MATHEMATICAL BIOSCIENCES
AND ENGINEERING
Volume **15**, Number **5**, October **2018**

doi:10.3934/mbe.2018053

pp. **1165–1180**

QUANTIFYING THE IMPACT OF EARLY–STAGE CONTACT TRACING ON CONTROLLING EBOLA DIFFUSION

Narges Montazeri Shahtori, Tanvir Ferdousi
Caterina Scoglio* and Faryad Darabi Sahneh

Department of Electrical and Computer Engineering
Kansas State University, Manhattan, KS 66506, USA

(Communicated by Dobromir T. Dimitrov)

Abstract. Recent experience of the Ebola outbreak in 2014 highlighted the importance of immediate response measure to impede transmission in the early stage. To this aim, efficient and effective allocation of limited resources is crucial. Among the standard interventions is the practice of following up with the recent physical contacts of the infected individuals — known as contact tracing. In an effort to understand the effects of contact tracing protocols objectively, we explicitly develop a model of Ebola transmission incorporating contact tracing. Our modeling framework is individual–based, patient–centric, stochastic and parameterizable to suit early–stage Ebola transmission. Notably, we propose an activity driven network approach to contact tracing, and estimate the basic reproductive ratio of the epidemic growth in different scenarios. Exhaustive simulation experiments suggest that early contact tracing paired with rapid hospitalization can effectively impede the epidemic growth. Resource allocation needs to be carefully planned to enable early detection of the contacts and rapid hospitalization of the infected people.

1. **Introduction.** Contact tracing is a mitigation strategy that aims at immediately detecting, testing, and treating the next-generation cases during the spreading of an infectious disease. Such local targeted control measure is very effective when the number of cases is limited, for example at the early stage of an outbreak. In 2014, West Africa experienced the most widespread Ebola epidemic in the history with more than 28,000 reported cases. Secondary infections were reported in several European countries and the United States. The Ebola virus is transmitted via physical contact with the infected individuals or their body fluids; the infected ones can transmit the virus to their contacts after becoming symptomatic [4]. In the case of the Ebola epidemic, the objective of contact tracing is to identify and monitor the individuals who have been exposed to the infectious ones for 21 days [27]. This procedure allows for a prompt isolation of the contacts of an infectious individual as soon as he/she becomes symptomatic. Contact tracing has shown effectiveness in several cases. In 2014, there was an Ebola virus disease (EVD) outbreak in Nigeria due to a traveler who returned from Liberia. An extensive contact tracing effort

2010 *Mathematics Subject Classification.* Primary: 92B05, 68U20; Secondary: 65C20.

Key words and phrases. Contact tracing, Ebola, compartmental model, activity-driven network, epidemic model.

This article is based on work supported by the National Science Foundation grants SCH-1513639 and CIF-1423411.

* Corresponding author: Caterina Scoglio.

took place starting from day 3 and a total of 894 contacts were traced, all linked to the single index case [21]. Compared to other regions of West Africa, the outbreak of Nigeria was better contained with only 19 confirmed and 1 probable EVD cases out of which 8 died. The improved outcomes can be attributed to the early detection of the index case and effective isolation of infectious individuals due to contact tracing [6]. In September 2014, a person in Dallas - TX, returning from Liberia, was diagnosed with EVD. All of his contacts were traced and monitored for 21 days. Two healthcare workers who provided care for the index case were also diagnosed positive and one of them took a round trip to Cleveland, OH before detection. This prompted the Centers for Disease Control and Prevention (CDC) to trace all the passengers of the two flights. Another case was detected when a person returned to New York from Guinea in October 2014 and contacts of that individual were traced as well. A total of 458 contacts were traced in Texas, Ohio, and New York [26]. Contact tracing was an appropriate approach to stop the transmission of Ebola in the USA as the number of cases reported was quite small [5]. In this paper, we attempt to quantify the effect of contact tracing such early stages of the epidemic.

In general, contact tracing can be carried out using different protocols, depending on the characteristics of the pathogen transmission. Definition of contact, duration and frequency of monitoring, are some examples of variables to consider while implementing contact tracing. Additionally, delays in implementing the contact tracing process are possible in realistic scenarios. Predicting the effectiveness of contact tracing as a function of the disease characteristics, disease stage, and protocol characteristics is a challenging task. Eames and Keeling have proposed a formula to correlate the effectiveness of contact tracing and the basic reproductive ratio by using detailed pairwise equations for a susceptible-infected-removed (SIR) model [5]. The basic reproductive ratio, R_0, is a key indicator in epidemiology and represents the expected number of secondary infections over all possible initial infections during their infectious period [8][3]. This ratio is a crucial tool for a quantitative measurement of the severity of a disease outbreak and helps the public health authorities to evaluate the risk of an outbreak in the emergence of an infectious disease.

Klinkenberg et al., evaluated the impact of time-related characteristics of the infection and the tracing process on the success of contact tracing [11]. They showed why contact tracing is effective for control of smallpox and SARS, only partially effective for foot-and-mouth disease and likely not effective for influenza [11]. The impact of contact pattern on the efficacy of contact tracing has also been studied. Researchers have concluded that not only the disease properties but also the contact network properties are crucial for the success of contact tracing. For example, Eames and Keeling indicated that contact tracing effectiveness increases with network clustering [5]. Kiss et al., showed that contact tracing is typically ineffective for random contact networks with high average node degrees and small clustering coefficients [10].

Researchers have also attempted to analyze the impact of intervention strategies on the recent Ebola epidemic using mean–field compartmental models, which can be either stochastic or deterministic in nature. Browne et al., used a deterministic version of the compartment models and separated the infected individuals into different compartments based on whether they are hospitalized or unreported.

They evaluated the impact of relevant epidemiological properties of Ebola on contact tracing efficiency and presented a formula to determine the minimum number of contacts to be traced per identified infectious individual in order to bring down the effective reproductive ratio below one [1]. In [16], Rizzo et al., adopted a susceptible–exposed–infected–removed (SEIR) compartmental model with additional compartments for hospitalized and dead people who had traditional funerals. Then, they adopted activity driven networks (ADN), where each individual has a network of contacts which depends on an activity potential and vary with time. ADN describes contact processes that evolve over time-varying networks [14]. The analysis of Rizzo et al., showed that contact tracing and other intervention policies adopted later in the West Africa would have drastically mitigated the epidemic spreading if used promptly.

Despite being a relatively new area of research, there have been several works involving ADNs. Starnini et al., used ADNs to study temporal percolation properties and showed how SIR models can be mapped to the percolation problem [22]. In another work, they explored the relation between network topology and activity potential distribution to obtain analytical expressions for several topological properties of the integrated social networks [23]. Mata et al., studied a power law distribution of activity potentials and found very slow relaxation dynamics and aging in random walks [13]. Sun et al., investigated ADNs with Markovian and non-Markovian dynamics and found that memory slows down the spreading process in SIR model and boosts the spreading process in SIS models [24]. Perra et al., experimented random walks in time-varying networks and found that results vary significantly. They concluded that the network dynamics should be considered to avoid misleading results in practical situations [15].

For a realistic study of contact tracing effectiveness in the early-stage of an Ebola outbreak, stochastic and individual-level models are needed. When considering a small number of cases, the localized and highly-structured contacts of infected individuals prominently influence the numbers, the timings, and the locations of the future cases. In this scenario, the accuracy of meta-population models, characterized by high levels of aggregation, dramatically deteriorates. The challenge is that successful modeling approaches to evaluate the effectiveness of contact tracing need to take into account the highly structured network of contacts and data on the network of contacts is often not available or too large. The real world networks are not static. The set of people with whom a person remain in contact changes with time. Temporal networks can incorporate these changes and accurately represent real behaviors in human populations. Agent-based models are accurate but computationally expensive. However, ADNs provide a tractable way to produce accurate results [18]. Our work focuses on the microscopic processes that occur at the beginning of an Ebola outbreak. We use ADNs to capture the contact dynamics using a constant underlying stochastic process. We also estimate the basic reproductive number of the disease spread in different scenarios.

In this paper, we evaluate the effectiveness of contact tracing using a novel modeling framework. Our modeling framework has several features to characterize early–stage Ebola transmission: 1) the network model is patient–centric because when the number of infected cases is small, only the myopic networks of infected individuals matter and rest of the possible social contacts are irrelevant, 2) the Ebola disease model is individual–based and stochastic because during the early stages

of a spreading process, the random fluctuations are significant and should be captured appropriately, 3) the contact tracing model is parameterizable to incorporate different critical aspects of the contact tracing protocols.

Our model is built on susceptible–exposed–infected–hospitalized–removed compartments ($SEIHR$), where susceptible, exposed and infected individuals may become monitored–susceptible, monitored–exposed, and monitored–infected respectively as a consequence of contact tracing. We propose an activity driven network approach to consider the inherent time–varying nature of the contagion process in a host population, in the form of variations in connectivity pattern of contacts. Activity driven networks are characterized by an activity firing rate assigned to each node at each time step, so that a fraction of the nodes create new links with others and the contagion process develops over those new paths. This is a general model for evaluating contact tracing, intertwined within the transmission model, which can be applied to a wide variety of diseases beyond the specific case of Ebola. Using this modeling framework, we perform extensive simulations varying important delays: identification delay (local), starting delay (global), and hospitalization delay. Through simulations, we quantify the effectiveness of contact tracing and compute R_0.

The remainder of this paper is organized as follows. In section 2, we propose a compartmental model for Ebola transmission incorporating contact tracing, discuss an overview of activity driven network (ADN) and explain it based on the proposed compartmental model. Section 3 presents a method to compute the basic reproductive number in a heterogeneous network. In section 4, we define true positive and false positive ratios based on the proposed model to plot the receiver operating characteristic (ROC) curve. Section 5 summarizes the main results of this article and section 6 contains the concluding remarks.

2. Mathematical modeling of Ebola disease spreading incorporating contact tracing.

Spreading of an infectious disease is a complex event with many interacting variables. One of the primary tools to analyze and predict the disease diffusion as well as the severity of infectious disease is the compartmental model. Compartmental models are the mathematical frameworks that can capture some major features of epidemic spreading such as pathogen transmission probabilities and host transition rates from one state to another [2]. In this work, we employ a discrete–time expression of the susceptible, exposed, infected, hospitalized and removed ($SEIHR$) compartmental model. Such model is compatible with the epidemiology of Ebola.

2.1. Compartmental model.

$SEIHR$ model is an extension of susceptible, exposed, infected and removed ($SEIR$) model [9] with an additional compartment H, where H stands for hospitalized. Each compartment variable denotes a fraction of individuals who belong to one of the following states: susceptible (S), exposed (E), infected (I), hospitalized (H) or removed (R). An individual can undergo transitions from one state to another during the disease evolution. To evaluate the impact of contact tracing for the detection of new Ebola patients, we add three more compartments: traced–susceptible (S_T), traced–exposed (E_T) and traced–infected (I_T) to the ($SEIHR$) model. We follow the contact tracing implementation guideline published by the World Health Organization (WHO) and the Centers for Disease Control and Prevention (CDC). In the guideline it is mentioned that when an infectious individual enters a hospital and his/her laboratory results come out positive,

any person who had contact with him/her in the last 21 days should be traced [27]. Therefore, in our proposed model, whenever an infectious individual enters the hospitalized (H) state, all the individuals exposed to the infected one will be identified and followed up for 21 days.

We classify transitions between different epidemiological compartments of the proposed model into two groups: node–based transition and edge–based transition. In a node–based transition, a node moves from one state to another individually and the transition does not depend on the states of the node's neighbors. Contrary to the nodal transition, the edge–based transition is dependent on the states of a node's neighbors. Based on these definitions, we describe the transition processes of our proposed model as follows:

- Edge–based transition: When a susceptible individual has contact with an infectious or hospitalized one, he/she moves to exposed state with probability β. The probability is multiplied if there are multiple infected or hospitalized individuals in contact.
- Node–based transition: An exposed individual undergoes an average incubation period of $1/\lambda$ before proceeding to the infected (I) state [19]. An infected individual moves to the hospitalized (H) state with average delay of probability $1/\gamma$ and their susceptible, exposed and infectious contacts move to S_T, E_T and I_T compartments respectively, with an average identification delay period of $1/\alpha$. Since a portion of the the contacts of the hospitalized individuals might be inaccessible or a portion of them might be unwilling to report all their contacts immediately, we assume that there is a delay to identify those contacts. An exposed individual who is traced, (referred to as the E_T compartment) undergoes an average incubation period $1/\lambda$ days before progressing to the infectious compartment where infections are traced (I_T). An infectious individual who is traced enters the hospitalized compartment with an average delay of $1/\gamma_T$ where $\gamma_T > \gamma$. Finally, a hospitalized individual moves to the removed compartment with an average delay of $1/\delta$.

A schematic of the epidemiological transition processes of the proposed model is depicted in figure 1.

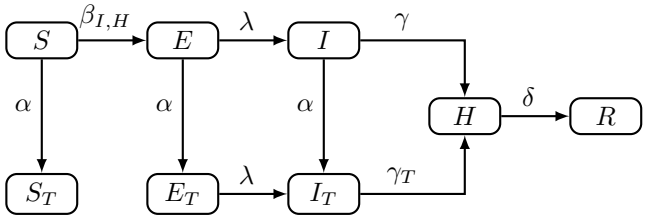

FIGURE 1. Schematic of the transition processes in the Ebola progression with contact tracing model.

In our model, we ignore demography and since the population is much greater than the number of infected people, we assume that $S \simeq 1$. In addition to that, we assume that no individual will die or recover without hospitalization, despite the fact that Ebola has shown high mortality rates in the West African outbreaks. This is a realistic scenario for small–scale outbreaks in the United States. We implement stochastic transitions in our simulation program, based on the above–mentioned state transition rules.

Based on the proposed model, we develop a quantitative approach to measure the effectiveness of contact tracing implementations. To asses the impact of contact tracing protocols in Ebola disease spreading before the epidemic phase, we propose two measures: missed–detection probability and contact tracing cost.

Definition 2.1. To assess the risk detection capabilities of contact tracing efforts for Ebola, we introduce the missed–detection probability. Missed–detection probability denotes the probability that a secondary infected individual is not detected before transmitting the virus to others. Based on our model, we propose the missed–detection probability as follows: $\frac{N_{E\to I}}{N_{E\to E_T}+N_{E\to I}}$, where, N_* represents the total number of individuals who move from one compartment to another indicated by the arrow.

Definition 2.2. The aim of contact tracing is to facilitate the detection of secondary infections from the contacts of an infected person. However, a large proportion of an infectious individual's contacts could remain uninfected (susceptible). We define contact tracing cost as the number of detected individuals who had contact with infections but were not infected. Based on the proposed model, the definition of contact tracing cost is: $Cost = N_{S\to S_T}$, where, $N_{S\to S_T}$ represents the total number of susceptible individuals who move to the S_T compartment.

2.2. **Activity driven network.** Disease contagious process and network structure are two important elements which can have significant impacts on disease spreading [5]. Many intervention strategies such as contact tracing, target strategy and egocentric strategy aim at controlling the contagious process based on interactions between individuals in a social network [12] [1]. In particular, the contact tracing strategy or the identification of individuals who have contact with infections is fundamentally linked to potential transmission paths in the network [10] [5]. The goal of contact tracing is to identify all the potential routes in the network and isolate all the new infected individuals, before they become infectious [10]. Here, we implement activity driven network (ADN) to capture interactions between nodes in a network over a specific period of time and assess effectiveness of contact tracing strategy for a temporal network based on Ebola contagious process. Activity driven network is a random and memoryless process which can capture structural features of a network such as the evolution of contact patterns over time [14].

Activity driven network considers an activity firing rate a_i for each node which is the probability of establishing links with other nodes per unit of time [12]. Activity firing rates are assigned according to a probability distribution $F(a)$, which can describe network dynamics and the corresponding structure [12]. Typically $F(a)$ is a heavy tail density function: $F(a) \propto a^{-c}$, where, $2 \leq c \leq 3$ and $a \in [\epsilon, 1]$ with $\epsilon = 10^{-3}$ [14]. At each time increment Δt, an active node generates m links with m other nodes that are selected randomly. The generative network process in an increment time Δt is listed as follows [12],

- At time t, the network $G_p(N, m)$ has N disconnected vertices.
- Each node i, with probability $p_i = a_i\eta_i\Delta t$, becomes active and generates m links with m other nodes. Here, η_i is a constant scaling factor for node i.
- At time $t + \Delta t$, all the edges in network G_p are removed and the process is repeated. The activity potentials (a_i) of nodes remain the same, so the underlying generator does not change.

2.3. **ADN for Ebola contagion process.** We implement the activity driven network (ADN) to generate a random network at each time step Δt. Then, we simulate Ebola contagion process using the proposed compartmental model. In our network generation process, we take discrete time steps with $\Delta t = 1$, and at each step only the nodes which are in susceptible, infected, exposed or hospitalized states can generate new links with probabilities denoted by p_i's. Here, $p_i \in P$, where P is the set of activation probabilities of the nodes that can become active. The contact tracing mechanism is constructed based on *"CDC emergency guidelines of implementation and management of contact tracing"* for Ebola virus disease [27]. Based on the guideline, any person who has a potential exposure to an Ebola Virus Disease (EVD) case, should go under observation for 21 days [27]. To implement contact tracing strategy in a temporal network such as ADN, we capture all the nodes that become neighbors of an infectious node j from the beginning. We also keep track of the time since the latest contact. We implement contact tracing after a delay of T_{CT} since the first case is identified. It runs until all the infected people have recovered and the contacts have been monitored for 21 days. Algorithm 1 sets the rules to produce and simulate Ebola virus spreading in a host population for discrete time $1 \leq t \leq T$, where T is the end time of the simulation. All the steps and transitions shown in algorithm 1 are done in a stochastic manner to simulate realistic disease dynamics.

3. **Reproductive number in heterogeneous network.** The basic reproductive ratio, R_0, is a descriptor of epidemic potential in the mathematical modeling of infectious diseases. This quantity helps the public health authorities to assess the risk of an outbreak in the emergence of an infectious disease [19]. Furthermore, early estimation of the basic reproductive number helps the healthcare authorities to plan appropriate control measures. A general definition of basic reproductive number is the expected number of secondary infections over all possible initial infections during their infectious period [8] [3]. Based on the general definition of reproductive number and characteristic of the heterogeneous network, we propose a suitable definition for R_0 in a heterogeneous network. In heterogeneous network, contact patterns tend to have a high variability in prevalence and so, besides high degree nodes, there are some low degree nodes which may have no contacts with others [20]. Based on this characteristic, to compute R_0 in a heterogeneous network, we only consider those initial infected nodes which establish links with other nodes and transmit infections. Therefore, we define R_0 as follows:

Definition 3.1. The basic reproductive number (R_0) is the expected number of secondary infectious cases over all initial infections that establish interaction with others during the infectious period. In our activity driven network which is a heterogeneous network, we compute R_0 as:

$$R_0 = \frac{\textit{Total number of hosts infected by } I_0}{\textit{Active subset of } I_0} \tag{1}$$

where, I_0 is the set of initially infected nodes at time $t = 0$. We take care of the fact that every infected node may not be able to transmit infection due to network heterogeneity. The infected nodes that do not have any links to others will not be able to transmit infection. We do not include them in our calculation and only count the active subset (infected nodes with links to others) of the initially infected hosts.

Algorithm 1 : ADN for Ebola Contagion Process

Set $N_A = \phi$, $N_I = \phi$, $I_{Neigh} = \phi$ and $t_{initial} = 0$
while $t \leq T$ **do**
  if $\exists\ i | x_i \in \{S, E, I, H\}$ **then**
    $N_A \leftarrow i$
  end if
  where x_i represents the state of node i. And N_A is the set of active nodes.
  1. Network generation:
  Generate a network $G_p(N, m)$, $w.r.t$ (P, N_A)
  2. Contact identification:
  if $\exists\ i | x_i \in \{H\}$ **then**
    $t_{initial} = t_{initial} + 1$
    $N_I \leftarrow i$
  end if
  where N_I is the set of identified nodes. $t_{initial}$ keeps track of the time since the first identified case.
  3. Contact tracing:
  if $t_{initial} \geq T_{CT}$ **then**
    for all $i \in N_I$ **do**
      Update the states of node i's current contacts and untraced past contacts in (I_{Neigh}) since it became infectious to their respective new states with probability α $(S \rightarrow S_T,\ E \rightarrow E_T,\ I \rightarrow I_T)$.
    end for
  end if
  4. Edge–based transition: Find susceptible nodes in contact with infectious nodes and update their state based on edge–based transition rule. Add all nodes that are neighbors of infected nodes to the set I_{Neigh}.
  5. Node–based transition: Update the states of nodes other than susceptible; $i | x_i \neq S$ based on node–based transition rules.
  6. Tracing removal: Remove nodes belonging to I_{Neigh} which were traced for 21 days but not detected. Return these nodes from S_T and E_T compartments to S and E compartments respectively.
  $t = t + 1$
end while

4. **Receiver operating characteristic.** A receiver operating characteristic or *ROC* curve is a fundamental method to illustrate the performance of a system such as separating true positive results from false positive results in a test or comparing two alternative tasks [7]. In a *ROC* curve, we plot $Sensitivity$ or true positive ratio (TPR) as a function of $(1 - Specificity)$ or false positive ratio (FPR). TPR is defined as the fraction of samples that are detected correctly and FPR is defined as the fraction of samples that are identified as positive, incorrectly.

The major aim of contact tracing is to identify exposed individuals before they become infectious, in order to halt the chain of pathogen transmission. We define the positive samples as those secondary infectious individuals who had contact with infections during the disease evolution. The true positives in the context of contact tracing are defined as the secondary infectious individuals who were traced. Similarly, false positives are defined as those individuals who were not infected but traced

as possible secondary infections. Therefore, based on the different epidemiological compartments in our proposed model, we define $Sensitivity$ and $1 - Specificity$ as the following:

Definition 4.1. We define the true positive ratio (TPR) or Sensitivity as,

$$TPR = \frac{Number\ of\ exposed\ hosts\ traced}{Total\ exposed\ hosts} \tag{2}$$

Definition 4.2. We define the false positive ratio or $1 - Specificity$ as,

$$FPR = \frac{Number\ of\ susceptible\ hosts\ traced}{Total\ susceptible\ hosts\ with\ infectious\ neighbors} \tag{3}$$

A point (p, q) in the ROC shows that with probability p, the susceptible individuals who had contact with infections could be identified as healthy and with probability q, the infected individuals who had contacts with infections could be identified as infectious.

5. **Results.** To generate realizations for Ebola disease spreading without any immunization strategy, parameters of our proposed model for contagious process are given in table 1. The parameter values used in our proposed model were inspired from the works of Rizzo et al.[16]. The time unit is day, and all the rate/probability parameters are given as day^{-1} values. We assume that the number of initially infected individuals is, $I_0 = 2$ and each active node can generate $m = 7$ links with other nodes where the total number of nodes is, $N = 1000$. In a usual case, sickness from infection causes a reduction in an individuals social interaction. Therefore, we assume the scaling factors of the activity firing rates for the hospitalized, infected, and susceptible individuals as following: $\eta_H << \eta_I < \eta_S$. Activity driven network's parameters are shown in table 2.

TABLE 1. Time–invariant parameters of Ebola contagion process

Parameter	Value
Transmission probability(β)	0.11
Incubation rate (λ)	0.095
Recovery/removal probability (δ)	0.1
Hospitalization probability in existence of contact tracing (γ_T)	0.9
Hospitalization probability (γ)	0.33

To assess the effectiveness of contact tracing in the early stage of the epidemic, we assume three different implementation–time scenarios for contact tracing. The first one is when we implement contact tracing from the beginning ($T_{CT} = 1$), the second scenario is when contact tracing is started on day 9 ($T_{CT} = 9$), and the third one is when contact tracing is implemented on day 22 ($T_{CT} = 22$). To evaluate the effectiveness of contact tracing in a more realistic situation, we consider five identification delay times, $\alpha^{-1} \in \{1, 2, 5, 10, 20\}$ $days$ for the three above mentioned scenarios of contact tracing implementation.

5.1. **Effectiveness of contact tracing.** To measure the effectiveness of contact tracing, we use the term epidemic attack rate (AR), which is the cumulative total of exposed/infected individuals during the disease evolution. In figure 2, we plot the attack ratio, AR^{α}/AR^{0} as a function of the identification delay, α^{-1}. Here, AR^{0} is

TABLE 2. Parameters of activity driven network generator

Parameter	Value
Density function exponent (c)	2.2
Links per active node (m)	7
Scaling factor for susceptible (η_S)	2.2
Scaling factor for infected (η_I)	1.1
Scaling factor for hospitalized (η_H)	0.005

the mean attack rate when no contact tracing strategy is used and AR^{α} is the mean attack rate for a contact tracing strategy with an identification delay of α^{-1}. The plots are the averaged results of 10,000 simulations. Figure 2 shows that contact tracing is more effective in the first and the second scenario when the identification delay, α^{-1}, is less than 10 days. In the third scenario, we still observe a reduction in the attack ratio, although not as influential as in the first two. Making the identification rate faster could bring the attack ratio down significantly if contact tracing is started early (< 10 days), otherwise, it is not so effective in controlling the epidemic.

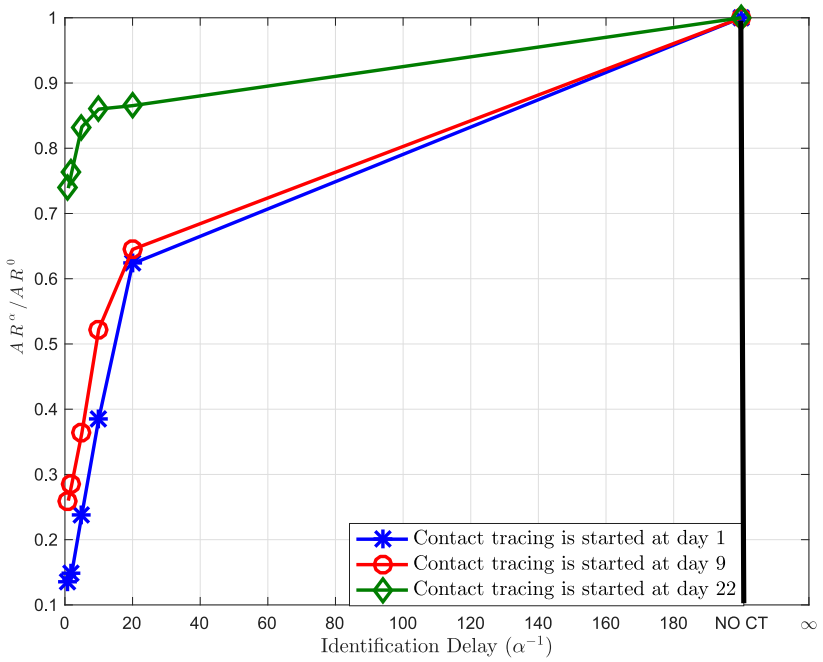

FIGURE 2. The epidemic attack ratio as a function of α^{-1} . The results are the averages of 10,000 simulations.

In figure 3, we study the impact of hospitalization delay, γ^{-1} on AR^{γ}/AR^{0}. Once again we perform 10,000 simulations and compute the average. Here, no contact tracing strategy has been used. AR^{γ} is the mean attack rate with a hospitalization probability of γ and AR^{0} is the mean attack rate for the hospitalization probability

given in table 1. The hospitalization delay is the average time it takes to hospitalize an infectious individual. Figure 3 shows the importance of immediate access to hospitals for infected individuals. From the figure, we can see that quick hospitalization can bring down the attack ratio significantly. Comparing figure 3 and figure 2 shows that the epidemic is more sensitive to the hospitalization delay, γ^{-1} than the identification delay, α^{-1}. Immediate hospitalization can keep the Ebola epidemic progression under control while contact tracing could be ineffective if it is started once the disease has progressed.

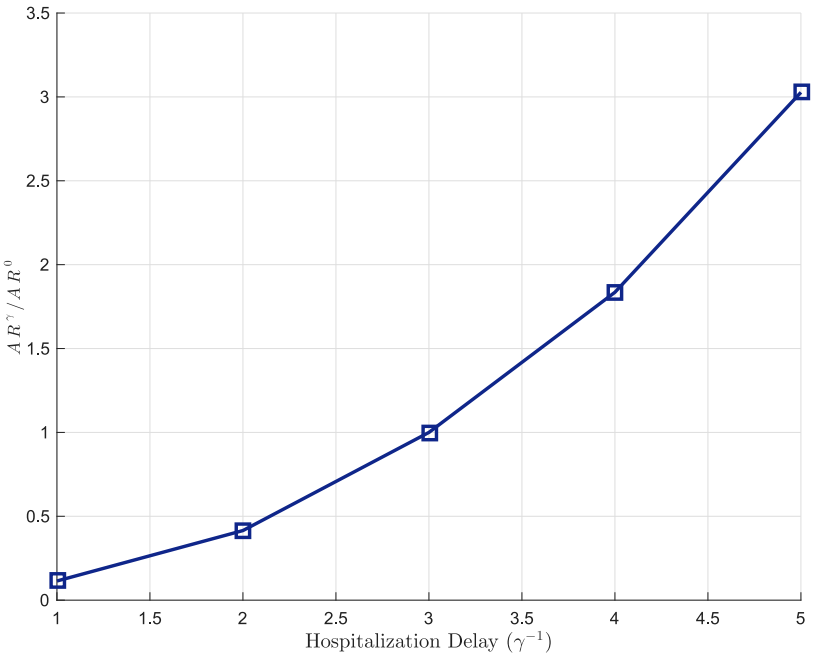

FIGURE 3. The epidemic attack ratio as a function of γ^{-1}. The results are the averages of $10,000$ simulations.

5.2. **Contact tracing performance.** To evaluate the performance of contact tracing on the Ebola contagious process, we employ the *ROC* curve approach. To plot the *ROC* curve, we compute the *Sensitivity* or TPR and $(1 - Specificity)$ or FPR in each iteration from equations 2 and 3. We compute the average of these two ratios in $10,000$ simulations. Figure 4 shows TPR as a function of FPR for the 5 identification delays, $\alpha^{-1} \in \{1, 2, 5, 10, 20\}$ *days*, in the three contact tracing implementation scenarios. We project the 3–D *ROC* plot to get a 2–D *ROC* plot, as shown in figure 5. In all those three scenarios, when α^{-1} increases, the probability to identify secondary infected individuals produced by an infectious individual decreases. Missed–detection probability is the number of exposed individuals who are not traced as defined previously. Therefore, missed–detection is equal to $(1 - Sensitivity)$. Figure 5 clearly shows that an increase in identification delay can increase the missed–detection probability. Furthermore, early implementation of contact tracing is needed for improving efficiency and reducing cost. It is evident

from the figure that the second and third scenarios produce a lot more false positives than the true positives. This implies that the costs of contact tracing could overshadow its benefits if contact tracing is started late.

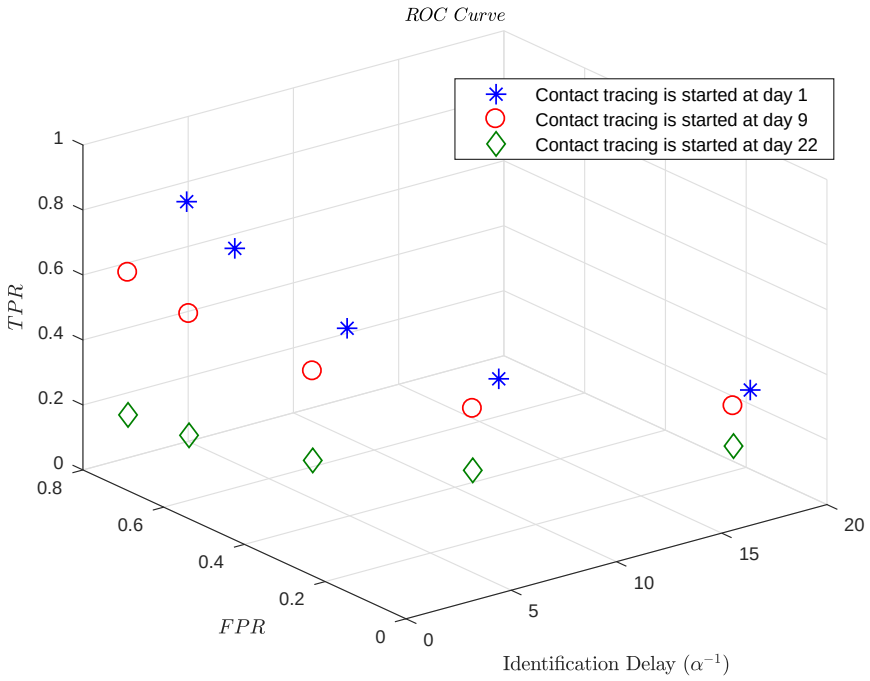

FIGURE 4. 3–D *ROC* curve of contact tracing with 5 identification delay implemented in three different scenarios. The results are the averages of 10,000 simulations.

5.3. **Basic reproductive number.** Using equation 1, we compute the basic reproductive number in a set of 10,000 simulations. In figure 6, we plot the average of the computed R_0. It shows that for the same identification rate, α, earlier contact tracing implementations allow better reductions in the value of R_0. However, even with the earliest contact tracing strategy, we never obtain a value of R_0 smaller than 1. In figure 7, the basic reproductive number is plotted as a function of the hospitalization delay, γ^{-1}. Figure 7 shows that a rapid hospitalization strategy can bring the value of R_0 below 1. If we can hospitalize infected individuals within 2 days ($\gamma^{-1} \leq 2$), the epidemic can be controlled effectively.

6. **Discussion and conclusion.** In this paper, we have simulated contact tracing on a compartmental model of Ebola in an activity driven network (ADN). We have performed simulations to analyze the effects of contact tracing initiation delay, contact identification delay, and hospitalization delay. Our results suggest that it is critical to start contact tracing within a few days (< 10 days), if not immediately after the disease emergence. In addition to that, quick identification of contacts can reduce the epidemic attack ratio up to 50% compared to delayed identification,

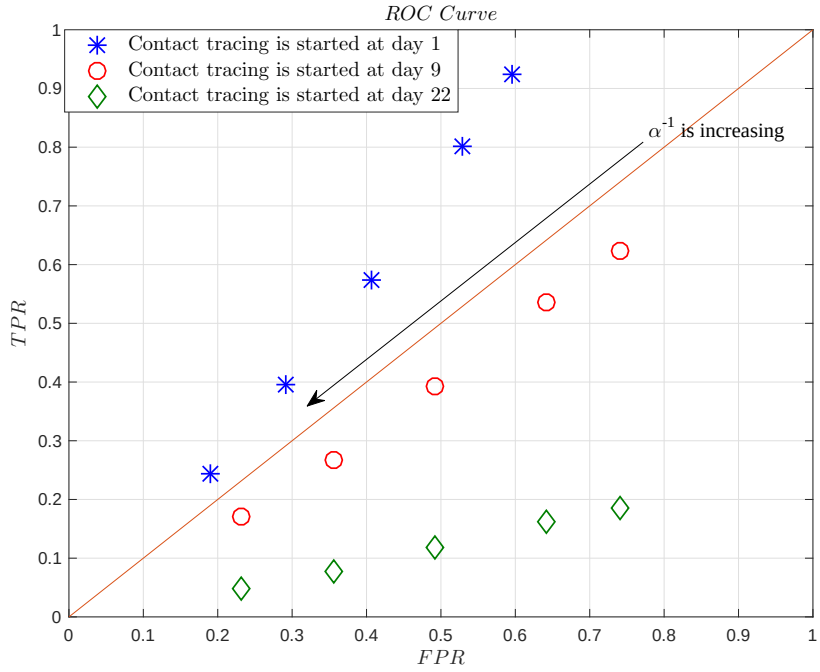

FIGURE 5. 2–D *ROC* curve of contact tracing implementation in three different scenarios. The area under the curve (AUC) values for contact tracing starting on day 1, day 9 and day 22 are respectively 0.6550, 0.4060 and 0.1207. The results are the averages of 10,000 simulations.

as shown in figure 2. Contact tracing is very effective when paired with immediate hospitalization in bringing down the reproductive ratio below one.

The contacts are usually traced up to the maximum incubation period for the disease [27]. The duration of incubation period has counteracting effects on contact tracing. The contacts need to be monitored longer for diseases with longer incubation periods, which is expensive in terms of resources required. When the incubation time is long, we do not gain much by allocating all resources on immediate identification and monitoring of contacts. On the other hand, longer incubation period provides the tracing agencies more time to identify the potential exposed contacts before they become infectious and start to spread pathogens to other people. On this regard, a long incubation period has a positive impact on the disease control. In our model, "identification" and "monitoring" of contacts happen simultaneously. However, these two processes can be separated. A long incubation time will help better identification. However, monitoring individuals for a longer time is expensive. Due to the long incubation period of Ebola, contact tracing could be inefficient. Hence, immediate hospitalization of the infected cases could be a crucial factor in disease control and infection containment.

A good collaboration between public health authorities and people can lead to rapid identification of secondary infections. Public health authorities should also keep the host population alert and run awareness campaigns to educate people about

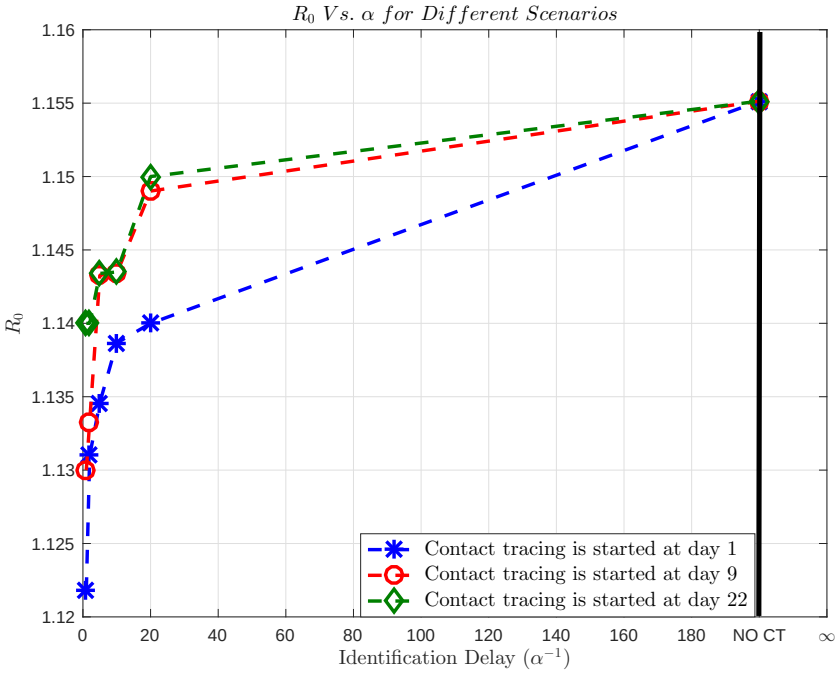

FIGURE 6. R_0 as a function of the identification delay, α^{-1} in three scenarios. The results are the averages of 10,000 simulations.

the disease. Since contact tracing protocols need to monitor all the contacts of the infected and hospitalized people, it cannot separate the exposed contacts from the healthy ones. Therefore, contact tracing might increase the financial burden on the public health authorities when many people are needed to be traced, as happened in the West African countries in 2014. Contact tracing is therefore, economically efficient during the early stage of the epidemic.

Our work can be extended in the future by modifying the activity potentials based on the states of nodes. Hence, the behavioral changes of individuals in response to the disease can be incorporated and properly modeled. It has been found that these changes have a controlling effect on the epidemic [17]. The model can be made even closer to the reality by using temporal networks with memory (non-Markovian link creation process). There is an alternative approach that can be used with ADNs. Instead of using continuous distribution of activity potential and discrete time-steps, we can use a discrete activity potential distribution with continuous time-steps. This can overcome some limitations of the continuous distribution discrete time ADNs and enhance our capabilities. For example, non-exponential inter-event times can be incorporated, and the partition of nodes in several classes based on their activity potentials can help studying the non mean-field dynamics [25].

When it comes to controlling invasion of a disease within a population, the best option is to contain the propagation processes in the early stage and at its source. Contact tracing is one of the important strategies towards this goal; and this applies to many diseases besides Ebola. Behavior of the early-stage dynamic process is very different from large scale outbreak. When number of cases are high, the infection

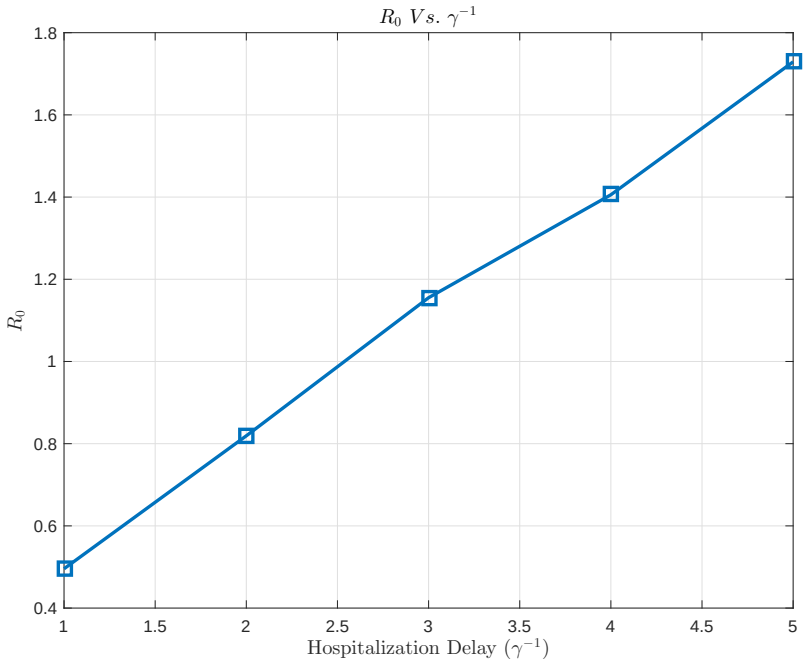

FIGURE 7. R_0 as a function of the hospitalization delay, γ^{-1}. The results are the averages of 10,000 simulations.

process possesses a stable momentum for spreading which in turn makes modeling easier because mean-field assumption applies. When the number of cases are low, however, the infection process is characterized by extreme randomness and dynamic fluctuations. Furthermore, contact network dynamism is very influential. As a result, mean-field models or models based on quenched/averaged contact networks are not viable candidates. Our modeling effort in this paper and the use of ADN framework calls for further work on efficient and accurate modeling of epidemic processes in heterogeneous populations during early stages after introduction of the infection.

REFERENCES

[1] C. Browne, H. Gulbudak and G. Webb, Modeling contact tracing in outbreaks with application to Ebola, *Journal of Theoretical Biology*, **384** (2015), 33–49.

[2] G. Chowell and C. Viboud, Is it growing exponentially fast?-Impact of assuming exponential growth for characterizing and forecasting epidemics with initial near-exponential growth dynamics, *Infectious Disease Modelling*, **1** (2016), 71–78.

[3] O. Diekmann, J. A. P. Heesterbeek and J. A. J. Metz, On the definition and the computation of the basic reproduction ratio R_0 in models for infectious diseases in heterogeneous populations, *Journal of Mathematical Biology*, **28** (1990), 365–382.

[4] M. G. Dixon and I. J. Schafer, Ebola Viral Disease Outbreak - West Africa, 2014, *MMWR Morb Mortal Wkly Rep*, **63** (2014), 548–551.

[5] K. T. Eames and M. J. Keeling, Contact tracing and disease control, *Proceedings of the Royal Society of London B: Biological Sciences*, **270** (2003), 2565–2571.

[6] F. O. Fasina, A. Shittu, D. Lazarus, O. Tomori, L. Simonsen, C. Viboud and G. Chowell, Transmission dynamics and control of Ebola virus disease outbreak in Nigeria, July to September 2014, *Eurosurveillance*, **19** (2014), 20920.

[7] M. Greiner, D. Pfeiffer and R. D. Smith, Principles and practical application of the receiver-operating characteristic analysis for diagnostic tests, *Preventive Veterinary Medicine*, **45** (2000), 23–41.
[8] J. M. Heffernan, R. J. Smith and L. M. Wahl, Perspectives on the basic reproductive ratio, *Journal of the Royal Society Interface*, **2** (2005), 281–293.
[9] M. J. Keeling and P. Rohani, *Modeling Infectious Diseases in Humans and Animals*, Princeton University Press, Princeton, NJ, 2008.
[10] I. Z. Kiss, D. M. Green and R. R. Kao, Disease contact tracing in random and clustered networks, *Proceedings of the Royal Society of London B: Biological Sciences*, **272** (2005), 1407–1414.
[11] D. Klinkenberg, C. Fraser and H. Heesterbeek, The effectiveness of contact tracing in emerging epidemics, *PloS One*, **1** (2006), e12.
[12] S. Liu, N. Perra, M. Karsai and A. Vespignani, Controlling contagion processes in activity driven networks, *Physical review letters*, **112** (2014), 118702.
[13] A. S. da Mata and R. Pastor-Satorras, Slow relaxation dynamics and aging in random walks on activity driven temporal networks, *The European Physical Journal B*, **88** (2015), Art. 38, 8 pp.
[14] N. Perra, B. Gonçalves, R. Pastor-Satorras and A. Vespignani, *Activity Driven Modeling of Time Varying Networks*, Scientific Reports, 2012.
[15] N. Perra, A. Baronchelli, D. Mocanu, B. Gonc'calves, R. Pastor-Satorras and A. Vespignani, Random walks and search in time-varying networks, *Physical review letters*, **109** (2012), 238701.
[16] A. Rizzo, B. Pedalino and M. Porfiri, A network model for Ebola spreading, *Journal of theoretical biology*, **394** (2016), 212–222.
[17] A. Rizzo, M. Frasca and M. Porfiri, Effect of individual behavior on epidemic spreading in activity-driven networks, *Physical Review E*, **90** (2014), 042801.
[18] A. Rizzo and M. Porfiri, Toward a realistic modeling of epidemic spreading with activity driven networks, in *Temporal Network Epidemiology* (N. Masuda and P. Holme), Springer, (2017), 317–319.
[19] N. M. Shahtori, C. Scoglio, A. Pourhabib and F. D. Sahneh, Sequential Monte Carlo filtering estimation of Ebola progression in West Africa, *American Control Conference(ACC)*, (2016), 1277–1282.
[20] M. D. Shirley and S. P. Rushton, The impacts of network topology on disease spread, *Ecological Complexity*, **2** (2005), 287–299.
[21] F. Shuaib, R. Gunnala, E. O. Musa, F. J. Mahoney, O. Oguntimehin, P. M. Nguku, S. B. Nyanti, N. Knight, N. S. Gwarzo, O. Idigbe, A. Nasidi and J. F. Vertefeuille, Ebola virus disease outbreak-Nigeria, July–September 2014, *MMWR Morb Mortal Wkly Rep*, **63** (2014), 867–872.
[22] M. Starnini and R. Pastor-Satorras, Temporal percolation in activity-driven networks, *Physical Review E*, **89** (2014), 032807.
[23] M. Starnini and R. Pastor-Satorras, Topological properties of a time-integrated activity-driven network, *Physical Review E*, **87** (2013), 062807.
[24] K. Sun, A. Baronchelli and N. Perra, Contrasting effects of strong ties on SIR and SIS processes in temporal networks, *The European Physical Journal B*, **88** (2015), Art. 326, 8 pp.
[25] L. Zino, A. Rizzo and M. Porfiri, Continuous-Time Discrete-Distribution Theory for Activity-Driven Networks, *Physical Review Letters*, **117** (2016), 228302.
[26] *Cases of Ebola Diagnosed in the United States*, 2014. Available from: `https://www.cdc.gov/vhf/ebola/outbreaks/2014-west-africa/united-states-imported-case.html`.
[27] *Implementation and Management of Contact Tracing for Ebola Virus Disease*, Emergency Guideline by the World Health Organization, 2015. Available from: `https://www.cdc.gov/vhf/ebola/pdf/contact-tracing-guidelines.pdf`.

Received September 15, 2017; Accepted January 27, 2018.

E-mail address: `nargesmsh92@ksu.edu`
E-mail address: `tanvirf@ksu.edu`
E-mail address: `caterina@ksu.edu`
E-mail address: `faryad@ksu.edu`