Journal of Theoretical Biology 384 (2015) 33–49

Contents lists available at ScienceDirect

Journal of Theoretical Biology

journal homepage: www.elsevier.com/locate/yjtbi

Modeling contact tracing in outbreaks with application to Ebola

Cameron Browne [a,*], Hayriye Gulbudak [b,c], Glenn Webb [a]

[a] Department of Mathematics, Vanderbilt University, United States
[b] School of Biology, Georgia Institute of Technology, United States
[c] School of Mathematics, Georgia Institute of Technology, United States

HIGHLIGHTS

- We develop a novel mechanistic *SEIR*-type model of contact tracing in Ebola outbreaks.
- We consider effect of variable tracing protocols on effective reproduction number, $\mathcal{R}_e$.
- We formulate $\mathcal{R}_e$ completely in terms of tracing and reported case observables.
- Tracing and case data from West Africa are utilized for weekly estimates of $\mathcal{R}_e$.
- Analysis and simulations quantify impact of contact tracing on the epidemic.

ARTICLE INFO

Article history:
Received 14 May 2015
Received in revised form
29 June 2015
Accepted 7 August 2015
Available online 18 August 2015

Keywords:
Mathematical modeling
Epidemiology
Contact tracing
Ebola

ABSTRACT

Contact tracing is an important control strategy for containing Ebola epidemics. From a modeling perspective, explicitly incorporating contact tracing with disease dynamics presents challenges, and population level effects of contact tracing are difficult to determine. In this work, we formulate and analyze a mechanistic SEIR type outbreak model which considers the key features of contact tracing, and we characterize the impact of contact tracing on the effective reproduction number, $\mathcal{R}_e$, of Ebola. In particular, we determine how relevant epidemiological properties such as incubation period, infectious period and case reporting, along with varying monitoring protocols, affect the efficacy of contact tracing. In the special cases of either perfect monitoring of traced cases or perfect reporting of all cases, we derive simple formulae for the critical proportion of contacts that need to be traced in order to bring the effective reproduction number $\mathcal{R}_e$ below one. Also, in either case, we show that $\mathcal{R}_e$ can be expressed completely in terms of *observable reported case/tracing quantities*, namely $\mathcal{R}_e = k((1-q)/q)+k_m$ where k is the number of secondary traced infected contacts per primary *untraced* reported case, k_m is the number of secondary traced infected contacts per primary *traced* reported case and $(1-q)/q$ is the odds that a reported case is not a traced contact. These formulae quantify contact tracing as both an intervention strategy that impacts disease spread and a probe into the current epidemic status at the population level. Data from the West Africa Ebola outbreak is utilized to form real-time estimates of $\mathcal{R}_e$, and inform our projections of the impact of contact tracing, and other control measures, on the epidemic trajectory.

1. Introduction

Contact tracing has recently gained public attention because of its importance as a control strategy in the 2014–2015 Ebola outbreaks. Contact tracing is a potentially powerful disease control strategy in which the close contacts of reported/isolated cases are traced and monitored so that if they become symptomatic they can be efficiently isolated and, in turn, cause reduced transmissions. There are numerous studies about contact tracing (also known as active case finding) over the past two decades. However, from a theoretical point of view, explicit modeling of the contact tracing process has been challenging due to the complexities in reconciling forward dynamics of an epidemic with the action of tracers working through a transmission chain, along with accounting for particular disease characteristics and public health capabilities. Thus, the formulation of mechanistic models of contact tracing which are analytically tractable and epidemiologically relevant is an important problem in epidemiology.

Because Ebola is typically transmitted through direct contact with bodily fluids of a symptomatic individual and the incubation period is relatively long (average around 11 days), contacts that have been exposed to Ebola virus can be identified, monitored, and, when symptomatic, be isolated to limit spread (WHO Ebola Response Team, 2014; Fraser et al., 2004). Previous outbreaks have been rapidly controlled with contact tracing and isolation, along

* Corresponding author.
E-mail address: cambrowne@louisiana.edu (C. Browne).

http://dx.doi.org/10.1016/j.jtbi.2015.08.004
0022-5193/

with limiting hospital and funeral transmission (Faye et al., 2015). However, the failure of initial containment and the subsequent unprecedented scale of the West Africa Ebola outbreak in 2014–2015 have challenged public health authorities to employ effective control measures. As of June 2015, there have been over 27,000 reported cases in the outbreak, however the incidence has decreased markedly over the past six months due to enhanced control efforts (WHO Ebola Response Team et al., 2015). Therefore it is vital to evaluate how different interventions, such as contact tracing, have affected the epidemic and can bring the outbreak to an end. Direct measurement of the impact of contact tracing on an outbreak has recently been considered in relation to tuberculosis (Guzzetta et al., 2015), but a general modeling framework for measuring the population-level effect of contact tracing with epidemic data is needed for Ebola and other emerging pathogens.

Previous works about contact tracing have used a range of modeling methods from individual based models on specific networks to compartmental ordinary differential equations at the population level. While networks are a natural setting for contact tracing (Kiss et al., 2005), their connection with traditional epidemic compartmental models (through a mean-field approximation) should be emphasized. Therefore it is desirable to have a modeling framework which can work in both settings with sufficient detail, mechanism and simplicity. Also, branching process models (Ball et al., 2011; Müller et al., 2000; Klinkenberg et al., 2006) have been utilized for explicit contact tracing structure, but lack both the simplicity and compartmental details inherent in the differential equation model we formulate in this paper. Many differential equation models have incorporated contact tracing implicitly (Rivers et al., 2014; Mubayi et al., 2010), though Hyman et al. (2003) considered as a deterministic model with explicit contact tracing for HIV, a different setting than an emerging outbreak such as Ebola. Mathematical modeling of Ebola has been considered by many authors, (e.g. Althaus, 2014; WHO Ebola Response Team, 2014; Chowell and Nishiura, 2014; Chowell et al., 2015; Camacho et al., 2015; Chowell et al., 2004; Chowell, 2014; Fisman et al., 2014; Merler et al., 2015; Kiskowski, 2014; Kupferschmidt, 2014; Legrand et al., 2007; Towers et al., 2014; Weitz and Dushoff, 2015), and several of Ebola modeling studies have implicitly incorporated effects of contact tracing (along with other interventions) (Rivers et al., 2014; Pandey et al., 2014; Chowell et al., 2015, 2004; Webb et al., 2015). However implicit inclusion of contact tracing fails to capture the true effect of tracing on the effective reproduction number $\mathcal{R}_e$, a key quantity of interest for epidemiologists.

In this work, we develop a deterministic outbreak model of contact tracing particularly applicable to Ebola epidemics, which explicitly links tracing back to transmissions, and incorporates disease traits and control together with monitoring protocols. We calculate the effective reproduction number, $\mathcal{R}_e$, and simulate the model under different control scenarios. In particular, we perform sensitivity analysis to determine how disease characteristics, variable monitoring protocols, case reporting and timing of intervention affect the efficacy of contact tracing in controlling the epidemic. In the special case where either traced contacts are always prevented from causing further infections (perfect monitoring) or 100% of cases are reported (perfect reporting), we derive simple formulae for the critical proportion of contacts that need to be traced in order to bring $\mathcal{R}_e$ below one.

Furthermore, from the explicit linking of tracing and transmission in our model, we derive novel formulae directly relating the effective reproduction number $\mathcal{R}_e$ to contact tracing observables. Indeed, define k as the average number of secondary infected contacts traced per primary reported *untraced* case, and q as the fraction of reported cases which are traced contacts. Then, in the case of *perfect monitoring* of traced contacts and the general setting of unknown underreporting with distinct reported/unreported case infectious periods, we show that the following formula holds

$$\mathcal{R}_e = k\left(\frac{1-q}{q}\right)$$

Thus, $\mathcal{R}_e$ is simply the product of the average number of secondary infected traced contacts per untraced reported case and the odds that a reported case is not a traced contact. If contact monitoring is *imperfect*, but case reporting is assumed to be perfect (100% of cases reported), then $\mathcal{R}_e$ can also be expressed simply in terms of contact tracing observables. In this instance, define k_m as the average number of secondary infected contacts traced per primary reported *traced* case, then:

$$\mathcal{R}_e = k\left(\frac{1-q}{q}\right) + k_m$$

Utilizing current data and this formula, we form weekly estimates of $\mathcal{R}_e$ for the Ebola outbreaks in Sierra Leone and Guinea, with the main goal of determining the impact of contact tracing on the epidemics. Taken together, our model and results quantify contact tracing as both a dynamic intervention strategy impacting disease spread and a probe into the current epidemic status at the population level.

2. Model and methods

2.1. Base SEIR model

We begin with an SEIR-type base model consisting of compartments representing susceptible (S), exposed or incubating (E), and two distinct infectious groups, namely infectious individuals which will be hospitalized/reported (I_h) and infectious individuals which will not be hospitalized and unreported (I_u), along with the decoupled compartment of cumulative hospitalized/reported cases (H). The following differential equation system models the dynamics of these populations:

$$\begin{aligned}
S'(t) &= -\beta S(t)(I_h(t)+I_u(t))\\
E'(t) &= \beta S(t)(I_h(t)+I_u(t)) - \frac{1}{\tau}E(t)\\
I_h'(t) &= \rho\frac{1}{\tau}E(t) - \frac{1}{T_h}I_h(t)\\
I_u'(t) &= (1-\rho)\frac{1}{\tau}E(t) - \frac{1}{T_u}I_u(t)\\
H'(t) &= \frac{1}{T_h}I_h(t)
\end{aligned} \tag{1}$$

The parameter β represents transmission rate for infectious individuals, τ is mean incubation period, ρ is fraction of hospitalized cases, T_h is time from infectiousness (symptom) onset until hospitalization/isolation and reporting, and T_u is the mean infectious period for an unhospitalized case. Note that we consider an infectious case being hospitalized, isolated and reported as the same, whether or not the individual is treated in a hospital or placed in an isolation unit. We assume that such a case is reported at the time of hospitalization and neglect any possibility of hospital transmission. While transmission in a health-care setting poses significant risk to workers and visitors during Ebola outbreak, community transmission accounts for the vast majority of cases. In addition, the main focus of our paper is a detailed model of contact tracing, so we elect to make the model simpler by not including hospital transmission. For this reason, we also neglect another route of transmission particular to Ebola; post-death transmission due to improperly handled deceased (Weitz and Dushoff, 2015), and leave incorporation of these features into contact tracing models for future work.

The distinction between reported cases and unreported cases is important when considering contact tracing since only reported cases can trigger contact tracing. We explicitly separate infectious