

SIMULATION OF VIRAL INFECTION PROPAGATION THROUGH AIR TRAVEL

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EXECUTIVE SUMMARY

There is direct evidence that commercial air travel spreads common infectious diseases including influenza, SARS, tuberculosis, and measles. This has motivated calls for restrictions on air travel, for example, during the 2014 Ebola outbreak. Such restrictions, however, carry considerable economic and human costs. Ideally, decision-makers ought to take steps to mitigate the likelihood of an epidemic without imposing the above costs. Science-based policy analysis can yield useful insight to decision-makers.

The effectiveness of a policy depends on human response to it. Given inherent uncertainties in human behavior, we simulate a variety of scenarios and identify the vulnerability of policies under these potential scenarios. Supercomputing is used to deal with the large number of scenarios and the need for a short response time in case of national emergencies. Our results identify new boarding procedures that can result in substantial reduction in the risk of the spread of Ebola and SARS.

RESEARCH CHALLENGE

Our goal is to develop models and a novel methodology that can provide insight to decision-makers on policies and procedures that will reduce the likelihood of infection spread during air travel. In addition, our research contributions promise major advances in the disciplinary areas of our expertise—pedestrian movement modeling, mathematics, epidemic modeling, computer science, and bioinformatics—with a consequent transformative effect on transportation infrastructure and management.

METHODS & CODES

We modeled pedestrian movement during air travel as particles based on a force-field approach proposed by Helbing, et al. [1]. Both pedestrian density and speed of immediate neighbor in a pedestrian line determine pedestrian speed and trajectory [2–3]. Our modifications incorporate these aspects into the pedestrian movement model. The pedestrian trajectory information is then integrated with a discrete-time stochastic Susceptible–Infected (SE) model for infection transmission. When i_0^i infectives come into contact with m_i susceptibles estimated by the pedestrian movement model, the newly infected and the probability of their infection

can be estimated using a binomial distribution approximated as Poisson distribution. This accounts for demographic stochasticity and variations in susceptibility of the population. This approach (see Fig. 1) provides insight into the consequences of policy choices that change a passenger’s behavior. We input this information to a global phylogeography model to assess the impact of these policies at global scale. Several airports (Phoenix, Tallahassee, and Daytona Beach) have expressed interest in collaborating with us on developing feasible policies.

Since inherent uncertainties in human behavior and insufficient data during the initial stages of an epidemic make prediction difficult, we parameterize the sources of uncertainty and evaluate vulnerability under different possible scenarios. Even if individual parameters cannot be reliably estimated due to identifiability issues, it may still be possible to precisely estimate a compound quantity of interest, such as the reproductive numbers. We use Blue Waters to deal with the computational load that arises from a large parameter-space.

We link the results of this fine-scale model with a phylogeography model, which uses genetic mutation information and geographic locations of viruses to model the spread of epidemics across large

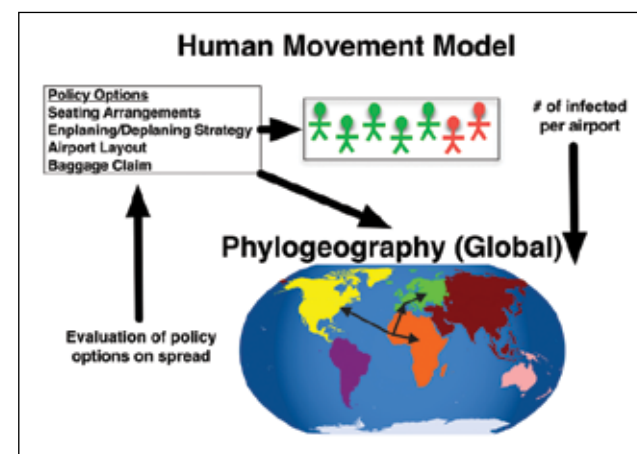


Figure 1: Schematic for combining fine-scale model at airport level with global level phylogeography model. The impact of airport-level public health policies on global disease spread can be evaluated through this approach.

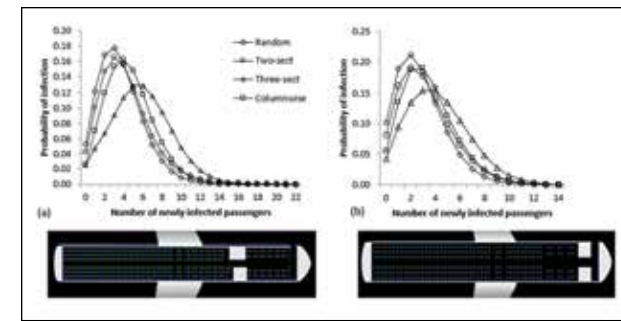


Figure 2: Infection distribution profile at different boarding strategies for: (a) Boeing 757–200 capable of 182 passengers, (b) Airbus A320 capable of 144 passengers. The pictures on the bottom show the corresponding aircraft seating configurations with seats (blue dots) and pedestrians (green dots).

geographic scales. For the phylogeography work, we used Blue Waters to analyze 264 full-genome Ebola sequences from Guinea, Liberia, Sierra Leone, Italy, the United Kingdom, and the U.S., then used the BEAST software on Blue Waters to implement the phylogeography model. As part of this, we specified a generalized linear model (GLM) to study predictors of spread between discrete locations. We used five predictors: worst-case (infection) scenario, best-case scenario, airplane passenger flux between airports, and sample size from the origin and destination. We ran multiple Bayesian Markov-chain Monte Carlo simulations to produce posterior estimates, and also implemented a traditional discrete phylogeographic run without a GLM that evaluated the transmission rate between locations and estimated the routes with strongest support

RESULTS & IMPACT

In prior work, we used the above approach with Ebola, studying the impact of different procedures for boarding, disembarkation, and seat assignment on infection spread. Our results show promise for substantial impact from such choices. For example, we showed that on a 182-passenger Boeing 757 airplane, random boarding can lead to substantial reduction in infection transmission compared with current zone-wise boarding (see Fig. 2). We obtained similar results showing the potential for changes in in-plane movement, deplaning procedure, seating arrangement, and plane sizes in reducing the likelihood of infection transmission. The improvements obtained for individual flights by these policy changes can be of substantial benefit over the course of an epidemic. Based on the transportation data from 2013, if unrestricted air travel were to have occurred during the 2014 Ebola epidemic, then the probability of generating 20 infectives per month from air travel could have been reduced from 67% to 40% using better pedestrian movement strategies. This could further be reduced to 13% by exclusively using smaller 50-seat airplanes. The approach is generic and can be used for other directly transmitted diseases such as SARS.

WHY BLUE WATERS

In a new emergency, due to lack of data, one usually needs to model for a variety of scenarios. This leads to a large parameter space of uncertainties, which requires a large computational effort. In addition, the models typically need fine-tuning, which leads to an iterative process where the model is repeatedly tuned based on results from its previous validation steps. Consequently, rapid turnaround time is critical, which requires massive parallelism. Such parallelism becomes even more crucial during the course of a decision meeting, where results are typically needed in the span of a couple of minutes.

Thus cloud computing is not effective in national emergencies because of the large parameter space and need for quick runtimes during policy decision meetings. After extensive optimization (with support from the Blue Waters team) the simulation time per run is currently around 20 minutes. This can be reduced further only by parallelizing an individual simulation, which is communication-intensive. Again, a cloud environment is not useful.

Among supercomputers available to us, only Blue Waters and Stampede provide the necessary computing power. However, Stampede’s queuing policy prevents large-scale parallelism except in an emergency. An optimized scalable infrastructure cannot be set up unless there is access to large-scale parallelism ahead of the emergency.

PUBLICATIONS AND DATA SETS

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