# The Limits to Learning a Diffusion Model

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#### Abstract

This paper provides the first sample complexity lower bounds for the estimation of simple diffusion models, including the Bass model (used in modeling consumer adoption) and the SIR model (used in modeling epidemics). We show that one cannot hope to learn such models until quite late in the diffusion. Specifically, we show that the time required to collect a number of observations that exceeds our sample complexity lower bounds is large. For Bass models with low innovation rates, our results imply that one cannot hope to predict the eventual number of adopting customers until one is at least two-thirds of the way to the time at which the rate of new adopters is at its peak. In a similar vein, our results imply that in the case of an SIR model, one cannot hope to predict the eventual number of infections until one is approximately two-thirds of the way to the time at which the infection rate has peaked. These limits are borne out in both product adoption data (Amazon), as well as epidemic data (COVID-19).

# 1. Introduction

Diffusion models are simple reduced form models (typically described by a system of differential equations) that seek to explain the diffusion of an epidemic in a network. The Susceptible-Infected-Recovered (SIR) model is a classic example, proposed nearly a century ago (Kermack and McKendrick 1927). The SIR model remains a cornerstone for the forecasting of epidemics. The so-called Bass model (Bass 1969), proposed over fifty years ago is similarly another example that remains a basic building block in forecasting consumer adoption of new products and services. The durability of these models arises from the fact that they have shown an excellent fit to data, in numerous studies

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spanning both the epidemiology and marketing literatures. Somewhat paradoxically, using these same models as reliable forecasting tools presents a challenge.

While we are ultimately motivated by the problem of forecasting a diffusion model, this paper asks a more basic question that is surprisingly unanswered: *What are the limits to learning a diffusion model?* We answer this question by characterizing sample complexity lower bounds for a class of stochastic diffusion models that encompass both the Bass model and the SIR model. We show that the time to collect a number of observations that exceeds these lower bounds is too large to allow for accurate forecasts early in the process. In the context of the Bass model our results imply that when adoption is driven by imitation, one cannot hope to predict the eventual number of adopting customers until one is at least two-thirds of the way to the time at which the rate of new adopters is at its peak. In a similar vein, our results imply that in the case of an SIR model, one cannot hope to predict the eventual number of infections until one is approximately two-thirds of the way to the time at which the infection rate has peaked. Our analysis is conceptually simple and relies on the Cramer-Rao bound. The core technical difficulty in our analysis rests in characterizing the Fisher information in the observations available due to the fact that they have a non-trivial correlation structure.

Maximum likelihood estimation of diffusion models on product adoption datasets (for products on Amazon.com), and epidemic data (from the ongoing COVID-19 epidemic) illustrate precisely the behavior predicted by our theory. As a byproduct of our analysis, we see that the difficulty in learning a diffusion model stems solely from uncertainty in a single unknown 'effective population size' parameter. In particular, other parameters, including those related to the 'rate of imitation' (in the Bass model) or the 'reproduction number' (in the SIR model) are easy to learn. This suggests that estimators that rely on an (informative) bias in this population size parameter *can* in fact overcome the limitations presented by our analysis. Although not a primary contribution of the present work, we describe a heuristic procedure used to construct such a biased estimator that yielded one of the first US county-level forecasters available for COVID-19.

**Related Literature:** Diffusion models find broad application in at least two key domains: epidemiology and marketing science. While there is surprisingly little literature that cuts across the two application domains, the dominant themes are quite similar.

The SIR model (Kermack and McKendrick 1927) is perhaps the best known and most widely analyzed and used diffusion model in the epidemiology literature. For instance, the plurality of COVID-19 modeling efforts are founded on SIR-type models (eg. Calafiore et al. (2020), Gaeta (2020), Giordano et al. (2020), Binti Hamzah et al. (2020), Kucharski et al. (2020), Wu et al. (2020), Anastassopoulou et al. (2020), Biswas et al. (2020), Chikina and Pegden (2020), Massonnaud et al. (2020), Goel and Sharma (2020)). It is common to consider generalizations to the SIR model that add additional states or 'compartments' (Giordano et al. (2020) is a nice recent example); not surprisingly, learning gets harder with as the number of states increases (Roosa and Chowell 2019). In a similar fashion, the Bass model (Bass 1969) remains the best known and most widely analyzed diffusion model in the marketing science literature. The model has found application in a staggering variety of industries over the past fifty years. Surveys such as Bass (2004), Mahajan et al. (2000), Hauser et al. (2006) provide a sense of this breadth showing that the model and its generalizations have found application in tasks ranging from forecasting the adoption of technologies, brands and products to describing information cascades on services such as Twitter (Bakshy et al. 2011). Just as in the case of the SIR model, a number of generalizations of the Bass model have been proposed over the years, including Peterson and Mahajan (1978), Bass et al. (1994), Van den Bulte and Joshi (2007).

Estimation in SIR Models: The identifiability of the stochastic SIR model (Bartlett 1949, Darling et al. 2008) is not well understood in the literature. In fact, even identification of the deterministic model is a non-trivial matter (Evans et al. 2005). Specifically, calibrating a vanilla SIR model to data requires learning the so-called infectious period and basic reproduction rate. Both these parameters are relatively easy to calibrate with limited data; this is supported both by the present paper, but also commonly observed empirically; see for instance Roosa and Chowell (2019). In addition to these parameters, however, one needs to measure both the initial number of infected individuals and the size of the susceptible population. Estimating the number of infected individuals poses a challenge in the presence of limited testing and asymptomatic carriers. Indeed, epidemiological models for COVID-19 typically assume that measured infections are some fraction of true infections; eg. Calafiore et al. (2020), Giordano et al. (2020). This challenge is closely related to that of measuring the true fraction of cases that lead to fatalities (or the so-called Infection Fatality Rate) (Basu 2020). Our main theorem shows that having to learn the true initial prevalence of the infection presents a fundamental difficulty to learning SIR models with limited data; this is complemented by heretofore unexplained empirical work (Chowell 2017, Capaldi et al. 2012).

Estimation in Bass Models: The Bass model has traditionally been estimated using a variety of weighted least squares estimators; Srinivasan and Mason (1986), Jain and Rao (1990) are popularly used examples. The key parameters that must be estimated here are the so-called coefficient of imitation (the analogue of the reproduction number in the SIR model) and the coefficient of innovation (which does not have an analogue in the SIR model). In addition one must estimate the size of the eventual population that will adopt (arguably one of the key quantities one would care to forecast). It has been empirically observed that existing estimation approaches are 'unstable' in the sense that estimates of the size of the population that adopts can vary dramatically even half-way through the diffusion model (Van den Bulte and Lilien 1997, Hardie et al. 1998) among other undesirable features. This has been viewed as a limitation of the estimators employed, and has led to corrections to the estimators that purport to address some of these issues (Boswijk and Franses 2005). In contrast, our results imply that this behavior is fundamental; as one example we show that no unbiased estimator of the Bass model can hope to learn the population size until at least two-thirds of the way through the diffusion model.

# 2. Model

We first define a general deterministic diffusion model using a system of ODEs. Our paper focuses on two parameter regimes of this model, which represent the Bass model (Section 2.2) and the SIR model (Section 2.3). We then describe a stochastic variant of the diffusion model in Section 2.4; our main result in Section 3 describes the limits to learning the parameters of this stochastic model.

# 2.1. Deterministic Diffusion Model

We define a general diffusion model with three 'compartments' over an 'effective' population of size N. Let s(t), i(t) and r(t) be the size of susceptible, infected, and recovered populations respectively, as observed at time t, where s(t) + i(t) + r(t) = N for all  $t \ge 0$ . The model is defined by the following system of ODEs, specified by the tuple of parameters  $(N, \beta, \gamma, p)$ :

(1) 
$$\frac{ds}{dt} = -\beta \frac{s}{N}i - ps, \qquad \qquad \frac{di}{dt} = \beta \frac{s}{N}i - \gamma i + ps, \qquad \qquad \frac{dr}{dt} = \gamma i$$

We assume that all parameters are non-negative, and that  $\beta > \gamma$ . The parameters here that we may need to estimate include  $\beta, \gamma, p$  and N.

# 2.2. Bass Model ( $\gamma = 0$ )

The Bass model is the special case of the diffusion model above where  $\gamma = 0$  and as already discussed has been variously used to describe the diffusion of a new product, technology, or even information in a population. *i* and *s* represent the number of people who have and have not adopted the product respectively by time *t*. Since  $\gamma = 0$ , there is effectively no *r* compartment.  $\beta \frac{s}{N}i$  represents the instantaneous growth rate in adoption contributed by individuals 'imitating' existing adopters, while *ps* represents the the instantaneous growth rate in adoption contributed by 'innovators' who adopt the product without the influence of existing adopters. The parameter  $\beta^1$  is often called the *coefficient of imitation*, while *p* is called the *coefficient of innovation*.

In the Bass model, the eventual number of adopters i.e.,  $\lim_{t\to\infty} i(t) = N$ , is often an important quantity of interest. As such, N is a key, unknown parameter to estimate in this setting. We define an additional parameter  $a \triangleq pN$ . Since  $s \approx N$  initially, a represents the growth rate of innovators near the beginning of the process.

# **2.3.** SIR Model (p = 0)

The SIR model is the simplest compartmental model in epidemiology that models how a disease spreads amongst a population, and it can be described by the diffusion model in the case that p = 0. The parameter  $\gamma$  specifies the rate of recovery;  $1/\gamma$  is frequently referred to as the *infectious period*.  $\beta > 0$  quantifies the rate of transmission;  $\beta/\gamma \triangleq R_0$  is also referred to as the *basic reproduction* number.

In using the SIR model to model an epidemic where only a fraction of all infections are observed (due to, for example, asymptomatic cases and limited testing) the N parameter is effectively the actual population of the region being modeled multiplied by the fraction of observed infections. If the fraction of observed infections is unknown (which it typically is), then N is effectively unknown. Specifically, the following proposition shows that the quantities corresponding to observing a constant fraction of an SIR model also constitutes an SIR model with the same parameters  $\beta$  and  $\gamma$ :

**Proposition 2.1.** Let  $\{(s'(t), i'(t), r'(t)) : t \ge 0\}$  be a solution to (1) for parameters  $N = N', \beta = \beta', \gamma = \gamma'$  and initial conditions i(0) = i'(0), s(0) = s'(0). Then, for any  $\eta > 0$ ,  $\{(\eta s'(t), \eta i'(t), \eta r'(t)) : t \ge 0\}$  is a solution to (1) for parameters  $N = \eta N', \beta = \beta', \gamma = \gamma'$  and  $i(0) = \eta i'(0), s(0) = \eta s'(0)$ .

<sup>&</sup>lt;sup>1</sup>The marketing science literature will frequently use the letter q in place of  $\beta$ .

In words, suppose a disease spreads according to an SIR model amongst the entire population of (known) size N'. Suppose we only observe a constant fraction from this process, where this fraction  $\eta$  is unknown. The proposition above states that the observed process is also an SIR model with the same parameters  $\beta$  and  $\gamma$ , and an effectively unknown population  $N = \eta N'$ . It is known that both cumulative and peak infections scale with N (Weiss 2013). As these are often the key quantities of interest, estimating N accurately is a critical task.

### 2.4. Stochastic Diffusion Model

In the deterministic diffusion model, all parameters are identifiable if i(t) is observable over an *infinitesimally small* period of time in either of the two regimes. Specifically:

**Proposition 2.2.** Suppose either p = 0 or  $\gamma = 0$ . Let i(t) be observed over some open set in  $\mathbb{R}_+$ . Then the parameters  $(N, \beta, \gamma, p)$  are identifiable.

Noise — an essential ingredient of any real-world model — dramatically alters this story. We describe next a natural continuous-time Markov chain variant of the deterministic diffusion model, proposed at least as early as Bartlett (1949). Specifically, the stochastic diffusion model,  $\{(S(t), I(t), R(t)) : t \ge 0\}$ , is a multivariate counting process, with RCLL paths, determined by the parameters  $(N, \beta, \gamma, p)$ . The jumps in this process occur at the rate in (3), and correspond either to a new observed infection or adopter (where I(t) increments by one, and S(t) decrements by one) or to a new observed recovery (where I(t) decrements by one, and R(t) increments by one). Let C(t) = I(t) + R(t) denote the cumulative number of infections or adoptions observed up to time t. Denote by  $t_k$  the time of the kth jump, and let  $T_k$  be the time between the (k-1)st and kth jumps. Finally, let  $I_k \triangleq I(t_k)$ , and similarly define  $R_k, S_k$  and  $C_k$ . The stochastic diffusion model is then completely specified by:

(2) 
$$C_k - C_{k-1} \sim \text{Bern}\left\{\frac{S_{k-1}(\beta I_{k-1} + pN)}{S_{k-1}(\beta I_{k-1} + pN) + N\gamma I_{k-1}}\right\}$$

(3) 
$$T_k \sim \operatorname{Exp}\left\{\frac{\beta S_{k-1}}{N}I_{k-1} + pS_{k-1} + \gamma I_{k-1}\right\}.$$

It is well known that solutions to the deterministic diffusion model (1) provide a good approximation to sample paths of the diffusion model (described by (2), (3)) in the so-called fluid regime; see Darling et al. (2008).

The next section analyzes the rate at which one may hope to learn the unknown parameters

 $(N, \beta, \gamma, p)$  as a function of k; our key result will illustrate that in large systems, N is substantially harder to learn than  $\beta$  or  $\gamma$ . In turn this will allow us to show that we cannot hope to learn the stochastic diffusion model described above until quite late in the diffusion.

# 3. Limits to Learning

This section characterizes the rate at which one may hope to learn the parameters of the stochastic diffusion model, simply from observing the process.

**Observations:** Define the stopping time  $\tau = \inf\{k : I_k = 0 \text{ or } I_k = N\}$ ; clearly  $\tau$  is bounded. For clarity, when  $k > \tau$ , we define  $C_k = C_{k-1}$ ,  $I_k = I_{k-1}$ , and  $T_k = \infty$ . Note that  $I_k$  and  $R_k$  are deterministic given  $C_k$ ,  $I_0$ , and  $R_0$ . We define the *m*-th information set  $O_m = (I_0, R_0, T_1, C_1, \ldots, T_m, C_m)$  for all  $m \ge 1$ .

**Evaluation Metric:** For any parameter  $\theta$ , suppose  $\hat{\theta}_m$  is an estimator based on the observations  $O_m$ . We define the *relative error* of  $\hat{\theta}_m$  as:

RelError
$$(\hat{\theta}_m, \theta) \triangleq \frac{(\hat{\theta}_m - \theta)^2}{\theta^2}.$$

A relative error of 1 implies that the absolute error of the estimator is the same size as the true parameter. Therefore, in order to estimate a parameter  $\theta$ , it is reasonable to require that the relative error be at most 1, and ideally shrinking to 0. Our goal is to find the regime of m relative to Nsuch that RelError( $\hat{\theta}_m, \theta$ ) = o(1).

Our main theorem lower bounds the relative error of any unbiased estimator of the parameter N. We first state the exact assumptions necessary for the two regimes:

Assumption 3.1 (Bass Model). Assume  $\gamma = 0$ ,  $I_0 = 1$ ,  $R_0 = 0$ , and assume  $\beta$  and a = pN are known. Consider a sequence of systems of increasing size, where  $N \to \infty$ . Let m = o(N).

Assumption 3.2 (SIR Model). Assume p = 0, and assume  $\beta$  and  $\gamma$  are known. Assume  $I_0 \ge D$ , where D is a constant that depends on  $\beta$  and  $\gamma$ . Consider a sequence of systems of increasing size, where  $N \to \infty$ , and  $\beta$  and  $\gamma$  are constant. Let m = o(N), and  $I_0, R_0 \le m$ .

We now state our main result.

**Theorem 3.3.** Under Assumption 3.1 or Assumption 3.2, if  $\hat{N}_m$  is any unbiased estimator of N

based on the observations  $O_m$ ,

(4) 
$$\mathbb{E}[RelError(\hat{N}_m, N)] = \Omega\left(\frac{N^2}{m^3}\right).$$

This result implies that to have  $\mathbb{E}[\text{RelError}(\hat{N}_m, N)] = o(1)$ , we must have  $m = \omega(N^{2/3})$  observations. The next section analyzes how long it takes to reach  $N^{2/3}$  observations. Although  $N^{2/3}$  is a vanishing quantity compared to N, we show in Section 3.1 that in many parameter regimes, the time it takes to reach  $N^{2/3}$  observations is a constant portion (e.g., two thirds) of the time it takes to reach the peak infection rate of the process. In Section 3.2, we analyze the relative error for the other parameters of the model, and we show that these other parameters are much easier to learn than N.

Theorem 3.3 is a direct consequence of applying the Cramer-Rao bound to the following theorem, which characterizes the Fisher information of  $O_m$  relative to N as N grows large.

**Theorem 3.4.** Under Assumption 3.1 or Assumption 3.2, the Fisher information of  $O_m$  relative to N is

(5) 
$$\mathcal{J}_{O_m}(N) = \Theta\left(\frac{m^3}{N^4}\right)$$

The proof of Theorem 3.4 can be found in Section 4. It is notable that the result above provides a precise rate for the Fisher information as opposed to simply an upper bound. This further allows us to conclude that the relative error rate in Theorem 3.3 is precisely the rate achieved by an efficient unbiased estimator for N.

### 3.1. Time to Learn

Theorem 3.3 implies that at least  $N^{2/3}$  observations are needed before we can learn N. Here we characterize how long the diffusion model takes to reach this point relative to the time it takes to reach the point when the rate of new infections is at its peak. In both settings, the peak corresponds to a time in which a constant fraction of the population has been infected.

### 3.1.1. Bass Model.

One way to characterize the time at which the rate of new adopters in the Bass model peaks is to identify the first epoch at which the expected time until the next adoption increases. That is, defining

$$k^* = \inf\{k : \mathbb{E}[T_k] \ge \mathbb{E}[T_{k-1}]\},\$$

 $t_{k^*}$  corresponds to the (random) time at which this peak in the rate of new adoptions occurs. We denote by  $t_{k^{CR}}$  (where  $k^{CR} \triangleq \lceil N^{2/3} \rceil$ ) the earlier time at which we have sufficiently many observations to estimate N accurately per Theorem 3.3. The following result characterizes the ratio  $\mathbb{E}[t_{k^{CR}}]/\mathbb{E}[t_{k^*}]$  as  $N \to \infty$ :

**Proposition 3.5.** Suppose  $\gamma = 0, I_0 = 1, \frac{p}{\beta} < c$  for some constant c < 1. Suppose  $\frac{p}{\beta} = \Theta(\frac{1}{N^{\alpha}})$ .

$$\lim_{N \to \infty} \frac{\mathbb{E}[t_{k^{\mathrm{CR}}}]}{\mathbb{E}[t_{k^*}]} = \begin{cases} 0 & \alpha \leq \frac{1}{3} \\ \frac{\alpha - \frac{1}{3}}{\alpha} & \frac{1}{3} < \alpha < 1 \\ \frac{2}{3} & \alpha \geq 1. \end{cases}$$

Treating  $\beta$  as a constant, we see that the fraction of time until peak by which we can hope to learn the Bass model,  $\mathbb{E}[t_{k^{CR}}]/\mathbb{E}[t_{k^*}]$ , depends on  $p/\beta$ . This latter quantity provides a measure of the relative contribution of innovators and imitators to the instantaneous rate of overall adoption. What the result above shows is that if adoption is driven largely by imitation (the case for many products that rely on word-of-mouth or network effects, and certainly for information) so that  $p/\beta$ is small ( $\alpha \geq 1$ ), we need to wait at least two-thirds of the way until peak to collect enough samples to learn N.

#### 3.1.2. SIR Model.

For the SIR model, characterizing the random time in which the process hits either the peak infection rate or  $N^{2/3}$  observations appears to be a difficult task. Therefore, we analyze the analogs of  $t_{k^{\text{CR}}}$  and  $t_{k^*}$  in the deterministic model (1). Specifically, let  $t_{\text{CR}}^d = \inf \left\{ t : c(t) \ge N^{2/3} \right\}$  and  $t_*^d = \inf \left\{ t : d^2s/dt^2 > 0 \right\}$  for the process defined by (1).

**Proposition 3.6.** Suppose p = 0 and  $\beta, \gamma$  are fixed. If  $c(0) = O(\log(N))$ ,

$$\liminf_{N \to \infty} \frac{t_{\mathrm{CR}}^d}{t_*^d} \ge \frac{2}{3}.$$

This suggests that the sampling requirements made precise by Theorem 3.3 can only be met at such time where we are close to reaching the peak infection rate. Unlike the Bass model, this ratio

**Table 1:** Summary of parameter estimation results for the Bass and SIR models. The first row shows the relative error of estimating each parameter with m observations. The second row shows  $\operatorname{argmin}_{m}\{\operatorname{RelError}(\hat{\theta}_{m},\theta) \leq 1\}$ , the number of observations needed so that the relative error is less than 1. For the Bass model, a = pN, and  $a = \Theta(N^{1-\alpha})$  for  $\alpha \geq 0$ .

	Bass		SI	R
N*	$\beta$	$a^{**}$	$\beta$	$\gamma$
$\begin{array}{c c c c c c c c c c c c c c c c c c c $	$ \begin{bmatrix} \tilde{O}\left(\frac{1}{m} + \frac{N^{2(1-\alpha)}}{m^3}\right) \\ \tilde{O}\left(\max\{1, N^{\frac{2}{3}}(1-\alpha)\}\right) \end{bmatrix} $	$\tilde{O}\left(\frac{1}{m} + \frac{1}{N^{(1-\alpha)}}\right)$ $\tilde{O}\left(1\right)$	$\begin{array}{ c } O\left(\frac{\log m}{m}\right) \\ O\left(1\right) \end{array}$	$O\left(\frac{\log m}{m}\right)$ $O\left(1\right)$

\*The column for N represents the *expected* relative error, whereas the other parameters are high-probability results. \*\*We note that the results for the parameter a hold only for  $\alpha < 1$ .

is not specific to a parameter regime for the model.

# 3.2. Estimating Other Parameters

We now turn our attention to learning the other parameters of the model. The high level message here is that parameters other than the population N are in general easier to learn, and this is best understood through Table 1. Specifically, the second row in that table shows the number of observations needed for a relative error less than one. Our earlier analysis provides lower bounds on this quantity for the estimation of N. Here we construct explicit estimators for the remaining parameters yielding upper bounds on the number of observations required to learn those parameters with a relative error less than one.

We immediately see that for the SIR model, we can accomplish this task with a number of observations that *does not scale* with the population size parameter. In the case of the Bass model the story is more nuanced: it is always easier to learn the the coefficient of imitation,  $\beta$ . On the other hand when the rate of innovation is very low, learning a := pN is hard, but also not relevant to tasks related to forecasting N. We next present formal results that support the quantities in Table 1.

#### 3.2.1. Bass Model.

For the Bass model, we construct estimators for the parameters  $\beta$  and a := pN:

**Theorem 3.7.** Suppose  $\gamma = 0$  and  $I_0 = 1$ . Let a = pN. Suppose  $m \leq N^{2/3} \log^{1/3}(N)$ . There exist

estimators  $\hat{a}_m$ ,  $\hat{\beta}_m$  based on the observations  $O_m$  such that with probability  $1 - O(\frac{1}{N})$ ,

$$RelError(\hat{\beta}_m, \beta) = O\left(\frac{\log N}{m} + \frac{a^2}{\beta^2} \frac{\log N}{m^3}\right),$$
$$RelError(\hat{a}_m, a) = O\left(\frac{\log N}{m} + \frac{\beta}{a} \log N\right).$$

The above result demonstrates that learning the coefficient of imitation,  $\beta$ , is always easier than estimating N. This is also the case for a when  $p/\beta = \omega(1/N)$ ; when  $p/\beta = O(1/N)$ , the number of innovators who adopt is negligible compared to the number of imitators and it is not possible to estimate a.

#### 3.2.2. SIR Model.

For the SIR model we construct estimators for the parameters  $\beta$  and  $\gamma$ :

**Theorem 3.8.** Suppose p = 0 and  $\beta > \gamma$ . Let  $C_0, m, N$  satisfy  $m(m+C_0) \leq N$ , and  $\frac{\beta}{\beta+\gamma} \frac{N-m-C_0}{N} > \frac{1}{2}(\frac{\beta}{\beta+\gamma}+\frac{1}{2})$ . Then, there exist estimators  $\hat{\beta}_m$  and  $\hat{\gamma}_m$ , both functions of  $O_m$ , such that with probability  $1 - \frac{8}{m} - B_1 e^{-B_2 I_0}$ ,

$$RelError(\hat{\beta}_m, \beta) \le M_1\left(\frac{\log m}{m}\right),$$
$$RelError(\hat{\gamma}_m, \gamma) \le M_2\left(\frac{\beta^2}{\gamma^2}\frac{\log m}{m}\right),$$

where  $M_1, M_2 > 0$  are absolute constants and  $B_1, B_2 > 0$  depends only on  $\beta$  and  $\gamma$ .

When  $\beta$  and  $\gamma$  do not scale with the size of the system N (which is the case for epidemics), this result shows that the relative error for both estimators is  $O(\log m/m)$ , i.e. independent of N. Consequently, to achieve any desired level of accuracy, we simply need the number of observations m to exceed a constant that is independent of the size of the system. This is in stark contrast to Theorem 3.3, in which m needs to scale at least as  $\omega(N^{2/3})$  in order to learn N.

# 4. Proof of Theorem 3.4

Recall that  $O_m = (I_0, R_0, T_1, C_1, \dots, T_m, C_m)$ . We will take advantage of conditional independence to decompose the Fisher information  $\mathcal{J}_{O_m}(N)$  into smaller pieces. We first define the conditional Fisher information and state some known properties. **Definition 4.1.** Suppose X, Y are random variables defined on the same probability space whose distributions depend on a parameter  $\theta$ . Let  $g_{X|Y}(x, y, \theta) = \frac{\partial}{\partial \theta} \log f_{X|Y;\theta}(x|y)^2$  be the square of the score of the conditional distribution of X given Y = y with parameter  $\theta$  evaluated at x. Then, the conditional Fisher information is defined as  $\mathcal{J}_{X|Y}(\theta) = \mathbb{E}_{X,Y} \left[ g_{X|Y}(X, Y, \theta) \right]$ .

**Property 4.2.**  $\mathcal{J}_{X_1,...,X_n}(\theta) = \mathcal{J}_{X_1}(\theta) + \sum_{i=2}^n \mathcal{J}_{X_i|X_1,...,X_{i-1}}(\theta).$ 

**Property 4.3.** If X is independent of Z conditioned on Y,  $\mathcal{J}_{X|Y,Z}(\theta) = \mathcal{J}_{X|Y}(\theta)$ .

**Property 4.4.** If X is deterministic given Y = y,  $g_{X|Y}(X, y, \theta) = 0$ .

**Property 4.5.** If  $\theta(\eta)$  is a continuously differentiable function of  $\eta$ ,  $\mathcal{J}_X(\eta) = \mathcal{J}_X(\theta(\eta))(\frac{d\theta}{dn})^2$ .

Since  $I_0$  and  $R_0$  are known and not random, the Fisher information of  $O_m$  is equal to the Fisher information of  $(T_1, C_1, T_2, C_2, \ldots, T_m, C_m)$ . Then, Property 4.2 implies

(6) 
$$\mathcal{J}_{O_m}(N) = \mathcal{J}_{T_1}(N) + \mathcal{J}_{C_1|T_1}(N) + \mathcal{J}_{T_2|T_1,C_1}(N) + \mathcal{J}_{C_2|T_1,C_1,T_2}(N) + \dots + \mathcal{J}_{C_M|T_1,C_1,\dots,T_m}(N).$$

**Bass Model:** The above expression simplifies greatly for the Bass model since every event corresponds to a new infection. That is, we know  $C_k = I_k = I_0 + k$  and  $S_k = N - k - I_0$ deterministically. Therefore, Property 4.4 implies that  $\mathcal{J}_{C_k|}(N) = 0$  for all k. Moreoever, since  $T_k \sim \exp(\beta \frac{S_{k-1}}{N} I_{k-1} + \frac{a}{N} S_{k-1})$  is independent of  $T_1, C_1, \ldots, C_{k-1}, \mathcal{J}_{T_k|T_1, C_1, \ldots, C_{k-1}}(N) = \mathcal{J}_{T_k}(N)$ . This yields

(7) 
$$\mathcal{J}_{O_m}(N) = \sum_{k=1}^m \mathcal{J}_{T_k}(N).$$

By letting  $\lambda_k(N) = \left(\frac{\beta}{N}(k+I_0) + \frac{a}{N}\right)(N-k-I_0)$ , since  $T_k \sim \exp(\lambda_k(N))$ , Property 4.5 says that  $\mathcal{J}_{T_k}(N) = \mathcal{J}_{T_k}(\lambda_k) \left(\frac{d\lambda_k}{dN}\right)^2$ . Using that the Fisher Information of an exponential distribution with parameter  $\lambda$  is  $\frac{1}{\lambda^2}$ , a couple lines of algebra yields  $\mathcal{J}_{T_k}(N) = \frac{(k+I_0)^2}{N^2(N-k-I_0)^2}$ . Plugging back into (7), we get

(8) 
$$\mathcal{J}_{O_m}(N) = \frac{1}{N^2} \sum_{k=1}^m \frac{(k+I_0)^2}{(N-k-I_0)^2}.$$

Using  $I_0 = 1$  and m = o(N) from Assumption 3.1, we get the desired result  $\mathcal{J}_{O_m}(N) = \Theta\left(\frac{m^3}{N^4}\right)$ .

**SIR Model:** The analysis for the SIR model is more complicated since  $C_k$  is not deterministic and the distribution of  $T_k$  depends on  $C_{k-1}$ . Moreover, there is a non-zero probability that the process has terminated before the k'th jump for any k. Define the indicator variable  $E_k = \mathbb{1}\{\tau > k\}$ on the event which the SIR process has not terminated after k jumps. The following lemma states that both  $E_k$  and  $I_k$  can be determined from  $C_k$ ,  $I_0$ , and  $R_0$ , which will allow us to decouple variables in  $O_m$  in the analysis of the Fisher information. The result follows from the definitions of  $\tau$ ,  $E_k$ , and  $C_k$ ; the details can be found in the Appendix.

**Lemma 4.6.** Define  $r_k \triangleq \frac{I_0 + k + 2R_0}{2}$  for all  $k \ge 0$ . For all k,  $E_k = \mathbb{1}\{C_k > r_k\}$ . Moreover, when  $E_k = 1$ ,  $I_k = 2C_k - k - I_0 - 2R_0 > 0$ .

The next lemma writes an exact expression for  $\mathcal{J}_{O_m}(N)$ , analogous of (8) for the Bass model: Lemma 4.7. The Fisher information of the observations  $O_m$  with respect to the parameter N is

(9) 
$$\mathcal{J}_{O_m}(N) = \sum_{k=1}^m \Pr(E_{k-1} = 1) \mathbb{E}\left[\frac{C_{k-1}^2}{N^2(N - C_{k-1})(N - C_{k-1} + \frac{\gamma}{\beta}N)} \middle| E_{k-1} = 1\right].$$

Proof. We start from (6). Note that for any k,  $C_k$  and  $T_k$  only depend on  $C_{k-1}$ . Indeed, since  $C_{k-1}$  determines  $E_{k-1}$ , if  $E_{k-1} = 0$  (the stopping time has passed), then  $C_k = C_{k-1}$  and  $T_k = \infty$ . When  $E_{k-1} = 1$ , the distributions of  $C_k$  and  $T_k$  are given in (2)-(3). Since  $\beta, \gamma, I_0, R_0$  are known,  $S_{k-1} = P - C_{k-1}$ , and  $I_{k-1}$  can be determined from  $C_{k-1}$  (Lemma 4.6), the distributions of  $C_k$  and  $T_k$  are determined by  $C_{k-1}$ . Therefore, we use Property 4.3 to simplify (6) to

$$\mathcal{J}_{O_m}(N) = \sum_{k=1}^m (\mathcal{J}_{C_k|C_{k-1}}(N) + \mathcal{J}_{T_k|C_{k-1}}(N)),$$

where we used  $\mathcal{J}_{T_1}(N) = \mathcal{J}_{T_1|C_0}(N)$ ,  $\mathcal{J}_{C_1}(N) = \mathcal{J}_{C_1|C_0}(N)$ . Moreover, when  $E_{k-1} = 0$ ,  $C_k$  and  $T_k$  are deterministic conditioned on  $C_{k-1}$ , which implies the score in this case is 0 (Property 4.4). Therefore, we can condition on  $E_{k-1} = 1$  to write

$$\mathcal{J}_{O_m}(N) = \sum_{k=1}^m \mathbb{E}[g_{C_k|C_{k-1}}(C_k, C_{k-1}, N) + g_{T_k|C_{k-1}}(T_k, C_{k-1}, N)|E_{k-1} = 1]\Pr(E_{k-1} = 1).$$

The last step is to evaluate  $g_{C_k|C_{k-1}}(C_k, C_{k-1}, N)$  and  $g_{T_k|C_{k-1}}(T_k, C_{k-1}, N)$ . When  $E_{k-1} = 1$ , the distributions of  $C_k$  and  $T_k$  conditioned on  $C_{k-1}$  have a simple form provided in (2)-(3). Property 4.5 allows for straight-forward calculations, resulting in (9). See Appendix A.3 for details of this last step.

What remains is to upper and lower bound (9). The upper bound  $\mathcal{J}_{O_m}(N) = O\left(\frac{m^3}{N^4}\right)$  follows from upper bounding  $\Pr(E_{k-1})$  by 1 and the fact that  $C_{k-1}$  is small relative to N (details of this step are in Appendix A.4). As for the lower bound, we first show a lower bound for  $Pr(E_{k-1} = 1)$  using the following lemma:

**Lemma 4.8.** Let  $p = \frac{1}{2} \left( \frac{\beta}{\beta + \gamma} + \frac{1}{2} \right) > \frac{1}{2}$ . There exists a constant D that only depends on  $\beta$  and  $\gamma$  such that if  $\frac{\beta(P-m-C_0)}{\beta(P-m-C_0)+P\gamma} > p$  and  $I_0 \ge D$ , then  $\Pr(E_m = 1) \ge \frac{1}{2}$ .

This result relies on an interesting stochastic dominance argument and can be found in the Appendix. Then, similarly to the upper bound,  $\mathcal{J}_{O_m}(N) = \Omega\left(\frac{m^3}{N^4}\right)$  follows from using  $\Pr(E_m = 1) \geq \frac{1}{2}$  and the fact that  $C_k \geq \frac{k+I_0+2R_0}{2}$  when  $E_k = 1$  (Lemma 4.6).

# 5. Numerical Results

We run experiments on real-world datasets for both the Bass and SIR models to demonstrate how the theoretical results from Section 3 manifest in practice. We describe two sets of empirical results:

- Section 5.2 mirrors the theory in this paper and makes two points: First, the relative error one sees in real-world datasets on quantities of interest as a function of the number of observations closely hews to that predicted by our results. Second, the time at which predictions of key quantities 'turn accurate' is late in the diffusions and again matches our theory.
- Our analysis demonstrates that one way to potentially produce accurate forecasts *early* in a diffusion would be the use of an estimator with an informative bias on N. In Section 5.3, we describe how this insight was used in a broader effort to build one of the first broadly distributed county-level forecasts available for COVID-19.

#### 5.1. A Discrete-Time Diffusion Model

First, we describe the standard Euler-Maruyama discretization of our stochastic diffusion model; this discretization better aligns with aggregated (as opposed to event level) data. Real-world data is often stored as arrival counts  $\Delta C_i[t]$  over a set of discrete time periods  $t \in [T]$  and problem instances  $i \in \mathcal{I}$ . We model these counts as the following Poisson process, obtained by approximately discretizing the exponential arrival process (3). Precisely, we divide the time horizon into T epochs of length 1, where at each epoch  $t \in [T]$  we observe random variables:

(10)  
$$\Delta C_i[t] \sim \text{Poisson}(\lambda_{i,t}(a_i, \beta_i, N_i))$$
$$\Delta R_i[t] \sim \text{Poisson}(\gamma I_i[t-1])$$

where  $\lambda_{i,t}(a,\beta,N) = (a + \beta I[t-1]) \frac{S[t-1]}{N}$ , and  $\Delta C_i[t]$  and  $\Delta R_i[t]$  are independent. Essentially, we evaluate the arrival rate of (3) at the beginning of each epoch, and assume that it remains constant over the course of the epoch. This arrival process is then split into  $\Delta C_i[t]$  and  $\Delta R_i[t]$  according to the probabilities in (2). The state space then evolves according to:

(11)  

$$S_{i}[t] = S_{i}[t-1] - \Delta C_{i}[t]$$

$$I_{i}[t] = I_{i}[t-1] + \Delta C_{i}[t] - \Delta R_{i}[t]$$

$$R_{i}[t] = R_{i}[t-1] + \Delta R_{i}[t]$$

For the datasets we study,  $\gamma$  is known a priori, (i.e. from clinical data for the ILINet flu datasets; for the Bass model  $\gamma = 0$ ). We then obtain maximum likelihood estimates  $\hat{a}_i[t], \hat{\beta}_i[t], \hat{N}_i[t]$  for the remaining parameters by solving the problem:

(12) 
$$\max_{a,\beta,N\in[0,N_{\max}]} \sum_{\tau=1}^{t} \log p(\Delta C_i[\tau]; \lambda_{i,\tau}(a,\beta,N))$$

where  $p(x; \lambda) = \frac{\lambda^x \exp(-\lambda)}{x!}$  denotes the Poisson PMF with rate parameter  $\lambda$ , and  $N_{\text{max}}$  is an upper bound on N known a priori. This reflects that loose upper bounds on N (e.g., the entire population of a geographic region, for epidemic forecasting) are typically known in real-world problems.

### 5.2. MLE Performance on Benchmark Datasets

In this section, we fit the Bass and SIR models to real-world datasets and compare the empirical results to the theoretical results from Section 3.

**Datasets** We fit the Bass model to a dataset of Amazon product reviews from Ni et al. (2019), which we take as a proxy for product adoption. Here t indexes weeks since the product's first

review, *i* indexes the product, and  $I_i[t]$  represents cumulative number of reviews for product *i*. For the SIR model, we use the CDC's ILINet database of patient visits for flu-like illnesses. Here, *t* indexes weeks, *i* indexes geographic regions, and  $I_i[t]$  represents infected patients. See Appendix E for further details on these datasets.

Comparing Actual Relative Error to Predicted Relative Error Here we fit diffusion models to products from the Amazon data, as well as individual seasons from the ILINet data, while varying the number of observations used to fit the model. We compare the observed relative error in predicting the effective population size N in each to the error predicted by Theorem 3.3. We find that Theorem 3.3 provides a valuable lower bound despite potential model mis-specification, aggregated data, and the fact that we jointly estimate the  $a, \beta$  and N parameters.

Specifically, let  $T_i$  be the time index of the last observation we have for product *i*. We take  $\hat{N}_i[T_i]$  to be the ground truth parameter for product *i*. Figure 1 is a scatter plot of the mean (over instances *i* and times *t*) observed relative error RelError $(\hat{N}_i[t], \hat{N}_i[T_i])$  against the Cramer-Rao lower bound of Theorem 3.3,  $M\hat{N}_i[T_i]^2/C_i[t]^3$ , where *M* is a lower bound on the constant suppressed in the statement of Theorem 3.3. In addition to providing a lower bound, we find that the slope of the relationship is close to one in both datasets as the error grows small. It is worth re-emphasizing that this is the case despite the fact that the data here is not synthetic so that the Bass and SIR models are almost certainly not a perfect fit to the data.

Time to accuracy of peak predictions As discussed earlier, predicting the peak of the infection process is a key task in the SIR model (as is predicting the peak in new adoptions in the Bass model). Here we show, through the ILINet data, that the time at which our prediction of the peak number<sup>2</sup> of infections in an epidemic 'turns accurate' is close to the peak and matches what our theory suggests. Specifically, let  $I_i^* = \max_{t \in [T_i]} I_i[t]$  be the maximal number of infections. Given estimates  $\hat{\beta}, \hat{N}$  of the diffusion parameters, we define a point estimate for the peak number of infections

$$\hat{I}_i^*(\hat{\beta}, \hat{N}) = \mathbb{E}\left[\max_{\tau \in [T_i]} I_i[\tau] \, | \, \hat{\beta}, \hat{N}\right].$$

The solid line in Figure 2 depicts errors for the estimator  $I_i^*(\hat{\beta}_i[t], \hat{N}_i[t])$ , where  $\hat{\beta}_i[t], \hat{N}_i[t]$  are

 $<sup>^{2}</sup>$ In Section 3.1 the peak was defined as the time of the peak *rate* of infections rather than the peak number. Both peak definitions refer to a time when a constant fraction of the total population has been infected, and we use the peak number in these experiments as it is a time that is well-defined even with noisy, real-world data.



(a) Bass model fit on Amazon product reviews.

(b) SIR model fit on ILINet patient visits.

**Figure 1:** Each figure shows the mean of RelError $(\hat{N}_i[t], \hat{N}_i[T_i])$  over instances  $i \in \mathcal{I}$  and times  $t \in [T]$  (error bars show 95% CIs), vs. the Cramer-Rao bound  $\frac{M\hat{N}_i[T_i]^2}{C_i[t]^3}$ , where M is a lower bound on the constant suppressed in the statement of Theorem 3.3. We also show the y = x line (dashed gray) for comparison. As predicted, the Cramer-Rao bound provides a lower bound on RelError $(\hat{N}_i[t], \hat{N}_i[T_i])$ , and the slope of this relationship is close to 1 as the error grows small.

the MLE using data up to time t. At 66% of time to peak<sup>3</sup>, around of 50% of instances predict peak infections with >50% error. By the time the peak actually occurs, around 40% of instances still suffer prediction error in this range. Errors then drop off sharply after this point.

For comparison, let  $\hat{\beta}_i[t]$  be the solution to the MLE problem (12) fixing  $N = \hat{N}_i[T_i]$ ; that is, the MLE for  $\beta$  if we knew the ground-truth value of N a priori. The dashed line in Figure 2 shows errors for the peak estimate  $I^*(\tilde{\beta}_i[t], \hat{N}_i[T_i])$ . Errors for this estimator drop off much more quickly, with almost 90% of instances achieving < 50% error by 66% of time to peak. This bears out the predictions of Theorem 3.8 that once N is known, the remaining parameters of the SIR process are easy to estimate.

### 5.3. Working Around the Limits to Learning in the COVID-19 Pandemic

Our theory demonstrates that if we are to produce a valuable forecast early in a diffusion, we must rely on an estimator that places an informative bias on the effective population parameter, N. Here we briefly describe a heuristic to construct such a biased estimator that we used to produce one of the first broadly available county-level forecasts for COVID-19.

As above, we would like to forecast infections  $C_i[t]$  for a set of regions  $i \in \mathcal{I}$ . Recall that the

<sup>&</sup>lt;sup>3</sup>For reference, the median peak time is 20 weeks.



**Figure 2:** % of instances with with relative prediction error  $|\hat{I}_i^*(\hat{\beta}, \hat{N}) - I_i^*| / I_i^* > 0.5$ , vs. % of time to peak on the ILINet dataset. For "N estimated", we evaluate the MLE at time  $t \hat{I}^*(\hat{\beta}_i[t], \hat{N}_i[t])$ . Errors for this estimator remain unreasonably large until around the peak occurs – after which it drops dramatically. For "N known", we evaluate the estimator  $\hat{I}^*(\hat{\beta}_i[t], \hat{N}_i[T_i])$ ; that is, we assume N known and estimate  $\beta$  via MLE. Here, most instances estimate the peak accurately after 66% of time to peak, reflecting the ease of estimating  $\beta$  given N.

effective population  $N_i$  for region i is the product of the actual population of the region (which is obviously known) and the fraction of infections that are actually observed (which is not). To arrive at a useful bias for  $N_i$ , we exploit hetereogeneity in the timing of infections in each region. Specifically, infections start at different times in each region, and we typically have access to some set  $P[t] \subseteq \mathcal{I}$  of regions that have already experienced enough infections to reliably estimate  $N_i$  for  $i \in P[t]$  via MLE. At a high level, our strategy will be to identify the set P[t], estimate  $N_i$  for  $i \in P[t]$ , then extrapolate these estimates (e.g., via matching on region-level covariates) to obtain  $N_i$  for  $i \notin P[t]$ . We describe this methodology in detail in Appendix E.3.

To identify the set P[t] of regions for which the variance of  $\hat{N}$  may be small, we simply look for regions that have passed its peak rate of new infections. Concretely, we define P[t] as:

(13) 
$$P[t] = \{i \in \mathcal{I} : C_i[t] - C_i[t-1] \le \gamma_1 \max_{\tau \le t} (C_i[\tau] - C_i[\tau-1])\},\$$

where  $\gamma_1 \in (0, 1)$  is a hyperparameter.

#### 5.3.1. Experimental results

We show the results of applying this methodology for forecasting in the COVID-19 pandemic. Our dataset consists of daily cumulative COVID-19 infections  $C_i[t]$  at the level of sub-state regions  $i \in \mathcal{I}$ ,

from March to May 2020. The dataset also includes a rich set of covariates for each region, which we use to extrapolate the fits  $N_i : i \in P[t]$  to other regions.

We compare the effectiveness of our heuristic (dubbed *Two-Stage*) to two extremes: *MLE* simply applies an approximate version of the MLE (the maximum likelihood problem here is substantially harder due to the recovery process being latent) to the data available and *Idealized* cheats by using a value of  $N_i$  learned by looking into the future. Figure 3 shows weighted mean absolute percentage error (WMAPE) over regions, with weights proportional to infections on the last day in our dataset (May 21, 2020), for two metrics relevant to decision making: cumulative infections by May 21, 2020 and maximum daily infections, for regions that have peaked by May 21, 2020. Model vintages vary along the x-axis so that moving from left to right models are trained on an increasing amount of data.



**Figure 3:** Prediction errors by model vintage, for regions that have peaked by May 21, 2020. Colors denote different approaches to learning  $N_i$ .

At one extreme, *Idealized* exhibits consistently low error even for early model vintages. This bears out the prediction of Theorem 3.8: given N,  $\beta$  is easy to learn even early in the infection with few samples. *MLE* performs poorly until close to the target date of May 21 at which point sufficient data is available to learn N. This empirically illustrates the difficult of learning N, as described in Theorem 3.3. Finally, we see that *Two-Stage* significantly outperforms *MLE* far away from the test date. Close to the test date the two approaches are comparable. For maximum daily infections, *MLE* drastically underperforms *Two-Stage* far from the test date. Our approach to learning from peaked regions significantly mitigates the difficulty of learning N. Further details on this study can be found in Appendix E.3.

# 6. Conclusion

In this paper, we have shown fundamental limits to learning for the SIR and Bass models, two models that often serve as building blocks for epidemic and product adoption modeling. In particular, we proved that in common parameter regimes, the time at which one has enough samples to reliably learn key parameters of the model is later than two-thirds of the way to the peak of the process. This implies that predictions from before this point in time (i.e., early on in the process) can be wildly inaccurate, and therefore one must be cautious in using such early-stage forecasts.

Fortunately, it is important to note that our results do not imply that it is *impossible* to have accurate forecasts early on. As our main theorem only pertains to unbiased estimators based on the observations of the diffusion model, a natural method to work around the lower bound is to either build *biased* estimators, make use of other information (i.e. increase the information set  $O_m$ ), or some combination thereof. We demonstrated one heuristic to do this for COVID-19 forecasting by taking advantage of the heterogeneity of the timing of the infection in different regions. Going forward, we believe that formally analysing methods such as this or developing new methods that work around the lower bound is a valuable avenue for future research.

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Appendices A, B and C contain the proofs of Theorems 3.4, 3.7 and 3.8 respectively. Appendix D contains the proofs of Propositions 2.1, 2.2, 3.5 and 3.6, each in their own subsections. Appendix E provides details on the datasets used in Section 5, and Appendix F contains a detailed description of the COVID-19 forecasting model from Section 5.3.

# A. Proof of Theorem 3.4

We finish the sections of the proof that were not included in the main paper. This includes the proof of Lemma 4.6, Lemma 4.8, calcuations for Lemma 4.7, and details regarding the final step of the proof.

We define  $\lambda(N, k-1, C_{k-1}) = \left(\frac{\beta(N-C_{k-1})}{N} + \gamma\right) I_{k-1}$  and  $\eta(N, C_{k-1}) = \frac{\beta(N-C_{k-1})}{\beta(N-C_{k-1}) + N\gamma}$ . Thus, for  $k \leq \tau$ ,  $\lambda(N, k-1, C_{k-1})$  is the mean of the k-th inter-arrival time and  $\eta(N, C_{k-1})$  is the probability that the arrival in the k-th instance is a new infection rather than a recovery.

### A.1. Proof of Lemma 4.6

*Proof.* Suppose  $k < \tau$  i.e  $E_k = 1$ . Then, k is equal to total number of jumps that have occurred so far (the number of movements from S to I and from I to R). The number of individuals that have moved from S to I is  $C_k - I_0 - R_0$ , and the number of movements from I to R is  $C_k - I_k - R_0$ . Therefore,  $k = 2C_k - I_0 - I_k - 2R_0$ . Since  $I_k > 0$ ,  $C_k > r_k$ .

Suppose  $k \ge \tau$  i.e  $E_k = 0$ . Then, k is greater than or equal to the total number of jumps, which is still equal to  $2C_k - I_0 - I_k - 2R_0$ . Hence  $C_k \le r_k$  in this case.

# A.2. Proof of Lemma 4.8

*Proof.* Let  $X_k \stackrel{iid}{\sim} \text{Bern}(p)$  for  $k = 1, 2, \dots$  Let  $\{A_k : k \ge 0\}$  be a stochastic process defined by:

$$A_k = \begin{cases} C_0 & \text{if } k = 0\\ C_0 + X_1 + \dots + X_k & \text{if } A_i > r_i \ \forall i < k\\ A_{k-1} & \text{otherwise.} \end{cases}$$

Let  $\tau_A = \min\{k : A_k \leq r_k\}$  be the "stopping time" of this process.

Claim A.1.  $Pr(\tau \leq m) \leq Pr(\tau_A \leq m)$ .

The proof of this claim involves showing the process  $\{A_k\}$  is stochastically less than  $\{C_k\}$ ; the proof can be found in Section A.2.1. We now upper bound  $\Pr(\tau_A \leq m)$ .  $\tau_A \leq m$  if and only if  $A_k \leq r_k$  for some  $k \leq m$ . Before this happens,  $A_k = C_0 + X_1 + \cdots + X_k$ . Therefore, if  $\tau_A \leq m$ , it must be that  $C_0 + X_1 + \cdots + X_k \leq \frac{k+I_0+2R_0}{2}$  for some  $k \leq m$ .

$$\Pr(\tau_A \le m) \le \sum_{k=1}^{m} \Pr\left(C_0 + X_1 + \dots + X_k \le \frac{k + I_0 + 2R_0}{2}\right)$$
$$= \sum_{k=1}^{m} \Pr\left(X_1 + \dots + X_k < pk\left(1 - \frac{2pk - k + I_0}{2pk}\right)\right)$$

Since  $\mathbb{E}[X_1 + \cdots + X_k] = pk$ , using the Chernoff bound (multiplicative form:  $\Pr(\sum_{i=1}^k X_i \le (1-\delta)\mu) \le \exp(-\delta^2\mu/2))$  gives

$$\begin{aligned} \Pr(\tau_A \le m) \le \sum_{k=1}^m \exp\left(-\frac{pk}{2}\left(\left(1 - \frac{1}{2p}\right) + \frac{I_0}{2pk}\right)^2\right) \\ = \sum_{k=1}^m \exp\left(-\frac{pk}{2}\left(1 - \frac{1}{2p}\right)^2 - \frac{I_0}{2}\left(1 - \frac{1}{2p}\right) - \frac{I_0^2}{8pk}\right) \\ \le \sum_{k=1}^m \exp\left(-\frac{pk}{2}\left(1 - \frac{1}{2p}\right)^2 - \frac{I_0}{2}\left(1 - \frac{1}{2p}\right)\right) \\ \le \exp\left(-\left(\frac{1}{2} - \frac{1}{4p}\right)I_0\right)\sum_{k=1}^m \exp\left(-\frac{pk}{2}\left(1 - \frac{1}{2p}\right)^2\right) \\ \le C_1 \exp(-C_2 I_0), \end{aligned}$$

for constants  $C_1 = \sum_{k=1}^{\infty} \exp\left(-\frac{pk}{2}\left(1-\frac{1}{2p}\right)^2\right), C_2 = \frac{1}{2}-\frac{1}{4p} > 0.$  ( $C_1$  is a constant since it is a geometric series with a ratio smaller than 1, since p > 1/2.) Let D be the solution to  $C_1 \exp(-C_2 D) = \frac{1}{2}$ . Then, if  $I_0 \ge D$ ,  $\Pr(E_m) = 1 - \Pr(\tau \le m) \ge 1 - \Pr(\tau_A \le m) \ge \frac{1}{2}$ .

### A.2.1. Proof of Claim A.1.

(14)

**Definition A.2.** For scalar random variables X, Y, we say that X is *stochastically less than* Y (written  $X \leq_{st} Y$ ) if for all  $t \in \mathbb{R}$ ,

$$\Pr(X > t) \le \Pr(Y > t).$$

For random vectors  $X, Y \in \mathbb{R}^n$  we say that  $X \leq_{st} Y$  if for all increasing functions  $\phi : \mathbb{R}^n \to \mathbb{R}$ ,

$$\phi(X_1,\ldots,X_n) \leq_{st} \phi(Y_1,\ldots,Y_n).$$

We make use of the following known result for establishing stochastic order for stochastic processes.

**Theorem A.3** (Veinott 1965). Suppose  $X_1, \ldots, X_n, Y_1, \ldots, Y_n$  are random variables such that  $X_1 \leq_{st} Y_1$  and for any  $x \leq y$ ,

$$(X_k|X_1 = x_1, \dots, X_{k-1} = x_{k-1}) \leq_{st} (Y_k|Y_1 = y_1, \dots, Y_{k-1} = y_{k-1})$$

for every  $2 \leq k \leq n$ . Then,  $(X_1, \ldots, X_n) \leq_{st} (Y_1, \ldots, Y_n)$ .

**Proof of Claim A.1.** Because of the condition  $\frac{\beta(N-m-C_0)}{\beta(N-m-C_0)+N\gamma} > p$ , for  $k \leq m$  and  $k \leq \tau$ ,  $C_k - C_{k-1} \sim \text{Bern}(q)$  for q > p. First, we show  $(A_0, A_1, \ldots, A_m) \leq_{st} (C_0, C_1, \ldots, C_m)$  using Theorem A.3.  $C_0 \leq_{st} A_0$  since  $C_0 = A_0 = I_0$ . We condition on  $A_{k-1} = x$  and  $C_{k-1} = y$  for  $x \leq y$ , and we must show  $A_k \leq_{st} C_k$ . (We do not need to condition on all past variables since the both processes are Markov.) If  $x \leq r_{k-1}$ , then  $A_k = A_{k-1} = x \leq y = C_{k-1} \leq C_k$ . Otherwise, the process

 $A_k$  has not stopped, and neither has  $C_k$  since  $y \ge x$ . Then,  $A_k \sim x + \text{Bern}(p)$  and  $C_k \sim y + \text{Bern}(q)$  for some  $q \ge p$ . Clearly,  $A_k \le_{st} C_k$  in this case. We apply Theorem A.3, which implies  $A_m \le_{st} C_m$ .

Define the function  $u : \mathbb{R}^{m+1} \to \{0,1\}, u(x_0, x_1, \dots, x_m) = \mathbb{1}\{\bigcup_{k=1}^m \{x_k \leq r_k\}\}$ . Then,  $u(A_0, A_1, \dots, A_m) = 1$  if and only if  $\tau_A \leq m$ , and  $u(C_0, C_1, \dots, C_m) = 1$  if and only if  $\tau \leq m$ . u is a decreasing function. Therefore,  $u(A_0, A_1, \dots, A_m) \geq_{st} u(C_0, C_1, \dots, C_m)$ . Then,  $\Pr(\tau \leq m) = \Pr(u(C_0, C_1, \dots, C_m) \geq 1) \leq \Pr(u(A_0, A_1, \dots, A_m) \geq 1) = \Pr(\tau_A \leq m)$  as desired.  $\Box$ 

#### A.3. Calculations for Lemma 4.7

We define  $\lambda(N, k - 1, C_{k-1}) = \left(\frac{\beta(N-C_{k-1})}{N} + \gamma\right) I_{k-1}$  and  $\eta(N, C_{k-1}) = \frac{\beta(N-C_{k-1})}{\beta(N-C_{k-1}) + N\gamma}$ . Thus, for  $k \leq \tau$ ,  $\lambda(N, k - 1, C_{k-1})$  is the mean of the k-th inter-arrival time and  $\eta(N, C_{k-1})$  is the probability that the arrival in the k-th instance is a new infection rather than a recovery.

**Derivation of**  $\mathbb{E}_{C_k}[g_{C_k|C_{k-1}}(C_k, C_{k-1}, N)|E_{k-1} = 1]$ . When  $E_{k-1} = 1$ , we have  $C_k \sim C_{k-1} + \text{Bern}(\eta(N, C_{k-1}))$ . Therefore,  $\mathbb{E}_{C_k}[g_{C_k|C_{k-1}}(C_k, C_{k-1}, N)|E_{k-1} = 1] = \mathcal{J}_{C_k \sim \text{Bern}(\eta(N, C_{k-1}))}(N)$ . We reparameterize to write the Fisher information as:

$$\mathbb{E}_{C_k}[g_{C_k|C_{k-1}}(C_k, C_{k-1}, N)|E_{k-1} = 1] = \mathcal{J}_{C_k \sim \operatorname{Bern}(\eta)}(\eta) \left(\frac{\partial}{\partial N}\eta(N, C_{k-1})\right)^2$$
$$= \frac{1}{\eta(1-\eta)} \left(\frac{\partial}{\partial N}\eta(N, C_{k-1})\right)^2.$$

Use  $\eta(N, C_{k-1}) = \frac{\beta(N-C_{k-1})}{\beta(N-C_{k-1})+N\gamma}$  to derive

$$\frac{\partial}{\partial N}\eta(N,C_{k-1}) = \frac{\beta(\beta(N-C_{k-1})+\gamma N) - \beta(N-C_{k-1})(\beta+\gamma)}{(\beta(N-C_{k-1})+\gamma N)^2}$$
$$= \frac{\beta\gamma C_{k-1}}{(\beta(N-C_{k-1})+\gamma N)^2}.$$

Also,  $\frac{1}{\eta(1-\eta)} = \frac{(\beta(N-C_{k-1})+N\gamma)^2}{(N-C_{k-1})\beta N\gamma}$ . Substituting,

$$\mathbb{E}_{C_k}[g_{C_k|C_{k-1}}(C_k, C_{k-1}, N)|E_{k-1} = 1] = \frac{(\beta(N - C_{k-1}) + N\gamma)^2}{(N - C_{k-1})\beta N\gamma} \left(\frac{\beta\gamma C_{k-1}}{(\beta(N - C_{k-1}) + \gamma N)^2}\right)^2 \\ = \frac{\beta\gamma C_{k-1}^2}{(N - C_{k-1})N(\beta(N - C_{k-1}) + \gamma N)^2}$$

**Derivation of**  $\mathbb{E}_{T_k}[g_{T_k|C_{k-1}}(T_k, C_{k-1}, N)|E_{k-1} = 1]$ . Similarly, conditioned on  $E_{k-1} = 1, T_k \sim \exp(\lambda(N, k - 1, C_{k-1}))$ . Therefore,  $\mathbb{E}_{T_k}[g_{T_k|C_{k-1}}(T_k, C_{k-1}, N)] = \mathcal{J}_{T_k \sim \exp(\lambda(N, k - 1, C_{k-1}))}(N)$ . We

reparameterize to write

$$\mathbb{E}_{T_k}[g_{T_k|C_{k-1}}(T_k, C_{k-1}, N)] = \mathcal{J}_{T_k \sim \operatorname{Exp}(\lambda)}(\lambda) \left(\frac{\partial}{\partial N}\lambda(N, k-1, C_{k-1})\right)^2$$
$$= \frac{1}{\lambda^2} \left(\frac{\partial}{\partial N}\lambda(N, k-1, C_{k-1})\right)^2.$$

Use  $\lambda(N, k-1, C_{k-1}) = \left(\frac{\beta(N-C_{k-1})}{N} + \gamma\right)(2C_{k-1} - (k-1) - I_0 - 2R_0)$  to derive

$$\frac{\partial}{\partial N}\lambda(N,k-1,C_{k-1}) = \frac{\beta C_{k-1}(2C_{k-1}-(k-1)-I_0-2R_0)}{N^2}$$
$$\frac{1}{\lambda(N,k-1,C_{k-1})} = \frac{N}{(\beta(N-C_{k-1})+\gamma N)(2C_{k-1}-(k-1)-I_0-2R_0)}$$

Substituting,

$$\mathbb{E}_{T_k}[g_{T_k|C_{k-1}}(T_k, C_{k-1}, N)] = \left(\frac{\beta C_{k-1}}{N(\beta(N - C_{k-1}) + \gamma N)}\right)^2$$

**Derivation of**  $\mathcal{J}_{O_m}(N)$ . Using the expressions derived above for  $\mathbb{E}_{C_k}[g_{C_k|C_{k-1}}(C_k, C_{k-1}, N)|E_{k-1}]$ 1 and  $\mathbb{E}_{T_k}[g_{T_k|C_{k-1}}(T_k, C_{k-1}, N)],$  we get

$$\begin{split} \mathbb{E}_{C_k}[g_{C_k|C_{k-1}}(C_k, C_{k-1}, N)|E_{k-1} = 1] + \mathbb{E}_{T_k}[g_{T_k|C_{k-1}}(T_k, C_{k-1}, N)] \\ &= \frac{\beta\gamma C_{k-1}^2}{(N - C_{k-1})N(\beta(N - C_{k-1}) + \gamma N)^2} + \left(\frac{\beta C_{k-1}}{N(\beta(N - C_{k-1}) + \gamma N)}\right)^2 \\ &= \frac{C_{k-1}^2}{(N - C_{k-1})N^2(N - C_{k-1} + \frac{\gamma}{\beta}N)} \end{split}$$

Thus,

$$\mathcal{J}_{O_m}(N) = \sum_{k=1}^m \mathbb{E}[g_{C_k|C_{k-1}}(C_k, C_{k-1}, N) + g_{T_k|C_{k-1}}(T_k, C_{k-1}, N)|E_{k-1} = 1] \Pr(E_{k-1} = 1)$$
$$= \sum_{k=1}^m \mathbb{E}\left[\frac{C_{k-1}^2}{(N - C_{k-1})N^2(N - C_{k-1} + \frac{\gamma}{\beta}N)} \middle| E_{k-1} = 1\right] \Pr(E_{k-1} = 1).$$

#### **Details of Final Step of Theorem 3.4** A.4.

Define  $p \triangleq \frac{1}{2}(\frac{\beta}{\beta+\gamma} + \frac{1}{2}) > \frac{1}{2}$  as in Lemma 4.8. Assume N is large enough so that  $m + C_0 \leq \frac{N}{2}$  and  $\frac{\beta(N-m-C_0)}{\beta(N-m-C_0)+P\gamma} > p$  (this is possible since  $\frac{\beta}{\beta+\gamma} > p$  and m = o(N)). For the upper bound, we have that  $C_k \leq k + I_0 + R_0$  by definition. Since  $I_0, R_0 \leq m$  by assumption,  $C_k \leq 3m$ . Moreover, by assumption,  $C_k \leq m + C_0 \leq \frac{N}{2}$ . Plugging these into (9) results

in

$$\mathcal{J}_{O_m}(N) \le \sum_{k=0}^{m-1} \Pr(E_{k-1} = 1) \frac{(3m)^2}{N^2 (N - \frac{1}{2}N)((N - \frac{1}{2}N) + \frac{\gamma}{\beta}N)} \le H_1 \frac{m^3}{N^4},$$

for a constant  $H_1$ .

Then, similarly to the upper bound,  $\mathcal{J}_{O_m}(N) \ge H_2 \frac{m^3}{N^4}$  follows from using  $\Pr(E_m = 1) \ge \frac{1}{2}$  and the fact that  $C_k \ge \frac{k+I_0+2R_0}{2} \ge \frac{k}{2}$  when  $E_k = 1$  (Lemma 4.6):

$$\mathcal{J}_{O_m}(N) \ge \sum_{k=0}^{m-1} \frac{1}{2} \frac{\left(\frac{k}{2}\right)^2}{N^4} \ge H_2 \frac{m^3}{N^4},$$

Combining the upper and lower bounds finish the proof.

# B. Proof of Theorem 3.7

*Proof.* For simplicity, assume m = 2k. Let  $A_i = \min(T_i, T_{m-i}), 1 \le i \le k$ . It is easy to see that  $A_i \sim \exp(l_i)$  where

$$l_i := (2a + \beta m) - (a + i\beta)\frac{i}{N} - (a + (m - i)\beta)\frac{m - i}{N}$$

Consider  $S = \sum_{i=1}^{m/2} A_i$ . Then by Theorem 5.1 in Janson (2018), for any  $\delta > 0$ 

$$\Pr(S \ge (1+\delta)\mu) \le e^{-l_*\mu(\delta - \ln(1+\delta))}$$

where  $\mu = E[S], l_* \leq \min_{i=1}^{m/2} l_i$ . It is easy to check that

$$\frac{N-m}{N}(2a+\beta m) \le l_i \le 2a+\beta m.$$

We can let  $l_* = (2a + \beta m) \frac{N-m}{N}$ . Furthermore, we can also obtain bounds for  $\mu = \sum_{i=1}^{m/2} \frac{1}{l_i}$ .

$$\frac{1}{2}\frac{m}{2a+m\beta} \le \mu \le \frac{1}{2}\frac{N}{N-m}\frac{m}{2a+m\beta}.$$

Take  $\delta = O(\sqrt{\frac{\log(N)}{m}})$ . Note that  $\delta - \ln(1+\delta) = O(\frac{\log(N)}{m})$ . We will have

$$\Pr(\frac{S}{m} \ge (1+\delta)\frac{\mu}{m}) \le e^{-l_*\mu(\delta - \ln(1+\delta))} = e^{-\frac{(N-m)m}{N}O(\frac{\log(N)}{m})} = O(\frac{1}{N^2}),$$

using the assumption  $\frac{N-m}{N} \geq \frac{1}{2}$ . Similar bounds can be obtained for the lower bound. Then one

can verify that, with probability  $1 - O(1/N^2)$ , we have, for some constant  $C_1$ 

$$\frac{m}{2S} - (2a + m\beta) \bigg| \le C_1 \left( \min(2a + m\beta, m/2S) \left( \frac{m}{N} + \sqrt{\frac{\log(N)}{m}} \right) \right)$$
$$\le C_1 \left( a \sqrt{\frac{\log(N)}{m}} + \sqrt{m\beta} \sqrt{\log(N)} \right).$$

Similarly, let  $S' = \sum_{i=1}^{m/4} \min(T_i, T_{m/2-i})$ . One can verify that with probability  $1 - O(1/N^2)$ ,

$$\left|\frac{m}{4S'} - \left(2a + \frac{m}{2}\beta\right)\right| \le C_1\left(a\sqrt{\frac{\log(N)}{m}} + \sqrt{m}\beta\sqrt{\log(N)}\right).$$

One can verify for any  $\hat{\alpha}, \hat{\beta}$  satisfy the following inequality

$$\left|\frac{m}{2S} - \left(2\hat{a} + m\hat{\beta}\right)\right| \le C_1 \left(\frac{m}{2S} \left(\frac{m}{N} + \sqrt{\frac{\log(N)}{m}}\right)\right)$$
$$\left|\frac{m}{4S'} - \left(2\hat{a} + \frac{m}{2}\hat{\beta}\right)\right| \le C_1 \left(\frac{m}{4S'} \left(\frac{m}{N} + \sqrt{\frac{\log(N)}{m}}\right)\right).$$

Then, we will have

$$|\hat{\beta} - \beta| = O\left(a\sqrt{\frac{\log(N)}{m^3}} + \beta\sqrt{\frac{\log(N)}{m}}\right)$$
$$|\hat{a} - a| = O\left(a\sqrt{\frac{\log N}{m}} + \sqrt{m}\beta\sqrt{\log N}\right)$$

In order to obtain the optimal estimators, we consider a union of estimators where  $S_k = \sum_{i=1}^{k/2} \min(T_i, T_{k-i})$ . We find the estimator  $\hat{\alpha}, \hat{\beta}$  such that for every k,

$$\left|\frac{k}{2S} - \left(2\hat{a} + k\hat{\beta}\right)\right| \le C_1 \left(\frac{k}{2S} \left(\frac{m}{N} + \sqrt{\frac{\log(N)}{m}}\right)\right).$$

This will guarantee, with probability 1 - O(1/N),

$$\begin{aligned} |\hat{\beta} - \beta| &= O\left(a\sqrt{\frac{\log(N)}{m^3}} + \beta\sqrt{\frac{\log(N)}{m}}\right) \\ |\hat{a} - a| &= O\left(\min_{1 \le k \le m} \left(a\sqrt{\frac{\log N}{k}} + \sqrt{k}\beta\sqrt{\log N}\right)\right) = O\left(a\sqrt{\frac{\log N}{m}} + \sqrt{\beta a}\sqrt{\log N}\right), \end{aligned}$$

as desired.

# C. Proof of Theorem 3.8

Fix an instance in which the assumptions of the theorem statement hold. Let  $p \triangleq \frac{1}{2} \left( \frac{\beta}{\beta+\gamma} + \frac{1}{2} \right) > \frac{1}{2}$ . Let  $\hat{A} = \frac{C_m - C_0}{m}$  be an estimator for  $\frac{\beta}{\beta+\gamma}$ ,  $\hat{B} = \frac{\tilde{S}_m}{m}$  be an estimator for  $\frac{1}{\beta+\gamma}$  for  $\tilde{S}_m = \sum_{k=1}^{\min(m,\tau)} I_{k-1}T_k$ . Let  $\hat{\beta} = \hat{A}/\hat{B}$  and  $\hat{\gamma} = 1/\hat{B} - \hat{\beta}$ .

This first lemma follows from (14) of the proof of Lemma 4.8.

**Lemma C.1.** If  $\frac{\beta}{\beta+\gamma} \frac{N-m-C_0}{N} > p$ ,  $\Pr(\tau < m) \leq B_1 e^{-B_2 I_0}$ , where  $B_1, B_2 > 0$  are constant that depend only on  $\beta$  and  $\gamma$ .

The next two lemmas give a high probability confidence bound for estimators  $\hat{A}$  and  $\hat{B}$ .

**Lemma C.2.** For any  $m, I_0$  where  $\frac{\beta}{\beta+\gamma} \frac{N-m-C_0}{N} > \frac{1}{2}$ , for any  $\delta > 0$ ,

$$\Pr\left(\frac{C_m - C_0}{m} \notin \left[\frac{\beta}{\beta + \gamma}(1 - \delta)\frac{N - m - C_0}{N}, \frac{\beta}{\beta + \gamma}(1 + \delta)\right], \tau \ge m\right) \le 2\exp(-m\delta^2/(4 + 2\delta)).$$

**Lemma C.3.** Let  $\tilde{S}_m = \sum_{k=1}^{\min(m,\tau)} I_{k-1}T_k$ . Then

$$\Pr\left(\frac{\tilde{S}_m}{m} \notin [\frac{(1-\delta)}{\beta+\gamma}, \frac{(1+\delta)}{\beta+\gamma} \frac{N}{N-m-C_0}], \tau \ge m\right) \le 2e^{-m\frac{N-m-C_0}{N}(\delta-\ln(1+\delta))}.$$

The next proposition combines the two estimators from the above lemmas and into estimators  $\hat{\beta}$ and  $\hat{\gamma}$ .

**Proposition C.4.** Assume  $\beta > \gamma > 0$ . Let  $I_0 \le m < N$  such that  $\frac{\beta}{\beta+\gamma} \frac{N-m-C_0}{N} > p$ . Let  $z = \frac{N-m-C_0}{N}$ . Then, for any  $0 < \delta < 1$ , with probability  $1 - 4e^{-m(\delta-\ln(1+\delta))} - 4e^{-m\delta^2/(4+2\delta)} - 2B_1e^{-B_2I_0}$ ,

(15) 
$$\hat{\beta} \in \left[\beta \frac{(1-\delta)z^2}{1+\delta}, \beta \frac{1+\delta}{1-\delta}\right]$$

(16) 
$$\hat{\gamma} \in \left[\gamma \frac{z}{1+\delta} + \beta \frac{(1-\delta)z - (1+\delta)^2}{(1+\delta)(1-\delta)}, \gamma \frac{1}{1-\delta} + \beta \frac{1+\delta - (1-\delta)^2 z^2}{(1-\delta)(1+\delta)}\right],$$

where  $B_1, B_2 > 0$  are constants that depend on  $\beta$  and  $\gamma$ .

We first show Theorem 3.8 using these results. We then prove Lemma C.2, Lemma C.3, and Proposition C.4 in Appendix C.2.

# C.1. Proof of Theorem 3.8

*Proof.* Let  $\delta = \sqrt{\frac{5 \log m}{m}}$ . First, we claim that the probability in Proposition C.4 is greater than  $1 - \frac{8}{m} - 2B_1 e^{-B_2 I_0}$ . Note that  $\ln(1+\delta) \leq \delta - \frac{\delta^2}{2} + \delta^3$ , implying  $\delta - \ln(1+\delta) \geq \delta^2(\frac{1}{2} - \delta)$ . Since  $\delta \leq \frac{1}{4}$ ,

$$4e^{-m(\delta-\ln(1+\delta))} \le 4e^{-m\frac{\delta^2}{4}} \le \frac{4}{m}$$

Using  $\delta \leq \frac{1}{4}$  again,

$$4e^{-m\delta^2/(4+2\delta)} \le 4e^{-m\frac{\delta^2}{5}} = \frac{4}{m}.$$

Hence, the bound in C.4 holds with probability greater than  $1 - \frac{8}{m} - 2B_1 e^{-B_2 I_0}$ . Since we assume  $m(m + C_0) \leq N$  and  $z = 1 - \frac{m+C_0}{N}$ ,

(17) 
$$1-z \le \frac{1}{m}.$$

From here on, assume the confidence bounds (15)-(16) hold. Note that  $\frac{1+\delta}{1-\delta} \leq 1+3\delta$  and  $\frac{1-\delta}{1+\delta} \geq 1-3\delta$  for  $\delta < \frac{1}{4}.$  Then,

$$\begin{aligned} (\hat{\beta} - \beta)^2 &\leq \beta^2 \left( 1 + 3\delta - (1 - 3\delta)z^2 \right)^2 \\ &\leq \beta^2 \left( (1 - z) + 3\delta(1 + z) \right)^2 \\ &\leq \beta^2 \left( \frac{1}{m} + 6\sqrt{\frac{5\log m}{m}} \right)^2 \\ &\leq \beta^2 M_3 \frac{\log m}{m} \end{aligned}$$

for an absolute constant  $M_3 > 0$ . The second last step uses (17) and  $1 + z \leq 2$ . Therefore, RelError $(\hat{\beta}, \beta) \leq M_1 \frac{\log m}{m}$ . Similarly,

(18) 
$$(\hat{\gamma} - \gamma)^2 \le \left(\gamma \left(\frac{1}{1-\delta} - \frac{z}{1+\delta}\right) + \beta \left(\frac{1+\delta - (1-\delta)^2 z^2}{(1-\delta)(1+\delta)} - \frac{(1-\delta)z - (1+\delta)^2}{(1+\delta)(1-\delta)}\right)\right)^2.$$

Using the fact that  $(1 - \delta)(1 + \delta) \ge \frac{1}{2}$ ,

$$\frac{1}{1-\delta} - \frac{z}{1+\delta} \le 2((1-z) + \delta(1+z)) \le 2\left(\frac{1}{m} + 2\sqrt{\frac{5\log m}{m}}\right).$$

$$\begin{aligned} \frac{1+\delta-(1-\delta)^2 z^2}{(1-\delta)(1+\delta)} &- \frac{(1-\delta)z-(1+\delta)^2}{(1+\delta)(1-\delta)} = \frac{(1+\delta)-(1-\delta)z+(1+\delta)^2-(1-\delta)^2 z^2}{1-\delta^2} \\ &\leq 2(1-z)+4\delta(1+z)+\frac{1+\delta}{1-\delta}-\frac{1-\delta}{1+\delta}z^2 \\ &\leq 2(1-z)+8\delta+(1+3\delta)-(1-3\delta)z^2 \\ &\leq 2(1-z)+8\delta+(1-z^2)+6\delta(1+z^2) \\ &\leq (1-z)(3+z)+\delta(8+6(1+z^2)) \\ &\leq \frac{4}{m}+20\sqrt{\frac{5\log m}{m}}. \end{aligned}$$

Substituting back into (18) results in

$$(\hat{\gamma} - \gamma)^2 \le \left(\gamma \left(\frac{2}{m} + 4\sqrt{\frac{5\log m}{m}}\right) + \beta \left(\frac{4}{m} + 20\sqrt{\frac{5\log m}{m}}\right)\right)^2$$
$$\le M_2 \beta^2 \frac{\log m}{m},$$

for an absolute constant  $M_2$ , since  $\beta > \gamma$ . This implies the desired result.

# C.2. Proofs of Intermediate Results

### C.2.1. Proof of Lemma C.2.

*Proof.* Fix m, let  $z := \frac{N-m-C_0}{N}$ ,  $p = \frac{\beta}{\beta+\gamma}z$ . Then  $p > \frac{1}{2}$ . Define three stochastic processes  $\{A_k : k \ge 0\}, \{B_k : k \ge 0\}, \{\tilde{C}_k : k \ge 0\}$ :

$$A_{k} = \begin{cases} C_{0} & \text{if } k = 0\\ A_{k-1} + \text{Bern}(p) & \text{otherwise.} \end{cases}$$
$$B_{k} = \begin{cases} C_{0} & \text{if } k = 0\\ B_{k-1} + \text{Bern}(p/z) & \text{otherwise.} \end{cases}$$
$$\tilde{C}_{k} = \begin{cases} C_{0} & \text{if } k = 0\\ \tilde{C}_{k-1} + \text{Bern}\left\{\frac{\beta(N-\tilde{C}_{k-1})}{\beta(N-\tilde{C}_{k-1})+N\gamma}\right\} & \text{otherwise} \end{cases}$$

Note that  $\tilde{C}_k$  is a modified version of  $C_k$  where  $\tilde{C}_k$  still evolves after the stopping time.

**Claim C.5.**  $A_m$  is stochastically less than  $\tilde{C}_m$   $(A_m \leq_{st} \tilde{C}_m)$ ;  $\tilde{C}_m$  is stochastically less than  $B_m$   $(\tilde{C}_m \leq_{st} B_m)$ ; that is, for any  $\ell \in \mathbb{R}$ ,

$$\Pr(B_m \le \ell) \le \Pr(C_m \le \ell) \le \Pr(A_m \le \ell).$$

This claim follows from Theorem A.3, using a similar argument to Claim A.1.

Let  $A_k = C_0 + X_1 + X_2 + \ldots X_k$  where  $X_i \sim \text{Bern}(p)$  are independent. We provide the left tail bound for  $C_m$ . Note that when  $\tau \ge m$ ,  $C_m \stackrel{d}{=} \tilde{C}_m$ . Hence,

$$\Pr(C_m \le mp(1-\delta) + C_0, \tau \ge m) = \Pr(\tilde{C}_m \le mp(1-\delta) + C_0, \tau \ge m)$$
$$\le \Pr(\tilde{C}_m \le mp(1-\delta) + C_0)$$
$$\le \Pr(A_m \le mp(1-\delta) + C_0).$$

Using the Chernoff bound gives,

(19)

$$\Pr(A_m \le mp(1-\delta) + C_0) = \Pr(C_0 + X_1 + \dots + X_m \le pm(1-\delta) + C_0)$$
$$= \Pr(X_1 + \dots + X_m \le mp(1-\delta))$$
$$\le \exp\left(-\frac{mp}{2}\delta^2\right).$$

Therefore,

$$\Pr\left(\frac{C_m - C_0}{m} \le \frac{p}{z}(1 - \delta)z, \tau \ge m\right) = \Pr\left(C_m \le mp(1 - \delta) + C_0, \tau \ge m\right)$$
$$\le \exp\left(-\frac{mp}{2}\delta^2\right) \le \exp(-m\delta^2/4).$$

Let  $B_k = C_0 + Y_1 + \ldots + Y_k$  where  $Y_i \sim \text{Bern}(p/z)$  are independent. Similarly, for the upper tail bound, we have

$$\Pr\left(\frac{C_m - C_0}{m} \ge \frac{p}{z}(1+\delta), \tau \ge m\right) = \Pr(C_m \ge mp/z(1+\delta) + C_0, \tau \ge m)$$
$$\le \Pr(B_m \ge mp/z(1+\delta) + C_0)$$
$$\le \Pr(C_0 + Y_1 + \dots + Y_m \ge mp/z(1+\delta) + C_0)$$
$$\le \exp(-\frac{mp/z}{2+\delta}\delta^2) \le \exp(-m\delta^2/(4+2\delta))$$

due to the multiplicative Chernoff bound  $\Pr(Z \ge E[Z](1+\delta)) \le e^{-\frac{Z}{2+\delta}\delta^2}$  where Z is the sum of i.i.d Bernoulli random variables.

Combine upper and lower tail bounds and note that  $p/z = \frac{\beta}{\beta+\gamma}$ . Then, we can conclude, for any  $\delta > 0$ ,

$$\Pr\left(\frac{C_m - C_0}{m} \notin \left[\frac{\beta}{\beta + \gamma}(1 - \delta)z, \frac{\beta}{\beta + \gamma}(1 + \delta)\right], \tau \ge m\right) \le 2\exp(-m\delta^2/(4 + 2\delta)).$$

### C.2.2. Proof of Lemma C.3.

*Proof.* Conditioned on  $(I_0, C_0, I_1, C_1, \ldots, I_{m-1}, C_{m-1})$  with  $\tau \ge m$ , we have

$$I_{k-1}T_k \sim \exp\left(\beta \frac{N - C_{k-1}}{N} + \gamma\right)$$

are independent exponential random variables.

Theorem 5.1 in Janson (2018) gives us a tail bound for the sum of independent exponential random variables: let  $X = \sum_{i=1}^{n} X_i$  with  $X_i \sim \text{Exp}(a_i)$  independent, then for  $\delta > 0$ ,

(20) 
$$\Pr(X \ge (1+\delta)\mu) \le \frac{1}{1+\delta} e^{-a_*\mu(\delta - \ln(1+\delta))} \le e^{-a_*\mu(\delta - \ln(1+\delta))}$$

(21) 
$$\Pr(X \le (1-\delta)\mu) \le e^{-a_*\mu(\delta - \ln(1+\delta))}$$

where  $\mu = E[X], a_* = \min_{1 \le i \le n} a_i$ .

Let  $\tilde{S}_{m|\vec{C},\vec{I}}$  be  $\tilde{S}_m$  conditioned on  $(I_0, C_0, I_1, C_1, \dots, I_{m-1}, C_{m-1})$  with  $\tau \geq m$ . Let  $\mu = E[\tilde{S}_{m|\vec{C},\vec{I}}] = \sum_{k=1}^m \frac{1}{\beta(N-C_{k-1})/N+\gamma}$ ,  $a_* = \min_{1 \leq k \leq m} \beta(N-C_{k-1})/N+\gamma$ . It is easy to verify the

following facts

$$\begin{split} \mu a_* \geq \sum_{k=1}^m \frac{a_*}{(\beta+\gamma)} \geq m \frac{N-m-C_0}{N} \\ \frac{1}{\beta+\gamma} \leq \frac{\mu}{m} \leq \frac{1}{\beta+\gamma} \frac{N}{N-m-C_0}. \end{split}$$

Combining these with Eqs. (20) and (21), we have

$$\Pr\left(\frac{\tilde{S}_{m|\vec{C},\vec{I}}}{m} \notin \left[\frac{(1-\delta)}{\beta+\gamma}, \frac{(1+\delta)}{\beta+\gamma} \frac{N}{N-m-C_0}\right]\right) \leq \Pr\left(\frac{\tilde{S}_{m|\vec{C},\vec{I}}}{m} \notin \left[\frac{\mu(1-\delta)}{m}, \frac{\mu(1+\delta)}{m}\right]\right) \\ \leq 2e^{-m\frac{N-m-C_0}{N}(\delta-\ln(1+\delta))}.$$

Therefore,

$$\Pr\left(\frac{\tilde{S}_m}{m} \notin I, \tau \ge m\right) = \int_{\vec{C}, \vec{I} \mid \tau \ge m} \Pr\left(\frac{\tilde{S}_m}{m} \notin I \mid \vec{C}, \vec{I}, \tau \ge m\right) f(\vec{C}, \vec{I} \mid \tau \ge m) \Pr(\tau \ge m)$$
$$\leq 2e^{-m\frac{N-m-C_0}{N}(\delta - \ln(1+\delta))} \Pr(\tau \ge m)$$
$$\leq 2e^{-m\frac{N-m-C_0}{N}(\delta - \ln(1+\delta))}.$$

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# C.2.3. Proof of Proposition C.4.

*Proof.* Let  $\hat{\beta} = \frac{C_m - C_0}{\tilde{S}_m}, z = \frac{N - C_0 - m}{N}$ . Suppose  $x \in \frac{\beta}{\beta + \gamma}[(1 - \delta)z, 1 + \delta], y \in \frac{1}{\beta + \gamma}[1 - \delta, (1 + \delta)1/z]$ . Then,

(22) 
$$\frac{x}{y} \in \left[\beta \frac{(1-\delta)z^2}{1+\delta}, \beta \frac{1+\delta}{1-\delta}\right]$$

Similarly, let  $\hat{\gamma} = \frac{m}{\tilde{S}_m} - \hat{\beta}$ . Suppose  $a \in (\beta + \gamma)[\frac{z}{1+\delta}, \frac{1}{1-\delta}], b \in \beta[\frac{(1-\delta)z^2}{1+\delta}, \frac{1+\delta}{1-\delta}]$ . Then

(23) 
$$a - b \in \left[\gamma \frac{z}{1+\delta} + \beta \frac{(1-\delta)z - (1+\delta)^2}{(1+\delta)(1-\delta)}, \gamma \frac{1}{1-\delta} + \beta \frac{1+\delta - (1-\delta)^2 z^2}{(1-\delta)(1+\delta)}\right]$$

Then, for any sets  $U_1, U_2$ ,

$$\begin{aligned} \Pr(\hat{\beta} \in U_1, \hat{\gamma} \in U_2) &\geq 1 - \Pr(\hat{\beta} \notin U_1) - \Pr(\hat{\gamma} \notin U_2) \\ &\geq 1 - \Pr(\hat{\beta} \notin U_1, \tau > m) - \Pr(\hat{\beta} \notin U_2, \tau > m) - 2\Pr(\tau < m) \\ &\geq 1 - 4e^{-m(\delta - \ln(1 + \delta))} - 4e^{-m\delta^2/(4 + 2\delta)} - 2B_1 e^{-B_2 I_0}, \end{aligned}$$

where the last step uses Lemma C.1, Lemma C.2 and Lemma C.3, using the intervals (22) and (23) for  $U_1$  and  $U_2$  respectively.

# D. Proofs of Propositions

# D.1. Proof of Proposition 2.1

*Proof.* As in Miller (2017, 2012), the solution  $\{(s'(t), i'(t), r'(t)) : t \ge 0\}$  can be written as:

$$s'(t) = s'(0)e^{-\xi'(t)}$$
  

$$i'(t) = N' - s'(t) - r'(t)$$
  

$$r'(t) = r(0) + \frac{\gamma' N'}{\beta'} \xi'(t)$$
  

$$\xi'(t) = \frac{\beta'}{N'} \int_0^t i'(t^*) dt^*$$

Making the appropriate substitutions yields the following equivalent system:

(24) 
$$i'(t) = N' - s'(0) \exp\left(-\frac{\beta'}{N'}\xi(t)\right) - r(0) - \frac{\gamma'N'}{\beta'}\xi'(t)$$

(25) 
$$\xi'(t) = \frac{\beta'}{N'} \int_0^t i'(t^*) dt^*.$$

Therefore, it remains to show that for  $\eta > 0$ ,  $\{(s(t), i(t), r(t)) : t \ge 0\} \triangleq \{(\eta s'(t), \eta i'(t), \eta r'(t)) : t \ge 0\}$  is a solution for (24) and (25) where N' is replaced with  $\eta N'$ . Starting with (24),

$$i'(t) = N' - s'(0) \exp(-\xi'(t)) - r'(0) - \frac{\gamma'N'}{\beta'}\xi'(t)$$
  

$$\eta i'(t) = \eta \left(N' - s'(0) \exp(-\xi'(t)) - r'(0) - \frac{\gamma'N'}{\beta'}\xi'(t)\right)$$
  

$$= \eta N' - \alpha s'(0) \exp(-\xi(t)) - \eta r(0) - \frac{\gamma'\eta N'}{\beta'}\xi(t)$$

where  $\xi(t) = \xi'(t) = \frac{\beta'}{N'\eta} \int_0^t \eta i'(t^*) dt^*$ . Noting that  $\xi'(t) = \xi(t)$  and substituting  $i(t) = \eta i'(t)$  yields the equations below, clearly showing that  $\{(s(t), i(t), r(t)) : t \ge 0\}$  satisfy (24) and (25):

$$i(t) = \eta N' - s(0) \exp(-\xi(t)) - r(0) - \frac{\gamma' \eta N'}{\beta'} \xi(t)$$
  
$$\xi(t) = \frac{\beta'}{N' \eta} \int_0^t i(t^*) dt^*.$$

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### D.2. Proof of Proposition 2.2

#### D.2.1. SIR Model

*Proof.* Consider initial conditions (s(0), i(0), 0), as in Miller (2017, 2012), the analytical solution is given by

$$s(t) = s(0)e^{-\xi(t)},$$
  

$$i(t) = N - s(t) - r(t),$$
  

$$r(t) = \frac{\gamma N}{\beta}\xi(t),$$
  

$$\xi(t) = \frac{\beta}{N} \int_0^t i(t')dt'.$$

Consider two SIR models with parameters  $(N, \beta, \gamma)$  and  $(N', \beta', \gamma')$ , and initial conditions  $(s_0, i_0, 0)$ and  $(s'_0, i'_0, 0)$  respectively. We claim that infection trajectories i(t) and i'(t) being identical on an open set [0, T) implies the parameters and initial conditions are identical as well.

Assume i(t) = i'(t) for all  $t \in [0, T)$ ; then, given the exact solution above it follows that

$$N - s_0 e^{-\frac{\beta}{N}x} - \gamma x = N' - s'_0 e^{-\frac{\beta'}{N'}x} - \gamma' x, \qquad \text{for all } x \in \left[0, \int_0^T i(t)dt\right]$$

As functions of x, both the RHS and LHS in the equality above are holomorphic, and hence, using the identity theorem, we then have for all  $x \in \mathbb{R}$ , there is  $N - s_0 e^{-\frac{\beta}{N}x} - \gamma x = N' - s'_0 e^{-\frac{\beta'}{N'}x} - \gamma' x$ .

Then the following implies  $\gamma = \gamma'$ :

$$-\gamma = \lim_{x \to +\infty} \frac{N - s_0 e^{-\frac{\beta}{N}x} - \gamma x}{x} = \lim_{x \to +\infty} = \frac{N' - s'_0 e^{-\frac{\beta'}{N'}x} - \gamma' x}{x} = -\gamma'.$$

Hence for all  $x \in \mathbb{R}$ ,  $N - s_0 e^{-\frac{\beta}{N}x} = N' - s'_0 e^{-\frac{\beta'}{N'}x}$ . Again, by taking x to infinity, we can conclude N = N' by the following

$$N = \lim_{x \to +\infty} \left( N - s_0 e^{-\frac{\beta}{N'}x} \right) = \lim_{x \to +\infty} \left( N' - s'_0 e^{-\frac{\beta'}{N'}x} \right) = N'.$$

Furthermore, by taking x = 0, we can also get  $s_0 = s'_0$  and then  $\beta = \beta'$  follows. This completes the proof.

#### D.2.2. Bass Model

*Proof.* Consider the initial condition i(0) = 0. By the analytic solution given by Bass (1969), we have

$$i(t) = N \frac{1 - e^{-(p+\beta)t}}{\frac{\beta}{p}e^{-(p+\beta)t} + 1}.$$

Consider two bass models with parameters  $(N, \beta, p)$  and  $(N', \beta', p')$  and initial conditions i(0) = 0, i'(0) = 0 respectively. We claim that trajectories i(t) and i'(t) being identical on an open

set [0, T) implies the parameters are identical as well.

Assume i(t) = i'(t) for all  $t \in [0, T)$ ; then, given the exact solution above it follows that

(26) 
$$N\frac{1-e^{-(p+\beta)t}}{\frac{\beta}{p}e^{-(p+\beta)t}+1} = N'\frac{1-e^{-(p'+\beta')t}}{\frac{\beta'}{p'}e^{-(p'+\beta')t}+1}, \qquad \text{for all } t \in [0,T)$$

As functions of t, both the RHS and LHS in the equality above are holomorphic, and hence, using the identity theorem, we then have Eq. (26) holds for all  $t \in \mathbb{R}$ .

By taking t to infinity, we can easily obtain N = N'. Furthermore, taking the derivative for t on both sides of Eq. (26), one can obtain

(27) 
$$\frac{(p+\beta)^2}{p} \frac{e^{-(p+\beta)t}}{(\beta/p \cdot e^{-(p+\beta)t}+1)^2} = \frac{(p'+\beta')^2}{p'} \frac{e^{-(p'+\beta')t}}{(\beta'/p' \cdot e^{-(p'+\beta')t}+1)^2}.$$

By taking t = 0 on both sides of Eq. (27), one can verify that p = p'. Furthermore, let g(t) = $\frac{(p+\beta)^2}{p} \frac{e^{-(p+\beta)t}}{(\beta/p \cdot e^{-(p+\beta)t}+1)^2} \text{ and } g'(t) = \frac{(p'+\beta')^2}{p'} \frac{e^{-(p'+\beta')t}}{(\beta'/p' \cdot e^{-(p'+\beta')t}+1)^2}.$ Note that

$$-(p+\beta) = \lim_{t \to +\infty} \frac{\ln(g(t))}{t} = \lim_{t \to +\infty} \frac{\ln(g'(t))}{t} = -(p'+\beta')$$

We then can conclude  $\beta = \beta'$ . This completes the proof.

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#### D.3. **Proof of Proposition 3.5**

*Proof.* Note that  $\mathbb{E}[T_i] = \frac{N}{pN(N-i)+\beta i(N-i)}$ . Then

$$\mathbb{E}[t_{k^{\text{CR}}}] = \mathbb{E}\left[\sum_{i=1}^{N^{2/3}-1} T_i\right] = \sum_{i=1}^{N^{2/3}-1} \frac{N}{pN(N-i) + \beta i(N-i)}$$

Let  $f(x) = \frac{N}{pN(N-x)+\beta x(N-x)}$ , we use f(x) as a proxy to bound  $\mathbb{E}[t_{k^{CR}}]$ . Easy to verify that f(x) is decreasing when  $x \in (0, \mathring{r}]$  where  $\mathring{r} = (1 - p/\beta)N/2$ . Note that  $p/\beta < c$  for some constant c. Hence when  $N \to \infty$ , we have  $\mathring{r} \gg N^{2/3}$  and

$$\begin{split} \sum_{i=1}^{N^{2/3}-1} \frac{N}{pN(N-i) + \beta i(N-i)} &\geq \int_{x=1}^{N^{2/3}} f(x) dx \\ &= \frac{\ln(\beta x + Np) - \ln(N-x)}{p+\beta} \Big|_{x=1}^{N^{2/3}} \\ &= \frac{\ln(\beta N^{2/3} + Np) - \ln(\beta + Np) + \ln(N-1) - \ln(N-N^{2/3})}{p+\beta} \\ &\geq \frac{\ln(\beta N^{2/3} + Np) - \ln(\beta + Np)}{p+\beta}. \end{split}$$

Similarly, for  $t_{k^*}$ , we have

$$E[t_{k^*}] = \sum_{i=1}^{\hat{m}-1} \frac{N}{pN(N-i) + \beta i(N-i)}$$

$$\leq f(1) + \int_{x=1}^{\hat{r}} f(x)dx$$

$$\leq f(1) + \frac{\ln(\beta N + Np) - \ln(pN + \beta) + \ln\frac{1}{1-c}}{p+\beta}$$

$$\leq \frac{\ln(\beta N + Np) - \ln(pN + \beta) + c'}{p+\beta}$$

for some absolute constant c'.

Let  $\frac{\beta}{p} = C \cdot N^{\alpha}$  for some constant C. We then have

$$\frac{E[t_{k^{\mathrm{CR}}}]}{E[t_{k^*}]} \geq \frac{\ln(\beta N^{2/3} + Np) - \ln(\beta + Np)}{\ln(\beta N + pN) - \ln(pN + \beta) + c'}$$
$$\geq \frac{\ln\left(\frac{CN^{2/3 + \alpha} + N}{CN^{\alpha} + N}\right)}{\ln\left(\frac{CN^{1 + \alpha} + N}{CN^{\alpha} + N}\right) + c'} =: k_N.$$

Then, it is easy to verify that when  $\frac{1}{3} < \alpha \leq 1$ ,  $\lim_{N \to \infty} k_N = \frac{\alpha - 1/3}{\alpha}$ . When  $\alpha > 1$ ,  $\lim_{N \to \infty} k_N = \frac{2}{3}$ .

Note that we also have  $\mathbb{E}[t_{k^{CR}}] \leq f(1) + \int_{x=1}^{N^{2/3}} f(x) dx$  and  $\mathbb{E}[t_{k^*}] \geq \int_{x=1}^{r} f(x) dx$ . Similarly, one can verify that

$$\limsup_{N \to \infty} \frac{\mathbb{E}[t_{k^{\mathrm{CR}}}]}{\mathbb{E}[t_{k^*}]} \le \begin{cases} 0 & \alpha \le \frac{1}{3} \\ \frac{\alpha - \frac{1}{3}}{\alpha} & \frac{1}{3} < \alpha \le 1 \\ \frac{2}{3} & \alpha > 1 \end{cases}$$

This completes the proof.

# D.4. Proof of Proposition 3.6

Let  $t_*^d = \inf\{t : \beta(s)t/N < \gamma\}$  be the time when the number of infections is at its peak. It is easy to show that  $t_2^d \le t_*^d$ . We show the analog of Proposition 3.6 with the peak defined instead as  $t_*^d$  — i.e. we show  $\liminf_{N \to \infty} \frac{t_{CR}^d}{t_*^d} \ge \frac{2}{3}$ . Then, the desired result follows since  $t_2^d \le t_*^d$ .

First, we prove  $t_2^d \leq t_*^d$ . We can write  $\frac{d^2s}{dt^2}$  as

(28)  
$$\frac{d^2s}{dt^2} = \frac{-\beta}{N} \left(\frac{ds}{dt}i + \frac{di}{dt}s\right)$$
$$= \frac{-\beta}{N} \left(\frac{-\beta s}{N}i^2 + \left(\frac{\beta s}{N} - \gamma\right)is\right)$$
$$= \frac{\beta^2 is}{N^2} \left(i - s + \frac{\gamma}{\beta}N\right).$$

From (28), we see that  $\frac{d^2s}{dt^2} > 0$  if and only if

$$s < \frac{\gamma}{\beta}N + i$$

By definition,  $t^d_*$  occurs at a time when

$$s < \frac{\gamma}{\beta} N.$$

Since s is decreasing and i is non-negative, clearly  $t_2^d$  occurs before  $t_*^d$ .

Next, we prove  $\liminf_{N\to\infty} \frac{t_{CR}^d}{t_*^d} \geq \frac{2}{3}$ . The crux of the problem is summarised in two smaller results, bounding  $t_{CR}^d$  and  $t_*^d$  respectively. Let  $\rho_1 = 1 - \frac{1}{\log \log N}$  and  $\rho_2 = \frac{\gamma}{\beta}$ .

**Proposition D.1.** There exists a constant  $\nu_1$  that only depends on  $\gamma, \beta$  such that

$$t_{\rm CR}^d \ge \frac{1}{\beta - \gamma} \left( \frac{2}{3} \log \frac{\nu_1 N}{c(0)^{3/2}} + \log \frac{\nu_1^{2/3}}{c(0)} \left( 1 - \frac{c(0)}{N^{2/3}} \right) \right).$$

**Proposition D.2.** There exists a constant  $\nu_2$  that only depends on  $\gamma, \beta$  and a constant C = O(1), such that

$$t^d_* \leq \frac{1}{\beta\rho_1-\gamma}\log\frac{\nu_2N}{i(0)} + \frac{C}{1-\rho_1}$$

The argument follows directly by taking the limit of the bounds we provide in Propositions D.1-D.2. Specifically, using that the constants  $\nu_1, \nu_2$  do not depend on N, we arrive at

$$\begin{split} \limsup_{N \to \infty} \frac{t_*^d}{t_{\mathrm{CR}}^d} &\leq \limsup_{N \to \infty} \frac{\frac{1}{\beta \rho_1 - \gamma} \log \frac{\nu_2 N}{i(0)} + \frac{C}{(1 - \rho_1)}}{\frac{1}{\beta - \gamma} \left(\frac{2}{3} \log \frac{\nu_1 N}{c(0)^{3/2}} + \log \frac{\nu_1^{2/3}}{c(0)} \left(1 - \frac{c(0)}{N^{2/3}}\right)\right)} \\ &= \limsup_{N \to \infty} \frac{\beta - \gamma}{\beta \rho_1 - \gamma} \cdot \frac{\log N + \log \nu_2 - \log i(0)}{\frac{2}{3} \log N + \frac{4}{3} \log \nu_1 - 2 \log c(0) + \log \left(1 - \frac{c(0)}{N^{2/3}}\right)} \\ &+ \limsup_{N \to \infty} \frac{(\beta - \gamma) C \log \log N}{\frac{2}{3} \log N + \frac{4}{3} \log \nu_1 - 2 \log c(0) + \log \left(1 - \frac{c(0)}{N^{2/3}}\right)} \end{split}$$

 $\rho_1 \to 1$  as  $N \to \infty$ , so  $\frac{\beta - \gamma}{\beta \rho_1 - \gamma} \to 1$ . Since  $c(0) = O(\log(N))$  by assumption (and  $i(0) \le c(0)$ ), and C = O(1) by Proposition D.2, the limits of the two summands above are 3/2 and 0 respectively, which concludes the proof.

# D.4.1. Proof of Proposition D.1.

**Proof of Proposition D.1.** Define  $\tilde{i}(t)$  such that  $\tilde{i}(0) = i(0)$  and  $\frac{d\tilde{i}}{dt} = (\beta - \gamma)\tilde{i}$ , implying

$$\tilde{i}(t) = i(0) \exp\{(\beta - \gamma)t\}.$$

Since  $\frac{d\tilde{i}}{dt} \ge \frac{di}{dt}$  for all  $t, \tilde{i}(t) \ge i(t)$  for all t. Then, for all t,

$$\frac{ds}{dt} = -\beta \frac{s}{N}i \ge -\beta i \ge -\beta \tilde{i}.$$

Hence we can write

$$\begin{split} s(t) &\geq s(0) + \int_0^t -\beta \tilde{i}(t')dt' \\ &= s(0) - \beta i(0) \int_0^t \exp\{(\beta - \gamma)t'\}dt' \\ &= s(0) - \frac{\beta i(0)}{\beta - \gamma} (\exp\{(\beta - \gamma)t\} - 1) \end{split}$$

Since  $s(0) - s(t_{CR}^d) = N^{2/3} - c(0)$ , setting  $t = t_{CR}^d$  and solving for  $t_{CR}^d$  in the inequality above results in

$$\begin{split} t_{\rm CR}^{d} &\geq \frac{1}{\beta - \gamma} \log \left( \frac{\beta - \gamma}{\beta i(0)} (N^{2/3} - c(0)) \right) \\ &\geq \frac{1}{\beta - \gamma} \log \left( \frac{\beta - \gamma}{\beta c(0)} (N^{2/3} - c(0)) \right) \\ &= \frac{1}{\beta - \gamma} \left( \log \frac{\beta - \gamma}{\beta c(0)} (N^{2/3}) + \log \frac{\beta - \gamma}{\beta c(0)} \left( 1 - \frac{c(0)}{N^{2/3}} \right) \right) \\ &= \frac{1}{\beta - \gamma} \left( \frac{2}{3} \log \frac{\nu_1 N}{c(0)^{3/2}} + \log \frac{\nu_1^{2/3}}{c(0)} \left( 1 - \frac{c(0)}{N^{2/3}} \right) \right) \end{split}$$

for  $\nu_1 = \left(\frac{\beta - \gamma}{\beta}\right)^{3/2}$  as desired.

### D.4.2. Proof of Proposition D.2.

For  $\rho \in [0, \frac{\gamma}{\beta}]$ , let  $t_{\rho}$  be the time t when  $\frac{s(t)}{N} = \rho$ .  $\rho$  will represent the fraction of the total population

that is susceptible. Since  $\rho \leq \frac{\gamma}{\beta}$ , *i* is increasing for the time period of interest. Let  $\beta > \gamma$ , *N* be fixed. Let  $\rho_1 = 1 - \frac{1}{\log \log N}$  and  $\rho_2 = \frac{\gamma}{\beta}$ . We assume *N* is large enough that  $\rho_1 > \rho_2$ , hence  $t_{\rho_1} < t_{\rho_2}$ .  $t_*^d = t_{\rho_2}$ .

**Lemma D.3.** For any  $\rho \in [0, \frac{\gamma}{\beta}]$ ,  $i(t_{\rho}) \geq N(1-\rho)\frac{\beta\rho-\gamma}{\beta\rho} - \frac{c(0)}{2}$ .

Fix  $\rho$ . At time  $t_{\rho}$ , the total number of people infected is  $c(t_{\rho}) = i(t_{\rho}) + r(t_{\rho}) =$ Proof of Lemma D.3.  $N(1-\rho)$ , by definition. At any time  $t \leq t_{\rho}$ , the rate of increase in *i* is  $\frac{\beta \frac{s(t)}{N} - \gamma}{\beta \frac{s(t)}{N}} \geq \frac{\beta \rho - \gamma}{\beta \rho}$  of the rate of increase in c. Therefore,  $i(t_{\rho}) - i(0) \ge \left(\frac{\beta\rho - \gamma}{\beta\rho}\right) (c(t_{\rho}) - c(0))$  and  $i(t_{\rho}) \ge \left(\frac{\beta\rho - \gamma}{\beta\rho}\right) N(1-\rho) - \frac{\beta\rho - \gamma}{\beta\rho} c(0) + \frac{\beta\rho - \gamma}{\beta\rho} (c(t_{\rho}) - c(0)) + \frac{\beta\rho - \gamma}{\beta\rho} (c(t_{\rho}) - c(0$ i(0). Using the fact that  $i(0) \geq \frac{c(0)}{2}$  and rearranging terms gives the desired result.

**Lemma D.4.** For  $t \in [t_{\rho_1}, t_{\rho_2}]$ , where  $\rho_2 > \rho_1$  for  $\rho_1, \rho_2 \in [0, \frac{\gamma}{\beta}]$ ,  $t_{\rho_2} - t_{\rho_1} \leq \frac{N(\rho_1 - \rho_2)}{\beta \rho_2 i(t_{\rho_1})}$ .

**Proof of Lemma D.4.** The difference in s between  $t_{\rho_1}$  and  $t_{\rho_2}$  is  $s(t_{\rho_1}) - s(t_{\rho_2}) = N(\rho_1 - \rho_2)$ . As a consequence of the mean value theorem,  $\frac{s(t_{\rho_2}) - s(t_{\rho_1})}{t_{\rho_2} - t_{\rho_1}} \leq \max_{t \in [t_{\rho_1}, t_{\rho_2}]} \{\frac{ds}{dt}\}$ . Using these two expressions,

$$\frac{N(\rho_1 - \rho_2)}{t_{\rho_2} - t_{\rho_1}} \ge \min\left\{-\frac{ds}{dt}\right\} = \min\left\{\beta\frac{s(t)}{N}i(t) : t \in [t_{\rho_1}, t_{\rho_2}]\right\} \ge \beta\rho_2 i(t_{\rho_1})$$

The desired expression follows from rearranging terms.

**Lemma D.5.** For any  $\rho \leq \min\{\frac{\gamma}{\beta}, 1/2\}, t_{\rho} \leq \frac{1}{\beta \rho - \gamma} \log \frac{\nu_2}{i(0)} N$ , for  $\nu_2 = \frac{2(\beta - \gamma)}{\beta}$ .

The proof of this lemma follows the exact same procedure as the proof of Proposition D.1.

**Proof of Lemma D.5.** We proceed in the same way as the proof of Proposition D.1 except in this case we will lower bound s(0) - s(t). We achieve this by letting  $\tilde{i}$  be defined to grow slower than i, so it is used as a lower bound. Define  $\tilde{i}(t)$  such that  $\tilde{i}(0) = i(0)$  and  $\frac{d\tilde{i}}{dt} = (\beta \rho - \gamma)\tilde{i}$ , implying

$$\tilde{i}(t) = i(0) \exp\{(\beta \rho - \gamma)t\}.$$

Since  $\frac{d\tilde{i}}{dt} \leq \frac{di}{dt}$  when ,  $\tilde{i}(t) \leq i(t)$  for all  $t < t_{\rho_2}$ . In addition, when  $t < t_{\rho_2}$ ,  $\frac{s}{N} \geq \frac{\gamma}{\beta} \geq \rho$ . Then, for  $t < t_{\rho_2}$ ,

$$\frac{ds}{dt} = -\beta \frac{s}{N}i \le -\beta \rho \tilde{i}.$$

Hence we can write

$$\begin{split} s(t) &\leq s(0) + \int_0^t -\beta\rho \tilde{i}(t')dt' \\ &= s(0) - \beta\rho i(0) \int_0^t \exp\{(\beta\rho - \gamma)t'\}dt' \\ &= s(0) - \frac{\beta\rho i(0)}{\beta\rho - \gamma} (\exp\{(\beta\rho - \gamma)t\} - 1) \end{split}$$

Since  $s(t_{\rho}) = \rho N$ ,

$$\rho N \le s(0) - \frac{\beta \rho i(0)}{\beta \rho - \gamma} (\exp\{(\beta \rho - \gamma)t_{\rho}\} - 1).$$

Solving for  $t_{\rho}$  results in

$$t_{\rho} \leq \frac{\log\left(\frac{\beta\rho - \gamma}{\beta\rho i(0)}(s(0) - \rho N) + 1\right)}{\beta\rho - \gamma} \leq \frac{1}{\beta\rho - \gamma}\log\left(\frac{\nu_2}{i(0)}N\right)$$

where  $\nu_2 = \frac{2(\beta - \gamma)}{\beta}$ , using the fact that  $\rho \le 1/2$ .

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**Proof of Proposition D.2.** Using the results from Lemmas D.3-D.5,

$$\begin{split} t_{\rho_2} &= t_{\rho_1} + (t_{\rho_2} - t_{\rho_1}) \\ &\leq \frac{1}{\beta \rho_1 - \gamma} \log \left( \frac{\nu_2}{i(0)} N \right) + \frac{N(\rho_1 - \rho_2)}{\beta \rho_2 i(t_{\rho_1})} \\ &\leq \frac{1}{\beta \rho_1 - \gamma} \log \left( \frac{\nu_2}{i(0)} N \right) + \frac{N(\rho_1 - \rho_2)}{\frac{\rho_2}{\rho_1} N(1 - \rho_1)(\beta \rho_1 - \gamma) - \frac{\beta \rho_2}{2} c(0)} \\ &= \frac{1}{\beta \rho_1 - \gamma} \log \left( \frac{\nu_2}{i(0)} N \right) + \frac{C}{1 - \rho_1}, \end{split}$$

where  $C = \frac{\rho_1 - \rho_2}{\frac{\rho_2}{\rho_1}(\beta \rho_1 - \gamma) - \frac{\beta \rho_2}{2} \frac{c(0)}{N(1 - \rho_1)}}$ . Note that, as required in the statement, C = O(1). Indeed,

$$C = \frac{(\rho_1 - \rho_2)}{\frac{\rho_2}{\rho_1}(\beta\rho_1 - \gamma) - \frac{\beta\rho_2}{2}\frac{c(0)}{N(1 - \rho_1)}} = \frac{1 - \rho_2 - \frac{1}{\log\log N}}{\beta\rho_2 - \frac{\gamma\rho_2}{1 - \frac{1}{\log\log N}} - \frac{\beta\rho_2}{2}\frac{c(0)\log\log N}{N}},$$

and so, as N grows large, C tends to  $(1 - \rho_2)/\rho_2(\beta - \gamma)$  (recall that  $c(0) = O(\log \log N)$ ).

# E. Datasets

Here we provide details on the datasets used in Section 5.

#### E.1. Amazon product reviews

For the Bass model, we use the Amazon product dataset of Ni et al. (2019), which contains product reviews for Amazon products over more than twenty years. We take these reviews as a proxy for sales. Products in Amazon's electronics category typically have review trajectories well-approximated by the Bass model, marked by slow initial adoption and a long tail of sales towards the end of the product lifecycle – see Figure 4 for examples of such trajectories. For our experiments, we randomly selected 100 products with over four years of reviews, and over 100 reviews by the fourth year. Review counts are taken at a weekly granularity. Here we use  $N_{\text{max}} = 1e5$  – an order of magnitude larger than any of the true product sales numbers in the dataset.

### E.2. CDC ILINet influenza database

For the SIR model, we use the CDC's ILINet database of patient visits for flu-like illnesses in the United States, broken down by Department of Health and Human Services region. Each instance in the dataset consists of weekly patient visits in a given region, over the course of one year. Each year starts in September, at the low point of the flu season. We use data from 2010 through 2019 for each of 10 regions, for 100 instances total. As the dataset only includes cumulative infections  $C_i[t]$ , rather than observations of infection and recoveries  $I_i[t], R_i[t]$ , we simulate these based on the dynamics (11).

Here, we take  $\gamma = 0.24$  as in Chowell et al. (2008), and *a* is assumed to be 0. We take  $N_{\text{max}}$  to be the total patient population (including for non-flu illnesses) in the dataset.



**Figure 4:** Cumulative weekly product reviews for randomly selected products from our subset of the Amazon dataset.

### E.3. COVID-19 Datasets

For observed COVID-19 cases, we use publicly available case data from the ongoing COVID-19 epidemic provided by Dong et al. (2020). We aggregate data into sub-state regions, corresponding broadly to public health service areas. The median state has seven regions. Here we take  $\gamma = 1/4$ .

The dataset contains static demographic covariates and time-varying mobility features that affect the disease transmission rate. The dynamic covariates proxy mobility by estimating the daily fraction of people staying at home relative to a region-specific benchmark of activity in early March before social distancing measures were put in place. We also include a regional binary indicator of the days when the fraction of people staying home exceeds the benchmark by 0.2 or more.

These data are provided by Safegraph, a data company that aggregates anonymized location data from numerous applications in order to provide insights about physical places. To enhance privacy, SafeGraph excludes census block group information if fewer than five devices visited an establishment in a month from a given census block group. Documentation can be found at Saf (2020).

The static covariates capture standard demographic features of a region that influence variation in infection rates. These features fall into several categories:

- Fraction of individuals that live in close proximity or provide personal care to relatives in other generations. These covariates are reported by age group by state from survey responses conducted by UMi (2020).
- Family size from U.S. Census data, aggregated and cleaned by Cla (2020).
- Fraction of the population living in group quarters, including colleges, group homes, military quarters, and nursing homes (U.S. Census via Cla (2020)).
- Population-weighted urban status (US Census via Cla (2020))
- Prevalence of comorbidities, such as cardiovascular disease and hypertension (CDC (2020a))

- Measures of social vulnerability and poverty (U.S. Census via Cla (2020); CDC (2020b))
- Age, race and occupation distributions (U.S. Census via Cla (2020))

# F. Detailed description of the COVID-19 model

### F.1. Approximating the arrival process with latent state

Recall the stochastic SIR process,  $(S(t), I(t), R(t)) : t \ge 0$ , a multi-variate counting process determined by parameters  $(N, \beta, \gamma)$ . We now allow  $\beta$  to be time-varying, yielding a counting process with jumps  $C_k - C_{k-1} \sim \text{Bern} \{\beta S_{k-1}/(\beta_k S_{k-1} + \gamma NI(t))\}.$ 

We obtain discrete-time diffusion processes,  $\{(S_i[t], I_i[t], R_i[t]) : t \in \mathbb{N}\}$  for instances  $i \in \mathcal{I}$  by considering the Euler-approximation to the stochastic diffusion process (3) (e.g. Jacod et al. (2005)). Specifically, let  $\Delta I[t] = I[t] - I[t-1]$ , and define  $\Delta S[t]$  and  $\Delta R[t]$  analogously. A discrete-time approximation to the SIR process is then given by:

(29)  
$$\Delta S_{i}[t+1] = -\beta_{i}[t](S_{i}[t]/N_{i})I_{i}[t] + \nu_{i,t}^{S}$$
$$\Delta I_{i}[t+1] = \beta_{i}[t](S_{i}[t]/N_{i})I_{i}[t] - \gamma I_{i}[t] + \nu_{i,t}^{I}$$
$$\Delta R_{i}[t+1] = \gamma I_{i}[t] + \nu_{i,t}^{R}$$

where  $\{\nu_{i,t}^S\}, \{\nu_{i,t}^I\}, \{\nu_{i,t}^R\}$  are appropriately defined martingale difference sequences.

In the real world, the SIR model is a latent process – we never directly observe any of the state variables  $S_i[t], I_i[t], R_i[t]$ . Instead, we observe  $C_i[t] = I_i[t] + R_i[t] = N_i - S_i[t]$ . The MLE problem for parameters  $(N, \beta)$  is simply  $\max_{(\beta, N)} \sum_{i,t} \log \mathbb{P}(C_i[t]|\beta, N)$ .

This is a difficult non-linear filtering problem (and an interesting direction for research). We therefore consider an approximation: Denote by  $\{(s_i[t], i_i[t], r_i[t]) : t \in \mathbb{N}\}$  the deterministic process obtained by ignoring the martingale difference terms in the definition of the discrete time SIR process. We consider the approximation  $C_i[t] = N_i - S_i[t] \sim (N_i - s_i[t])\omega_i[t]$ , where  $\omega_i[t]$  is log-normally distributed with mean 1 and variance  $\exp(\sigma^2) - 1$ .

Under this approximation, we have the log likelihood function

(30) 
$$\log p(C_i[t]|N,\beta) = (\log C_i[t] - \log (N_i - s_i[t]))^2$$

#### F.2. Two-Stage Estimation of the SIR model

We parameterize our estimates of N as  $\hat{N}_i(\phi, \delta) = \exp(\phi^\top Z_i + \delta_i)P_i$ , where  $Z_i$  are non-time-varying, region-specific covariates,  $P_i$  is the population of region i,  $\phi$  is a vector of fixed effects, and  $\delta_i \sim \mathcal{N}(0, \sigma_{\delta}^2)$  are region-specific random effects.

Demographic and mobility factors also influence the reproduction rate of the disease. To model these effects, we estimate  $\beta_i[t]$  as a mixed effects model incorporating covariates  $\beta_i[t] = \exp(X_i[t]^\top \theta) + \epsilon_i$ , where  $\theta$  is a vector of fixed effects, and  $\epsilon_i \sim \mathcal{N}(0, \sigma_{\epsilon}^2)$  is a vector of random effects.

Given observations up to time T, we then estimate the model parameters  $(\theta, \phi, \delta, \epsilon)$  in two stages:

1. Estimate the peak parameters  $\hat{\phi}, \hat{\delta}$  via MLE, for the regions  $i \in P[t]$ :

$$\hat{\phi}, \hat{\delta} = \arg\max_{\phi, \delta} \left\{ \max_{\theta, \epsilon} \left\{ \sum_{i \in P[t]} \sum_{t \in [T]} \log p\left(C_i[t] \mid \beta_i(\theta, \epsilon), \hat{N}_i(\phi, \delta)\right) + \log p(\epsilon, \delta) \right\} \right\}$$

where p is the likelihood defined in (30). We let  $\hat{\delta}_i = 0$  for  $i \notin P[t]$ .

2. Estimate the remaining parameters over all regions  $i \in \mathcal{I}$ :

(31) 
$$\hat{\theta}, \hat{\epsilon} = \arg \max_{\theta, \epsilon} \left\{ \sum_{i \in \mathcal{I}} \sum_{t \in [T]} \log p\left(C_i[t] \mid \beta_i(\theta, \epsilon), \hat{N}_i(\hat{\phi}, \hat{\delta}), \right) + \log p(\epsilon, \delta) \right\}$$

We note that (31) is differentiable with respect to the parameters  $(\theta, \epsilon, \phi, \delta)$ , and we solve it (or a weighted version) using Adam Kingma and Ba (2014).<sup>4</sup>

# F.3. Performance relative to other models

To contextualize the quality of the Two-Stage model, we compare our analyzed models to the widely used IHME model ihm (2020). We note that there exist comparable models that may serve as stronger baselines; we include these results merely to demonstrate that the Two-Stage model yields high-quality predictions, comparable to widely-cited models in the literature.

Figure 5 compares state-level<sup>5</sup> WMAPE for MLE, Two-Stage and IHME models, for vintages stretching back 28 days. The IHME model up to this date is, in effect, an SI model with carefully tuned parameters. We report published IHME forecasts; 10 vintages of that model were reported between April 21 and May 21. *Two Stage* dominates IHME across all model vintages.



**Figure 5:** WMAPE for predicting state-level cumulative cases on May 21, 2020, comparing MLE and the Two-Stage approach against IHME.

<sup>&</sup>lt;sup>4</sup>Adam was run for 20k iterations, with learning rate tuned over a coarse grid. A weighted version of the loss function in (31) with weights for (i, t)th observation set to  $C_i[t]$  worked well.

<sup>&</sup>lt;sup>5</sup>Due to IHME only providing state-level predictions. Additionally IHME only offers deaths predictions for these vintages; we show WMAPE on deaths for IHME and WMAPE on infections for MLE and Two-Stage.