

CONTAGIOUS DISEASE MODULE FOR THE JOINT EFFECTS MODEL

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ABSTRACT

This presentation describes an approach to modeling the spread of contagious diseases across a population-at-risk represented by the LandScan database used by the Joint Effects Model (JEM). We are implementing two models of disease transmission for this effort: 1) a cohort-based Susceptible-Exposed-Infectious-Removed (SEIR) model that uses historical epidemics and simulated outbreaks as the basis for its time-dependent transmission functions and 2) a small-world network model that defines probabilities of transmitting a disease to people within a local contact network as well as to others with whom there are chance encounters. The resulting module for JEM is designed to be fast-running, scaleable to different populations, and to provide a mechanism for accessing the effectiveness of contagious disease controls such as quarantine and prophylaxis. We are working with Sandia National Labs to use an agent-based model of disease transmission to study the effects agent type, weapon size, attack location, and population density have on disease transmission in order to ultimately develop a method that uses generalized transmission functions and probabilities that can be used across populations of varying sizes and structure.

INTRODUCTION

JEM is an atmospheric transport and health effects model that currently provides simulations for nine biological warfare agents and toxins, including smallpox and plague. Smallpox and plague are contagious diseases that lead to an additional load on medical facilities and resources resulting from the infectious spreading of the disease amongst the population at risk. In order to properly defend against an attack involving smallpox or plague, medical planners must have a robust model that predicts how the disease will spread throughout the population. Our proposed solution to this problem involves leveraging a SEIR model of disease transport as presented by Dr. John Bombardt of the Institute for Defense Analyses (IDA)¹ and a small-world network model of disease spread as presented by Jari Saramaki and Kimmo Kaski of the Helsinki University of Technology².

The two models are required in order to address the challenges introduced by JEM's LandScan population database. LandScan provides a world-wide population database that specifies the population density of 30-arc seconds (1km or finer) squares. JEM allows users to place biological releases anywhere on a map and calculate the hazard areas and health effects as a result of the biological dispersion. The task of creating models of disease spread unique to every region would require tremendous effort and, we hypothesize, unnecessary. By leveraging Sandia National Laboratory's high-fidelity agent-based model³ of disease spread within Portland,

we're studying the factors and parameters that can be generalized and utilized in our SEIR and small-world network models of disease spread so that they can be applied to additional population centers around the world. The task is to find ways to get at the factors that are relevant to a JEM user without resorting to slow-running agent-based models. The proposed factors are:

- The time at which the first generation of exposed individuals become infectious
- High-fidelity new-infection estimates for the beginning of the epidemic
- Epidemic peak in untreated situations
- Epidemic duration in untreated situations
- Total number of infections in untreated situations
- The estimated benefits of vaccination, prophylaxis, quarantine, and isolation

BACKGROUND

Bombardt's SEIR model was originally implemented in the Office of the Surgeon General's (OTSG's) Allied Medical Publication-8 (AMedP-8)⁴. The implementation applied transmission functions derived from historical epidemics of smallpox, plague, and influenza to small, secluded military populations. The model assumes a well-mixed population where each susceptible individual has an equal probability of becoming exposed. Once exposed, an individual has a disease-specific incubation period before becoming infectious and capable of spreading the disease to susceptible individuals. Eventually the individual becomes removed via death or the disease running its course; whatever the mechanism the individual can no-longer transmit the disease to susceptible individuals. The difference equations that guide this process are driven by transmission functions that were derived from historical outbreaks (Yugoslavia and Sweden for smallpox⁵, Mukden and Oakland for plague⁶, and Camp Custer for influenza⁷). The model, with modifications, was transitioned to the Joint Effects Federation (JOEF)⁸ in order to model the spread of disease within small, dynamic populations, but they cannot be transitioned "as is" to JEM due to the large civilian populations presented by the LandScan database.

In order to transition the model to JEM, we had to include a small-world network model of disease transmission. The small-world network is a scalable model that assumes an individual can infect their nearest neighbor (guided by one probability) and can also infect long-distance individuals via chance contacts (guided by another probability). The small-world network model can act on populations of varying sizes and the predicted disease spread won't be restricted to the time and magnitude features of a historical or pre-calculated outbreak. The small-world network model can therefore be used to estimate the peak, duration, and total infections resulting from the epidemic, three of the factors relevant to a medical planner.

Bombardt's SEIR model is able to account for the other factors (start date, high-fidelity estimates of the first several weeks, and the estimated benefits of countermeasures). The historical transmission functions used in AMedP-8 and JOEF do not provide transmission functions adaptable to JEM, however. The transmission functions were from small, isolated communities and do not accurately capture the nuances associated with larger populations. In order to adapt Bombardt's models to large population centers, we are working with Sandia to generate the appropriate transmission functions. The current study is looking at the effects attack point, attack size, and population density have on disease transmission with an eye towards coming up with a set of generalized rules that can be used to apply transmission functions to any large population center.

We are also looking at the effect population-segmentation has on disease spread. Portland is an ideal city for the study due to a large river running through its center. We are working with

Sandia to study how disease spreads across the river and developing an algorithm that clusters populations into subpopulations. The subpopulations will be treated as uniformly mixed populations and their will be transition functions derived to model the spread between subpopulations. The underlying models will be based on equations derived by Bombardt when studying the spread of influenza across separate units stationed at Camp du Valdahon during World War I⁷.

The benefit of Bombardt's model of disease transmission comes from the accurate reconstruction of the outbreaks that the transmission function is derived from. This feature provides us with the start date of the secondary infections as well as the high-fidelity prediction of disease spread during the first several weeks of the epidemic, two of the remaining three factors relevant to medical planners.

The remaining factor, benefit of countermeasures, is achieved by implementing models of population-wide, resource-limited vaccination, prophylaxis, quarantine, and isolation. The vaccination⁵ and prophylaxis⁶ models are adaptations of a model proposed by Bombardt that take into consideration the efficacy of the medications, the quantity available, and the rate at which vaccinations and prophylaxis can be supplied. The quarantine and isolation models are new to this project and are used to remove exposed and infectious individuals from the population at a rate deemed possible by the JEM user.

METHODS

In the first year we developed software modules based on the small-world network model and Bombardt's SEIR model with vaccination, prophylaxis, isolation, and quarantine included.

The current thrust of the program involves studying the effect attack point, attack size, and population density have on the spread of an infectious disease. In order to carry out this study, we are working with Sandia to use their agent-based model of disease transmission that models the daily interactions of routines of people living in Portland to carry out the following experiments:

- Vary the epidemic's starting location in order to study the effect different attack points have on the spread of disease,
- Vary the number of initial infections in order to study the effect different attack sizes have on the spread of disease,
- Randomly remove people from the population at risk in order to study the effect population density has on the spread of disease.

The study will allow us to generalize parameters that predict the spread of disease (the infection probabilities used within the small-world network model and the transmission functions used within the SEIR model). To date, we've begun studying the effect attack point has on the spread of disease. We have run eight different scenarios with different attack points north and south of the Columbia River and have observed a consistent transmission across the Columbia River that still needs to be quantified via transmission functions.

DISCUSSION

Figure 1 shows the output of the SEIR model using a historical transmission function derived from an outbreak in Sweden applied to a population of 50,000 people with 100 initial infections. Figure 2 shows the same outbreak with the following countermeasures turned on:

- 5000 vaccinations per day starting at day 18 up to a maximum of 20,000 vaccinations

- A maximum of 10,000 doses of prophylaxis per day for unvaccinated individuals from days 20 to 60
- 25% of the exposed and susceptible population quarantined with the ability to isolate 500 people

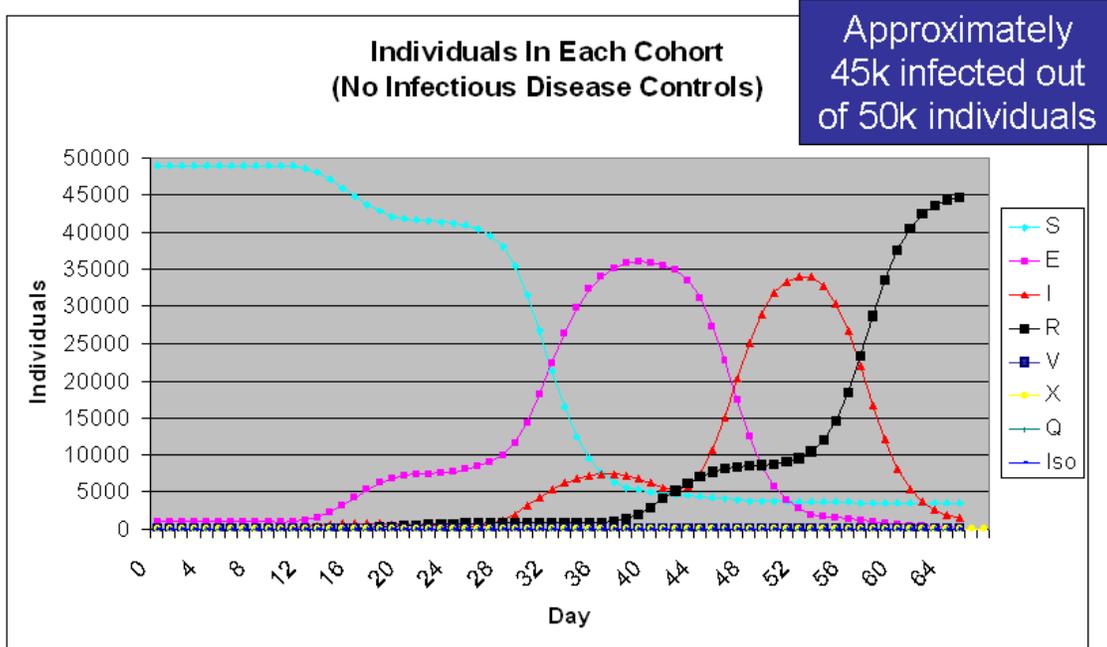


FIGURE 1 – SEIR output for an untreated smallpox epidemic.

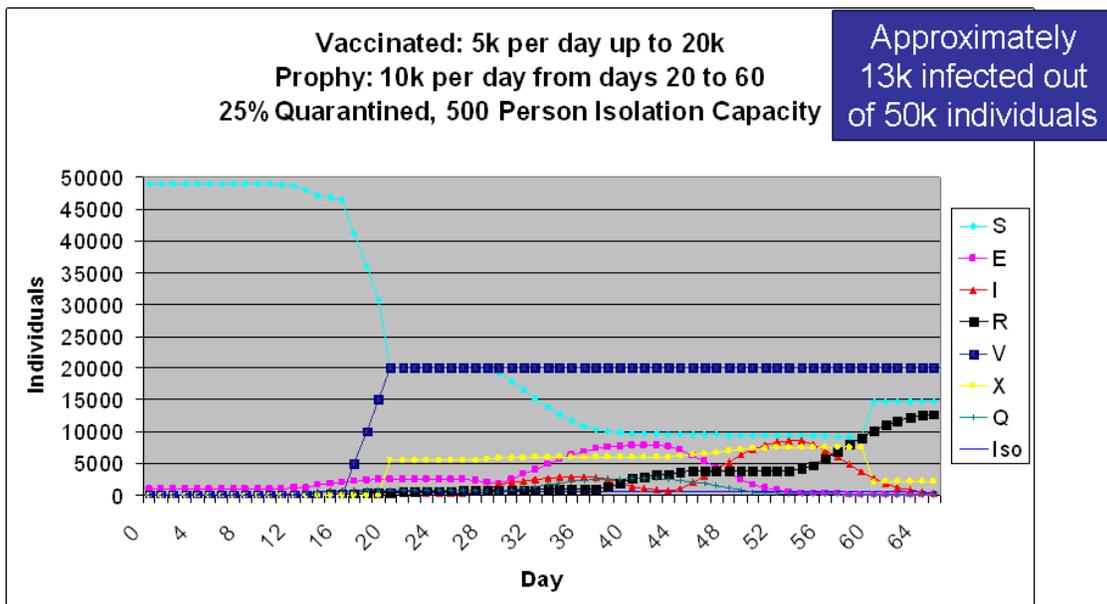


FIGURE 2 – SEIR output for a smallpox epidemic with countermeasures employed.

As evident in both runs, the nuances of the epidemic are represented using the SEIR model. We believe the high-fidelity nature of the epidemics will continue to be captured as we derive

transmission functions from Sandia's output. The above trials were compiled incredibly fast (less than a second for both simulations) and the run-time will not change as we move to larger populations based on the nature of the underlying difference equations.

Figure 3 shows the output from the current implementation of the small-world network model.

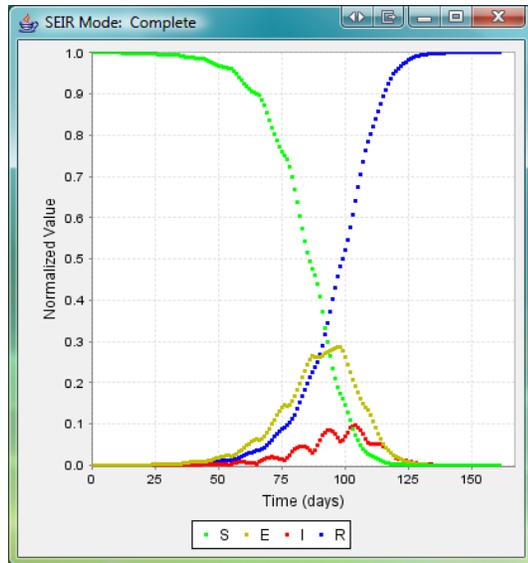


FIGURE 3 – Output from the small-world network model.

within the county of origin, slowly making its way into the other counties. Clark County, however, is much slower to pick up infections from the lower three counties and it is much slower at transmitting infections across to the other three counties. In Figures 5 and 6, where the epidemic begins south of the river, Clark County has a lower rate of new infections compared to the other counties. In Figure 6, where the epidemic starts in Clark County, the spread to neighboring counties is not as drastic as it is in Figures 5 and 6. This indicates that our decision to investigate the effect physical boundaries (in this case, the Columbia River) have on disease spread is justified. We recently ran simulations for five additional starting locations north and south of the Columbia River and that data is currently being processed.

As mentioned, the small-world network model will be used to estimate the duration of the epidemic in untreated cases as well as the day in which the epidemic is expected to peak. In the example illustrated in Figure 3, the epidemic lasts approximately 130 days and peaks at Day 95.

Figures 4 shows Portland and its surrounding counties that are being included in the disease transmission study. Clark County, in Washington State, is a major population center north of the Columbia River. Figures 5, 6, and 7 show the spread of smallpox (as simulated with the Sandia agent-based model) within the four counties (Clark, Multnomah, Washington, and Clackamas) for three different attack areas (Multnomah, Washington, and Clark County, respectively). Looking at the three figures we see that the disease tends to spread



FIGURE 4 – The four counties included in the disease transmission study. Clark County is north of the Columbia River

Starting Point: Multnomah County

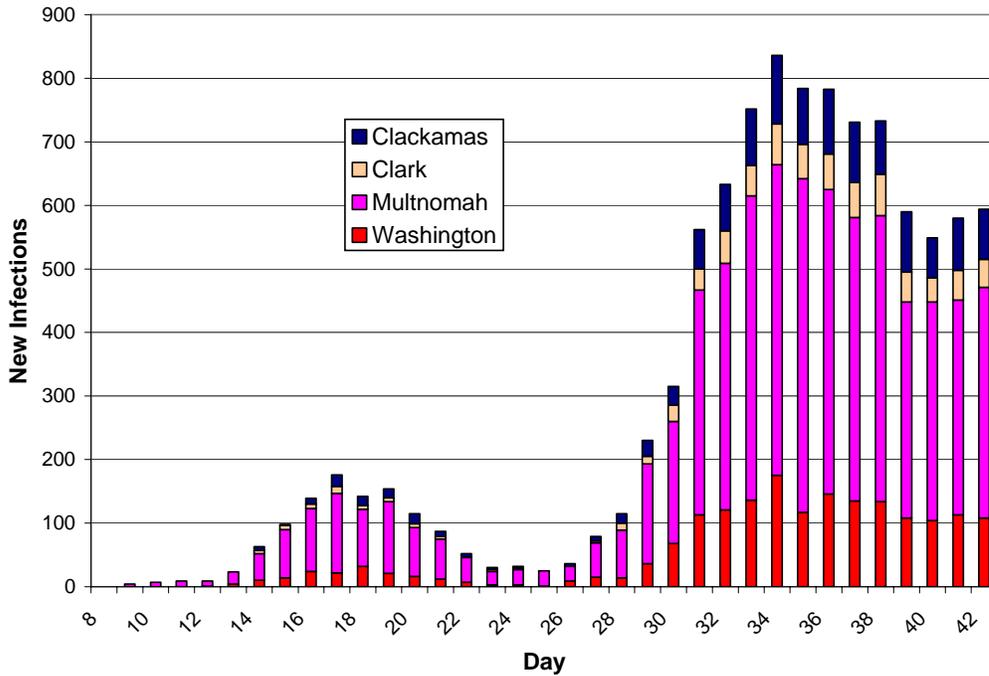


FIGURE 5 – New Infections by county for an epidemic beginning in Multnomah County. Notice Clark County (across the river) has the lowest number of new infections per day.

Starting Point: Washington County

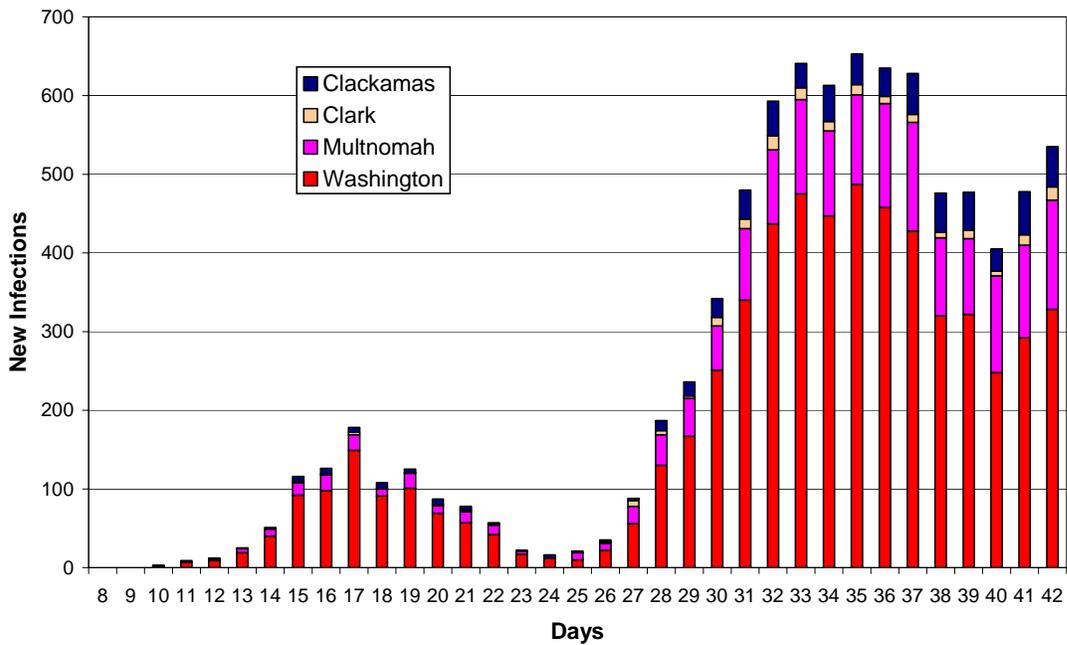


FIGURE 6 – New Infections by county for an epidemic beginning in Washington County. Notice Clark County (across the river) has the lowest number of new infections per day.

Starting Point: Clark County

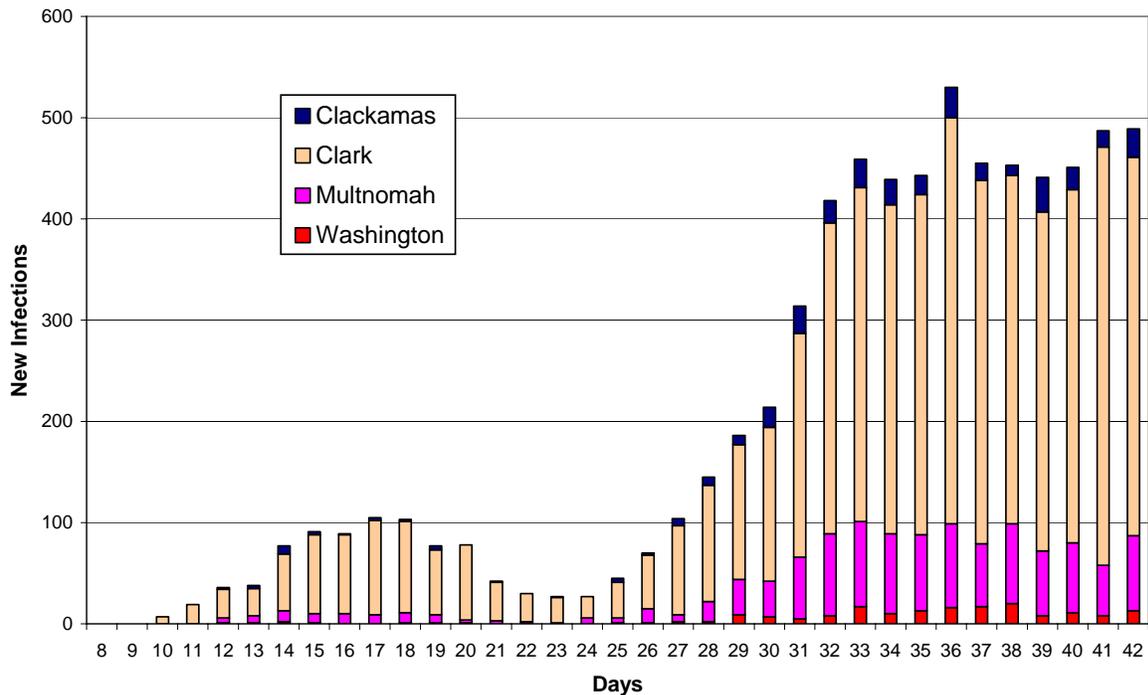


FIGURE 7 – New Infections by county for an epidemic beginning in Clark County. Notice the other three counties (across the river) have a much lower of new infections per day when compared to Figures 5 and 6.

CONCLUSION

The current implementation of the SEIR and small-world network model is in the testing and parameterization phase, guided by the current study of disease transmission in large populations. The software modules being developed are designed to address the challenges presented by JEM's population database. The final product will be a set of robust software modules that are capable of assessing population centers directly affected by a plume, segmenting the population into uniformly mixed subpopulations, and predicting the spread of disease via parameters derived from high-fidelity simulations.

ACKNOWLEDGEMENTS

This work is funded by DTRA/JSTO Project CB07MSB100 under Contract DTRA01-03-D-0066. Mr. Rick Fry of DTRA/CBI is the Contract Officer's Representative (COR). The authors would like to acknowledge Mrs. Stephanie Hamilton, DTRA/CBI and Dr. Rashid Chotani, who served until recently as an A&AS advisor to the effort, for their encouragement and support. This paper was prepared for the Chemical Biological Defense (CBD) Physical Science and Technology Conference held in New Orleans, Louisiana, 12-21 November 2008. Sandia is a multiprogram laboratory operated by the Sandia Corporation, a Lockheed Martin Company, for the United States Department of Energy's National Nuclear Security Administration under Contract DE-AC04-94-AL85000.

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