IOSR Journal of Mathematics (IOSR-JM)
e-ISSN: 2278-5728, p-ISSN: 2319-765X. Volume 13, Issue 5 Ver. 1 (Sep. - Oct. 2017), PP 70-74
www.iosrjournals.org

Modelling the Impact of Time of Case Detection and Control Strategy on Ebola Virus Disease (EVD) Spread on Graphs

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Abstract: *Ebola virus disease is dreadful and, therefore, the study of its transmission dynamics is worthwhile. The objective of this article is to investigate the impact of time of case detection and control strategy on Ebola virus disease epidemics. A dynamic graph that captures human contact interactions, wherein, the numbers of contact interactions are generated by a Poisson distribution, is constructed by the mechanism of configuration model. Ebola virus disease models were simulated on the graph, using varying time frames for case detection and commencement of control response. The results show that the earlier the time of case detection and control response, the smaller the size of the epidemic. This probably explains the reason for varying distributions of Ebola cases in some West African countries recently. Therefore, early case detection and control interventions are crucial for eliminating the disease.*

Keywords: *graph, network, Ebola virus disease, index case*

Date of Submission: 23-07-2017 Date of acceptance: 13-08-2017

I. Introduction

Ebola, previously known as Ebola hemorrhagic fever, is a rare and deadly disease caused by infection with one of the Ebola virus species. Ebola can cause disease in human and nonhuman primates (monkeys, gorillas and chimpanzees). Ebola is caused by a virus of the family filoviridae, genus Ebola virus. Ebola viruses are found in several African countries. Ebola was first discovered in 1976 near the Ebola River in what is now the Democratic Republic of the Congo. Since then, outbreaks have appeared sporadically in Africa. The natural reservoir of host of Ebola viruses remains unknown. However, on the basis of evidence and the nature of similar viruses, researchers believe that the virus is animal-borne and that bats are the most likely reservoir (Ebola Factsheet, 2015).

Ebola is spread through direct contact (through broken skin or unprotected mucous membranes in, for example, the eyes, nose, or mouth) with blood or body fluids (including but not limited to feces, saliva, sweat, urine, vomit, breast milk, and semen) of a person who is sick with Ebola, objects (like needles and syringes) that have been contaminated with the virus, infected fruit bats or primates (apes and monkeys), and possibly from contact with semen from a man who has recovered from Ebola (for example, by having oral, vaginal, or anal sex) (Ebola Factsheet, 2015).

As of 6 October 2015, WHO had reported 28 427 confirmed, probable and suspected cases of Ebola virus disease (EVD), including 11 297 deaths related to the West African epidemic (ECDC, 2015).

There is no treatment (like antiretroviral drugs) for Ebola disease neither is there any preventive vaccine. The only interventions are contact tracing, quarantine, isolation, and treatment of symptoms that may arise. The worse-hit countries for Ebola virus disease were Guinea, Sierra Leone and Liberia (Damon *et al*, 2015).

The plan of this article is as follows. Modeling is introduced in section 2. Section 3 is devoted to model description. Simulation set up is presented in section 4. Section 5 is for presentation of results. Discussion of results and conclusive remark are passed in sections 6 and 7 respectively.

II. Modelling

Classical models of Ebola disease using ODEs are available. In Conrad et al (2016), such models were proposed by Browne et al (2014); Camacho et al (2014); Chowell et al (2014); Rivers et al (2014); Gomes et al (2014); Martin et al (2014); Nishiura et al (2014). Graph or network-based models can be found in Arino et al (2003); Eubank et al (2004); Hyman and LaForce (2003); McMahon et al (2014); Xue et al (2012).

Branching process models have been used to study Ebola virus disease. For a survey of these models, see Drake *et al* (2015). Damon *et al* (2015) employed the theory of branching processes with a negative binomial offspring distribution to estimate the probability that new introductions would lead to outbreaks exceeding various sizes.

III. Model Description

At time t_0, the population is wholly susceptible. At time t_1, the population is susceptible except an index case of Ebola disease. Let t_c be the time when there is case detection and intervention starts. If case is detected immediately an index case invades the population, $t_1 = t_c$. When $t_1 < t_c$, there is no case detection, and it is assumed that members of the population exhibit their normal complex human contact interactions; and within this window, a member may be susceptible, exposed or infectious. It is assumed also that after time $t \geq t_c$, there is case detection and consequently, there is a change in human contact interactions and attendant provision of medical facility and safe burial of people that might die of Ebola disease. The simulation processes are outlined below.

i. Between time t_1 and t_c, a graph that captures the normal complex human contact interactions is generated. At every time step, a susceptible individual may be exposed with the probability ξ_1, an exposed individual may proceed to infectious state with probability ξ_2 and an infectious individual may recover with probability ξ_3 or die of the disease with probability ξ_4.
ii. At any time $t \geq t_c$, there is a change in human contact interactions influenced by the alarm of case detection and a graph that captures this is constructed. Within this time, a member of the population may be in any of these states: susceptible, exposed, infectious with the case managed at home or infectious with the case managed in a medical facility. At every time step, a susceptible may be exposed with probability $\lambda_1 < \xi_1$, an exposed individual proceed to an infectious state with probability $\lambda_{2,}$ an infectious individual remains at home with probability λ_3 or moves to a medical facility with probability $\lambda_{4.}$

These steps are repeated until statistical significance is obtained.

IV. Simulation

The following parameter values used in Conrad et al (2016) are adopted for our simulation experiments.

Symbol	Parameter description	Baseline
c_*^-	Number of contacts per day when $t < t_c$ $c_s^- = 30, c_e^- = 30, c_i^- = 8.1657, c_m^- = 5, c_f^- = 20, c_r^- = 30$	
c_s^+	Number of contacts per day when $t \geq t_c$ $c_s^+ = 30, c_e^+ = 30, c_i^+ = 3.0311, c_m^+ = 5, c_f^+ = 20, c_r^+ = 30$	
β_*	Probability of transmission per contact with state * $\beta_i = 0.017, \beta_m = 0.0005, \beta_f = 0.05$	
τ_e	Average days spent in exposed state	7
τ_i	Average days spent in I	20
p_{hr}	Probability an infectious person recovers at home	0.55
p_{mr}	Probability an infectious person recovers in a medical facility	0.75

For our simulation experiments, we consider varying times of case detection and control response: 30 days, 20 days, 15 days, 10 days, 5 days, 2 days and 1 day before case detection and control response. The results are shown in Figures 1 through 6 respectively.

V. Results

The results of our experiments showing the sizes of the epidemics at varying times are depicted in the following Figures.

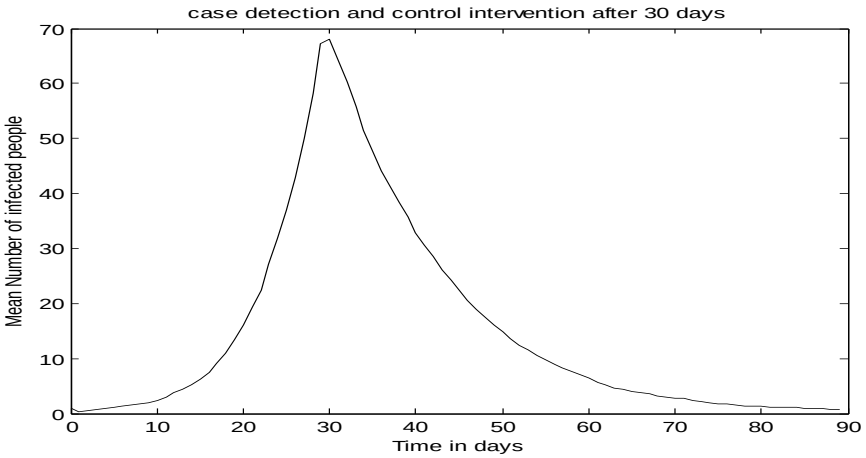

Figure 1: *Graph showing Ebola cases after* 30 *days of case detection and control response*

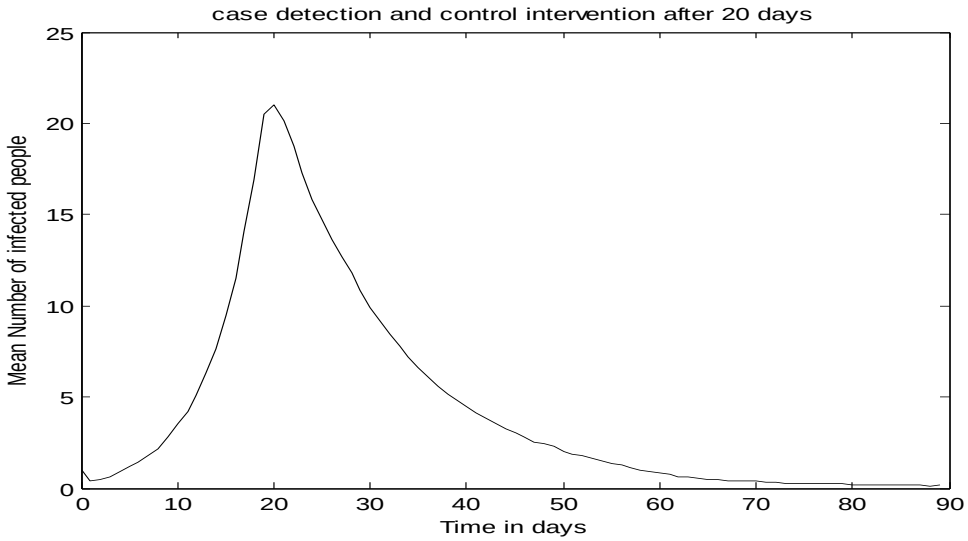

Figure 2: *Graph showing Ebola cases after* 20 *days of case detection and control response*

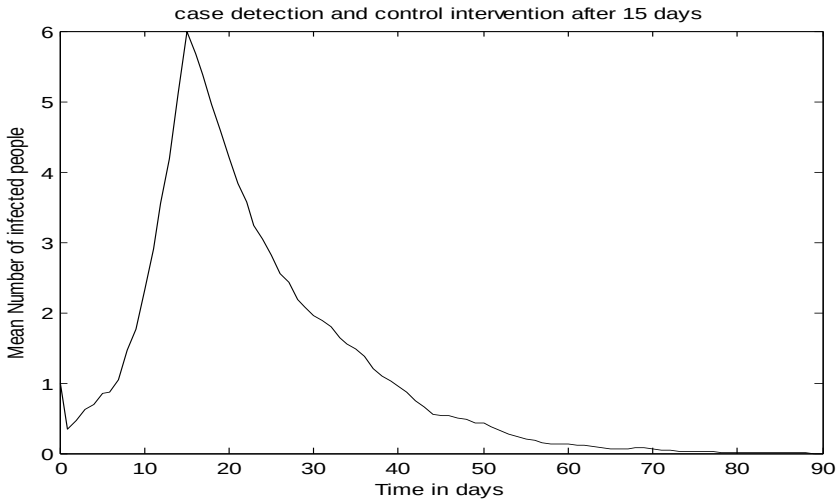

Figure 3: *Graph showing Ebola cases after* 15 *days of case detection and control response*

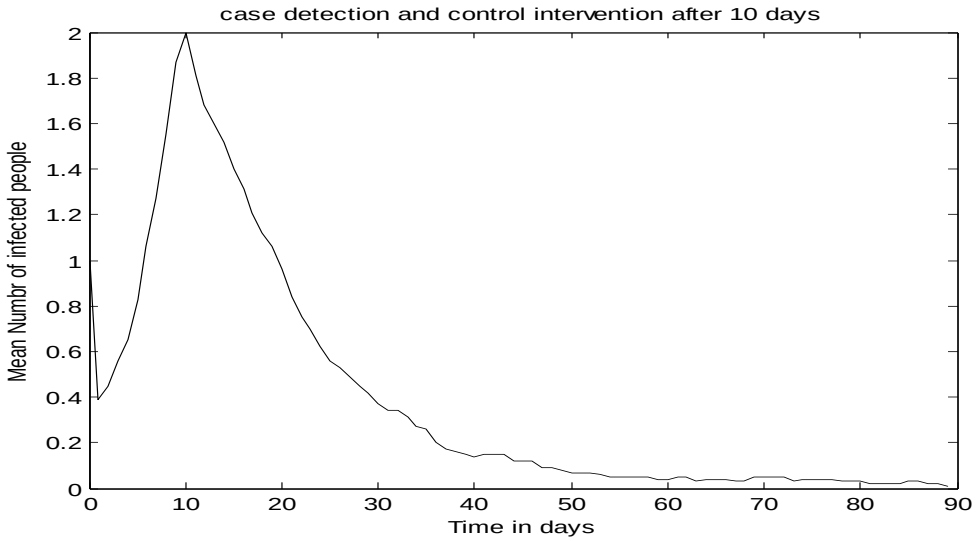

Figure 4: *Graph showing Ebola cases after* 10 *days of case detection and control response*

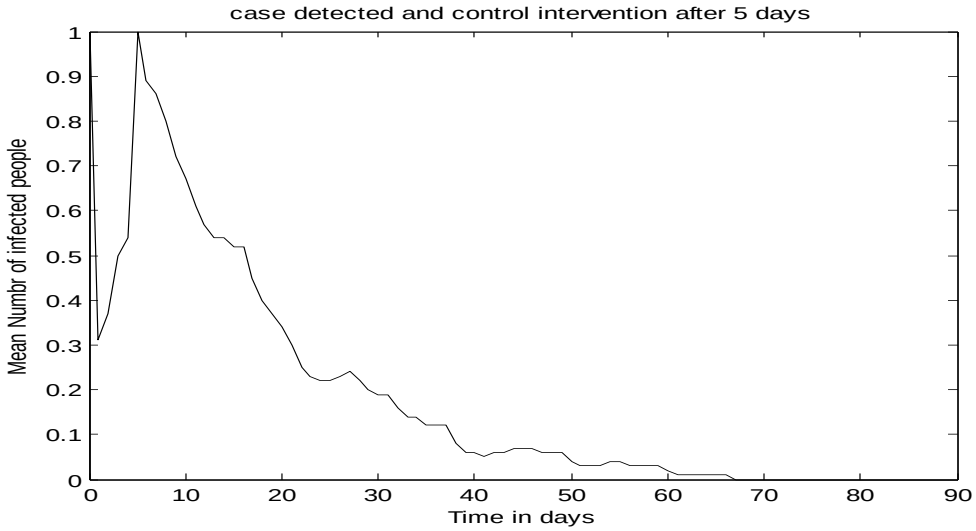

Figure 5: *Graph showing Ebola cases after* 5 *days of case detection and control response*

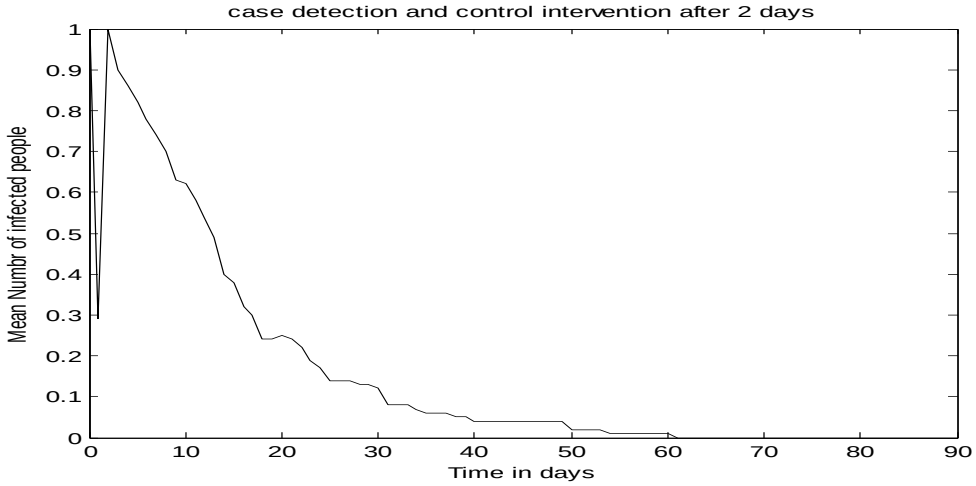

Figure 6: *Graph showing Ebola cases after* 2 *days of case detection and control response*

VI. Discussion

Ebola virus disease outbreaks in some countries in West Africa recently portray a high amount of variability across the region. One of the factors for this was the time the case was detected and interventions put in place. Another factor could be the level of complexity of human contact interactions among the members of the population. In this article, we have investigated the impact of the time of case detection and control response together with human contact interactions on the spread of Ebola virus disease. The results in Figures 1 through 6 explain this impact. The results show that the time of case detection and control response determines whether there should be an epidemic take- off and the size if there is an epidemic. In our case, the time detection and control response after 30 days precipitates the highest epidemic size. Thus, we have the least epidemic size when the time of case detection and control response is 10 days. Our results in Figures 5 and 6 show that case detection and control response at day 5 and day 2 does not lead to an outbreak, emphasizing the importance of early detection and control.

VII. Conclusion

In this article, we have developed a graph-based model to investigate the impact of the time of case detection and control response on the dynamics of transmission of Ebola virus disease. The main results are shown in Figures 1 through 6. Our findings highlight the importance of early detection and control of Ebola virus disease. These findings also highlight the importance of case detection gadgets.

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O. Abu. "Modelling the Impact of Time of Case Dete Ction and Control Strategy on Ebola Virus Disease (Evd) Spread on Graphs." IOSR Journal of Mathematics (IOSR-JM), vol. 13, no. 5, 2017, pp. 70–74.