Predicting the 2014 Ebola Outbreak in West Africa using Network Analysis

Milestone Report

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Abstract

The current Ebola outbreak in West Africa is the worst in history. Most traditional epidemiological models are compartmental models that have a random-mixing assumption. These models calculate the effective reproductive rate of an outbreak. We survey three of these models: the classic SIR (Susceptible, Infectious, Recovered) model and two extensions used in Ebola research.

Network models allow for avoiding the random-mixing assumption inherent in compartmental models. This is done by assigning each individual a finite set of permanent contacts. We review generated contact network models for SARS, including an urban network, a random network, and a scale-free network. We then review a worldwide network model that represents traffic flowing across transportation networks and consider approaches for predicting the extent of an Ebola outbreak.

I. Introduction

TODO: Add introduction

II. Related Work

Related work by (Gomes et al., 2014) attempts to predict the spread of Ebola to different parts of the world based on a model that incorporates both the compartmental approach and the use of world-wide air traffic flows.

In (Meyers et al., 2005), the authors model the spread of the 2002-2003 outbreak of SARS in Hong Kong and Canada using a contact network. A contact network model attempts to characterize every interpersonal contact that can potentially lead to disease transmission in the community, with each person in the community represented as a node and each contact represented as an edge between them.

The majority of research in epidemiological theory is based on the compartmental model, which is not a network model. In order to simply capture the dynamics of disease spread over time, the compartmental model employs a a population-wide random mixing assumption, meaning that each individual has a small and equal chance of coming into contact with any other individual in the population. To model the progress of an epidemic in a large population, the individuals in the population are compartmentalized according to the state of the disease. The most widely used such model is the SIR model introduced in (Kermack and McKendrick, 1932):

- **Susceptible (S):** Individuals who have not yet caught the disease from contact with an infectious individual.
- **Infectious (I):** Individuals who have the disease. They have some probability of infecting susceptible people.
- **Recovered (R):** Individuals who have experienced the full infectious period, and are now non-infectious and immune.

The changes among these states over time are represented by a set of differential equations. The basic reproductive number R_0 is defined as the average number of secondary cases generated by a primary case in a pool of mostly susceptible individuals, and is an estimate of epidemic growth at the start of an outbreak if everyone is susceptible.

In (Chowell et al., 2004), the authors model the effect of Ebola outbreaks in 1995 in Congo and in 2000 in Uganda using a compartmental model similar to the SIR model. However, a distinct feature of Ebola is that individuals exposed to the virus who become infectious do so after a mean incubation period. In order to reflect this feature, in the SIR model is extended with an additional "Exposed" compartment state. This SEIR model is summarized in Figure 1:

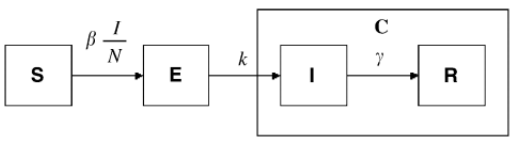


Fig. 1: SEIR model

In (Legrand et al., 2007), the Ebola outbreaks in Congo in 1995 and Uganda in 2000 are also studied. However, a major difference from (Chowell et al., 2004) is that (Legrand et al., 2007) models the spreading of disease in heterogeneous settings.

In order to gain better insight of the epidemic dynamics, the infectious phase is subdivided into three stages: infection in a community setting (I), infection in a hospital setting (H), and infection after death assuming a traditional funeral (F).

This SEIHFR compartmental model is summarized in Figure 2.

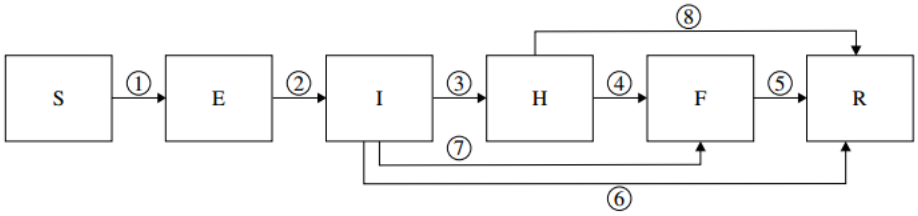


Fig. 2: SEIHFR model

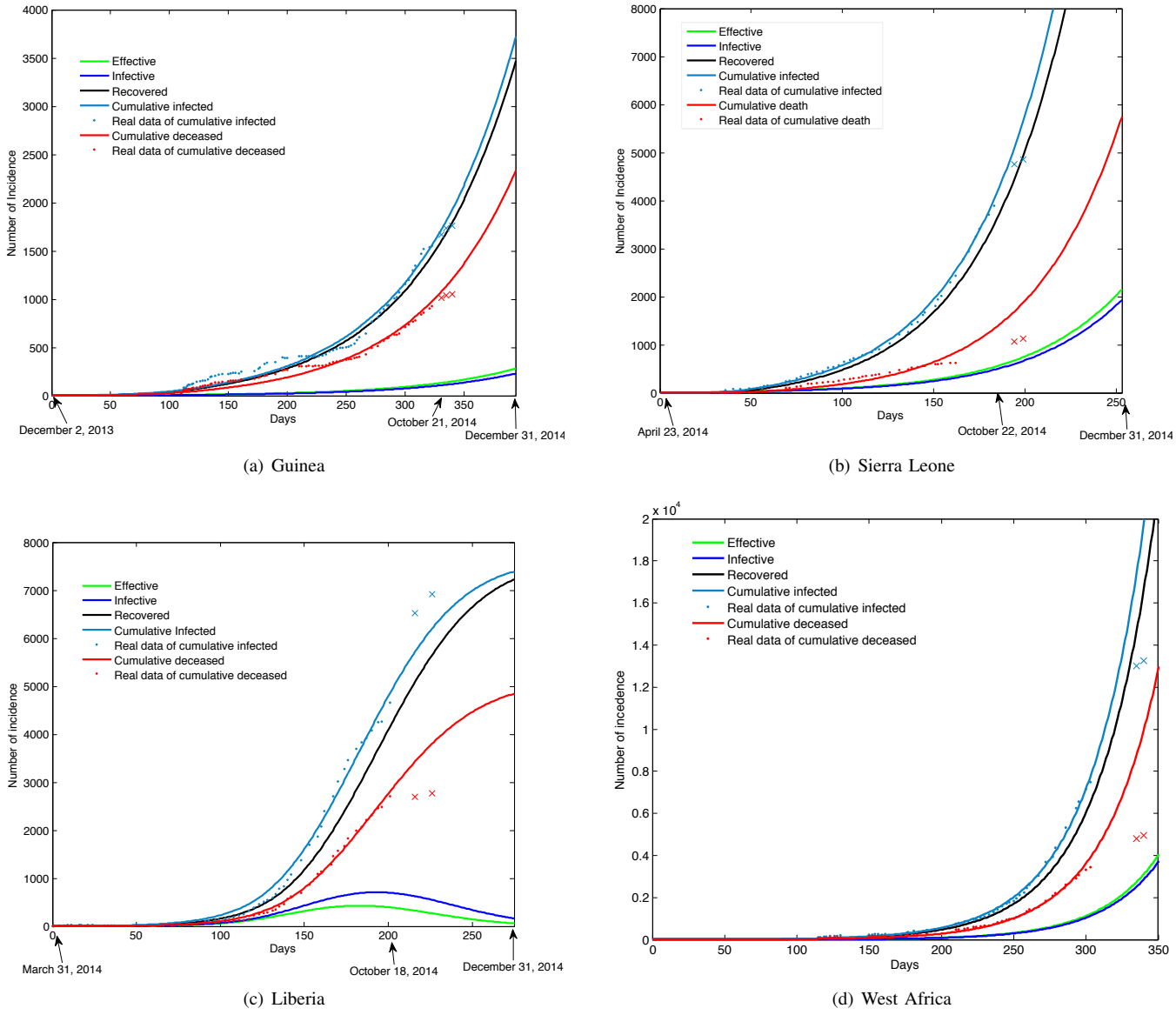
III. Modeling localized epidemic spread

Estimating model parameters and basic reproduction number for 2014 Ebola data using a random mixing model

In first phase of the project, to calculate the basic reproduction number of the current Ebola epidemic spread at different countries, we performed model fitting on the data we gathered from Rivers (2014). We considered the SEIR model described in Chowell et al. (2004). The SEIR model under consideration is a non-linear model with six parameters. The current Ebola epidemic is still spreading and depending on the preventative measures taken, the underlying dynamics of the spread can change drastically anytime. We fitted our model to three countries in the West Africa - Guinea, Sierra Leone and Liberia. In addition, we performed model fitting for the West Africa Region by adding up the data from these three countries. Given the limited number of data available, instead of fitting all six parameters to the model, we decided to fix some of the parameters based on the studies on previous Ebola epidemic. In Chowell et al. (2004), the incubation time of the Ebola $1/k$ is found to be varying between 1 to 21 days, with a mean time of 6.3 days for previous Ebola spread. For ease of data fitting, we set this parameter value to the mean value of 6.3 days. We note that, the dynamics of the current epidemic may differ from previous one, and therefore fixing a value based on the prior estimate may lead to some inaccuracy. To model the effect the intervention on the spread of the epidemic, a modified transmission rate β_1 is generally used instead of the initial transmission rate β_0 at later stage of the epidemic. The transition of β_0 to β_1 depends on intervention time τ and decaying factor q. The choice of intervention time is a very difficult problem. To this end, we looked into different sources like Wikipedia, WHO and CDC website to learn more about the timeline of the spread. In Guinea, a 2-year-old boy fell in December 2, 2013, later diagnosed as Ebola patient. We consider this incidence as the index case for Guinea and set t_0 to December 2. In March 2, the Government of Guinea informed WHO regarding the possibility of Ebola epidemic and declared national heath emergency. We considered this date as the intervention date and set τ to 110. In Sierra Leone, one person fell in April 2014. In June 12, 2014 the country declared emergency and closed borders with neighboring Guinea and Liberia. We consider the first date as t_0 and second date as intervention time, therefore set τ to 50. In Liberia, in March 31, 2014, there were official confirmation of two person getting infected from Ebola. We set this date to t_0 and set I_0 and C_0 in our model as 2. The Government of Liberia shut down all schools in July 30, 2014. We consider this date as the date of intervention and set τ to 120.

In order to fit the non-linear SEIR model to data, we used non-linear least square estimation. We use the reported data (t_i, c_i) for $i = 1, 2, \ldots, n$ where t_i denote the $i-th$ reporting time and c_i as the cumulative number of infectious cases from the beginning of outbreak time t_0 to time t_i. The optimization problem contains a large number of local minimas. Therefore, the choice of initial parameter estimate is an important consideration to get the global optimum solution. In order to find a good initial choice of the parameters as an input to the non-linear least square solver, we first perform a Latin hypercube sampling on the 4-dimensional parameter space. We grid up the hypercube with a number of grid points in each dimension. We then choose the sample that minimizes the least square error as the initial input. In order to calculate the 95% confidence interval of estimated parameter, we performed bootstrapping based on residual error.

The estimated parameters for the SEIR model of Guinea, Sierra Leone, Liberia, as well as West Africa region is presented in the appendix. In Figure 3, we presented the the number of incidence at different compartments of the SEIR model, as well as the cumulative number of infectious cases over time. Our model fit was based on the last data we collected in October 21, 2014. As of today, November 11, 2014, few additional data points are available; we also plotted those data points in the graph. In addition to that, we extrapolated the graph up to December 31, 2014. We note that, the forecasting to future cases may not be appropriate as the underlying factors of the Epidemic are changing rapidly with the increase in safety measures. We observe that, the prediction of the model to the cases up to November 11 is mostly in par with the observed data for Guinea and Sierra Leone. We note that, for Guinea epidemic, we have data for the longest range of days as the initial case was in December 2. The estimated model, therefore, captures most of the dynamics of the spread in Guinea in contrast to the other cases. In case of Liberia, our prediction under-estimated the observed data. Our guess is the estimated parameters for Libera may be overfitting the model. While performing some exploratory analysis on the Liberia data, we observed some



(a) Guinea (b) Sierra Leone

(c) Liberia (d) West Africa

Fig. 3: SEIR model fit results for 2014 Ebola epidemic data

discrepancies, e.g. decrease in cumulative value from the previous data points, which may somewhat distorted the model fitting parameters. For the West Africa region plot, our prediction number is much higher that the actual data. This is understandable, as the underlying assumption behind SEIR model is random mixing. Within a country without any movement restriction, this model is some what appropriate. However, for the aggregated model among multiple countries, this assumption is no longer valid due to stricter movement regulations between country borders. Therefore a model with random mixing assumption will over predict the infectious number of cases.

As an extension of the above approach, for find parameters for the model based on the current data, we designed and ran the simulation using mcmc approach with input as time series data for the various infected regions. Initial values for the various parameters were assumed as above for the prior distribution but the range based on the literature was used to find the most appropriate values for the current outbreak. For example β_0 had a range [0,1], β_1 had a range [0,1], infection time($1/\gamma$) had range [3.5,10.7], incubation time ($1/k$) had a range [5, 22] and (τ) had a range [100,150]. The simulation is currently running on a server and we will have results in the final report.

Mapping the compartmental model to the network based model

Due to some inherent challenges with the compartmental models as discussed above, we are using the reproductive rate calculated using above model to simulate the spread of Ebola in the network. We are using the mapping between a compartmental model and a network as proposed by (Chowell et al., 2004; Legrand et al., 2007). using the data provided at

http://networkdata.ics.uci.edu/data.php?id=108 to captures the permanence of many human relationships assuming the network to exist in west Africa impacted by Ebola. The undirected network has 4846609 nodes and 42851237 edges and average degree = 17.7. We calculated the Transmissibility T of a disease which is defined as the average probability that an infectious individual will transmit the disease to a susceptible individual with whom they have contact and also calculated the epidemic threshold T_c which is the minimum transmissibility required for an outbreak to become a large-scale epidemic. Using relation between the basic reproductive number R_0 and the transmissibility T and using values R_0=2.27 and k=17.7

$$R_0 = T\frac{\langle k^2\rangle}{\langle k\rangle - 1}$$

We get the value of Transmissibility as 0.1210.

We calculate the value of epidemic threshold T_c which is defined as

$$T_c = \frac{\langle k\rangle}{\langle k^2\rangle - \langle k\rangle}$$

Here, $\langle k\rangle$ and $\langle k^2\rangle$ are the mean degree and mean square degree of the network to be 0.0598 for the above network. We are using these results to predict average size of the outbreak and to compare more directly the relationships between random mixing model and network model.

IV. Predicting worldwide spread

Approach

TODO: We are looking at modeling using trade data.

Preparing data

TODO: Used public data from the UN and CIA...

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Appendix

TABLE I: Parameter estimation for Ebola SEIR model (Guinea & Sierra Leone)

	Guinea			**Sierra Leone**		
Incidence Dependent Parameters	*Value*		*Comments*	*Value*		*Comments*
Initial Case t_0	December 2, 2013		one person fell ill	April 23, 2014		one person fell ill
S_0	0		-	0		-
E_0	0		-	0		-
I_0	1		-	1		-
R_0	0		-	0		-
C_0	1		-	1		-
Intervention time	March 2, 2014		Gov. of Guinea informed WHO	June 12, 2014		Country declared emergency
τ	110		-	50		-
Estimated Parameters	*Value*	*95% CI*	*Comments*	*Value*	*95% CI*	*Comments*
Incubation Time $1/k$	6.3	-	based on previous works	6.3	-	based on previous works
Infection Time $1/\gamma$	5.4957	[5.43, 5.545]	-	6.36	[6.324, 6.396]	-
β_0	0.2407	[0.2374, 0.244]	-	0.357	[0.3525, 0.3613]	-
β_1	0.2084	[0.2033, 0.2135]	-	0.2012	[0.1994, 0.2028]	-
q	32	[0.1, 100]	-	34	[1.9, 110]	-
Fatality Rate	0.67	-	-	0.38	-	-
R_0	1.323	[1.295, 1.341]	-	2.27	[2.243, 2.298]	-
R_1	1.145	-	-	1.28	-	-

TABLE II: Parameter estimation for Ebola SEIR model (Liberia & West Africa overall)

	Liberia			**West Africa**		
Incidenced Dependent Parameters	*Value*		*Comments*	*Value*		*Comments*
Initial Case t_0	March 31, 2014		official confirmation two infected	December 2, 2013		one person fell ill in Guinea
S_0	0		-	0		-
E_0	0		-	0		-
I_0	2		-	1		-
R_0	0		-	0		-
C_0	2		-	1		-
Intervention time	July 30, 2014		School shutdown	March 2, 2014		Gov. of Guinea informed WHO
τ	120		-	110		-
Estimated Parameters	*Value*	*95% CI*	*Comments*	*Value*	*95% CI*	*Comments*
Incubation Time $1/k$	6.3	-	based on previous works	6.3	-	based on previous works
Infection Time $1/\gamma$	10.7	[8.9,10.7]	-	6.8	-	-
β_0	0.169	[0.168, 0.191]	-	0.2	-	-
β_1	0.0001	[0.0001, 0.1]	-	0	-	-
q	0.0085	[0.0072-0.0264]	-	0	-	-
Fatality Rate	0.67	-	-		-	-
R_0	1.808	-	-	1.36	-	-
R_1	0.001	-	-	-	-	-