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Likelihood Estimation for Stochastic Epidemics with Heterogeneous Mixing Populations

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Abstract—We consider a heterogeneously mixing SIR stochastic epidemic process in populations described by a general graph. Likelihood theory is developed to facilitate statistic inference for the parameters of the model under complete observation. We show that these estimators are asymptotically Gaussian unbiased estimates by using a martingale central limit theorem.

Keywords—statistic inference, maximum likelihood, epidemic model, heterogeneous mixing.

I. Introduction

Understanding the spread of an infectious disease is a highly crucial issue in order to prevent major outbreaks of an epidemic. Mathematical modeling of infectious disease has a long history; see e.g. [4], [13] and references therein.

In the last decades, there has been an increase in research activity regarding modeling epidemics among populations with various heterogeneities and their effects on disease propagation [3]. Epidemics with two levels of mixing have been introduced by [5], [6]. Such a model assumes two different kind of contacts; a local and a global. Apart from describing the infection process of such a model, the authors in [6] briefly consider statistical inference for their model. See also [10] on how to draw Bayesian inference for such type of models. Recently, [8] studied statistical inference for epidemics with three levels of mixing. Heterogeneities caused by social structures are also incorporated in relatively simple models by using random network models, e.g. [2], [9], [11]. Population age structures have also been addressed in [7].

In this paper, aiming to further extend the heterogeneities in the stochastic epidemic models, we treat the underlying population structure as an arbitrary graph and explore non-uniform mixing in the spreading of epidemics. Inferences for the infection rate and removal rate are drawn under complete observation by using the likelihood theory. Based on the likelihood theory for counting processes [1], we show that these estimators are asymptotically Gaussian unbiased estimates by using a martingale central limit theorem [14].

The rest of the paper is organized as follows. The model is described in detail in Section 2. In Section 3 the likelihood is derived for the case of complete observation of the epidemics. Section 4 contains our main results followed by some discussions.

II. The Model

Consider the SIR epidemic model with a closed population of $n+m$ individuals out of which m are initially infected and the n remaining individuals are susceptible to the disease in question. We shall model the population structure using a general network, G. Specifically, each individual in the population will be represented by a vertex in G and the adjacency of two vertices means contact between the two corresponding individuals. Furthermore, a Markovian epidemic process with heterogeneous mixing can be defined on G. We now describe the model in more detail.

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Let $G=(V,E)$ be a simple connected graph with vertex set $V=\{1,2,\cdots,n+m\}$, edge set E and $|V|=n+m$. Assume $m=\mu n$ with $\mu>0$, that is, a positive (usually small) proportion of population is initially infectious. For any $v\in V$, the neighborhood of vertex v is denoted by $\mathcal{N}_v$ and let $|\mathcal{N}_v|=d_v$. Thus $\mathcal{N}_v$ restricts the set of individuals with whom the individual v can make contact. The infectious periods of different individuals are assumed to be independently distributed according to exponential random variables I_v with means $(\beta\beta_v)^{-1}$, where $\beta_v>0$ is a deterministic function involving some individual specific characteristics, such as age, sex and physique. We refer to $\beta\beta_v>0$ as the removal rate.

An infective v will make contacts with a given neighbor in $\mathcal{N}_v$ at the time points of a homogeneous Poisson process with intensity $(\Gamma\Gamma_v)/d_v$, where $\Gamma_v>0$ is a deterministic function, which may contain individual properties like β_v do. The Poisson processes governing different infective-susceptible pairs are assumed to be independent of one another; they are also independent of the infectious periods I_v. Therefore, during his infectious period an infective makes contacts with his neighbors at the time points of a Poisson process with a constant intensity $\Gamma\Gamma_v>0$, where $\Gamma\Gamma_v$ is known as the infection rate.

If a contacted individual is still susceptible, then he becomes infectious and is immediately able to infect other individuals (in his neighborhood). An individual is considered removed once his infectious period has terminated, and is then immune to new infections, playing no further role in the epidemics. The epidemic continues until there are no more infectious individuals left in the population.

III. Maximum Likelihood Estimators

We assume the aforementioned SIR epidemic process is observed completely, i.e. the infection times τ_v and removal times ρ_v of all infected individuals are observed, up until some time s (see Remark 5). Consequently, the length of the infectious period $I_v=\rho_v-\tau_v$ is also known. Moreover, we assume that the functions Γ_v, β_v and the population structure incorporated in G are fully known. Based on the observed

data we want to draw inferences on the parameters Γ and β involving in the infection rate and removal rate, respectively, by means of Maximum Likelihood (ML) theory.

Let f_v and F_v denote, respectively, the density and distribution functions of the infectious period I_v. Define by $\mathcal{X}_n(t)$ and $\mathcal{Y}_n(t)$ the sets of susceptible and infectious individuals at time t, respectively. Hence, $X_n(t) := |\mathcal{X}_n(t)|$ and $Y_n(t) := |\mathcal{Y}_n(t)|$ are the numbers of susceptibles and infectives respectively at time t. Recall that $X_n(0) = n$ and $Y_n(0) = \mu n$. Define $I(t) = n - X_n(t)$, a counting process for the number of infections that have occurred in $(0, t]$, and $R(t) = n+m-X_n(t)-Y_n(t)$ a counting process for the number of removals in $(0, t]$.

The counting processes $I(t)$ and $R(t)$ have intensities $\sum_{v\in\mathcal{Y}_n(t)}(\Gamma\Gamma_v/d_v)|\mathcal{X}_n(t)\cap\mathcal{N}_v|$ and $\sum_{v\in\mathcal{Y}_n(t)} f_v(t-\tau_v)/(1-F_v(t-\tau_v))$, respectively [3]. From the likelihood theory for counting processes [1], it follows that the log-likelihood function can by expressed as

$$\begin{aligned} l_s(\Gamma,\beta) &= \int_0^s \ln\Big(\sum_{v\in\mathcal{Y}_n(t)}(\Gamma\Gamma_v/d_v)|\mathcal{X}_n(t)\cap\mathcal{N}_v|\Big)\mathrm{d}I(t) \\ &\quad - \sum_{v\in\mathcal{Y}_n(t)}(\Gamma\Gamma_v/d_v)|\mathcal{X}_n(t)\cap\mathcal{N}_v|\mathrm{d}t \\ &\quad + \sum_{v;\tau_v\le s<\rho_v}\ln(1-F_v(s-\tau_v)) \\ &\quad + \sum_{v;\rho_v\le s}\ln f_v(\rho_v-\tau_v). \end{aligned} \tag{1}$$

To estimate Γ we differentiate the log-likelihood (1) with respect to Γ

$$\begin{aligned} \frac{\partial l_s(\Gamma,\beta)}{\partial\Gamma} &= \int_0^s \frac{1}{\Gamma}\Big(\mathrm{d}I(t) \\ &\quad - \sum_{v\in\mathcal{Y}_n(t)}(\Gamma\Gamma_v/d_v)|\mathcal{X}_n(t)\cap\mathcal{N}_v|\mathrm{d}t\Big) \\ &= \frac{I(s)}{\Gamma} - \int_0^s\sum_{v\in\mathcal{Y}_n(t)}\frac{\Gamma_v|\mathcal{X}_n(t)\cap\mathcal{N}_v|}{d_v}\mathrm{d}t. \end{aligned}$$

Solving the likelihood equation $\partial l_s(\Gamma,\beta)/\partial\Gamma = 0$ hence gives the ML estimate

$$\hat{\Gamma} = \frac{I(s)}{\int_0^s\sum_{v\in\mathcal{Y}_n(t)}(\Gamma_v/d_v)|\mathcal{X}_n(t)\cap\mathcal{N}_v|\mathrm{d}t}. \tag{2}$$

It is straightforward to see the intensity for $R(t)$ is just $\beta\sum_{v\in\mathcal{Y}_n(t)}\beta_v$. The derivative of the likelihood with respect to β then becomes

$$\begin{aligned} \frac{\partial l_s(\Gamma,\beta)}{\partial\beta} &= \int_0^s\frac{1}{\beta}\Big(\mathrm{d}R(t) - \beta\sum_{v\in\mathcal{Y}_n(t)}\beta_v\mathrm{d}t\Big) \\ &= \frac{R(s)}{\beta} - \int_0^s\sum_{v\in\mathcal{Y}_n(t)}\beta_v\mathrm{d}t. \end{aligned}$$

Accordingly, the ML estimator is

$$\hat{\beta} = \frac{R(s)}{\int_0^s\sum_{v\in\mathcal{Y}_n(t)}\beta_v\mathrm{d}t}. \tag{3}$$

We will prove that the ML estimates $\hat{\Gamma}$ and $\hat{\beta}$ are asymptotically Gaussian unbiased estimators.

IV. Main Results

In this section, for $v \in V$, we assume that $1 \le d_v \le M$ for some $M < \infty$. For mathematical convenience we suppose that $\Gamma_v = \Gamma_u := \Gamma_i$ if $|\mathcal{N}_v| = |\mathcal{N}_u| = i$. Moreover, the number of different β_v, say N, is finite. We signify them as $\{\beta_k\}_{1\le k\le N}$. Without loss of generality, we assume

$$\mu = \sum_{i=1}^{M}\sum_{j=0}^{i}a_{ij} = \sum_{k=1}^{N}b_k, \tag{4}$$

for $a_{ij} \ge 0$ and $b_k \ge 0$. Thereby, $a_{ij}n$ represents the number of initial infectives that have i neighbors out of which j are susceptible, while $b_k n$ is the number of initial infectives with removal rate $\beta\beta_k$.

To prove the asymptotic normality of the estimators, we choose to use the density dependent jump Markovian framework developed in [3](Chap. 5) and [12](Chap. 11).

For each $n \ge 1$, define an $(M^2/2+3M/2+N)$-dimensional continuous-time Markov process

$$V_n(t) = \big(\{Q_k^{(n)}(t)\}_{1\le k\le N};\{Z_{ij}^{(n)}(t)\}_{1\le i\le M,0\le j\le i}\big), \tag{5}$$

with $Q_k^{(n)}(t)$ representing the number of infectives with removal rate $\beta\beta_k$ and $Z_{ij}^{(n)}(t)$ the number of infectives that have i neighbors out of which j are susceptible, respectively, at time t. From the definitions, it is clear that $Y_n = \sum_{i=1}^{M}\sum_{j=0}^{i}Z_{ij}^{(n)} = \sum_{k=1}^{N}Q_k^{(n)}$.

The process V_n in (5) can make two types of jumps:

(I) the process changes by $(0,\cdots,-1,\cdots,0;0,\cdots,-1,\cdots,0)$ with one -1 in the first N coordinations (say k-th) and another in the last $(M^2/2 + 3M/2)$ coordinations (say ij-th), implying an infective is removed.

(II) the process changes by $(0,\cdots,1,\cdots,0;0,\cdots,1,\cdots,0)$ with one 1 in the first N coordinations (say k-th) and another in the last $(M^2/2+3M/2)$ coordinations (say ij-th), implying a susceptible becomes infected.

It is easily shown that the (I)-type jump occurs at rate $\beta\beta_k Z_{ij}^{(n)}(t)$ while the (II)-type jump occurs at rate $(\Gamma\Gamma_i j/i)Z_{ij}^{(n)}(t)$.

Hence, from the definition ([3] pp. 40) the scaled jump rate functions for Markov process (5) are

$$\begin{aligned} &r_{(0,\cdots,-1,\cdots,0;0,\cdots,-1,\cdots,0)}\big(\{q_k\}_{1\le k\le N};\{z_{ij}\}_{1\le i\le M,0\le j\le i}\big) \\ &\qquad = \beta\beta_k z_{ij} \end{aligned} \tag{6}$$

with the typical locations of two -1 as specified in (I), and

$$\begin{aligned} &r_{(0,\cdots,1,\cdots,0;0,\cdots,1,\cdots,0)}\big(\{q_k\}_{1\le k\le N};\{z_{ij}\}_{1\le i\le M,0\le j\le i}\big) \\ &\qquad = (\Gamma\Gamma_i j/i)z_{ij} \end{aligned} \tag{7}$$

with the typical locations of two 1 as specified in (II), where $\sum_{k=1}^{N}q_k = \sum_{i=1}^{M}\sum_{j=1}^{i}z_{ij}$ holds.

Using (6) and (7) we may define the drift function F by

$$\begin{aligned} & F\big(\{q_k\}_{1\le k\le N};\{z_{ij}\}_{1\le i\le M,0\le j\le i}\big) \\ = & \sum_l l r_l\big(\{q_k\}_{1\le k\le N};\{z_{ij}\}_{1\le i\le M,0\le j\le i}\big) \\ = & \Big(\Big\{\sum_{i=1}^{M}\sum_{j=0}^{i}\Big(\frac{\Gamma\Gamma_i j}{i}z_{ij}-\beta\beta_k z_{ij}\Big)\Big\}_{1\le k\le N}; \\ & \Big\{\Big(\frac{\Gamma\Gamma_i j}{i}-\sum_{k=1}^{N}\beta\beta_k\Big)z_{ij}\Big\}_{1\le i\le M,0\le j\le i}\Big), \end{aligned} \tag{8}$$

where the summation in the first equation is over all the possible transitions l.

Now let's define the deterministic vector function

$$v(t)=\big(\{q_k(t)\}_{1\le k\le N};\{z_{ij}(t)\}_{1\le i\le M,0\le j\le i}\big)$$

as the solution to the integral equation

$$v(t)=v(0)+\int_0^t F(v(s))\mathrm{d}s, \tag{9}$$

where the initial value is given by $v(0)=\big(\{b_k\}_{1\le k\le N};\{a_{ij}\}_{1\le i\le M,0\le j\le i}\big)$.

The following lemma is concerning the almost uniform convergence of the Markov process (5) defined in the beginning of this section.

Lemma 1. *Consider our SIR epidemic process spreading on G with initial values $X_n(0)=n$, $Y_n(0)=\mu n$ and (4). We have*

$$\lim_{n\to\infty}\sup_{s\le t}\Big\|\frac{V_n(s)}{n}-v(s)\Big\|=0$$

almost surely, where $\|\cdot\|$ is l^1 norm and $v(t)$ is the unique solution to (9).

Proof: We apply Theorem 5.2 [3] to show that the process V_n/n converges to the deterministic function $v(s)$.

By employing (8) and the fact that the domain of interesting satisfies

$$0\le\{q_{k,1}\}_{1\le k\le N},\{z_{ij,1}\}_{1\le i\le M,0\le j\le i}\le 1+\mu$$

and

$$0\le\{q_{k,2}\}_{1\le k\le N},\{z_{ij,2}\}_{1\le i\le M,0\le j\le i}\le 1+\mu,$$

we obtain

$$\begin{aligned} & \big\|F\big(\{q_{k,1}\}_{1\le k\le N},\{z_{ij,1}\}_{1\le i\le M,0\le j\le i}\big) \\ & -F\big(\{q_{k,2}\}_{1\le k\le N},\{z_{ij,2}\}_{1\le i\le M,0\le j\le i}\big)\big\| \\ \le & \ 2\Gamma(1+\mu)\sum_{i=1}^{M}\sum_{j=0}^{i}\sum_{k=1}^{N}\Big(\frac{\Gamma_i j}{i}+\beta\beta_k\Big) \\ & \cdot\big\|\big(\{q_{k,1}\}_{1\le k\le N},\{z_{ij,1}\}_{1\le i\le M,0\le j\le i}\big) \\ & -\big(\{q_{k,2}\}_{1\le k\le N},\{z_{ij,2}\}_{1\le i\le M,0\le j\le i}\big)\big\|. \end{aligned}$$

Note that $\big(\{Q_k^{(n)}(0)\}_{1\le k\le N};\{Z_{ij}^{(n)}(0)\}_{1\le i\le M,0\le j\le i}\big)=\big(\{b_k\}_{1\le k\le N};\{a_{ij}\}_{1\le i\le M,0\le j\le i}\big)=v(0)$, which completes the proof by Theorem 5.2 [3]. ∎

To prove the asymptotical normality of ML estimates $\hat\Gamma$ and $\hat\beta$ we need another lemma on the martingale central limit theorems, c.f. [1], [14].

Lemma 2. *Consider our SIR epidemic process spreading on G with initial values $X_n(0)=n$, $Y_n(0)=\mu n$ and (4). Define the normed score processes $W_1^{(n)}(s)=n^{-1/2}\partial l_s(\Gamma,\beta)/\partial\Gamma$ and $W_2^{(n)}(s)=n^{-1/2}\partial l_s(\Gamma,\beta)/\partial\beta$, evaluated at the true parameter values (Γ_0,β_0). Hence,*

$$W_1^{(n)}\xrightarrow{D}W_1\quad\textit{and}\quad W_2^{(n)}\xrightarrow{D}W_2,$$

as $n\to\infty$, where $\xrightarrow{D}$ represents convergence in distribution and W_1 and W_2 are Gaussian martingales. The variances of W_1 and W_2, denoted by w_1 and w_2 respectively, are given by

$$w_1(s)=\frac{1}{\Gamma_0}\int_0^s\sum_{i=1}^{M}\sum_{j=0}^{i}\frac{\Gamma_i j}{i}z_{ij}(t)\mathrm{d}t$$

and

$$w_2(s)=\frac{1}{\beta_0}\int_0^s\sum_{k=1}^{N}\beta_k q_k(t)\mathrm{d}t$$

respectively, where $\{q_k\}$ and $\{z_{ij}\}$ constitute the solution to the deterministic equation (9) defined above.

Proof: We will apply a martingale limit theorem (see [14] or Theorem II.5.1 [1]) to prove the lemma.

First, we have

$$W_1^{(n)}(s)=\frac{1}{\sqrt{n}}\int_0^s\frac{1}{\Gamma_0}\Big(\mathrm{d}I(t)-\sum_{v\in\mathcal{Y}_n(t)}\Big(\frac{\Gamma_0\Gamma_v}{d_v}\Big)|\mathcal{X}_n(t)\cap\mathcal{N}_v|\mathrm{d}t\Big)$$

and

$$W_2^{(n)}(s)=\frac{1}{\sqrt{n}}\int_0^s\frac{1}{\beta_0}\Big(\mathrm{d}R(t)-\beta_0\sum_{v\in\mathcal{Y}_n(t)}\beta_v\mathrm{d}t\Big),$$

as discussed in Section 2.

Therefore, by Lemma 1, the associated predictable variation processes $<W_1^{(n)}>(s)$ and $<W_2^{(n)}>(s)$ satisfy

$$\begin{aligned} <W_1^{(n)}>(s) &= \frac{1}{n\Gamma_0^2}\int_0^s\sum_{v\in\mathcal{Y}_n(t)}\Big(\frac{\Gamma_0\Gamma_v}{d_v}\Big)|\mathcal{X}_n(t)\cap\mathcal{N}_v|\mathrm{d}t \\ &\xrightarrow{P} \frac{1}{\Gamma_0}\int_0^s\sum_{i=1}^{M}\sum_{j=0}^{i}\frac{\Gamma_i j}{i}z_{ij}(t)\mathrm{d}t \end{aligned}$$

and

$$\begin{aligned} <W_2^{(n)}>(s) &= \frac{1}{n\beta_0^2}\int_0^s\beta_0\sum_{v\in\mathcal{Y}_n(t)}\beta_v\mathrm{d}t \\ &\xrightarrow{P} \frac{1}{\beta_0}\int_0^s\sum_{k=1}^{N}\beta_k q_k(t)\mathrm{d}t \end{aligned}$$

respectively, where $\xrightarrow{P}$ represents convergence in probability.

Moreover, there will be no jumps larger than $\epsilon>0$ for n large enough since the size of all jumps are $n^{-1/2}$ for the normed score processes. Then the martingale limit theorem in [14] guarantees $W_1^{(n)}\xrightarrow{D}W_1$ and $W_2^{(n)}\xrightarrow{D}W_2$, as $n\to\infty$.

Also, since $<W_1>(s)=[W_1](s)=(1/\Gamma_0)\int_0^s\sum_{i=1}^{M}\sum_{j=0}^{i}(\Gamma_i j/i)z_{ij}(t)\mathrm{d}t$ and $W_1(0)=0$, we have $w_1(s)=(1/\Gamma_0)\int_0^s\sum_{i=1}^{M}\sum_{j=0}^{i}(\Gamma_i j/i)z_{ij}(t)\mathrm{d}t$, where $[W_1]$ is the optional variation process corresponding

to W_1 (see e.g. [1]). w_2 can be derived similarly, which then concludes the proof of the lemma. ∎

Now we are at the stage to prove our main result. It can be viewed as an extension of results in [15] with uniform mixing in a homogeneous population.

Theorem 1. *The ML estimates $\hat{\Gamma}$ and $\hat{\beta}$ are asymptotically Gaussian with asymptotic means Γ_0 and β_0 (the true parameter values) respectively. The asymptotic variance for $\hat{\Gamma}$ is $1/nw_1(s)$ and for $\hat{\beta}$ is $1/nw_2(s)$. Consistent estimators of the standard errors of $\hat{\Gamma}$ and the parameter $\hat{\beta^{-1}} = 1/\hat{\beta}$ (note $1/\hat{\beta}\beta_v$ is the average length of the infectious period for individual v) are $s.e.(\hat{\Gamma}) = \hat{\Gamma}/\sqrt{I(s)}$ and $s.e.(\hat{\beta^{-1}}) = \hat{\beta^{-1}}/\sqrt{R(s)}$ respectively.*

Proof: Since $\hat{\Gamma}$ is the solution to the likelihood equation $\partial l_s(\Gamma,\beta)/\partial\Gamma = 0$, we may multiply the likelihood equation by $\hat{\Gamma}/\sqrt{n}$ to yield

$$\begin{aligned} 0 &= \frac{1}{\sqrt{n}}\Big(I(s) - \int_0^s \sum_{v\in\mathcal{Y}_n(t)} \frac{\hat{\Gamma}\Gamma_v}{d_v}|\mathcal{X}_n(t)\cap\mathcal{N}_v|\mathrm{d}t\Big) \\ &= \Gamma_0 W_1^{(n)}(s) \\ &\quad + \frac{1}{\sqrt{n}}(\Gamma_0 - \hat{\Gamma})\int_0^s \sum_{v\in\mathcal{Y}_n(t)} \frac{\Gamma_v}{d_v}|\mathcal{X}_n(t)\cap\mathcal{N}_v|\mathrm{d}t. \end{aligned}$$

Consequently, we get

$$\sqrt{n}(\hat{\Gamma}-\Gamma_0) = \frac{W_1^{(n)}(s)}{\Gamma_0^{-1}n^{-1}\int_0^s\sum_{v\in\mathcal{Y}_n(t)}(\Gamma_v/d_v)|\mathcal{X}_n(t)\cap\mathcal{N}_v|\mathrm{d}t}.$$

By Lemma 2, $W_1^{(n)}(s)$ converges to a Gaussian random variable with mean zero and variance $w_1(s)$. According to Lemma 1, we have

$$\frac{1}{n\Gamma_0}\int_0^s \sum_{v\in\mathcal{Y}_n(t)} \frac{\Gamma_v}{d_v}|\mathcal{X}_n(t)\cap\mathcal{N}_v|\mathrm{d}t \xrightarrow{P} w_1(s).$$

Hence, from Slutsky's theorem the estimate $\hat{\Gamma}$ is asymptotically normal with prescribed mean and variance. The asymptotic distribution for $\hat{\beta}$ can be proved similarly.

For the consistent standard error of $\hat{\Gamma}$, we have

$$\begin{aligned} s.e.(\hat{\Gamma}) &= \sqrt{\frac{\hat{\Gamma}}{n\int_0^s\sum_{v\in\mathcal{Y}_n(t)}(\Gamma_v/nd_v)|\mathcal{X}_n(t)\cap\mathcal{N}_v|\mathrm{d}t}} \\ &= \frac{\hat{\Gamma}}{\sqrt{I(s)}}. \end{aligned}$$

To derive the consistent estimate of standard error of $\hat{\beta^{-1}}$, we note from the likelihood function that

$$0 = \frac{1}{\sqrt{n}}\Big(\frac{R(s)}{\hat{\beta}} - \int_0^s \sum_{v\in\mathcal{Y}_n(t)} \beta_v\mathrm{d}t\Big).$$

Thus we have $W_2^{(n)}(s) = (R(s)/\sqrt{n})\big(1/\beta_0 - 1/\hat{\beta}\big)$. Rearrange the formula yields

$$\frac{1}{\beta_0} - \frac{1}{\hat{\beta}} = \frac{\sqrt{n}W_2^{(n)}(s)}{R(s)}.$$

Therefore, we obtain

$$\begin{aligned} s.e.(\hat{\beta^{-1}}) &= s.e.\Big(\frac{1}{\hat{\beta}}\Big) = \frac{1}{R(s)}\sqrt{\frac{\int_0^s\sum_{v\in\mathcal{Y}_n(t)}\beta_v\mathrm{d}t}{\hat{\beta}}} \\ &= \frac{1}{\hat{\beta}\sqrt{R(s)}} = \frac{\hat{\beta^{-1}}}{\sqrt{R(s)}} \end{aligned}$$

as desired. ∎

Remark 1. *We have used the node-oriented or sender perspective in our model formulation in Section 1. A distinct feature of this perspective is that an infective v makes contacts with a given neighbor according to a Poisson process with intensity $\Gamma\Gamma_v/d_v$, splitting the (total) constant infection rate $\Gamma\Gamma_v$ of v.*

A natural alternative is to use the edge-oriented or receiver perspective. In such case, a susceptible v gets infected because of its neighbor $u \in \mathcal{N}_v$ at the time points of a homogenous Poisson process with rate $\gamma\gamma_u$. Therefore, the infection rate of an individual u amounts to $\gamma\gamma_u d_u$. We note the ML estimate $\hat{\gamma}$ is the same as equation (2) with Γ_v replaced by γ_v and d_v replaced by 1. The asymptotical normality can be proved in parallel.

Remark 2. *In this paper we only considered inference for fully observed epidemics. However, it is often the case, that neither the infection nor the removal times are available and only the number of the individuals who contracted the disease out of the total size of the initial susceptible population is known (c.f. [3], [4]). Hence, the problem of partial observation is more demanding and is our future work.*

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