A Computational Model For Flight-Based Propagation of Ebola

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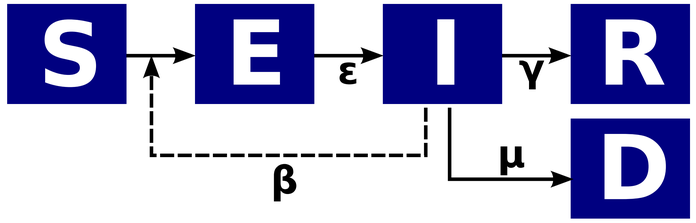
Objectives

- **Estimate the basic reproductive number (R_0) for the 2014 West African Ebola Outbreak.**
- **Simulate a pandemic of the 2014 West African Ebola Outbreak using flight routes.**



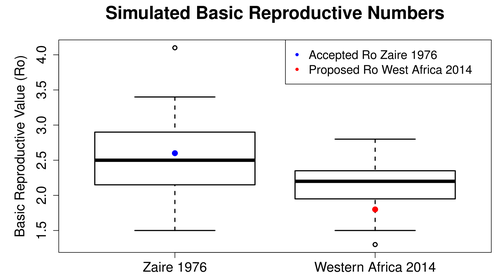


Figure 4 Distribution of the basic reproductive numbers for our model for both the 1976 Yambuku, Zaire and 2014 West African Ebola outbreaks. There was not a statistically significant difference between our model's R_0 values and the reported R_0 for the 1976 outbreak (t = -0.8702, df = 39, p = 0.3895). We found that our model's R_0 values were statistically greater than the estimated R_0 for the 2014 West African Ebola Outbreak (t = 4.6069, df = 22, p < 0.001).

Background

The 2014 West African Ebola Outbreak has been the largest recorded Ebola outbreak yet, with over 12,000 suspected cases and 5,000 recorded deaths. Caused by a strain of the Zaire ebolavirus, it has an average incubation period of 9.6 days and a worldwide mortality rate of 71% within 6 days of the onset of symptoms[1]. One metric for contagion is the basic reproductive number (R_0): a measure of the number of secondary infections caused by a single infectious individual in an otherwise susceptible population[2]. One estimate of R_0 for this strain of ebolavirus is approximately 1.8[3]. This estimate does not, however, take into consideration the possibility of exposed individuals transmitting the disease internationally by means of air travel. To better understand the spread of Ebola on a global scale, we developed a metapopulation network model to estimate the R_0 for Ebola.

Model

We constructed a stochastic, individual based infectious disease metapopulation network model, in which individuals can travel to geographically diverse subpopulations via air transportation. Subpopulations were estimated using a Gridded Population of the World [4]. These subpopulations were then connected by a flight-based transportation network constructed from historical flight data[5,6]. Based on the work of Legrand et al. we used an SEIRD compartment model in which individuals are classified as either susceptible, exposed, infectious, recovered, or deceased[7]. Our model simulates the spread of disease in discrete time steps of 30 minutes to properly capture the timescale of international flights. The spread of Ebola was validated using the R_0 of the 1976 Yambuku, Zaire outbreak and extrapolated using the transmission parameters for 2014 West African outbreak.

Results

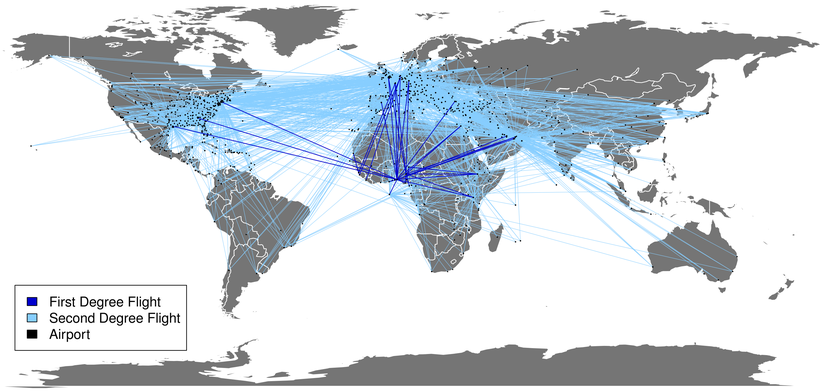


Figure 1 Primary and secondary flights connected to Guinea, Liberia, and Sierra Leone. Although there are a limited number of flights connected to the affected regions, secondary and tertiary connections can transport exposed and infectious individuals to nearly every country in the world.

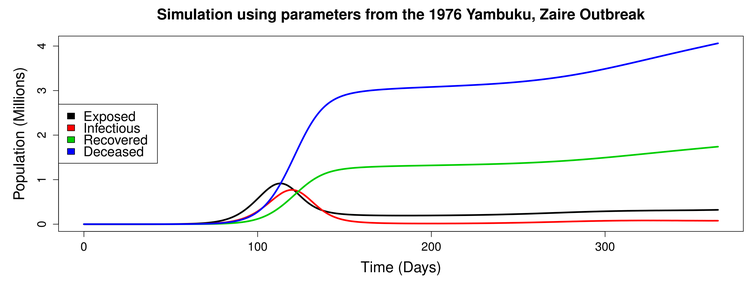


Figure 2 Simulated populations using disease parameters from the 1976 Yambuku, Zaire Ebola Outbreak. We used a mean incubation period of 6 days and a mean recovery time of 6.4 days. We simulated for 365 days at an integration of 30 minutes per time step. We found that the majority of infections occurred in a small number of subpopulations, with occasional importation events in other populations. As Ebola spreads it results in periods of little change in populations punctuated by exponential growth.

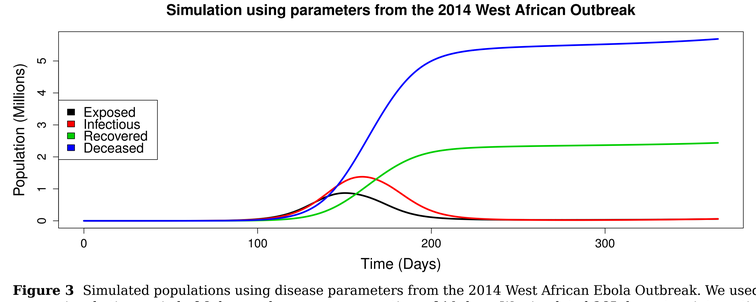


Figure 3 Simulated populations using disease parameters from the 2014 West African Ebola Outbreak. We used a mean incubation period of 6 days and a mean recovery time of 10 days. We simulated 365 days at an integration of 30 minutes per time step. We found that the majority of infections occurred in a small number of subpopulations, with occasional importation events in other populations. It should be noted that the total number of infections is greater in the 2014 outbreak than the 1976 outbreak.

Discussion

For the 1976 outbreak of Ebola in Yambuku, Zaire, our model predicted an R_0 of 2.5. We did not find statistical significance in the difference between our predicted R_0 and the accepted R_0 of 2.6 (t = -0.8702, df = 39, p-value = 0.3895). Based on these results, we are confident that our model accurately predicts the R_0 for other Ebola outbreaks. When we extrapolated our model to the 2014 outbreak of Ebola in Western Africa, our model predicted an R_0 of 2.1. This result is statistically greater than the current R_0 estimate of 1.8 (t = 4.6069, df = 22, p-value < 0.001). We also found that this specific strain of Ebola spreads on average to 1.6 distinct subpopulations per initial infected individual. Our results suggest that there is a high risk that Ebola can become pandemic if the international community does not implement adequate precautionary measures.

Acknowledgments

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