence, when all healing triggers of the leaves trigger in this time interval at least once, the infection dies out. Therefore, the last of these healing triggers after $T'$ is an upper bound for $T$. By Lemma 3.1, the expected time for this last trigger to happen is at most $\ln(n) + 2$. That gives us

$$E[T - T_0] = E[T - T' + T' - T_0] = E[T - T'] + E[T' - T_0] \leq \ln(n) + 3.$$ 

Next, we lower bound the probability that starting with an infected center, the infection dies out before the center gets infected again. We use that later to get an upper bound on the number of times that the center gets infected in total.
Lemma 3.3. Let \( G \) be a star with \( n \in \mathbb{N}_{>0} \) leaves and let \( C \) be a contact process in the SIRS model on \( G \) with infection rate \( \lambda \) and with deimmunization rate \( \varphi \). Let \( t_0 \in \mathbb{R}_{\geq 0} \) be a time at which the center is infected. Further, let \( E_0 \) be the event that the infection dies out after \( t_0 \) before the center gets infected again. Then for sufficiently large \( n \) it holds that \( \Pr[E_0] \geq \frac{1}{2} n^{-4\varphi} \).

Proof. In order for either the center to get infected again after being healthy or the infection to die out, the center has to recover first. Let \( t_1 \in \mathbb{R} \) be the first time after \( t_0 \) at which the center recovers. As long as the center is in the recovered state, no vertex gets infected as all edges of the graph are incident to the center. If all leaves heal before the center leaves the recovered state, the infection dies out. To bound the probability of that, we consider the first time \( T \in \mathbb{R} \) after \( t_1 \) at which the center gets susceptible and the first time \( T' \in \mathbb{R} \) after \( t_1 \) at which all of the healing triggers of the leaves trigger at least once in the interval \((t_1, T')\). In particular, we use that all leaves heal before the center leaves the recovered state if \( T' - t_1 < 4 \ln(n) \) and \( T - t_1 \geq 4 \ln(n) \).

By Lemma 3.1, it holds that \( \mathbb{E} [T' - t_1] \leq \ln(n) + 2 \). By Markov’s inequality it holds for sufficiently large \( n \) that \( \Pr[T' - t_1 \geq 4 \ln(n)] \leq \Pr[T' - t_1 \geq 2 \mathbb{E} [T' - t_1]] \leq \frac{1}{2} \).

All vertices lose their immunity at a rate of \( \varphi \). Hence, \( T - t_1 \) is exponentially distributed with parameter \( \varphi \). Using the exponential probability distribution, we get

\[
\Pr[T - t_1 \geq 4 \ln(n)] = e^{-4\varphi \ln(n)} = n^{-4\varphi}.
\]

Now using the fact that the infection dies out when all leaves heal before the center gets susceptible and that \( T - t_1 \) and \( T' - t_1 \) are independent, we get

\[
\Pr[E_0] \geq \Pr[T' - t_1 < T - t_1] \\
\geq \Pr[T' - t_1 < 4 \ln(n) \land T - t_1 \geq 4 \ln(n)] \\
= \Pr[T' - t_1 < 4 \ln(n)] \cdot \Pr[T - t_1 \geq 4 \ln(n)] \\
\geq \frac{1}{2} n^{-4\varphi}.
\]

Using the previous bounds, we now upper bound the expected survival time of an SIRS contact process on a star.

Theorem 3.4. Let \( G \) be a star with \( n \in \mathbb{N}_{>0} \) leaves, and let \( C \) be a contact process in the SIRS model on \( G \) with infection rate \( \lambda \) and with deimmunization rate \( \varphi \). Let \( T \) be the survival time of \( C \). Then \( \mathbb{E}[T] \in O(n^{4\varphi} \ln(n)) \).

Proof. Let \( S \) be the random variable that counts the number of times that the center gets infected before the infection dies out. For all \( i \in \mathbb{N}_{\leq S+1} \), let \( X_i \) be the \( i \)-th time at which either the center gets infected or the infection dies out (we define \( X_0 = 0 \)). It then holds that \( T = X_{S+1} = \sum_{i=0}^{S} X_{i+1} - X_i \). We aim to bound the expectation of that value using the generalized Wald’s equation (Theorem 2.5).
Let \((\mathcal{F}_t)_{t \in \mathbb{R}_{\geq 0}}\) be the natural filtration of \(C\). By Lemma 3.2, it holds for all \(i \in \mathbb{N}_{\leq S}\) that 
\[0 \leq E \left[ X_{i+1} - X_i \bigg| \mathcal{F}_{t} \right] \leq \ln(n) + 3.\] Hence, the expectations of all of the summed random variables are bounded. By Lemma 3.3, for all \(i \in \mathbb{N}_{\geq 1}\), the \(i\)-th infection of the center has a probability of at least \(\frac{1}{2} n^{-4\theta}\) to be the last one if there is an \(i\)-th infection of the center. Therefore, \(S\) is dominated by a geometrically distributed random variable \(A \sim \text{Geom}(\frac{1}{2} n^{-4\theta})\). Hence, \(\sum_{i=0}^{\infty} X_{i+1} - X_i\) is integrable. By Theorem 2.5, we get

\[
E[T \mid \mathcal{F}_0] = E \left[ \sum_{i=0}^{S} X_{i+1} - X_i \bigg| \mathcal{F}_0 \right] \\
= E \left[ \sum_{i=0}^{S} E \left[ X_{i+1} - X_i \bigg| \mathcal{F}_{X_i} \right] \bigg| \mathcal{F}_0 \right] \\
\leq E \left[ \sum_{i=0}^{S} \ln(n) + 3 \bigg| \mathcal{F}_0 \right] \\
= (\ln(n) + 3) E \left[ \sum_{i=0}^{S} 1 \bigg| \mathcal{F}_0 \right] \\
\leq (\ln(n) + 3)(2n^{4\theta} + 1).
\]

## 4 SIRS Clique

In this section, we consider the SIRS model for infections on cliques. In particular, we give a super-polynomial survival threshold for these contact processes when the deimmunization rate is constant. We begin in Section 4.1 by analyzing basic properties of the process, such as the transition rates between all of the states and the exact number of susceptible, infected and recovered vertices in the equilibrium state.

In Section 4.2 we show that the expected survival time of the considered contact processes is super-polynomial if, for some constant \(c \in \mathbb{R}_{>1}\), it holds that \(\lambda = \frac{c}{n}\). To this end, we first prove that the process reaches a state with at least \(cn^2\) infected vertices with sufficiently high probability. We then provide a lower bound for the expected survival time starting at this state. To this end, we define a potential over the state space that has a constant negative drift away from the all healthy state in a specific region. We then translate this region into bounds for the potential, allowing us to apply the negative drift theorem to get a super-polynomial expected survival time.

### 4.1 The SIRS Contact Process

Let \(G = (V, E)\) be a clique with \(n\) infected vertices. Consider a contact process \(C\) with infection rate \(\lambda\) and deimmunization rate \(\varphi\) on \(G\). We define for all \(t \in \mathbb{N}\) the random variables

\[P_{r_t} = S_{r_t} + \frac{\varphi}{\lambda}\]

and \(Q_{r_t} = R_{r_t} + \frac{\varphi}{\lambda}\). We use these two random variables to define the potential later. Note that, at
all times $t$, $S_t + I_t + R_t = n$, since every vertex of $G$ is always in exactly one of these three sets. Additionally, $P_t + I_t + R_t = n + \frac{c}{\lambda} = n'$.

For all $t \in \mathbb{N}$, one of the following three events occurs at step $t + 1 (\tau_{t+1})$: either a susceptible vertex is infected, which we call $E_{s,i,t}$; or an infected vertex recovers in the event $E_{i,r,t}$; or a recovered vertex loses its immunity which is called $E_{r,s,t}$. At the time point $\tau_t$, vertices get infected at a rate of $r_{s,i,t} = \lambda I_t P_t - q I_t$, because every infected vertex infects each susceptible vertex at a rate of $\lambda$. Vertices recover from an infection at a rate of $r_{i,r,t} = I_t$ and lose their immunity at a rate of $r_{r,s,t} = q R_t$. Now let $r_t = r_{s,i,t} + r_{i,r,t} + r_{r,s,t}$. We get

$$p_{s,i,t} = \Pr[E_{s,i,t}] = \frac{r_{s,i,t}}{r_t} = \frac{\lambda I_t P_t - q I_t}{r_t},$$

$$p_{i,r,t} = \Pr[E_{i,r,t}] = \frac{r_{i,r,t}}{r_t} = \frac{I_t}{r_t}, \quad \text{and}$$

$$p_{r,s,t} = \Pr[E_{r,s,t}] = \frac{r_{r,s,t}}{r_t} = \frac{q R_t}{r_t}.$$

Note that we only consider these probabilities in states in which at least one vertex is infected, hence $r_t \neq 0$, hence the above probabilities are well-defined. We now define $S^*, P^*, I^*, R^*$ and $Q^*$ as the values of the process at the equilibrium state where all of the three events are equally likely. We calculate $S^*$ and $P^*$ by solving $p_{s,i,t} = p_{i,r,t}$ for $S_t$, or $P_t$, respectively. The values for $I^*$ and $R^*$ are then calculated with the equations $I^* + R^* = n - S^*$ and $P_{i,r,t} = p_{r,s,t}$. We get

$$S^* = \frac{1}{\lambda},$$

$$P^* = \frac{1 + q}{\lambda},$$

$$I^* = \frac{q (n - \frac{1}{\lambda})}{1 + q},$$

$$R^* = \frac{(n - \frac{1}{\lambda})}{1 + q}, \quad \text{and}$$

$$Q^* = R^* + \frac{q}{\lambda}.$$

### 4.2 Super-polynomial survival threshold

We now aim to show that the infection becomes epidemic when $\lambda = \frac{c}{n}$ for some $c \in \mathbb{R}_{>1}$ that is constant with respect to $n$. We start by proving that, when starting with one infected vertex, the infection reaches a state with at least $en$ infected vertices with sufficiently large probability.

- **Lemma 4.1.** Let $G$ be a clique of size $n \in \mathbb{N}_{>0}$ and let $C$ be a contact process in the SIRS model on $G$ with infection rate $\lambda = \frac{c}{n}$ for a constant $c \in \mathbb{R}_{>1}$ and with constant deimmunization rate $q$. Also let $C$ start with exactly one infected vertex and no recovered vertices. Then there exists an
\( \varepsilon \in \mathbb{R}_{>0} \), such that for sufficiently large \( n \), the probability that there exists a \( t \in \mathbb{N} \) with \( I_{t_\varepsilon} \geq \varepsilon n \) is at least \( \frac{1}{n^2} \).

**Proof.** Let \( c' = c - 1 \). Note that \( c' \) is positive because \( c > 1 \). Let \( \varepsilon = \frac{c'}{2 + c'} \). We define for all \( t \in \mathbb{N} \) the potential \( H_t = H(I_{t_\varepsilon}, R_{t_\varepsilon}) = I_{t_\varepsilon} - \frac{c'}{2 + c'} R_{t_\varepsilon} \). Additionally, we define the stopping time \( T = \inf \{ t \in \mathbb{N} \mid H_t \leq 0 \lor S_{t_\varepsilon} < \frac{2}{2 + c'} n \} \) and the natural filtration \( (F_t)_{t \in \mathbb{N}_0} \) of \( C \). We aim to show that \( (H_t)_{t \in \mathbb{N}} \) is a sub-martingale until \( T \). This allows us to apply the optional stopping theorem (Theorem 2.1) to lower bound \( E[H_T] \). The law of total expectation then gives us a lower bound of \( \frac{1}{n^2} \) for \( \Pr[H_T > 0] \). We conclude the proof by showing that if \( H_T > 0 \), then \( I_{t_\varepsilon} \geq \varepsilon n \).

We first bound for all \( t \in \mathbb{N} \) the drift \( E[(H_{t+1} - H_t) \cdot 1_{t < T} \mid F_{t_\varepsilon}] \). To improve readability, we omit the multiplicative \( 1_{t > T} \) in all of the terms.

\[
E[H_{t+1} - H_t \mid F_{t_\varepsilon}] = p_{st,t}(H(I_{t_\varepsilon} + 1, R_{t_\varepsilon}) - H_t) + p_{tr,t}(H(I_{t_\varepsilon} - 1, R_{t_\varepsilon} + 1) - H_t) + p_{rs,t}(H(I_{t_\varepsilon}, R_{t_\varepsilon} - 1) - H_t)
\]

\[
= p_{st,t} - p_{tr,t} \left( 1 + \frac{c'}{2 + c'} \right) + p_{rs,t} \frac{c'}{2 + c'}
\]

\[
= \left( \lambda S_{t_\varepsilon} I_{t_\varepsilon} - I_{t_\varepsilon} \left( 1 + \frac{c'}{2 + c'} \right) + \varrho R_{t_\varepsilon} \frac{c'}{2 + c'} \right) / r_t
\]

\[
\geq \left( \frac{1 + c'}{2 + c'} \frac{2}{c'} - n I_{t_\varepsilon} - I_{t_\varepsilon} \left( 1 + \frac{c'}{2 + c'} \right) + \varrho R_{t_\varepsilon} \frac{c'}{2 + c'} \right) / r_t
\]

\[
= \frac{\varrho R_{t_\varepsilon} c'}{(2 + c') r_t}
\]

\[
\geq 0.
\]

Now it holds \( E[T] < \infty \) because in each step \( t \in \mathbb{N} \), there is a non-zero probability (independent of \( t \)) to heal a vertex, hence there is always a non-zero probability to heal all vertices within the next \( n \) steps, which stops the process. Therefore, by applying the optional stopping theorem (Theorem 2.1) we get \( E[H_T] \geq E[H_0] \).

By the law of total expectation, we get that

\[
E[H_T] = E[H_T \mid H_T \leq 0] \cdot \Pr[H_T \leq 0] + E[H_T \mid H_T > 0] \cdot \Pr[H_T > 0]
\]

\[
= E[H_T \mid H_T \leq 0] \cdot (1 - \Pr[H_T > 0]) + E[H_T \mid H_T > 0] \cdot \Pr[H_T > 0].
\]

Because of the definition of \( T \) and the fact that \( H \) changes by at most \( 1 + \frac{c'}{2 + c'} \leq 2 \) in one step, we get that \( H_T \geq -2 \). We also know that \( H_T \leq n \) as \( I_{t_\varepsilon} \leq n \). By definition of \( C \), it holds \( H_0 = 1 \). By substituting \( E[H_T] \) in \( E[H_T] \geq E[H_0] \) and solving for \( \Pr[H_T > 0] \) we get

\[
\Pr[H_T > 0] \geq \frac{1 - E[H_T \mid H_T \leq 0]}{E[H_T \mid H_T > 0] - E[H_T \mid H_T \leq 0]}
\]
\[ \geq \frac{1}{n+2}. \]

Now assume \( H_T > 0 \). By the definition of \( T \), it then holds \( S_{\tau_T} < \frac{2}{2+c'}n \). Therefore

\[ I_{\tau_T} + R_{\tau_T} = n - S_{\tau_T} > \frac{c'}{2+c'}n. \]

With \( H_T > 0 \) we then get \( I_{\tau_T} > \frac{c'}{2+c'}R_{\tau_T} \) which implies

\[ (1 + \frac{2+c'}{c'})I_{\tau_T} > \frac{c'}{2+c'}n. \]

To show that the infection survives long from that point onwards, we define a potential function for the states and analyze its drift. The potential function is an extended version of the Lyapunov function of [KW02]. We first define a helper function \( f \).

**Definition 4.2.** We define \( f \) such that, for all \( x, x' \in \mathbb{R}_{>0} \), we have

\[ f(x',x) = x'\left(\frac{x}{x'} - \ln \frac{x}{x'} - 1\right). \]

Note that the derivative \( \frac{df(x',x)}{dx} = 1 - \frac{x'}{x} \), hence for a given \( x' \in \mathbb{R}_{>0} \), \( x = x' \) is the only local optimum of \( f(x',x) \) and it is a global minimum. We now define the potential function that we use in the following lemmas.

**Definition 4.3.** Let \( G \) be a clique of size \( n \in \mathbb{N}_{>0} \) and let \( C \) be a contact process in the SIRS model on \( G \) with infection rate \( \lambda = \frac{c}{n} \) for a constant \( c \in \mathbb{R}_{>1} \) and with constant deimmunization rate \( \varphi \). Let \( n' = n + \frac{\varphi}{\lambda} \) and let

\[ \alpha = \frac{(1+\varphi)^2 n}{c^2 \varphi n'} \left(1 + \frac{c}{1+\varphi}\right), \]

\[ \beta = \frac{\varphi}{c}. \]

For all \( t \in \mathbb{N} \), we define \( F_t \) as

\[ F_t = F(P_{\tau_t}, I_{\tau_t}, Q_{\tau_t}) = \alpha f(P^*, P_{\tau_t}) + f(I^*, I_{\tau_t}) + \beta f(Q^*, Q_{\tau_t}). \]

Let \( (\mathcal{F}_t)_{t \in \mathbb{R}_{\geq0}} \) be the natural filtration of \( C \). We define for all \( t \in \mathbb{N} \) the drift \( D_t \) as

\[ D_t = \mathbb{E}[F_{t+1} - F_t \mid \mathcal{F}_t]. \]
The potential \( F \) is minimized at the equilibrium state and becomes larger at states further away. We aim to show that the process tends to drift towards the equilibrium state. To calculate the differences of the \( F \) values in the drift, we first have a look at \( f \).

**Lemma 4.4.** Let \( x^* \in \mathbb{R}_{>0} \) and \( x \in \mathbb{R}_{>2} \). Then

\[
\begin{align*}
    f(x^*, x + 1) - f(x^*, x) &\leq 1 - \frac{x^*}{x} + \frac{x^*}{x(x + 1)} \\
    \text{and } f(x^*, x - 1) - f(x^*, x) &\leq -\left(1 - \frac{x^*}{x} - \frac{x^*}{x(x - 1)}\right).
\end{align*}
\]

*Proof.* We use that for all \( y \in \mathbb{R}_{>1} \) holds

\[
\frac{1}{y + 1} < \ln(y + 1) - \ln(y) < \frac{1}{y}.
\]

Together with the definition of \( f \), we have

\[
\begin{align*}
    f(x^*, x + 1) - f(x^*, x) &= x^*\left(\frac{x + 1}{x^*} - \ln\frac{x + 1}{x^*} - 1\right) - x^*\left(\frac{x}{x^*} - \ln\frac{x}{x^*} - 1\right) \\
    &= 1 - x^*(\ln(x + 1) - \ln(x)) \\
    &\leq 1 - \frac{x^*}{x + 1}.
\end{align*}
\]

For the second part we get

\[
\begin{align*}
    f(x^*, x - 1) - f(x^*, x) &= x^*\left(\frac{x - 1}{x^*} - \ln\frac{x - 1}{x^*} - 1\right) - x^*\left(\frac{x}{x^*} - \ln\frac{x}{x^*} - 1\right) \\
    &= -1 + x^*(\ln(x) - \ln(x - 1)) \\
    &\leq -(1 - \frac{x^*}{x - 1}).
\end{align*}
\]

Noting that \( \frac{x^*}{x + 1} = \frac{x^*}{x} - \frac{x^*}{x(x + 1)} \) and \( \frac{x^*}{x - 1} = \frac{x^*}{x} + \frac{x^*}{x(x - 1)} \) concludes the proof.

We now show the following lemma that states that the drift \( D_t \) is upper bounded by a negative constant for states in which the random variables are far enough away from the equilibrium and from 0.

**Lemma 4.5.** Let \( G \) be a clique of size \( n \in \mathbb{N}_{>0} \) and let \( C \) be a contact process in the SIRS model on \( G \) with infection rate \( \lambda = \frac{\ell}{n} \) for a constant \( c \in \mathbb{R}_{>1} \) and with constant deimmunization rate \( \varphi \).

Let \( t \in \mathbb{N} \) and \( \epsilon, \delta \in (0, 1) \) be constants. We define \( \Delta S_t, \Delta I_t \) and \( \Delta R_t \) such that

\[
P_{r_t} = P^* + \Delta S_t \cdot n, \quad I_{r_t} = I^* + \Delta I_t \cdot n, \quad R_{r_t} = R^* + \Delta R_t \cdot n.
\]
Now assume that the following conditions hold

\[ I_{rr} \geq cn, \]
\[ |\Delta S_t| + |\Delta I_t| + |\Delta R_t| \geq \delta. \]

Then there exists a constant \( d \in \mathbb{R}_{>0} \) such that \( D_t \leq -d \) for sufficiently large \( n \).

**Proof.** For this proof, we first use the law of total expectation and Lemma 4.4 to get a large formula as an upper bound for \( r_tD_t \). We split that bound into two parts and simplify each part separately. We show that, with the given conditions, one of the parts is upper bounded by a constant and the other part is at most \(-mn\) for some constant \( m \in \mathbb{R}_{>0} \). We conclude the proof by bounding \( r_t \) and dividing the obtained bound for \( r_tD_t \) by it.

Using the law of total expectation and Lemma 4.4, we get

\[
\begin{align*}
r_t \cdot D_t &= r_{sl,t} \cdot (F(P_{rr} - 1, I_{rr} + 1, Q_{rr}) - F(P_{rr}, I_{rr}, Q_{rr})) \\
&\quad + r_{ir,t} \cdot (F(P_{rr}, I_{rr} - 1, Q_{rr} + 1) - F(P_{rr}, I_{rr}, Q_{rr})) \\
&\quad + r_{rs,t} \cdot (F(P_{rr} + 1, I_{rr}, Q_{rr} - 1) - F(P_{rr}, I_{rr}, Q_{rr})) \\
&\leq r_{sl,t} \cdot \left( \alpha \left( 1 - \frac{\gamma^*}{I_{rr}} + \frac{\gamma^*}{I_{rr}(I_{rr} + 1)} \right) - \alpha \left( 1 - \frac{\gamma^*}{P_{rr}^*} - \frac{\gamma^*}{P_{rr}(P_{rr} - 1)} \right) \right) \\
&\quad + r_{ir,t} \cdot \left( \beta \left( 1 - \frac{Q^*}{Q_{rr}} + \frac{Q^*}{Q_{rr}(Q_{rr} + 1)} \right) - \alpha \left( 1 - \frac{\gamma^*}{I_{rr}} - \frac{\gamma^*}{I_{rr}(I_{rr} - 1)} \right) \right) \\
&\quad + r_{rs,t} \cdot \left( \alpha \left( 1 - \frac{\gamma^*}{P_{rr}^*} + \frac{\gamma^*}{P_{rr}(P_{rr} + 1)} \right) - \beta \left( 1 - \frac{Q^*}{Q_{rr}} - \frac{Q^*}{Q_{rr}(Q_{rr} - 1)} \right) \right) \\
&= \alpha \left( 1 - \frac{\gamma^*}{I_{rr}} \right) (r_{sl,t} - r_{ir,t}) + \left( 1 - \frac{\gamma^*}{P_{rr}^*} \right) (r_{rs,t} - r_{sl,t}) + \beta (1 - \frac{Q^*}{Q_{rr}}) (r_{ir,t} - r_{rs,t}) \\
&\quad + \frac{\alpha r_{sl,t} \gamma^*}{I_{rr}(I_{rr} + 1)} + \frac{\alpha r_{sl,t} \gamma^*}{P_{rr}(P_{rr} - 1)} + \frac{\alpha r_{ls,t} \gamma^*}{Q_{rr}(Q_{rr} + 1)} + \frac{\alpha r_{ls,t} \gamma^*}{I_{rr}(I_{rr} - 1)} + \frac{\alpha r_{ls,t} \gamma^*}{P_{rr}(P_{rr} + 1)} + \frac{\beta r_{rs,t} \gamma^*}{Q_{rr}(Q_{rr} - 1)}.
\end{align*}
\]

For ease of notation, we define \( A_t \) and \( B_t \) such that \( r_tD_t \leq A_t + B_t \) as

\[
A_t = \alpha \left( 1 - \frac{\gamma^*}{I_{rr}} \right) (r_{sl,t} - r_{ir,t}) + \left( 1 - \frac{\gamma^*}{P_{rr}^*} \right) (r_{rs,t} - r_{sl,t}) + \beta (1 - \frac{Q^*}{Q_{rr}}) (r_{ir,t} - r_{rs,t})\]

and

\[
B_t = \frac{\alpha r_{sl,t} \gamma^*}{I_{rr}(I_{rr} + 1)} + \frac{\alpha r_{sl,t} \gamma^*}{P_{rr}(P_{rr} - 1)} + \frac{\beta r_{ir,t} \gamma^*}{Q_{rr}(Q_{rr} + 1)} + \frac{\alpha r_{ls,t} \gamma^*}{I_{rr}(I_{rr} - 1)} + \frac{\alpha r_{ls,t} \gamma^*}{P_{rr}(P_{rr} + 1)} + \frac{\beta r_{rs,t} \gamma^*}{Q_{rr}(Q_{rr} - 1)}.
\]

We first upper bound \( B_t \). Note that with the given conditions, all values of \( P_{rr}, I_{rr}, Q_{rr}, P^*, I^* \) and \( Q^* \) are in \( \Theta(n) \). All of \( r_{sl,t}, r_{ir,t} \) and \( r_{rs,t} \) are in \( O(n) \). As both \( \alpha \) and \( \beta \) are constants, \( B_t \) is the sum of six terms that are all in \( O(1) \) and is thus upper bounded by a constant \( b \in \mathbb{R} \).

We now bound \( A_t \). We first simplify the first summand of \( A_t \) by plugging in the rates, some of
the values of $I^*$ and $P^*$ and using that $P_{t_2} + I_{t_2} + R_{t_2} = n'$. We get

$$(1 - \frac{I^*}{P_{t_2}})(r_{sl,t} - r_{ir,t}) + (1 - \frac{P^*}{P_{t_2}})(r_{rs,t} - r_{sl,t})$$

$$= (1 - \frac{I^*}{P_{t_2}})(\lambda I_{t_2} P_{t_2} - \theta I_{t_2} - I_{t_2}) + (1 - \frac{P^*}{P_{t_2}})(\theta R_{t_2} - \lambda I_{t_2} P_{t_2} + \theta I_{t_2})$$

$$= (1 - \frac{I^*}{P_{t_2}})(\lambda I_{t_2} P_{t_2} - (1 + \theta) I_{t_2}) + (1 - \frac{P^*}{P_{t_2}})(\theta n' - \theta P_{t_2} - \lambda I_{t_2} P_{t_2} - \theta n' P_{t_2} + \theta P^* + \lambda I_{t_2} P^*)$$

$$= -\frac{\theta (c - 1)}{1 + \theta} P_{t_2} + \theta (n - \frac{n}{c}) + \theta n' - \theta P_{t_2} - \theta n' P_{t_2} + \frac{\theta (1 + \theta)n}{c}$$

By their definitions, we get

$$\lambda I_{t_2} P_{t_2} - (1 + \theta) I_{t_2} - \lambda P^* P_{t_2} + (1 + \theta) I^* + \theta n' - \theta P_{t_2} - \lambda I_{t_2} P_{t_2} - \theta n' P_{t_2} + \theta P^* + \lambda I_{t_2} P^*$$

Note that these calculations are the same as the calculations in [KW02] as the considered term is exactly the derivative of their Lyapunov function. We aim to represent $A_t$ by using $\Delta S_t$, $\Delta I_t$ and $\Delta R_t$. By their definitions, we get

$$\frac{P_{t_2}}{P^*} = 1 + \frac{\Delta S_t \cdot n}{P^*} = 1 + \frac{\Delta S_t \cdot n}{1 + \theta}$$

and

$$1 - \frac{Q^*}{Q_{t_2}} = \frac{\Delta R_t \cdot n}{Q^* + \Delta R_t \cdot n} = \frac{\Delta R_t \cdot n}{\frac{c - 1}{(1 + \theta)c} + \frac{\theta}{c} + \Delta R_t}.$$ 

Note that $I^* = \theta R^*$. With these equations and the definition of $\alpha$ and $\beta$, we get

$$A_t = -\alpha n' \frac{P^*}{P_{t_2}} \left(1 - \frac{P_{t_2}}{P^*}\right)^2 + \beta (1 - \frac{Q^*}{Q_{t_2}})(I_{t_2} - \theta R_{t_2})$$

$$= -\alpha n' \left(\frac{\Delta S_t \cdot c}{1 + \Delta S_t \cdot c/(1 + \theta)} \right)^2 + \beta \left(\frac{c - 1}{(1 + \theta)c} + \frac{\theta}{c} + \Delta R_t\right)n.$$
\[
= -(1 + \frac{c}{1 + q}) \frac{\Delta S_t^2}{1 + \Delta S_t \cdot c / (1 + q)} n + \beta \frac{\Delta R_t}{(c-1) \gamma} + \frac{\Delta R_t}{c} (\Delta I_t - q \Delta R_t) n.
\]

We aim to simplify this formula by substituting the \(\Delta S_t\) and \(\Delta R_t\) in the denominator. By definition of \(\Delta S_t\), it holds that
\[
\frac{1}{c} = \frac{S^*}{n} \leq \Delta S_t < 1.
\]

Therefore, the first term of the previous equation is always negative and we upper bound it by substituting the \(\Delta S_t\) in the denominator by 1. We also split up the second term for easier calculations later. We get
\[
A_t \leq -\Delta S_t^2 n + \beta \frac{\Delta R_t \cdot \Delta I_t}{(c-1) \gamma} n - \beta \frac{\Delta R_t^2}{c} \frac{\Delta R_t}{(c-1) \gamma} n.
\]

By definition of \(\Delta R_t\) it holds
\[
-\frac{c - 1}{(1 + q)c} = \frac{R^*}{n} \leq \Delta R_t < 1.
\]

Note that the latter inequality implies that \(\frac{c - 1}{(1 + q)c} + \frac{\Delta R_t}{c}\) is positive. We now make a case distinction depending on the sign of \(\Delta R_t \cdot \Delta I_t\), as this sign decides whether we use the lower bound or the upper bound of \(\Delta R_t\) to upper bound the second term. For both cases, note that \(\Delta S_t + \Delta I_t + \Delta R_t = 0\) as every vertex is always in exactly one of \(S_t, I_t\), or \(R_t\). Together with the constraint \(|\Delta S_t| + |\Delta I_t| + |\Delta R_t| \geq \delta\) this means that of these three values, one or two are positive and add up to at least \(\frac{\delta}{2}\) and one or two are negative and add up to at most \(-\frac{\delta}{2}\).

**Case \(\Delta R_t \cdot \Delta I_t < 0\):** The second term of the bound of \(A_t\) is negative. Therefore we get an upper bound by substituting the \(\Delta R_t\) in the denominator by its upper bound 1. We get
\[
A_t \leq -\Delta S_t^2 n + \beta \frac{\Delta R_t \cdot \Delta I_t}{c} n - \beta \frac{\Delta R_t^2}{c} \frac{\Delta R_t}{c} n
\]
\[
\leq -\Delta S_t^2 n - \beta \frac{\Delta R_t^2}{c} \frac{\Delta R_t}{c} n.
\]

By the pigeonhole principle, one of \(|\Delta S_t|\) and \(|\Delta R_t|\) has to be at least \(\frac{\delta}{4}\) in order to fulfill \(\Delta S_t + \Delta I_t + \Delta R_t = 0\) and \(|\Delta S_t| + |\Delta I_t| + |\Delta R_t| \geq \delta\). Therefore we get
\[
A_t \leq \frac{\delta^2}{16} \min \left(1, \frac{\beta q}{(c-1) \gamma + \frac{\Delta R_t}{c} + \frac{\Delta R_t^2}{c} + 1}\right) \cdot n.
\]
Case $\Delta R_t \cdot \Delta I_t \geq 0$: The second term of the bound of $A_t$ is non-negative. Therefore we get an upper bound by substituting the $\Delta R_t$ in the denominator by its lower bound $\frac{c-1}{(1+\varphi)c}$. We get

$$A_t \leq -\Delta S_t^2 n + \beta \frac{\Delta R_t \cdot \Delta I_t}{\frac{c-1}{(1+\varphi)c} + \frac{\varphi}{\zeta} + \Delta R_t} n - \beta \frac{\varphi \Delta R_t^2}{\frac{c-1}{(1+\varphi)c} + \frac{\varphi}{\zeta} + \Delta R_t} n$$

$$\leq -\Delta S_t^2 n + \beta \frac{\Delta R_t \cdot \Delta I_t}{\frac{c-1}{(1+\varphi)c} + \frac{\varphi}{\zeta} + \frac{c-1}{(1+\varphi)c}} n$$

$$= (-\Delta S_t^2 + \Delta R_t \cdot \Delta I_t)n.$$

Because $\Delta S_t + \Delta I_t + \Delta R_t = 0$ and $\Delta R_t$ and $\Delta I_t$ have the same sign or one of them is 0, we know that $|\Delta S_t| = |\Delta R_t + \Delta I_t|$. Also because $|\Delta S_t| + |\Delta I_t| + |\Delta R_t| \geq \delta$, by the pigeonhole principle one of $|\Delta I_t|$ and $|\Delta R_t|$ has to be at least $\frac{\delta}{4}$. Using these insights, we get

$$A_t \leq (-\Delta S_t^2 + \Delta R_t \cdot \Delta I_t)n$$

$$= (-\delta^2 + \Delta R_t \cdot \Delta I_t)n$$

$$= (-\delta^2 - \Delta R_t \cdot \Delta I_t - \Delta I_t^2)n$$

$$\leq -\frac{\delta^2}{16} n.$$

Let

$$m = \frac{\delta^2}{16} \min \left(1, \frac{\beta \varphi}{\frac{c-1}{(1+\varphi)c} + \frac{\varphi}{\zeta} + 1} \right).$$

We showed that in all cases $A_t \leq -mn$. For sufficiently large $n$ we then get

$$r_tD_t \leq A_t + B_t$$

$$\leq -mn + b$$

$$\leq -\frac{mn}{2}.$$

We know that $r_t = \lambda I_{t_t} S_{t_t} + I_{t_t} + \varphi R_{t_t} \leq \lambda n^2 + n + \varphi n = (c + 1 + \varphi)n$. As also $r_t \geq I_{t_t} \geq \epsilon n > 0$, by dividing the inequality for $D_t$ by $r_t$ we get

$$D_t \leq -\frac{mn}{2r_t}$$

$$\leq -\frac{mn}{2(1 + \varphi + \epsilon)n}.$$


As all of the constants on the right side of that inequality are positive, choosing $d = \frac{m}{2(1 + q + c)}$ concludes the proof.

We aim to apply the negative drift theorem (Theorem 2.2) to bound the survival time of the infection. In Lemma 4.5, we showed a constant negative drift of the potential in a region of the state space. To apply the drift theorem, we first transform the state space restrictions into restrictions on the value of the potential.

**Lemma 4.6.** Let $G$ be a clique of size $n \in \mathbb{N}_{>0}$ and let $C$ be a contact process in the SIRS model on $G$ with infection rate $\lambda = \frac{c}{n}$ for a constant $c \in \mathbb{R}_{>1}$ and with constant deimmunization rate $q$. Let $t \in \mathbb{N}$ and $\varepsilon \in (0, 1)$ be constants such that $I_{tr} \geq \varepsilon n$. It then holds

$$F_t \in O(n).$$

**Proof.** We aim to upper bound $F_t$ by writing it as a sum and upper bounding the individual summands. To this end, we first bound the terms that appear in the summands. By the definition of our random variables and the fact that there are only $n$ vertices that are in any of the states, we get

$$
\max(P_{tr}, I_{tr}, Q_{tr}, P^*, I^*, Q^*) \leq n', \\
\min(P_{tr}, I_{tr}, Q_{tr}) \geq \min(\varepsilon, q/c)n.
$$

Applying these bounds to $F_t$ results in

$$
F_t = a(f(P_{tr}, P_{tr}) + f(I_{tr}, I_{tr})) + \beta f(Q^*, Q_{tr}) \\
= a\left(P^*\left(P_{tr} - \ln P_{tr} - 1\right) + I^*\left(I_{tr} - \ln I_{tr} - 1\right)\right) + \beta Q^*\left(Q_{tr} - \ln Q_{tr} - 1\right) \\
\leq a\left(P_{tr} + P^* \ln P_{tr} - P_{tr} + I_{tr} + I^* \ln I_{tr} - I_{tr}\right) + \beta Q_{tr} + Q^* \ln Q_{tr} \\
\leq (2\alpha + \beta) \cdot (n' + n' \ln \frac{n'}{\min(\varepsilon, q/c)n}).
$$

As $n' = (1 + q/c)n$, the calculated upper bound for $F_t$ is linear in $n$ and therefore it holds $F_t \in O(n)$.

**Lemma 4.7.** Let $G$ be a clique of size $n \in \mathbb{N}_{>0}$ and let $C$ be a contact process in the SIRS model on $G$ with infection rate $\lambda = \frac{c}{n}$ for a constant $c \in \mathbb{R}_{>1}$ and with constant deimmunization rate $q$. Let $t \in \mathbb{N}$ and $\varepsilon \in (0, I^*/n)$ be constants such that $1 \leq I_{tr} \leq \varepsilon n$. It then holds
Proof. We aim to lower bound \( F_t \) by lower bounding the \( f \) values in its definition. Recall that for a given \( x^* \in \mathbb{R}_{>0} \), the function \( f(x^*, x) \) is minimized for \( x = x^* \), which is the only local extreme value for \( x \in \mathbb{R}_{>0} \). Therefore, we get for all \( x, x^* \in \mathbb{R}_{>0} \)

\[
f(x^*, x) \geq f(x^*, x^*) = 0.
\]

Using \( 1 \leq I_t \leq \varepsilon n \) and the fact that for all \( x^* \in \mathbb{R}_{>0} \), \( f(x^*, x) \) decreases monotone in \( x \) while \( x < x^* \), we now get

\[
F_t = \alpha f(P^*, P_t) + f(I^*, I_t)) + \beta f(Q^*, Q_t)
\geq 0 + \alpha f(I^*, \varepsilon n) + 0
\geq \alpha \left( \frac{en}{I^*} - \ln \frac{en}{I^*} - 1 \right)
\geq \alpha \left( \ln \frac{1}{\varepsilon} + \ln \frac{I^*}{n} - 1 \right).
\]

\[\]
To this end, we define a stopping time that is dominated by the number of steps until survival time $T$. Then for the survival time $T$ of $\mathbb{E}^{-1}$, we use the previous lemmas to show that all of the conditions for the drift theorem are satisfied. Note that for sufficiently large $n$, we get that $\min(P_{r,t} - 1, I_{r,t} - 1, Q_{r,t} - 1) \geq \varepsilon n/2$. We get

$$
|F(P_{r,t} + \Delta P, I_{r,t} + \Delta I, Q_{r,t} + \Delta Q) - F(P_{r,t}, I_{r,t}, Q_{r,t})| \\
= |\alpha f(P^*, P_{r,t} + \Delta P) + \alpha f(I^*, I_{r,t} + \Delta I) + \beta f(Q^*, Q_{r,t} + \Delta Q) - \alpha f(P^*, P_{r,t}) - \alpha f(I^*, I_{r,t}) - \beta f(Q^*, Q_{r,t})| \\
\leq |\alpha f(P^*, P_{r,t} + \Delta P) - \alpha f(P^*, P_{r,t})| + |\alpha f(I^*, I_{r,t} + \Delta I) - \alpha f(I^*, I_{r,t})| + |\beta f(Q^*, Q_{r,t} + \Delta Q) - \beta f(Q^*, Q_{r,t})| \\
\leq \alpha \left(1 + \frac{P^*}{P_{r,t} - 1}\right) + \alpha \left(1 + \frac{I^*}{I_{r,t} - 1}\right) + \beta \left(1 + \frac{Q^*}{Q_{r,t} - 1}\right) \\
\leq (2\alpha + \beta) \left(1 + \frac{n}{\varepsilon n/2}\right) \\
\leq (2\alpha + \beta) \left(1 + 2(1 + q/c)\varepsilon^{-1}\right).
$$

\[\square\]

**Lemma 4.9.** Let $G$ be a clique of size $n \in \mathbb{N}_{>0}$ and let $C$ be a contact process in the SIRS model on $G$ with infection rate $\lambda = \frac{c}{n}$ for a constant $c \in \mathbb{R}_{>1}$ and with constant deimmunization rate $\varrho$. Let $E_{\varepsilon}$ be the event that there exists a $t \in \mathbb{N}$ such that $I_{r,t} \geq \varepsilon_0 n$. Then for the survival time $T$ of $C$ holds that $\mathbb{E}[T \mid E_{\varepsilon}] = 2^{\Omega(n)}$.

**Proof.** We assume that $E_{\varepsilon}$ happens. Let $(\mathcal{F}_t)_{t \in \mathbb{R}_{>0}}$ be the natural filtration of $C$ and let $t \in \mathbb{N}$ such that $I_{r,t} \geq \varepsilon_0 n$. We aim to apply the negative drift theorem (Theorem 2.2) to get the desired bound. To this end, we define a stopping time that is dominated by the number of steps until $T$, and we use the previous lemmas to show that all of the conditions for the drift theorem are satisfied. Note that we shift the time to start at $t$ instead of 0. We then translate the bound on the number of steps into a bound on the survival time.

As $I_{r,t} \geq \varepsilon_0 n$, by Lemma 4.6 there exists a constant $a \in \mathbb{R}_{>0}$ such that $F_t \leq an$. We define $T_1 = \inf\{i \in \mathbb{N}_{\geq t} \mid F_i > 2an\}$.

We first show that for all $i \in \mathbb{N}$ with $t \leq i < T_1$ holds that $I_{r,t}$ is large enough such that Lemma 4.8 is applicable. Let $\varepsilon_1 \in (0, 1/n)$ be a constant low enough such that $a \frac{P_n}{\varepsilon_1} (\ln \frac{1}{\varepsilon_1} + \ln \frac{P_n}{\varepsilon_1} - 1) > 2a$. Such an $\varepsilon_1$ exists as $a, \frac{P_n}{\varepsilon_1}$ and $a$ are positive constants. Then by the contraposition of Lemma 4.7 for all $i \in \mathbb{N}$, $F_i \leq 2an$ implies that $I_{r,t} \geq \varepsilon_1 n$.

To show that condition 2 of Theorem 2.2 is satisfied, let $s = (2\alpha + \beta) (1 + 2(1 + q/c)\varepsilon^{-1})$. For all $i \in \mathbb{N}$ with $t \leq i < T_1$ holds $F_i \leq 2an$ and therefore $I_{r,t} \geq \varepsilon_1 n$. Hence by Lemma 4.8, for all $i \in \mathbb{N}_{\geq t}$ holds that $|F_{i+1} - F_i| \cdot 1\{i < T_1\} \leq s \cdot 1\{i < T_1\}$. Therefore for all $i \in \mathbb{N}_{\geq t}$ and $j \in \mathbb{R}_{>0}$ holds that $\Pr[|F_{i+1} - F_i| \geq j \mid \mathcal{F}_t] \cdot 1\{i < T_1\} \leq \frac{s}{2\varepsilon_1} \cdot 1\{i < T_1\}$. Note that $2^a$ is a constant.

We now show that condition 1 is satisfied as well. Let $\delta \in (0, 1)$ such that $\delta \varepsilon \leq a$. Also, for all time steps $i \in \mathbb{N}$, we define $\Delta S_i, \Delta I_i$ and $\Delta R_i$ such that

\[\leq |\Delta x| + |x^* \ln \left(\frac{x + \Delta x}{x}\right)| \leq 1 + \frac{x^*}{x - 1}.\]
\[ P_{\tau_i} = P^r + \Delta S_{i} \cdot n, I_{\tau_i} = I^r + \Delta I_{i} \cdot n, R_{\tau_i} = R^r + \Delta R_{i} \cdot n. \]

Recall that \( F(P^r, I^r, Q^r) = 0 \). Let \( i \in \mathbb{N} \). By Lemma 4.8 if \( I_{\tau_i} \geq \epsilon n \cdot \frac{1}{\delta} \), \( |\Delta S_{i}| + |\Delta I_{i}| + |\Delta R_{i}| \leq \frac{1}{n} \) implies \( F_i \leq s \). By induction on \( k \in \mathbb{N} \) we get that if \( I_{\tau_i} \geq \epsilon n \cdot \frac{1}{\delta} \), \( |\Delta S_{i}| + |\Delta I_{i}| + |\Delta R_{i}| \leq \frac{k}{n} \) implies \( F_i \leq ks \). By choosing \( k = \delta n \), the contradiction of the previous statement results in the fact that if \( I_{\tau_i} \geq \epsilon n \cdot \frac{1}{\delta} \), \( F_i > an \cdot \frac{1}{\delta} \), \( s \) implies \( |\Delta S_{i}| + |\Delta I_{i}| + |\Delta R_{i}| > \delta \). Hence, for all \( i \in \mathbb{N} \) with \( an < F_i < 2an \), the conditions for Lemma 4.5 are fulfilled and we get that there exists a constant \( F \) for all \( i \in \mathbb{N} \).

Now all of the conditions of Theorem 2.2 are satisfied and we get that there exists a constant \( c^* \in \mathbb{R}_{>0} \) such that

\[
\Pr\left[ T_1 - t \leq 2^{c^*an/2^s} \mid \mathcal{F}_{\tau_i} \right] \cdot \mathbf{1}\{F_i \leq an\} = 2^{-\Omega(an/2^s)} \cdot \mathbf{1}\{F_i \leq an\}.
\]

Note that this probability goes towards 0 as \( n \) goes towards infinity. Hence, \( E[T_1 \mid \mathcal{F}_{\tau_i}] \cdot \mathbf{1}\{F_i \leq an\} \leq 2^{\Omega(n)} \cdot \mathbf{1}\{F_i \leq an\} \). We therefore get

\[
E[T_1 \mid \mathcal{F}_{\tau_i}] \cdot \mathbf{1}\{I_{\tau_i} \geq \epsilon n\} = 2^{\Omega(n)} \cdot \mathbf{1}\{I_{\tau_i} \geq \epsilon n\}.
\]

We showed that for all \( i \in \mathbb{N} \) with \( \tau_1 \leq T_1 \) holds \( I_{\tau_i} \geq \epsilon n > 0 \). Therefore, \( T \) dominates \( \tau_{\tau_i} \).

In \( C \) there are \( n \) healing clocks with a rate of 1 each and \( n(n-1) \) infection clocks with a rate of \( \frac{c}{n} \) each. Therefore, all of the clocks trigger at a rate of at most \( (c+1)n \) and the expected time for each trigger is at least the inverse of that. By Wald’s equation, we get that

\[
E[T \mid \mathcal{F}_0] \cdot \mathbf{1}\{E_{e_0}\} \geq E[T \mid \mathcal{F}_0] \cdot \mathbf{1}\{E_{e_0}\} \geq \frac{1}{cn} 2^{\Omega(n)} \cdot \mathbf{1}\{E_{e_0}\}.
\]

We now prove the main theorem.

\textbf{Theorem 4.10.} Let \( G \) be a clique of size \( n \in \mathbb{N}_{>0} \), and let \( C \) be a contact process in the SIRS model on \( G \) with infection rate \( \lambda = \frac{c}{n} \) for a constant \( c \in \mathbb{R}_{>1} \) and with constant deimmunization rate \( q \). Further, let \( C \) start with exactly one infected vertex and no recovered vertices, and let \( T \) be the survival time of \( C \). Then for sufficiently large \( n \), we have \( E[T] = 2^{\Omega(n)} \).

\textbf{Proof.} Let for all \( \epsilon \in (0, 1) \), \( E_{\epsilon} \) be the event that there exists a \( t \in \mathbb{N} \) such that \( I_{\tau_i} \geq \epsilon n \). By Lemma 4.1, there exists an \( \epsilon \in \mathbb{R}_{>0} \) such that for sufficiently large \( n \) holds \( \Pr[E_{\epsilon}] \geq \frac{1}{n^2} \). By Lemma 4.9 it holds that \( E[T \mid E_{\epsilon}] = 2^{\Omega(n)} \). Using the law of total expectation, we get

\[
E[T] = \Pr[E_{\epsilon}] E[T \mid E_{\epsilon}] + \Pr[E_{\overline{\epsilon}}] E[T \mid E_{\overline{\epsilon}}] \\
\geq \Pr[E_{\epsilon}] E[T \mid E_{\epsilon}] \\
\geq \frac{1}{n^2} 2^{\Omega(n)}
\]
2^n = 2^{Ω(n)}.

5 SIS Clique

In this section, we give a lower and an upper bound for the epidemic threshold of the SIS contact process on a clique. To this end, we first analyze some basic properties of the process like the transition probabilities between the states and the equilibrium state in Section 5.1. We then show in Section 5.2 that when the infection goes above the equilibrium value, it returns to that value quickly again. In Section 5.3 and Section 5.4, we derive an upper and lower bound respectively for the probability of the infection to die out when starting at the equilibrium. That gives us a bound for the expected survival time.

5.1 The SIS Contact Process

Consider an SIS contact process $C$ on a clique $G$ with $n$ vertices with an infection rate $\lambda$. For all $t \in \mathbb{N}$, one of the following two events occurs at step $t + 1 (\tau_{t+1})$: either a susceptible vertex is infected, which we call $E_{is,t}$; or an infected vertex recovers in the event $E_{is,t}$. At the time point $\tau_t$, vertices heal at a rate of $r_{is,t} = I_{\tau_t}$ and new vertices get infected at a rate of $r_{si,t} = \lambda I_{\tau_t} S_{\tau_t}$. Let $r_t = r_{is,t} + r_{si,t} = I_{\tau_t} + \lambda I_{\tau_t} S_{\tau_t}$. While $I_{\tau_t} > 0$, we get

$$p_{is,t} = \Pr[E_{is,t}] = \frac{r_{is,t}}{r_t} = \frac{I_{\tau_t}}{I_{\tau_t} + \lambda I_{\tau_t} S_{\tau_t}}$$

$$p_{si,t} = \Pr[E_{si,t}] = \frac{r_{si,t}}{r_t} = \frac{\lambda I_{\tau_t} S_{\tau_t}}{I_{\tau_t} + \lambda I_{\tau_t} S_{\tau_t}}.$$

In the proofs, we consider infection rates of the form $\lambda = \frac{1}{n^{\alpha}}$ for some $\alpha \in (0, n)$. As $S_{\tau_t} = n - I_{\tau_t}$, by expanding the fractions by $(n - \alpha)/I_{\tau_t}$, we get

$$p_{is,t} = \frac{n - \alpha}{2n - \alpha - I_{\tau_t}}$$

$$p_{si,t} = \frac{n - I_{\tau_t}}{2n - \alpha - I_{\tau_t}}.$$

Note that these two probabilities are exactly the same for $I_{\tau_t} = \alpha$. Therefore, we call $\alpha$ the equilibrium value for the contact process. Note that we assume in the proofs that $\alpha$ is a natural number, such that there is a state with exactly $\alpha$ infected vertices. As the expected survival time increases monotone with $\alpha$, the results extend to real values of $\alpha$ as well.
5.2 The Process Above the Equilibrium

To show that $I_t$ quickly drops back to the equilibrium value after getting higher than it, we use following theorem. It is the application of a more general theorem of [GMT05] on the clique.

**Corollary 5.1 ([GMT05] Theorem 3.1).** Let $G$ be a clique with $n \in \mathbb{N}_{>0}$ vertices and let $C$ be a contact process in the SIS model on $G$ with infection rate $\lambda$. Let $T \in \mathbb{N}$ be the first step at which no vertex is in the infected state. Let $\lambda < \frac{1}{n-1}$. Then

$$E[\tau_T] \leq \frac{\ln(n) + 1}{1 - (n - 1)\lambda}.$$

We now apply this theorem.

**Lemma 5.2.** Let $G$ be a clique with $n \in \mathbb{N}_{>0}$ vertices and let $C$ be a contact process in the SIS model on $G$ with infection rate $\lambda = \frac{1}{n - \alpha}$ for some $\alpha \in \mathbb{N}_{<n}$. Let $t_0$ be a time step with $I_{t_0} > \alpha$ and let $T \in \mathbb{N}$ be the first time step after $t_0$ with $I_T = \alpha$. Then

$$E[\tau_T - \tau_{t_0}] \leq (\ln(n - \alpha) + 1) \cdot (n - \alpha).$$

**Proof.** We aim to apply Corollary 5.1. To this end, we consider the random process $(X_t)_{t \in \mathbb{N}}$ with $X_t = I_t - \alpha$ for all $t \in \mathbb{N}$. Also, let $n' = n - \alpha$. For each $t \in \mathbb{N}$, $X$ increases by 1 in the next step with probability $p_{is,t}$ and decreases by one with probability $p_{si,t}$. While the infection has not died out yet, we get

$$p_{is,t} = \frac{n - \alpha}{2n - \alpha - I_t}, \quad p_{si,t} = \frac{n - I_t}{2n - \alpha - I_t}.$$

Now consider an SIS contact process $C'$ on a clique $G'$ with $n'$ vertices that has an infection rate of $\lambda' = \frac{1}{n'}$ and starts with $I_{t_0} - \alpha$ infected vertices. Note that if for $t, t' \in \mathbb{N}$ holds $X_t = I_{t'} > 0$ then $X_{t+1} - X_t$ and $I'_{t+1} - I'_t$ are distributed exactly the same as the transition probabilities are the same. Further note that for these steps, $\tau_{t+1} - \tau_t$ follows an exponential distribution with a higher rate than the exponential distribution $\tau_{t+1}' - \tau'_t$ as $C$ has $\alpha$ more vertices which are all infected, so there are strictly more triggers that heal vertices. Hence, $C$ and $C'$ can be coupled in a way such that for all $t \in \mathbb{N}$ with $t_0 \leq t \leq T$ holds that $X_t = I'_t$ and $\tau_t - \tau_{t_0} \leq \tau'_t$. As for all $t \in \mathbb{N}$ with $t_0 \leq t \leq T$ holds that $X_t = I'_{t-t_0}$ by definition of $T$, $T - t_0$ it is the first step in which there is no infected vertex in $C'$. Therefore Corollary 5.1 is applicable and we get

$$E[\tau_T - \tau_{t_0}] \leq E[\tau'_{T-t_0}].$$
\[ \ln(n') + 1 \leq 1 - (n' - 1) \frac{1}{n'} \]
\[ = (\ln(n') + 1)n'. \]

### 5.3 Upper Bound for the Epidemic Threshold

To give an upper bound for the epidemic threshold, we show that the considered process \( C \) has a super-polynomial expected survival time if for some \( \epsilon \in (0, 1) \), \( \alpha \geq n^{1/2+\epsilon} \). To this end, we show that the process gets to a state with at least \( \alpha/2 \) infected vertices with sufficient probability and that it is very unlikely from that point on that the infection dies out fast.

**Lemma 5.3.** Let \( G \) be a clique with \( n \in \mathbb{N}_{>0} \) vertices and let \( C \) be a contact process in the SIS model on \( G \) with infection rate \( \lambda = \frac{1}{n-a} \) for some \( \alpha \in \mathbb{N}_{<n/2} \). Further, let there be a constant \( \epsilon \in (0, 1/2) \) such that \( \alpha \geq n^{1/2+\epsilon} \). Let \( t_0 \) be a time step with \( I_{\tau_{t_0}} = \alpha/2 - 1 \) and let \( T \) be the first step after \( t_0 \) with \( I_{\tau_T} = 0 \) or \( I_{\tau_T} = \alpha/2 \). Then

\[
\Pr[I_{\tau_T} = 0] \leq \frac{1}{1.5^\alpha - 1}.
\]

**Proof.** For all \( t \) with \( t_0 \leq t < T \) holds \( 0 < I_{\tau_t} < \alpha/2 \) and therefore \( p_{i,s,t} = \frac{n-a}{2n-a-I_{\tau_t}} \leq \frac{n-a}{2n-\frac{1}{2}a} \). As this bound holds independently for all steps and because each step changes the number of infected vertices by 1 in either direction, in the time interval \( [\tau_{t_0}, \tau_T] \) the discrete version of the process dominates a gambler’s ruin instance \( (P_t)_{t \in \mathbb{N}} \) with a probability of \( \frac{n-a}{2n-\frac{1}{2}a} \) to win. Let \( T' \) be the first time that \( P_t \) either reaches the lower bound 0 or the upper bound \( \alpha/2 \) when starting at \( P_0 = \alpha/2 - 1 \). Then \( \Pr[I_{\tau_T} = 0] \leq \Pr[P_{T'} = 0] \) because of the domination. We bound \( \Pr[P_{T'} = 0] \) with Theorem 2.6. Note that \( \frac{1}{1-p} = \frac{n-a}{n-a} = 1 + \frac{a}{2(n-a)} \). We also use the bounds for \( \alpha \) and the fact that for all \( x \in \mathbb{R}_{\geq 1} \) and \( y \in \mathbb{R} \) with \( |y| \leq x \) holds \( (1 + \frac{y}{x})^x \geq 1 + y \) to get that

\[
\Pr[I_{\tau_T} = 0] \leq \Pr[P_{T'} = 0] = \left( 1 - \frac{\alpha}{2(n-a)} \right) \frac{1}{1 - (1 + \frac{\alpha}{2(n-a)})^{\frac{3}{2}}} = \frac{1}{(1 + \frac{\alpha}{2n-a})^{\frac{3}{2}} - 1} \leq \frac{1}{(1 + \frac{n-a}{2})^{\frac{3}{2}} - 1} \leq \frac{1}{(1 + \frac{n-a}{2})^{\frac{3}{2}} - 1} \leq 1
\]

\[
\leq \frac{n^{1/2+\epsilon}}{2^{n^{1/2+\epsilon}}} - 1
\]

\[ = (\ln(n') + 1)n'. \]
We use the previous lemma to get an upper bound for the epidemic threshold on cliques.

**Theorem 5.4.** Let $G$ be a clique with $n \in \mathbb{N}_{>0}$ vertices, and let $C$ be a contact process in the SIS model on $G$ with infection rate $\lambda = \frac{1}{n^a}$, for some $a \in \mathbb{N}_{<n/2}$, that starts with at least one infected vertex. Further, let there be a constant $\varepsilon \in (0, 1/2)$ such that $\alpha \geq n^{1/2+\varepsilon}$. Let $T$ be the survival time of $C$. Then

$$E[T] \in \Omega(1.5^{\frac{n^a}{n}}).$$

**Proof.** We aim to apply Lemma 5.3 to lower bound the survival time after reaching a state with $\alpha$ infected vertices. To get a bound on the overall survival time we first lower bound the probability to reach such a state. Let $T'$ be the first step with $I_{r_{t'}} = 0$ or $I_{r_{t'}} = \alpha/2$. For all time steps $t \in \mathbb{N}$ with $I_{r_t} \leq \alpha$ holds $p_{st,t} = \frac{n-I_{r_t}}{2n-\alpha-I_{r_t}} \geq \frac{1}{2}$. Hence until $T'$, the discrete version of $I_{r_t}$ dominates an unbiased gamblers ruin instance. Therefore, we get $\Pr[I_{r_{t'}} = \alpha/2] \geq \frac{2}{\alpha}$.

Let $A$ be the random variable that counts the number of time steps $t \in \mathbb{N}$ that exist with $I_{r_t} = \alpha/2$. Assume that $I_{r_{t'}} = \alpha/2$. As each step changes the number of infected vertices by 1, by Lemma 5.3 $A$ dominates a random variable $B \sim \text{Geom}\left((1.5^{\frac{n^a}{n}} - 1)^{-1}\right)$. Returning to $\alpha/2$ infected vertices $A$ times takes at least $A$ steps. In $C$ there are $n$ healing clocks with a rate of 1 each and $n(n-1)$ infection clocks with a rate of $\lambda \leq \frac{2}{n}$ each. Therefore, all of the clocks trigger at a rate of at most $\frac{3}{2}n$ and the expected time for each trigger is at least the inverse of that. Applying these insights on the expected survival time together with the law of total expectation results in

$$E[T] \geq \Pr[I_{r_{t'}} = \alpha/2] \cdot E[T \mid I_{r_{t'}} = \alpha/2]$$

$$\geq \frac{2}{\alpha} \cdot \frac{2}{3n} E[A \mid I_{r_{t'}} = \alpha/2]$$

$$\geq \frac{4}{n} \cdot \frac{2}{3n} (1.5^{\frac{n^a}{n}} - 1).$$

### 5.4 Lower Bound for the Epidemic Threshold

To give a lower bound for the epidemic threshold, we show that the considered process $C$ has a polynomial expected survival time if $\alpha \leq n^{1/2}$. To this end, we use Lemma 5.2 to bound the time spent above $\alpha$ infected vertices and we lower bound the probability to die out when below $\alpha$. The proof of the probability bound below $\alpha$ is very similar to the proof of Lemma 5.3.
Lemma 5.5. Let $G$ be a clique with $n \in \mathbb{N}_{>0}$ vertices and let $C$ be a contact process in the SIS model on $G$ with infection rate $\lambda = \frac{1}{n^2}$ for some $\alpha \in \mathbb{N}_{>0}$ with $\alpha \leq n^{1/2}$. Let $t_0 \in \mathbb{N}$ be a time step with $I_{t_0} = \alpha$ and let $T \in \mathbb{N}_{>t_0}$ be the first step after $t_0$ with $I_T = 0$ or $I_T = \alpha + 1$. Then

\[ \Pr[I_T = 0] \geq \frac{1}{n \cdot (2e^2 - 1)} \]

and $E[\tau_T - \tau_{t_0}] \leq 4(n - \alpha + 1)$.

Proof. We first bound the probability for the infection to die out. For all $t \in \mathbb{N}$ with $t_0 \leq t < T$ holds $0 < I_t$, and therefore $p_{t+1,t} = \frac{n-\alpha}{2n-\alpha-I_t} \geq \frac{n-\alpha}{2n-2\alpha}$. As this bound holds independently for all steps and because each step changes the number of infected vertices by 1 in either direction, in the time interval $[\tau_{t_0}, \tau_T)$ the discrete version of the process is dominated by a gamblers ruin instance $(P_t)_{t \in \mathbb{N}}$ with a probability of $p = \frac{n}{2n-2\alpha}$ to win. Let $T'$ be the first time that $P$ either reaches the lower bound 0 or the upper bound $\alpha + 1$ when starting at $P_0 = \alpha$. Then $\Pr[I_{T'} = 0] \geq \Pr[P_{T'} = 0]$ because of the dominance. We bound $\Pr[P_{T'} = 0]$ with Theorem 2.6. Note that $\frac{p}{1-p} = \frac{n}{2n-2\alpha} = 1 + \frac{\alpha}{n-\alpha}$. We get

\[
\Pr[I_{T'} = 0] \geq \Pr[I_{T'} = 0] \\
= \frac{1 - (1 + \frac{\alpha}{n-\alpha})^1}{1 - (1 + \frac{\alpha}{n-\alpha})^{\alpha+1}} \\
= \frac{1 + \frac{\alpha}{n-\alpha} - 1}{(1 + \frac{\alpha}{n-\alpha})^{\alpha+1} - 1} \\
\geq \frac{1}{n \cdot ((1 + \frac{2\alpha}{n})^{\alpha+1} - 1)} \\
\geq \frac{1}{n \cdot (2(1 + \frac{\alpha}{n})^\alpha - 1)} \\
\geq \frac{1}{n \cdot (2\sqrt{n})^\sqrt{\alpha} - 1)} \\
\geq \frac{1}{n \cdot (2e^2 - 1)}.
\]

To bound $E[\tau_T - \tau_{t_0}]$, we bound the number of times that we reach a state with exactly $\alpha$ infected vertices and the time between those states. Let $S$ be the random variable that counts the number of time steps $t \in \mathbb{N}$ with $t_0 \leq t < T$ and $I_t = \alpha$. For all $i \in \mathbb{N}_{\leq S+1}$, let $X_i$ be the $i$-th time step from $t_0$ to $T$ at which the number of infected vertices is either 0, $\alpha$ or $\alpha + 1$. It then holds that $\tau_T - \tau_{t_0} = \tau_{X_{S+1}} - \tau_{X_1} = \sum_{i=1}^{S} \tau_{X_{i+1}} - \tau_{X_i}$. We aim to bound the expectation of that value using the generalized Wald’s equation (Theorem 2.5).

We first bound $S$. Let $t \in \mathbb{N}$ with $t_0 \leq t < T$ and $I_t = \alpha$. Then $p_{s=t} = \frac{n-I_t}{2n-2\alpha-I_t} = \frac{1}{2}$. Hence, with
a probability of $\frac{1}{2}$, it holds $I_{t+1} = \alpha + 1$ which implies that $T = t + 1$ and that $t$ is the last step before $T$ with $\alpha$ infected vertices. Therefore, $S$ is dominated by a geometrically distributed random variable $A \sim \text{Geom}(\frac{1}{2})$.

Let $(\mathcal{F}_t)_{t \in \mathbb{N}}$ be the natural filtration of $C$. Let $t \in \mathbb{N}$ with $1 \leq t \leq S$. To bound $E\left[ X_{t+1} - X_t \mid \mathcal{F}_{X_t} \right]$, we first bound $E\left[ X_{t+1} - X_t \mid \mathcal{F}_{X_t} \right]$. We know that $I_{X_t} = \alpha$. As the number of infected vertices changes by exactly 1 in each step, there are two possibilities for $I_{X_t+1}$. Let $E$ be the event that $I_{X_t+1} = \alpha - 1$. If $E$ does not occur, it holds $I_{X_t+1} = \alpha + 1$, which implies $X_{t+1} = X_t + 1$, and therefore $X_{t+1} - X_t = 1$. We now bound $X_{t+1} - X_t$ in the case that $E$ happens using the additive drift theorem (Theorem 2.3).

We define the random process $(Y_i)_{i \in \mathbb{N}}$ with $Y_i = 1\{I_{t+1} = 0\} \cdot (\alpha - I_{t+1})$ for all $i \in \mathbb{N}$ and the stopping time $T' = \inf(i \in \mathbb{N} \mid Y_i \leq 0)$. Note that this process is basically shifted in time to start at $X_t$ and that the process reaches 0 when the number of infected vertices at the shifted time point is either 0 or $\alpha$. Therefore, $T' = X_{t+1} - X_t - 1$. Let $(\mathcal{F}'_i)_{i \in \mathbb{N}}$ with $\mathcal{F}'_i = \mathcal{F}_{t+1,X_{t+1}}$ for all $i \in \mathbb{N}$ be the natural filtration of $Y_i$.

We now show that the two conditions of the additive drift theorem are satisfied. We start with the first condition. As we assume that $I_{X_t+1} = \alpha - 1$ and because we stop when we reach $\alpha$ infected vertices, the term $\alpha - I_{t+1} = \alpha - 1$ is non-negative until $T'$ for all $i \in \mathbb{N} \leq T$ which implies for all $i \in \mathbb{N}$ that $Y_i \cdot 1\{i \leq T'\} \geq 0$.

Now let $i \in \mathbb{N}$ and $i' = i + X_t + 1$. To bound the drift for condition 2, we use that that by definition of $Y$ it holds $(Y_{i+1} - Y_i) \cdot 1\{i < T'\} \leq (I_{t+1} - I_{t+1}) \cdot 1\{i < T'\}$. Note that $I_{t+1} \leq \alpha - 1$. We get the following inequality. Note that we omit the multiplicative $1\{i < T'\}$ in all of the terms for better readability.

$$E\left[ Y_i - Y_{i+1} \mid \mathcal{F}'_{i+1} \right] \geq E\left[ I_{t+1} - I_{t+1} \mid \mathcal{F}'_{i} \right]$$

$$= p_{i,i'} - p_{i,i'}$$

$$= (1 - p_{i,i'}) - p_{i,i'}$$

$$= 1 - 2\frac{n - \alpha}{2n - \alpha - I_{t+1}}$$

$$\geq 1 - 2\frac{n - \alpha}{2n - 2\alpha + 1}$$

$$= \frac{1}{2n - 2\alpha + 1}$$

Now all of the conditions of Theorem 2.3 are satisfied and as $Y_0 = 1$, we get

$$E\left[ T' \mid \mathcal{F}'_{T'} \right] \cdot 1\{E\} \leq (2n - 2\alpha + 1) \cdot 1\{E\}.$$  

As now depending on $E$, $X_{t+1} - X_t$ is either equal to 1 or $T' + 1$, we get
\[ E[X_{t+1} - X_t | \mathcal{F}_t] \leq E\left[ 1 \cdot 1\{E\} + (T' + 1) \cdot 1\{E\} \right] \mathcal{F}_t \]
\[ \leq 2n - 2\alpha + 2. \]

As long as the infection has not died out yet, the state of \( C \) changes at a rate of at least 1. Therefore, the expected time between two states is at most 1 and we get

\[ E[\tau_{X_{t+1}} - \tau_{X_t} | \mathcal{F}_{\tau_{X_t}}] \leq E[X_{t+1} - X_t | \mathcal{F}_{\tau_{X_t}}] \leq 2n - 2\alpha + 2. \]

As now for all \( t \in \mathbb{N} \), both \( S \) and \( E \) are upper bounded by some values independent of \( t \). \( \sum_{i=1}^S \tau_{X_{t+i}} - \tau_{X_t} \) is integrable and by Theorem 2.5 we get

\[ E[\tau_T - \tau_{\tau_{X_0}} | \mathcal{F}_{\tau_{X_0}}] = E\left[ \sum_{i=1}^S \tau_{X_{t+i}} - \tau_{X_t} \right] | \mathcal{F}_{\tau_{X_t}}] \]
\[ = E\left[ \sum_{i=1}^S E[\tau_{X_{t+i}} - \tau_{X_t} | \mathcal{F}_{\tau_{X_t}}] \right] | \mathcal{F}_{\tau_{X_t}}] \]
\[ \leq E\left[ \sum_{i=1}^S 2n - 2\alpha + 2 \right] | \mathcal{F}_{\tau_{X_t}}] \]
\[ = 2(n - \alpha + 1)E \left[ \sum_{i=1}^S 1 | \mathcal{F}_{\tau_{X_t}} \right] \]
\[ \leq 4(n - \alpha + 1). \]

We now use Lemma 5.2 and Lemma 5.5 to give a polynomial extinction threshold.

**Theorem 5.6.** Let \( G \) be a clique with \( n \in \mathbb{N}_{>0} \) vertices and let \( C \) be a contact process in the SIS model on \( G \) with infection rate \( \lambda = \frac{1}{n-\alpha} \) for some \( \alpha \in \mathbb{N}_{>0} \) with \( \alpha \leq n^{1/2} \) that starts with at least one infected vertex. Let \( T \) be the survival time of \( C \). Then

\[ E[T] \in O(n^2 \ln(n)). \]

**Proof.** Let \((\mathcal{F}_t)_{t \in \mathbb{R}_{\geq0}}\) be the natural filtration of \( C \). First note that adding more vertices to the set of initially infected vertices monotonically increases \( T \). To upper bound \( E[T | \mathcal{F}_0] \), we assume that \( I_0 = n \) as that gives us the largest survival time of the infection. We use Lemma 5.2 and Lemma 5.5 to upper bound the number of times that the number of infected vertices drops to \( \alpha \) and the expected time between these times. With the generalized Wald’s equation (Theorem 2.5), that upper bounds \( E[T | \mathcal{F}_0] \).
Let $S$ be the random variable that counts the number of times at which the number of infected vertices in $C$ drops from $\alpha + 1$ to $\alpha$. For all $i \in \mathbb{N}_{\leq S+1}$, let $X_i$ be the $i$-th time at which the number of infected vertices drops to either $\alpha$ or 0 (We define $X_0 = 0$). Note that the number of infected vertices can only drop to 0 once as the infection cannot leave the state with no infected vertices anymore. By the definition of $S$, the infection dies out at $X_{S+1}$. We get that $T = X_{S+1} - X_0 = \sum_{i=0}^{S} X_{i+1} - X_i$.

By Lemma 5.5 after each time that the number of infected vertices drops to $\alpha$, there is a probability of at least $\frac{1}{n(2e-1)}$ that the infection dies out before the number of infected vertices drops to $\alpha$ again. Therefore, $S$ is dominated by a geometrically distributed random variable $A \sim \text{Geom}\left(\frac{1}{n(2e-1)}\right)$.

Let $(\mathcal{F}_i')_{i \in \mathbb{N}}$ with $\mathcal{F}_i' = \mathcal{F}_{X_i}$ for all $i \in \mathbb{N}$ be the natural filtration of $X$. Further, let $i \in \mathbb{N}_{\leq S}$. We aim to upper bound $E[X_{i+1} - X_i \mid \mathcal{F}_i']$. Let $Y_i \in \mathbb{R}$ be the first time after $X_i$ with $I_{Y_i} = 0$ or $I_{Y_i} > \alpha$. Note that $X_i \leq Y_i \leq X_{i+1}$. If $i = 0$, it holds $Y_i - X_i = 0$. Otherwise Lemma 5.5 is applicable and we get $E[Y_i - X_i \mid \mathcal{F}_i'] \leq 4(n - \alpha + 1)$. If $I_{Y_i} = 0$ then $X_{i+1} - Y_i = 0$. Otherwise Lemma 5.2 is applicable and we get $E[X_{i+1} - Y_i \mid \mathcal{F}_i'] \leq (\ln(n - \alpha) + 1) \cdot (n - \alpha)$. We therefore have

$$E[X_{i+1} - X_i \mid \mathcal{F}_i'] = E[X_{i+1} - Y_i \mid \mathcal{F}_i'] + E[Y_i - X_i \mid \mathcal{F}_i']$$

$$\leq 4(n - \alpha + 1) + (\ln(n - \alpha) + 1) \cdot (n - \alpha)$$

$$\leq (\ln(n - \alpha) + 5) \cdot (n - \alpha + 1).$$

As we now have an upper bound for $S$ and for all $i \in \mathbb{N}_{\leq S}$ an upper bound for $E[X_{i+1} - X_i \mid \mathcal{F}_i']$, $\sum_{i=0}^{S} X_{i+1} - X_i$ is integrable and by Theorem 2.5 we get

$$E[T \mid \mathcal{F}_0] = E\left[\sum_{i=0}^{S} X_{i+1} - X_i \mid \mathcal{F}_0\right]$$

$$= E\left[\sum_{i=0}^{S} E[X_{i+1} - X_i \mid \mathcal{F}_i'] \mid \mathcal{F}_0\right]$$

$$\leq E\left[\sum_{i=0}^{S} (\ln(n - \alpha) + 5) \cdot (n - \alpha + 1) \mid \mathcal{F}_0\right]$$

$$= (\ln(n - \alpha) + 5) \cdot (n - \alpha + 1)E\left[\sum_{i=0}^{S} 1 \mid \mathcal{F}_0\right]$$

$$\leq (\ln(n - \alpha) + 5) \cdot (n - \alpha + 1)(n \cdot (2e^2 - 1) + 1).$$

**Acknowledgments**

Andreas Göbel was funded by the project PAGES (project No. 467516565) of the German Research Foundation (DFG). This project has received funding from the European Union’s Horizon 2020 research and innovation program under the Marie Skłodowska-Curie grant agreement No. 945298-
ParisRegionFP. This research was partially funded by the HPI Research School on Data Science and Engineering.

References

[BB+05] Noam Berger, Christian Borgs, Jennifer T Chayes, and Amin Saberi. “On the spread of viruses on the internet”. In: *ACM Symposium on Discrete Algorithms (SODA)* (2005), pp. 301–310 (see pages 2, 4, 5).

[BBD+20] Marian Boguna, Ivan Bonamassa, Manlio De Domenico, Shlomo Havlin, Dmitri Krioukov, and M. Angeles Serrano. “Network Geometry”. In: *arXiv:2001.03241* (2020). URL: https://arxiv.org/abs/2001.03241 (see page 8).

[BCG+10] Christian Borgs, Jennifer Chayes, Ayalvadi Ganesh, and Amin Saberi. “How to distribute antidote to control epidemics”. In: *Random Structures & Algorithms* 37.2 (2010), pp. 204–222. DOI: https://doi.org/10.1002/rsa.20315 (see pages 2, 5).

[BFK18] Thomas Bläsius, Tobias Friedrich, and Anton Krohmer. “Cliques in Hyperbolic Random Graphs”. In: *Algorithmica* 80 (2018), pp. 2324–2344. DOI: 10.1007/s00453-017-0323-3 (see page 8).

[BNN+21] Shankar Bhamidi, Dannz Nam, Oanh Nguyen, and Allan Sly. “Survival and extinction of epidemics on random graphs with general degree”. In: *The Annals of Probability* 49.1 (2021), pp. 244–286 (see pages 2, 4).

[BP10] Bancal, J.-D. and Pastor-Satorras, R. “Steady-state dynamics of the forest fire model on complex networks”. In: *Eur. Phys. J. B* 76.1 (2010), pp. 109–121. DOI: 10.1140/epjb/e2010-00165-7. URL: https://doi.org/10.1140/epjb/e2010-00165-7 (see page 3).

[DK22] Carola Doerr and Martin S. Krejca. “Run Time Analysis for Random Local Search on Generalized Majority Functions”. In: *CoRR* abs/2204.01793 (2022). DOI: 10.48550/ARXIV.2204.12770 (see page 11).

[Fel68] William Feller. *An introduction to probability theory and its applications*. 3rd ed. Vol. 1. John Wiley & Sons, Inc, 1968. ISBN: 978-0-471-25708-0 (see pages 10, 11).

[GMT05] Ayalvadi Ganesh, Laurent Massoulié, and Don Towsley. “The effect of network topology on the spread of epidemics”. In: *International Conference on Computer Communications (INFOCOM)*. Vol. 2. IEEE. 2005, pp. 1455–1466 (see pages 2–5, 7, 8, 28).

[Haj82] Bruce Hajek. “Hitting-time and occupation-time bounds implied by drift analysis with applications”. In: *Advances in Applied Probability* 14.3 (1982), pp. 502–525. DOI: 10.2307/1426671 (see page 6).

[Har74] T. E. Harris. “Contact Interactions on a Lattice”. In: *The Annals of Probability* 2.6 (1974), pp. 969–988. DOI: 10.1214/aop/1176996493. URL: https://doi.org/10.1214/aop/1176996493 (see page 2).
[OW11] Pietro S Oliveto and Carsten Witt. “Simplified drift analysis for proving lower bounds in evolutionary computation”. In: Algorithmica 59.3 (2011), pp. 369–386 (see pages 6, 10).

[OW12] Pietro S. Oliveto and Carsten Witt. “Erratum: Simplified Drift Analysis for Proving Lower Bounds in Evolutionary Computation”. In: CoRR abs/1211.7184 (2012). URL: http://arxiv.org/abs/1211.7184 (see page 10).

[PCM+15] Romualdo Pastor-Satorras, Claudio Castellano, Piet Van Mieghem, and Alessandro Vespignani. “Epidemic processes in complex networks”. In: Reviews of Modern Physics 87 (3 2015), pp. 925–979. DOI: 10.1103/RevModPhys.87.925 (see page 1).

[Pem92] Robin Pemantle. “The Contact Process on Trees”. In: Annals of Probability 20 (1992), pp. 2089–2116 (see page 2).

[Sai19] M Ali Saif. “Epidemic threshold for the SIRS model on the networks”. In: Physica A: Statistical Mechanics and its Applications 535 (2019), p. 122251 (see page 3).

[Sta96] A. M. Stacey. “The existence of an intermediate phase for the contact process on trees”. In: The Annals of Probability 24.4 (1996), pp. 1711–1726. DOI: 10.1214/aop/1041903203. URL: https://doi.org/10.1214/aop/1041903203 (see page 2).

[WCA+17] Yi Wang, Jinde Cao, Ahmed Alsaeedi, and Tasawar Hayat. “The spreading dynamics of sexually transmitted diseases with birth and death on heterogeneous networks”. In: Journal of Statistical Mechanics: Theory and Experiment 2017.2 (Feb. 2017), p. 023502. DOI: 10.1088/1742-5468/aa58a6. URL: https://doi.org/10.1088/1742-5468/aa58a6 (see page 3).