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# Stochastic SIR Model with Contact Tracing

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**Abstract**

This paper is about the study of a specific epidemic model accounting for the effect of contact tracing on the spread of an infectious disease. We consider the situation in which individuals identified as infected by the public health detection system may contribute to detecting other infections individuals by providing information related to persons with whom they have had possibly infectious contacts. The control strategy that consists examining each individual one has able to identify on the basis of the information collected within a certain period is expected to reinforce efficiently the standard random – screening based detection and slack considerably the epidemic. We consider modeling of the spread of a communicable infections disease, the population of interest evolves through demographic, infection and detection processes in a way that its temporal evolution is described by a stochastic Markov process. For adequate scaling of the demographic, infection and detection rates, it is shown to converge to the weak deterministic solution of a PDE system, as a parameter n interpreted as the population size which is large.
From the perspective of the analysis of infection disease data, this approximation result may serve a key tool for exploring the asymptotic properties of standard inference methods such as maximum likelihood estimation.

**Keywords:** Stochastic SIR model, contact – tracing, measure value markov process, large population approximation, central limit theorem.

**2000 Mathematics subject classification number :** 60G20

## Introduction:

In the area of public health practice, by contact – tracing one means the active detection mechanism that consists in asking individuals they have had possibly

infections contacts and the as the basics of the information provided in striving to find those persons in the scientific literature and in the health community within which they a generally considered as efficient guidance method for beginning the spread of sexually transmissible diseases under control. From the perspective public health guidance practice, mathematical modeling of epidemics in presence of a contact tracing strategy reinforcing a steering based detection system is a crucial stake, as it may help evaluating the impact of this costly control measure. In this frame work, epidemic models must naturally account for the fact that once detected, an infected person keeps on playing a role in the evolution of the epidemic for a certain time by helping towards identification of infectious individuals.

The main aim of this paper is to generalize the standard SIR model by incorporating a structure by age in the subpopulation of detected individuals, age being here the time since which a person has been identified as infected. At any time the 'R' class is described by a point measure, on which the contact – tracing detection rate is supposed to depend. In this manner the way an 'R' individual contribute to contact – tracing detection may be made strongly dependent on the time since her/his detection through a given weight function $\psi$ allowing for great flexibility in the modeling. Assuring in particular a large population in which the infections disease is spread properties of the mathematical model are thoroughly investigated and preliminary statistical questions are tackled.

In this paper we discuss about a Markov process with an age structured component is introduced for modeling the temporal evolution of an epidemic in the presence of contact – tracing. a short qualitative description is provided, aiming at giving a insight into how the dynamic is driven by a few key components. The process of interest is the solution of a stochastic differential equation (SDE) for which existence and uniqueness results are stated.

**The stochastic SIR Model with contact - tracing**

Epidemic problems really present a great challenge to probabilists and statisticians. Models for the spread of infections are based on hypothesis about such mechanisms as infection as detection. The huge diversity of possible hypothesis could give rise to an enormous variety of probabilities models with their specific features we shall deal with a stochastic epidemic model with reasonably simple structure, while covering some important aspects and keeping thus its pertinence from the perspective of practical applications.

The classical stochastic epidemic SIR is a well-studied model that, together with its generalizations, has been widely applied. At any time t, a population of size N is divided into three categories $S_i$ Susceptible, $I_i$ infectious and $R_i$ removed individuals. The model assumes that the population is homogeneously mixed. As time Passes, some infectives recover and go into the removed category. At the same time, infective make contact with susceptible so that $S_i$ decreases and $I_i$ increases A particular SIR model hypothesizes certain stochastic rates for these two processes. We add a third type of transition, Susceptibles are vaccinated and move directly to the removed class.

The stochastic Process ($S_i$, $I_i$) is a continuous time Markov chain. The states at time t are ($S_i$, $I_i$) = (Number of Susceptible, number of infectives). The initial state ($S_o$, $I_o$)

is (n, m). The rates of infection and recovery are

$(s,i) \rightarrow (s-1,i+1)$ *at rate* $\lambda si/N \quad \rightarrow (1)$

$(s,i) \rightarrow (s,i-1)$ *at rate* $i \rightarrow (2)$

Where N is the total population size $n+m$ . In addition $(s,i) \rightarrow (s-1,i)$ according to a related process which we give in detail as follows. When $(S_t, I_t) = (s,i)$ the total rate of stochastic evolution of the process is the sum of the rates in (1) and (2). Each infected person is ill for an exponentially distributed time with parameter which we take equal to 1, for notational convenience and then becomes immune and cannot have illness again. At time t, an infected person meets susceptible at a stochastic *rate* $\lambda S_t / N$ . At each such meeting time, a susceptible becomes infected, so that $S_t$ decreases by 1 and $I_t$ increases by 1. At the random transition times of the process $(S_t, I_t)$ authorities respond to the epidemic, Susceptible are vaccinated and leave the susceptible class at a rate $\theta$. The number $R_t$ of immune or recovered persons need not be modeled since $R_t = n+m-S_t-I_t$ . So over or later $I_t = 0$ for the first time or $S_t = 0$ . In either case the epidemic stops and the total epidemic size is the number of infections which have occurred, including the initial infectives.

**The Population Dynamics**

The Population is structured in to three classes corresponding to the different possible states with respect to the infective disease. We adopt the standard SIR terminology for denoting the current status of an individual with only differences that R stands here for the population of removed individuals willing to take part in the contact – tracing program and that it is structured according to the age of detection namely the time since a detected individual has been identified by the public health detection system as infected. Such a distinction allows for considering heterogeneity in the way earth R individual contributes to the contact tracing control. Hence at any time t ≥ O the class of removed individuals is described by $R_t(da) in M_P(R_+)$ the set of point measures on $R_+$ for all $O < a_1 < a_2 < \infty$, the quantity $R_t([a_1, a_2])$ represent the number of removed individuals who have been detected between $t-a_2$ *and* $t-a_1$ . Here and throughout we use the notation $\langle R, \psi \rangle = \int \psi(a) R(da), R$ being any positive measure on $R_+$ and $\psi$ any R-integrable functions In a more standard fashion, we shall denote by $S_t$ and $I_t$ the sizes of the classes of susceptible and infective individuals.

Individuals immigrate one at a time according to a poisson process of intensity $\lambda_o$ once in the population an individual becomes susceptible and may either leave the population without being contaminated or in dependently be infected. Emigrations occur in the population at time t ≥ O with the hazard rate $\mu_0$ $S_t$ and infections with the rate $\lambda_1(S_t, I_t)$ . Once infected an individual can be discovered by the detection system either by random screening or by contact – tracing or else emigrates / dies. The hazard

rates associated with these events are respectively $\lambda_2 I_t, \lambda_3\left(I_t, \langle R_t, \psi\rangle\right)$, Where $\psi : R_+ \to R_+$ is a bounded and measurable weight function that determines the contribution of a removed individual to the contact – tracing control according to the time a she / he has been detected and $\mu_1 I_t$ .

If detected an individual takes part in the contact – tracing system by providing useful information related to her/his (possibly) infectious contacts. we do not consider the emigration / death of detected individuals since it is the availability of the information that they have given rather than their presence in the system that plays a role in the contact – tracing process. In order to avoid possible misunderstanding due to the notation, we underline that $\lambda_1$ ( .,.) and $\lambda_3$ (.,.) here denote jump rate functions related to the SIR process and not the individual rates.

The events through which the sizes $S_t$, $I_t$ and the point measure $R_t$ evolve are numbered as follows.
Event E=O; recruitment of a susceptible.
Event E=1; death / emigration of a susceptible
Event E=2; Infection
Event E=3; Spontaneous detection of an infective
Event E=4; Detection of an infective by contact – tracing
Event E=5; death / emigration of an infection

**Definition 1**

Consider a probability space $(\Omega, F, P)$ , on which are defined

(1) a random vector $(S_0, I_0)$ with values in $\left(N^*\right)^2$ such that $E[S_0 + I_0] < +\infty$ (at t= O, we assume that no one has been detected yet),

(2) two *independent Poisson point measures on* $R_+^2, Q^s(dv,du)$ *and* $Q^1(dv,du)$ *with intensity* $dv \otimes du$ ,

the Lebesgue measure on $R_+^2$ , and independent from the initial conditions $(S_o, I_o)$.

Define $\left\{\left(S_t, I_t, R_t(da)\right)\right\}_{t\geq 0}$ as the Markov process solution of the following system of $SDE_s$;

$$S_t = S_0 + \int_{v=0}^{t}\int_{u=0}^{\infty}\left(1_{0\leq u\leq \lambda_0} - 1_{\lambda_0 < u\leq \lambda_0 + \mu_0 S_{v-} + \lambda_1\left(S_{v-}, I_{v-}\right)}\right) Q^s(dv,du)$$

$$I_t = I_0 + \int_{v=0}^{t}\int_{u=0}^{\infty} 1_{\lambda_0 < u\leq \lambda_0 + \lambda_1\left(I_{v-}, S_{v-}\right)} Q^s(dv,du)$$

$$- \int_{v=0}^{t}\int_{u=0}^{\infty} 1_{0\leq u\leq (\mu_1+\lambda_2) I_{v-} + \lambda_3\left(I_{v-}, (R_{v-}, \psi)\right)} Q^I(dv,du)$$

$$\langle R_t, f\rangle = \int_{v=0}^{t}\int_{u=0}^{\infty} f(0) 1_{0\leq u\leq \lambda_2 I_{v-} + \lambda_3\left(I_{v-}, \langle R_{v-}, \psi\rangle\right)} Q^i(dv,du) + \int_{v=0}^{t}\int_{u=0}^{\infty} \partial_a f(a) R_v(da)\, dv \quad \to (3)$$

for all $f \in C_b^1(R_+)$ the set of real bounded functions of class $C^1$ with bounded derivatives. We have denoted by $\partial_a f$ the gradient of $f$ *and by* $g(t-)$ the left limit in

t $\epsilon$ R of any cadlag functions g:R $\rightarrow$ R.
Under H 1 and of definition given above it may be seen that there exists a unique strong solution to SDE (3).
Where H1 is defined as follows.

**Assumptive H1:**
The rate functions $\lambda_1$ and $\lambda_3$ are assumed to being to $C^1$ ($R_+^2$), the set of real functions of class $C^1$ and $R_+^2$. We denote by $\partial_s \lambda_1$, $\partial_I \lambda_1, \partial_1\lambda_3$ and $\partial_R \lambda_3$, their partial derivatives. We also suppose that all these functions are locally lispchitz continuous and dominated by the mapping $\left(x,x^{'}\right)\in R_+^2 \rightarrow xx^{'}$ for K $\epsilon$ {1,3}, we assume that for every N > O, $\exists$ $L_k$ (N) > O such that
$\forall \left(x,x^{'}\right),\left(y,y^{'}\right)\in[0,\mathrm{N}]^2 ,\left|\lambda_k\left(x,x^{'}\right)-\lambda_k\left(y,y^{'}\right)\right|\le L_k\left(N\right)\left(\left|x-y\right|+\left|x^{'}-y^{'}\right|\right)$
and that $\exists\bar{\lambda}_k>0,\forall\left(x,x^{'}\right)\in R_+^2,\lambda_k\left(x,x^{'}\right)\le\bar{\lambda}_k xx^{'}$ . Finally the weight function $\psi$ is assumed measurable and bounded.

**Limiting behavior in long time assumptions**
**Proposition 1**
Assume that $f\left(a\right)\rightarrow 0$ as $a\rightarrow\infty$ considering the Markov process $\left\{\left(S_t,I_t,R_t\left(da\right)\right)\right\}_{t\ge0}$ introduced in definition 1, we have, whatever the initial conditions $\left(S_0,I_0\right)\in\left(N^*\right)^2$ , that $\left(S_t,I_t,\left\langle R_t\left(da\right),f\right\rangle\right)\rightarrow\left(S_\infty,0,0\right)$ in distribution as t $\rightarrow \infty$, denoting by $S_\infty$ a poisson random variable of Parameter $\lambda_o / \mu_o$.
The law of $S_\infty$ is the stationary distribution of the N – valued immigration and death process which jumps from k to k + 1 with rate $\lambda_o$ and from k to k-1 with rate $\mu_o$k. This result show that the time of extinctions of the epidemic is almost surely finite.
In the situation of long-lasting epidemics as in the HIV case, the long term behavior of the epidemic conditioned upon its non extinction may be refined by studying quasi-stationary measures.

**Renormalization:**
We consider a sequence $\left(\left\{(S_t^{(n)},I_t^{(n)},R_t^{(n)}\left(da\right))\right\}_{t\ge0},n\in N^*\right)$ , of SIR processes with contact – tracing. For n ≥ 1, $\left\{\left(S_t^{(n)},I_t^{(n)},R_t^{(n)}\left(da\right)\right)\right\}_{t\ge0}$ corresponds to the stochastic process described in Definition 1, starting from ($S_o^{(n)}$, $I_o^{(n)}$) of size proportional to n and with following rate modifications, the immigration rate is n $\lambda_o$, the infection jump rate function is n $\lambda_1$ ($S^{(n)}$/n, $I^{(n)}$/n), while the contact – tracing jump rate function is $n\lambda_3\left(I^{(n)}/n,\left\langle R^{(n)},\psi\right\rangle/n\right)$. We denote the $\left(s_t^{(n)},i_t^{(n)},r_t^{(n)}\left(da\right)\right)=\left(S_t^{(n)},I_t^{(n)},\mathrm{R}_t^{(n)}\left(da\right)/n\right)$ the randomized process obtained by re-weighting all individuals of the population by

1/n. We assume further that $\left(s_0^{(n)}, i_0^{(n)}\right)$ converges in probability to a deterministic couple $\left(s_0, i_0\right) \in R_+^{*2}$ *as* $n \to \infty$

Let $P > 2$

Moment assumption $M_p : \sup_{n \in N^*} E\left[\left(s_0^{(n)}\right)^P + \left(i_0^{(n)}\right)^P\right] < +\infty$ .

This moment assumption combined with Assumption H1 implies that the moments of order $\rho$ propagate on compact time intervals [o, T] with T > O. the renormalization given above is interpreted in the following example.

In the case of homogeneous rate functions, the eventual impact of the renormalization on the jump rates may be described as follows.

with $\lambda_0^{(n)} = n\lambda_0$ , the immigration / birth rate is assume to the initial population size.

If the form chosen for $\lambda_1\left(S, I\right)$ is either $\lambda_1 I$ *or* $\lambda_1 SI / \left(I + S\right)$ the renormalized infection rate function $\lambda_1 I^{(n)}$ *or* $\lambda_1 S^{(n)} I^{(n)} / \left(I^{(n)} + S^{(n)}\right)$ is not affected by the scaling, while of one takes $\lambda_1\left(S, I\right) = \lambda_1 SI$ the renormalized rate function $\lambda_1 S^{(n)} I^{(n)} / n$ decreases proportionately to 1/n. This reflects the fault that for large scaling the risk of being contaminated by a given infections individual is smaller that for small scaling.

The same remark holds for the contact – tracing rate function $\lambda_3\left(I, \langle R, \psi \rangle\right)$ .

**Proposition : 2**

Let $n \in N^*, t \geq 0$ *and* $f : (a,u) \to f_u(a)$ *a function in* $C_b^1\left(R_+^2\right)$. *Under H 1and the mome nt condition* $M_p$ *with* $P > 2$,

$$\begin{pmatrix} M_t^{s,(n)} \\ M_t^{i,(n)} \\ M_t^{r,(n)}(f) \end{pmatrix} = \begin{pmatrix} S_t^{(n)} - S_0^{(n)} - \lambda_0 t + \int_{u=0}^{t} \left\{\mu_0 S_u^{(n)} + \lambda_1\left(S_u^{(n)}, i_u^{(n)}\right)\right\} du \\ i_t^{(n)} - i_0^{(n)} - \int_{u=0}^{t} \left\{\lambda_1\left(S_u^{(n)}, i_u^{(n)}\right) - \left(\mu_1 + \lambda_2\right) i_u^{(n)} - \lambda_3\left(i_u^{(n)}, \langle r_u^{(n)}, \psi \rangle\right)\right\} du \\ \langle r_t^{(n)}, f_t \rangle - \int_{u=0}^{t} \left\{\langle r_u^n, \partial_a f_u + \partial_u f_u \rangle + f_u(0)\left(\lambda_2 i_u^{(n)} + \lambda_3\left(i_u^{(n)}, \langle r_u^{(n)}, \psi \rangle\right)\right)\right\} du \end{pmatrix}$$

is a cod lag $L^2$ – martingale, with predictable quadratic variation given by

$$\left\langle M^{s,(n)} \right\rangle_t = (1/n) \int_{u=0}^{t} \left\{\lambda_0 + \left\{\mu_0 s_u^{(n)} + \lambda_1\left(s_u^{(n)}, i_u^{(n)}\right)\right\}\right\} du$$

$$\left\langle M^{i,(n)} \right\rangle_t = (1/n) \int_{u=0}^{t} \left\{\lambda_1\left(s_u^{(n)}, i_u^{(n)}\right) + \left(\mu_1 + \lambda_2\right) i_u^{(n)} + \lambda_3\left(i_u^{(n)}, \langle r_u^{(n)}, \psi \rangle\right)\right\} du$$

$$\left\langle M^{r,(n)}(f) \right\rangle_t = (1/n) \int_{u=0}^{t} f_u^2(0)\left\{\lambda_2 i_u^{(n)} + \lambda_3\left(i_u^{(n)}, \langle r_u^{(n)}, \psi \rangle\right)\right\} du$$

$$\left\langle M^{s,(n)}, \mathrm{M}^{i,(n)} \right\rangle_t = -(1/n)\int_{u=0}^{t} \lambda_1\left(s_u^{(n)}, I_u^{(n)}\right) du, \quad \left\langle M^{s,(n)}, M^{r,(n)}(f) \right\rangle_t = 0$$

$$\left\langle M^{i,(n)}, M^{r,(n)}(f) \right\rangle_t = -(1/n)\int_{u=0}^{t} f_u(0)\left\{\lambda_2 i_u^{(n)} + \lambda_3\left(i_u^{(n)}, \left\langle r_u^{(n)}, \psi \right\rangle\right)\right\} du$$

This result follows from the representation given in Definition:1

**Conclusion:**

Since the quadratic variation of the martingale process displayed above is of order 1/n, results in a deterministic limit by letting n tend to infinity.

Consider the system of deterministic evolution equation obtained by equating to zero the martingale process in proposition 2

$$s_t = s_0 + \int_{u=0}^{t} \left(\lambda_0 - \mu_0 s_u - \lambda_1(s_u, i_u)\right) du$$

$$i_t = i_0 + \int_{u=0}^{t} \left(\lambda_1(s_u, i_u) - (\mu_1 + \lambda_2) i_u - \lambda_3\left(i_u, \langle r_u, \psi \rangle\right)\right) du$$

$$\langle r_t, f_t \rangle = \int_{u=0}^{t} \left\{ \int_{a=0}^{\infty} \left(\partial_u f(a,u) + \partial_a f(a,u)\right) r_u(da) + f(0,u)\left(\lambda_2 i_u + \lambda_3\left(i_u, \langle r_u, \psi \rangle\right)\right)\right\}$$

for all $f \in C_b^1\left(R_+^2\right)$ . There exist a unique solution to this deterministic system, to which the sequence.

$\left\{\left(s^{(n)}, i^{(n)}, r^{(n)}\left(da\right)\right)\right\}_{n\geq 1}$ converges in probability .

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