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Executive Summary

In 1994, the U.S. Army Office of the Surgeon General (OTSG) asked the Institute for Defense Analyses (IDA) to assume the role of maintaining, updating, and standardizing the methodology of the North Atlantic Treaty Organization (NATO) for estimating chemical, biological, radiological, and nuclear (CBRN) casualties. This methodology was documented in the *NATO Planning Guide for the Estimation of CBRN Casualties* (*AMedP-8(C)* and was promulgated by NATO in March 2011 as Standardization Agreement 2553.[1]

One component of this NATO methodology allows users to estimate the casualties that could result from the use of the contagious biological agents plague and smallpox against Allied forces. The current *AMedP-8(C)* contagious disease model considers a single population at risk where individuals are assumed to mix evenly. Military populations, however, are highly structured, and the patterns of movement between units are different from those within them. The IDA research team wanted to understand better whether or not casualty estimates would change if the team's calculations had considered movement and structure, and if the estimates had changed, whether the change was significant enough to warrant a change to the methodology.

In anticipation of this effort, IDA acquired a set of data from the Complex Operations Data Development Activity[2] at the U.S. Army Training and Doctrine Command (TRADOC) Analysis Center, Fort Leavenworth, Kansas, that provided geographic locations of military personnel in Afghanistan over the calendar year 2012. OTSG subsequently directed IDA to "identify and illustrate the application of *AMedP-8* epidemiological models to troop movement data collected in Afghanistan." Using this dataset, IDA developed an analytic representation of a military population (see the figure on the next page). Although the Afghan troop location data proved sufficient for this purpose, it is important to note that, while inspired by actual data, the resulting model is notional, for analytic purposes, and does not provide a realistic depiction of U.S. forces in Afghanistan in 2012.

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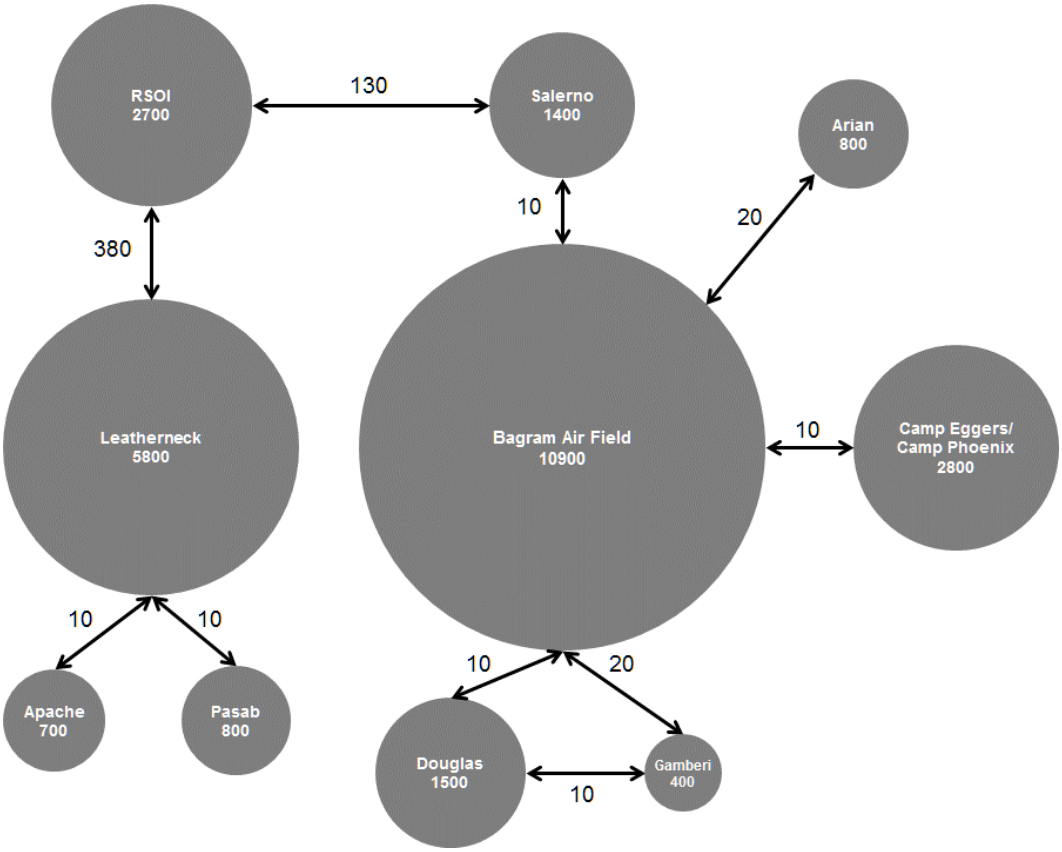
1 North Atlantic Treaty Organization (NATO), *AMedP-8(C): NATO Planning Guide for the Estimation of CBRN Casualties*, STANAG 2553 (Brussels: NATO, March 2011).

2 U.S. Army Training and Doctrine Command (TRADOC) Analysis Center, data excerpted from the Complex Operations Data Development Activity (Fort Leavenworth, Kansas: U.S. Army TRADOC Analysis Center, 2012).



RSOI – reception, staging, onward movement, and integration.

Analytic Representation of a Military Population and Daily Movement Results

To assess the effect of including structure and movement on the casualty estimate, the IDA research team developed a contagious disease model[3] that was able to account for structure and movement in a population. Using the aforementioned analytic representation of a military population, a series of model runs were conducted for smallpox and plague, while varying the number of initial infections and the subpopulation in which they were located, as shown in the following table.

[3] While similar in many respects to the model included in *AMedP-8(C)*, the contagious disease model used in this analysis lacks several features required for NATO casualty estimation. It is not intended to be included, in its current form, in the upcoming revision of *AMedP-8(C)*.

Contagious Disease Modeling Run Design Factor Matrix

No. of Primary Infections	Disease	Structure & Movement	Location of Initial Infections*
1	Plague	Single Population at Risk (PAR)	Bagram Air Field
10	Smallpox	Multiple PARs based on Afghan data	RSOI
100	—	—	Apache

* Considered only in the case of multiple PARs based on Afghan data.

The IDA team ran the model twice with a given set of input parameters: once considering structure and movement (referred to as the *test scenario*) and once without (referred to as the *baseline scenario*). Finally, the team measured the difference between the two sets of casualty estimates in terms of the following three metrics:

1. total numbers of expected casualties,
2. the overall duration of the modeled outbreak, and
3. the time to reach an overall casualty rate of 20%, considered for the purposes of this analysis as a surrogate for the time to reach combat ineffectiveness.

Together, these three comparisons describe differences in both the magnitude of the outbreak and its overall shape.

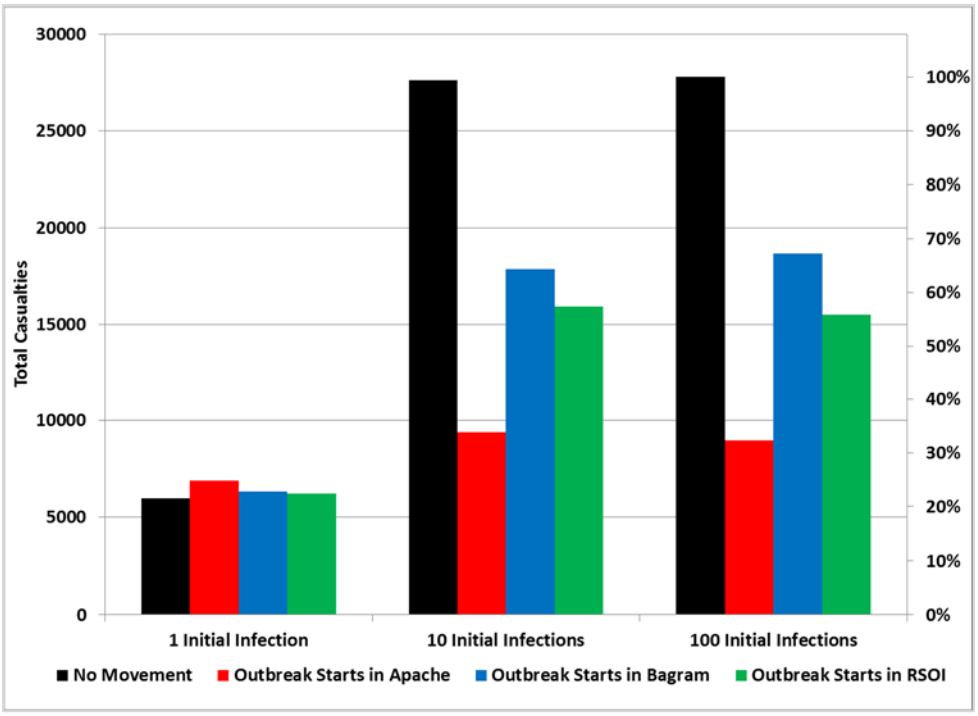
Finally, IDA evaluated the costs and benefits of incorporating population structure and movement into the larger NATO standard CBRN casualty estimation methodology, i.e., *AMedP-8(C)*. Four factors influenced this evaluation:

- mathematical complexity,
- input data requirements,
- time per model run, and
- the magnitude of difference in output casualty estimates.

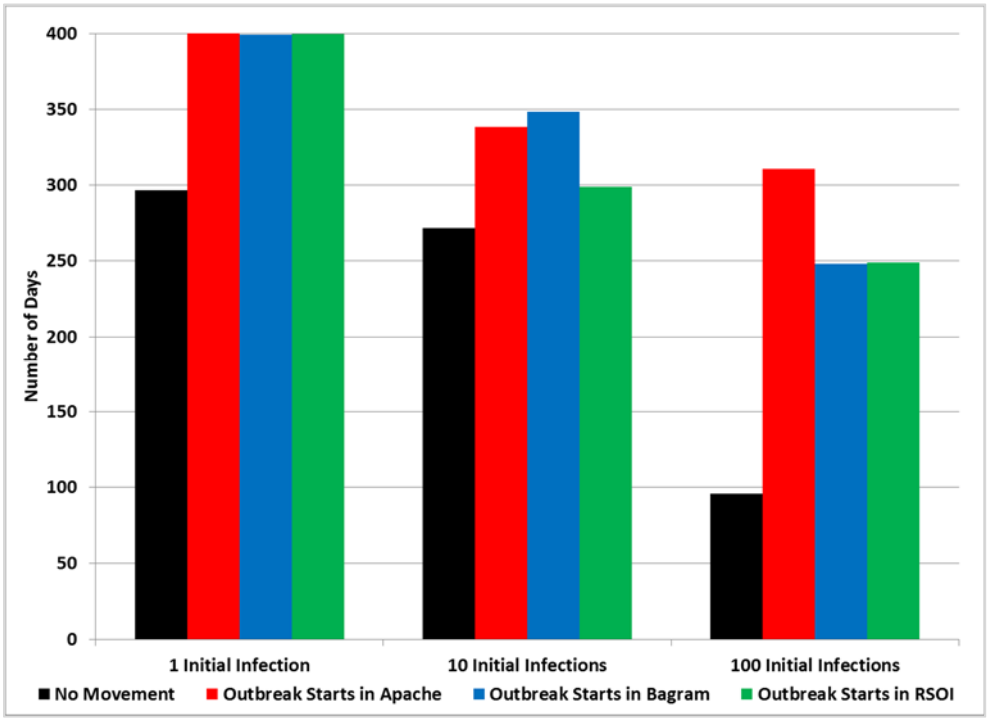
The next three figures show the three comparisons used to quantify the difference between the baseline and test scenarios for the plague projections.

- The first figure shows the total numbers of expected plague casualties.
- The second figure shows the duration of the modeled outbreak.
- The third figure shows the time to reach a casualty rate of 20%.

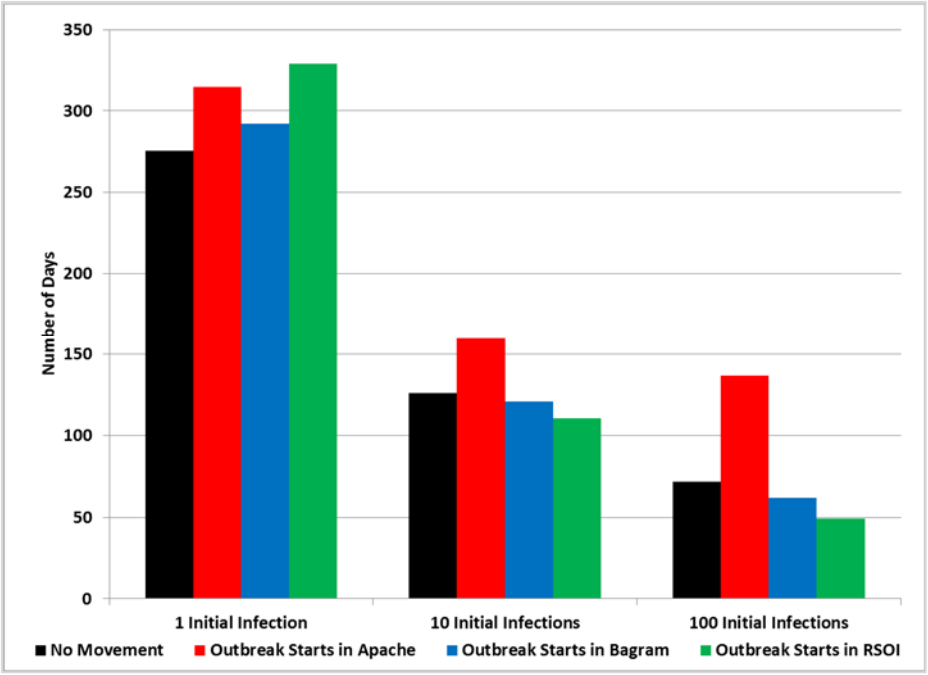
All three figures have in common the baseline and test scenarios for 1, 10, and 100 initial infections at the three locations.



Total Number of Expected Plague Casualties



Duration of Plague Outbreak



Time to Reach Combat Ineffectiveness (20% Plague Casualty)

Including structure and movement will result in a significantly different casualty estimate, as shown in the three comparisons. The total number of infections resulting from the baseline scenarios (without structure and movement) was always greater than those resulting from the test scenarios (with structure and movement). Additionally, the baseline scenarios resulted in shorter outbreaks. For some scenarios, the baseline scenario resulted in an outbreak that infected more than three times as many individuals, but only lasted a third as long as the corresponding test scenarios. The observed differences in the time to reach combat ineffectiveness were not as apparent:

- Some of the test scenarios became combat ineffective earlier than the baseline scenarios, while some became combat ineffective afterwards. This comparison was highly sensitive to the assumed casualty threshold for combat ineffectiveness.
- The large differences observed in the total number of infections and the duration of the outbreaks, including structure and movement, will tend to produce a different, less conservative casualty estimate (i.e., an estimation that predicts relatively longer outbreaks with fewer casualties and, consequently, an outbreak response that would require fewer resources).
- In addition, the ability to model structure and movement within a population allows planners to consider the operational effect of implementing restrictions of movement as a method of curtailing the outbreak.

The added benefits of a more situationally representative casualty estimate and the flexibility to model restrictions of movement associated with the model used in this analysis come at a cost of increased analytic and computational complexity.

- First, the enhanced model requires a user to create an analytic representation of structure and movement for the population at risk. The process of dividing a population of interest into evenly mixed subpopulations connected by specified movement rates is a challenging task. Even when data on populations and movements, such as the data on U.S. deployed forces in Afghanistan used in this analysis, are available, numerous simplifying assumptions must be made to incorporate the data into the model.
- Second, the implementation of movement between the single populations at risk (PARs) as a random process dramatically increases the computational complexity of the model. For each set of inputs, the model requires multiple executions to generate meaningful results. While the computational efficiencies of parallel processing were utilized, certain simulations required hours or days to complete.
- Furthermore, it is unclear how many runs are adequate to produce meaningful results for a given modeling scenario as well as how much variation is expected between individual trials. Both questions represent knowledge gaps that would require additional analysis to fill.

It is important to reiterate the fact that the methodology presented in this analysis is distinct from the contagious disease model in *AMedP-8(C)*. It is not intended to be included "as is" in an updated version of *AMedP-8(C)*: the methodology would need additional enhancements to account for all the features required in an updated version of *AMedP-8(C)* (e.g., medical treatment). Additionally, to overcome the acknowledged limitations of this model, alternative methods for considering population structure in a contagious disease model should be explored. Particular attention should be paid to the manner in which the time-varying disease transmission rates are calculated and employed.

On balance, the IDA team believes that the purpose of an updated version of *AMedP-8(C)*—support for medical planning—would be adequately served by the relatively conservative estimates generated without structure and movement, especially for small numbers of initial infections. Moreover, at the present time, the NATO casualty estimation methodology must be implemented manually, making the complexities of considering population structure and movement prohibitive at the moment. However, if casualty estimates are to reflect expected restrictions of movement in the population at risk, or if the casualties in a specific subpopulation are of a particular interest, then the advantages of structure and movement outweigh the costs associated with the analytic complexities.

Contents

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1. Introduction

In 1994, the U.S. Army Office of the Surgeon General (OTSG) asked the Institute for Defense Analyses (IDA) to assume the role of maintaining, updating, and standardizing the methodology of the North Atlantic Treaty Organization (NATO) for estimating chemical, biological, radiological, and nuclear (CBRN) casualties. This methodology is documented in the *NATO Planning Guide for the Estimation of CBRN Casualties* (*AMedP-8(C)*.[4] *AMedP-8(C)* was promulgated by NATO in March 2011 as Standardization Agreement 2553.

The current *AMedP-8(C)* contagious disease model considers a single population at risk, where individuals are assumed to mix evenly. Military populations, however, are highly structured, and the patterns of movement between units are different than those within them. As the IDA research team is now in the process of updating *AMedP-8(C)*, the team wanted to better understand (1) whether or not casualty estimates would change if their calculation considered movement and structure, and (2) if estimates changed, whether the change was significant enough to warrant a change to the methodology.

In anticipation of this effort, the IDA team acquired a set of data from the Complex Operations Data Development Activity at the Army Training and Doctrine Command Analysis Center[5] (TRADOC), Fort Leavenworth, Kansas, which provided geographic locations of military personnel in Afghanistan in the calendar year 2012. The sponsor subsequently directed IDA to "identify and illustrate the application of AMedP-8 epidemiological models to troop movement data collected in Afghanistan." Using this dataset, the team developed an analytic representation of a military population. Although the Afghan troop location data proved sufficient for this purpose, it is important to note that, while inspired by actual data, the resulting model is notional, for analytic purposes, and does not provide a realistic depiction of US forces in Afghanistan in 2012.

To assess the impact of including structure and movement on the casualty estimate, the team developed a contagious disease model[6] that was able to account for structure and

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4 North Atlantic Treaty Organization (NATO), *NATO Planning Guide for the Estimation of CBRN Casualties* (*AMedP-8(C)*), STANAG 2553 (Brussels: NATO, 2011).

5 U.S. Army Training and Doctrine Command (TRADOC) Analysis Center, data excerpted from the Complex Operations Data Development Activity (Fort Leavenworth, Kansas: U.S. Army TRADOC Analysis Center, 2012).

6 The contagious disease model used in this analysis and the model included in *AMedP-8(C)* share common antecedents but diverge in several important respects, as the latter is a simplified adaptation of the methodology, and is intended to meet the specific needs of the *AMedP-8(C)* intended users (see Appendix A). The model described in this document would also need additional functionality to meet

movement in a population. Using the aforementioned analytic representation of a military population, a series of model runs were conducted for two diseases (smallpox and plague), while varying the number of initial infections and subpopulations in which they were located. The team ran the model twice with a given set of input parameters: once considering structure and movement (referred to as the test scenario) and once without (referred to as the baseline scenario). Three comparisons were then used to quantify the difference between the two casualty estimates, as depicted in Figure 1:

- The first comparison is between the total number of people who became infected over the duration of the outbreak.
- The second is between the duration of the outbreak.
- The third is between the amount of time required for 20% of the population to become infected.

Together, these three comparisons describe differences in both the magnitude of the outbreak and its overall shape.

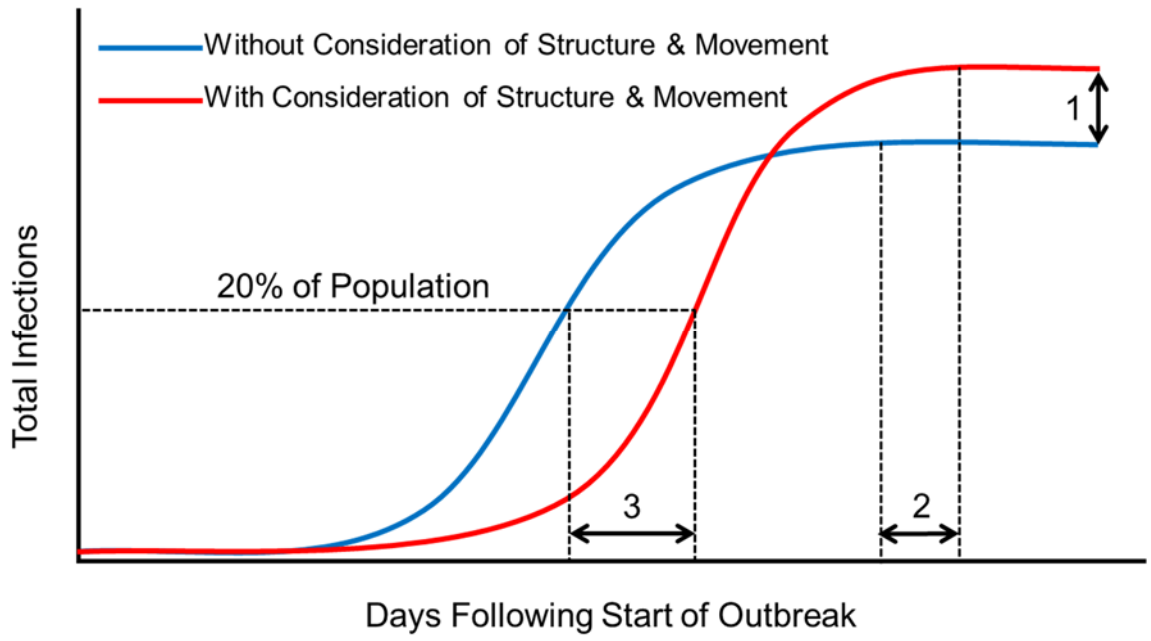

Figure 1. Notional Sets of Results: Cumulative Number of Infected People Resulting from a Casualty Estimate

the requirements of the upcoming revision of *AMedP-8(C)*, to be designated *AMedP-7.5*. The purpose of this analysis is, in fact, to determine whether the *addition of structure and movement* would be desirable for the contagious disease portion of the *AMedP-7.5* methodology.

Finally, IDA evaluated the costs and benefits of incorporating population structure and movement into the larger NATO standard CBRN casualty estimation methodology. Four factors influenced this evaluation:

- mathematical complexity,
- input data requirements,
- time per model run, and
- magnitude of difference in output casualty estimates.

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2. Methodology

A. Overview

The current *AMedP-8(C)* contagious disease model considers a PAR. It assumes that any susceptible member of the population is equally as likely to become infected as any other member. While this assumption of a single population may be valid in some scenarios, it may not realistically describe the organizational and geographical structure of a deployed military population, where interactions are highly structured, and where the patterns of movement between units are different than those within them. To assess the impact of incorporating structure and movement into the population on the casualty estimate, a new contagious disease model was developed.

The models of contagious disease incorporated into *AMedP-8(C)* are adapted from a set of models developed by Dr. John Bombardt and are already in general use at IDA for a variety of studies and analyses. These models rely on a traditional Susceptible-Exposed-Infectious-Removed (SEIR) epidemiological approach. A SEIR model classifies members of the population as being part of either

- S (susceptible to infection),
- E (exposed but non-contagious),
- I (infectious/contagious), or
- R (removed as source of infection) cohort.[7]

Additionally, these models incorporate a time-varying disease transmission rate, colloquially referred to by its variable name, β.

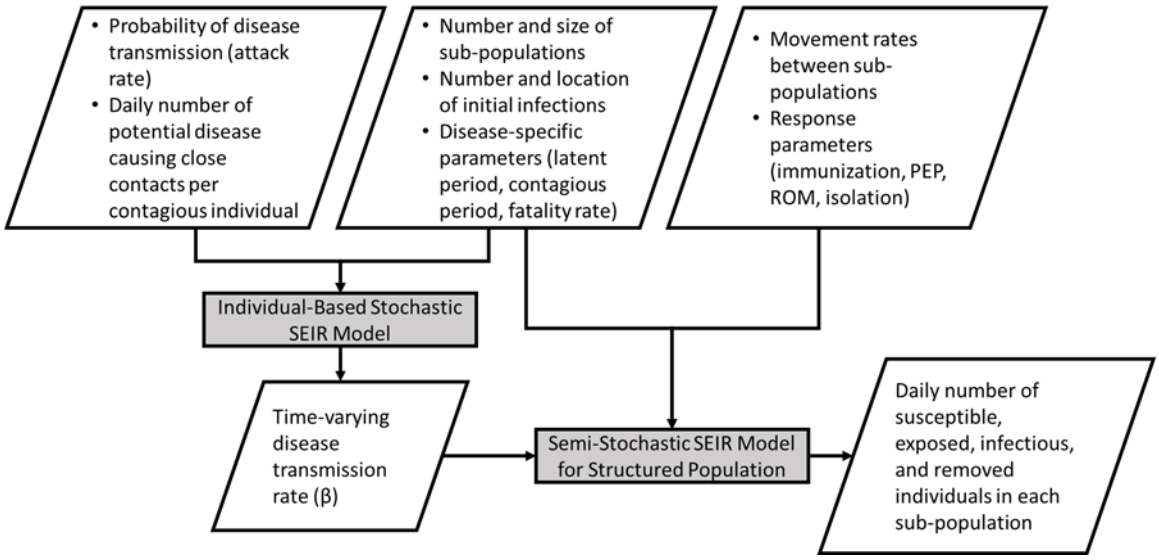
The contagious disease model used in this analysis was adapted from the "basic epidemic model for an unstructured population" model for SARS (Severe Acute Respiratory Syndrome) presented in Bombardt's most recently published work (hereafter

[7] The SEIR model and its variants are well described in the literature; the Bombardt work typically cites one well-known publication on the subject, D. T. Haydon, M. E. J. Woolhouse, and R. P. Kitching, "An Analysis of Foot-and-Mouth-Disease Epidemics in the UK," *IMA Journal of Mathematics Applied in Medicine & Biology* 14 (1997): 1–9.

referred to as Bombardt's SARS model).[8] The IDA team enhanced Bombardt's SARS model in two ways:

- First, a new method of determining the time-varying disease transmission rate was developed.
- Second, the model was adapted to allow for the consideration of any number of subpopulations with specifiable movement rates between each subpopulation.

Both of these enhancements are discussed in depth in subsequent sections of this chapter. An overview of the methodology used in this analysis is shown in Figure 2.



PEP – post-exposure prophylaxis. ROM – restriction of movement.

Figure 2. Methodological Flow of Contagious Disease Model

The first step is to obtain the input data and parameters for generating the time-varying disease transmission rate. These input parameters are

- the probability of disease transmission (often referred to as the attack rate);
- the daily number of potential disease causing close contacts per contagious individual (as observed in a historical outbreak);
- the number and size of the subpopulations;
- the number and location of the initial infections; and
- the disease-specific latent period, contagious period, and fatality rate.

[8] John N. Bombardt, "Congruent Epidemic Models for Unstructured and Structured Populations: Analytical Reconstruction of a 2003 SARS Outbreak," *Mathematical Biosciences* 203 (2006): 171–203.

The Individual-Based Stochastic SEIR Model uses this set of inputs to derive the time-varying disease transmission rate, β. The methodology then uses this β function, together with user-defined movement rates between subpopulations, and the parameters used to model response measures (e.g., immunization or post-exposure prophylaxis) as inputs to the Semi-Stochastic SEIR Model for Structured Population. This model determines the daily number of susceptible, exposed, infectious, and removed individuals in each subpopulation. The overall methodology can be used to generate the following:

- a simple casualty estimate (i.e., the cumulative number of symptomatic individuals over time), or
- a more sophisticated assessment of disease propagation (e.g., the time at which the disease first appears in a previously uninfected subpopulation).

Each of the two SEIR models shown previously in Figure 2 is discussed in the following sections.

B. Individual-Based Stochastic SEIR Model

As mentioned above, one of the adaptations that was made to Bombardt's model was a new method of calculating the time-varying disease transmission rate, β. In Bombardt's published work, as well as the methodology included in *AMedP-8(C)*, the time-varying disease transmission rate was calculated from a historical outbreak of the specific disease being modeled. The manner in which the β values were calculated resulted in a transmission rate strongly linked to the historical outbreak. This was done by backtracking from either *daily fatalities* or *daily symptom onsets* to determine the number of new infections per day.

As the result of the close relationship of the β values with the historical outbreak from which they are derived, the β values force the *modeled outbreak* to behave similarly to that of the *historical outbreak*. While this behavior was ideal for the purpose of recreating a past outbreak, its application towards a wide range of analytic scenarios was limited. In other words, the predictive utility of the model was dependent upon the similarities between the epidemiological circumstances of the historical outbreak and those of the scenario being modeled.

- To lessen the model's dependencies on the circumstances of historical outbreaks, for this analysis the IDA team used a new methodology for calculating a time-varying disease transmission rate. This new methodology is not entirely independent of an historical outbreak and still requires a well-documented outbreak for each disease.
- The new method for calculating β values is based on the standard incidence assumption, mean results from an individual-based stochastic SEIR model—in

which the population is tracked at the level of individual people—and the number of initial infections in the population.

Each infected individual has a randomly selected incubation and contagious period, as well as having a random chance of surviving the disease. Additionally, the transmission of the disease from one individual to another is also a random event.

The probability of any one contagious individual infecting a susceptible individual is calculated from two random variables:

- the daily number of close contacts per contagious person and
- the probability of disease transmission.

The values for these two random variables can be derived from the literature on historical outbreaks of disease and from other model parameters. The probability of disease transmission, sometimes referred to as the *attack rate*, can be found in the literature for certain disease outbreaks. Given the probability of disease transmission, the daily number of close contacts per contagious person can be calculated from historical outbreak data.[9] Once values for these two random variables are known, the stochastic SEIR model can be run and the resulting numbers of daily new infections, contagious individuals, and susceptible individuals, are used to calculate β.

Although the β values calculated from this new methodology have the same interpretation as those calculated using the Bombardt method—the daily rate at which each contagious person transmits the disease to members of the susceptible population— the numeric values themselves differ. Furthermore, the outbreak dynamics predicted by the SEIR model using these two different β values will differ dramatically. In other words, if one were to compare two modeled scenarios in which all parameters except for the β values were the same, the results of the SEIR models would be substantially different. The results of the scenario modeled using β values calculated using Bombardt's original methodology would appear similar to the historical outbreak. In the case that the modeled scenario had an identical number of initial infections as the historical outbreak, the model would reproduce the historical outbreak. However, the results of the scenario modeled using the newly developed method of calculating β values will be dissimilar to the historical outbreak. Since the epidemiological circumstances associated with a future outbreak may or may not be similar to those of a historical outbreak, the newly developed method of calculating β—which uses some inputs that are *disease specific* but not necessarily *outbreak specific*—may be more applicable to a range of analytic scenarios.

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[9] The process of calculating the daily number of close contacts per contagious individual requires an estimate of the daily number of contagious individuals (i.e., the I cohort) and the daily number of new infections for the historical outbreak.

C. Semi-Stochastic SEIR Model for Structured Population

The model used in this analysis further differs from Bombardt's SARS model in the consideration of population structure and movement. In Bombardt's SARS model, it was assumed that disease spread through a single PAR, wherein it is assumed that individuals are mixed uniformly—any susceptible individual has an equal chance of becoming exposed. To consider structure and movement within military populations, IDA took an alternative approach.

In lieu of a single PAR, the model used in this analysis subdivides the population into multiple subPARs, each of which can be thought of as a military unit, organizationally and/or geographically distinct from others. Each of these subPARs is assumed to be evenly mixed, and outbreaks of disease are evaluated separately for each subPAR. The rate at which the disease spreads within a PAR is determined by a set β values calculated for that specific PAR and number of initial infections.[10] Outputs are then summed over all subPARs for the population as a whole. This division of the population into subPARs is the way in which the model now represents *structure*.

Movement in the model is now represented by the removal of an individual from one cohort in one subPAR, and insertion of that individual into the same cohort in another subPAR, a process that is conceptually the same as that used to represent physical and medical control measures. Movement between subPARs can be defined in terms of rates or absolute numbers of individuals. These individuals are randomly selected from within a subPAR and can be from any cohort; the probability that an individual will be pulled from a given cohort at any given time is determined by the proportional representation of that cohort within the subPAR at that time. It is important to note that while only integer numbers of people can move between the subPARs, within each subPAR disease progression and transmission is not tracked on an individual basis.

The random selection of individuals from specific cohorts represents a significant departure from past contagious disease modeling conducted at IDA. All prior models were entirely deterministic (i.e., for a given set of input parameters the model will always produce the same results). By incorporating a random process, the selection of individuals to move from certain cohorts, the model now contains a stochastic element, and therefore each run of the model for a given set of input parameters will not return the same result.

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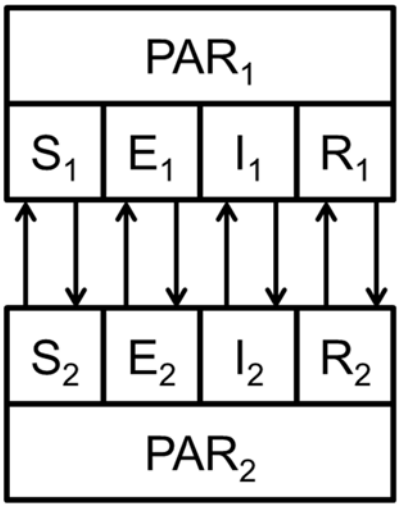
[10] The methodology used to calculate the β values for any population assumes that the infection is introduced into the population at a single point in time (Day Zero) in the form of a number of initial infections who are all on the first day of their latent period. However, each subPAR in the SEIR model will experience the arrival and departure of members of both the E and I cohorts on days following the start of the outbreak. These arrivals and departures are not accounted for in the methodology used to calculate the β values, and it is currently not clear to the research team how this inconsistency will affect the results of the model. Additional development of the model, namely the manner in which the β values are calculated, and employed, is necessary to fill this knowledge gap.

To capture the inherent variability with the random process, the model is run numerous times for a given set of input parameters and the results can be statistically assessed.

Figure 3 provides a notional representation of population structure and movement as now considered for military populations. Each rectangle represents an evenly mixed subPAR, while the arrows represent the specified movement between each subPAR. As suggested by Figure 3, this model allows individuals from any of the four cohorts (S, E, I, or R**)** to move from one subPAR to another, with the exception of those who died of their infection (i.e., fatalities).



Note: S (susceptible to infection); E (exposed but non-contagious);
I (infectious/contagious); R (removed as source of infection), a type of cohort.

Figure 3. Notional Depiction of Population Structure and Movement

Representation of structure and movement in this way is conceptually similar to the way military units are typically represented for modeling purposes—as groups of individuals sharing a common geographic location, with interactions between units at different locations. Therefore, required input data could be generated from the types of force laydowns used as inputs to other components of the *AMedP-8(C)* methodology, such as calculation of individual CBRN challenges.[11]

[11] Carl A. Curling and Sean M. Oxford, *NATO Allied Medical Publication 7.5 Study Draft 2 (AMedP-7.5 SD.2): NATO Planning Guide for the Estimation of CBRN Casualties*, IDA Paper NS P-5154 (Alexandria, VA: Institute for Defense Analyses, November 2014), 1-7.

D. Analytic Representation of Structure and Movement

To assess the difference in a casualty estimate that considers structure and movement within the population to one that does not, an analytic representation of structure and movement needed to be defined. Specifically, the population size of each subPAR and the number of people moving between each of the subPARs needed to be defined. For the analysis at hand, IDA used data acquired from TRADOC on U.S. forces deployed in Afghanistan for calendar year 2012. This data set was gathered via SPOT-JAMMS (Synchronized Predeployment and Operational Tracker – Joint Asset Movement Management System). SPOT-JAMMS captures location information for US military personnel, government civilians, and contractors at data collection points established in operational theaters. These data collection points are typically the locations where personnel swipe identification cards to gain access to facilities at a specified geographic location, such as a dining hall. SPOT-JAMMS used the identification card swipes to record the daily location of each individual service member while he or she was deployed in Afghanistan at a location with a data collection point.

TRADOC provided IDA with SPOT-JAMMS data in the form of twelve separate Microsoft Excel spreadsheets, one for each calendar month in 2012. Each spreadsheet provides unique individual swipes—one per person per day—for each of the 28 most populous locations in theater during that month. Movement among these locations could be derived from this data by tracking changes to the swiping locations of individual service members.

Although the data obtained from SPOT-JAMMS provides a detailed account of personnel locations and movements, there were several limitations in its ability to be used in this analysis.

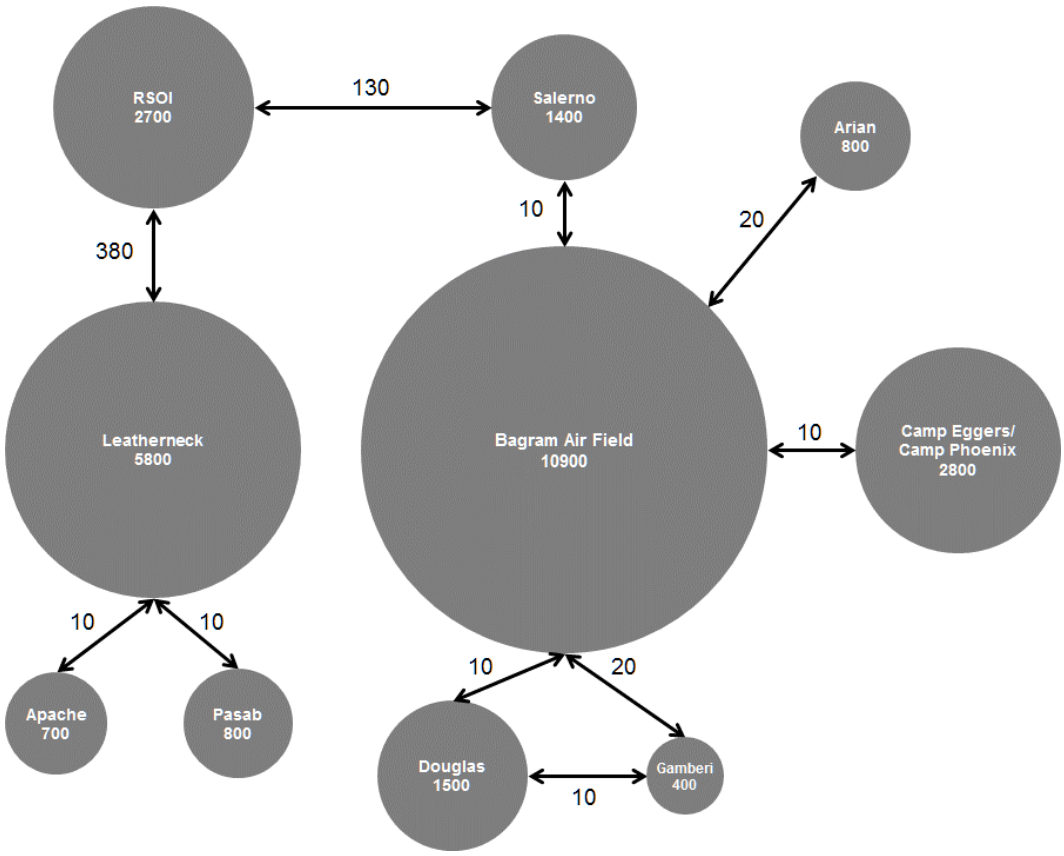
- First, individuals are likely to swipe their badge multiple times a day, and possibly at multiple locations; while SPOT-JAMMS only reports one swipe per person per day, to avoid overcounting individuals, the rules by which a swipe is selected for reporting are unclear. For example, an individual may routinely swipe at the same location each morning or evening, and at others throughout the day. Depending on which swipes were reported, a significant amount of individual movement could be unreported in the data set.
- Second, the location names used in the data set were often vague and ambiguous. Some of the locations were part of the same larger facility, for example dining facilities on an airbase. The IDA team made an effort to identify all such collocated data collection points. Some were found simply by the name used in the data set (e.g., “Camp Leatherneck #1” and “Camp Leatherneck #2”) but some required a review of open source literature. In some cases, location names were too ambiguous, and associating the name with an actual facility was

impossible. All locations that could not be associated with a larger facility were assumed to be geographically or organizationally separated.

- Finally, and most importantly, the SPOT-JAMMS data set provided to IDA is incomplete. SPOT-JAMMS data collection points are not present at all troop locations in theater, and the percent of deployed personnel locations captured by the system on a daily basis is unknown.
  - Although the data provided included personnel locations for the entire year, only an approximate third of all locations gathered by SPOT-JAMMS—the 28 most populous—were included for each month.
  - This limitation is a function of the format in which the data were provided—SPOT-JAMMS recorded over three million unique card swipes each month, but only about one million could be recorded in a single Microsoft Excel file because of the limits on the number of rows in each spreadsheet.
  - The locations included in each month's dataset varied from month to month. Because of the incompleteness of the data set, IDA was able to determine the total number of people present at only some of the locations for each day.
  - The only personnel movements that IDA could track were those between the 28 most populous SPOT-JAMMS collection locations. Movements to other locations—including many that collected SPOT-JAMMS data and all that did not—were not captured in the data set.

Even with these limitations, IDA was able to derive a notional representation of a military population from the SPOT-JAMMS data that could be used analytically for purposes of assessing the effect of structure and movement on casualty estimates. Shown in Figure 4, this representation is derived from a subset of SPOT-JAMMS data and includes the population at those locations that appear in a sufficient number of the provided spreadsheets such that a network of movement between locations could be established.[12]

[12] In other words, some locations had enough personnel to warrant inclusion in the analytic representation as shown in Figure 4 but none of those personnel moved to or from any other location in the analytic representation; because these locations would be completely isolated from disease within the model, they would have no impact on the outcome. Consequently, the IDA team chose to exclude them from consideration.



RSOI – reception, staging, onward movement, and integration.

Figure 4. Analytic Representation of a Military Population and Daily Movement Results

Each circle in the figure represents a location with its average daily population represented by the area of the circle as well as numerically; the total population across all locations is 27,800 personnel. The arrows and numbers between the circles represent the movement between the locations and the number of people moving each day. To ensure that the population of each location was constant during the modeled outbreak, it was assumed that the daily number of people exiting each location was exactly equal to the daily number of people arriving at each location.[13] For simplicity, the IDA team excluded movement between locations of fewer than ten people per day.

Although based on recorded movements of deployed military personnel, because of the significant limitations of the available SPOT-JAMMS data set, in no way should this

[13] In reality, the number of individuals present on a day at any one location will change with time, and movement between locations will vary. As modeled, however, variable movement rates would, eventually lead to a consolidation of the population within one large PAR, hence defeating the purposes of the analysis. Thus for analytical purposes, the IDA team assumed that the population at each location is constant over the duration of the outbreak.

representation be construed as a complete or realistic depiction of U.S. forces deployed in Afghanistan in 2012.

To understand the impact of structure and movement on casualty estimates, IDA designed and conducted a series of model runs, using the contagious disease model and the analytic representation of a military population described above. Model outputs included the number of individuals estimated to be in the S, E, I, and R cohorts by day and by subPAR. As shown in Table 1, the IDA team tested the sensitivity of outputs to various factors by modeling different diseases (smallpox or plague), the numbers of primary infections, and locations of primary infections.

Table 1. Contagious Disease Modeling Matrix

No. of Primary Infections	Disease	Structure & Movement	Location of Initial Infections*
1	Plague	Single PAR	Bagram Air Field
10	Smallpox	Multiple PARs based on Afghan data	RSOI
100	–	–	Apache

* Considered only in the case of multiple PARs based on Afghan data.

For each combination, the IDA team generated a set of baseline casualty estimates that considered the population at risk as a single entity, with a population of 27,800, equal to that of the combined population of all locations shown in Table 1 above. The team then generated a second set of casualty estimates that incorporated structure and movement, using the analytic representation shown in. Finally, the team measured the difference between the two sets of casualty estimates in terms of the following three metrics:

- total numbers of infections,
- the overall duration of the modeled outbreak, and
- the time to reach an overall casualty rate of 20%, considered for the purposes of this analysis as a surrogate for the time to reach combat ineffectiveness.

3. The Effect of Population Structure and Movement on Casualty Estimates

A. Plague Results

The baseline casualty estimates for 1, 10, and 100 initial plague infections, all occurring simultaneously on Day Zero, in a single population without considering structure and movement are shown in Figure 5. As modeled, without return to duty or replacement of personnel,[14] the entire population of 27,800 personnel would be expected to eventually become casualties as a result of either 10 or 100 initial infections.

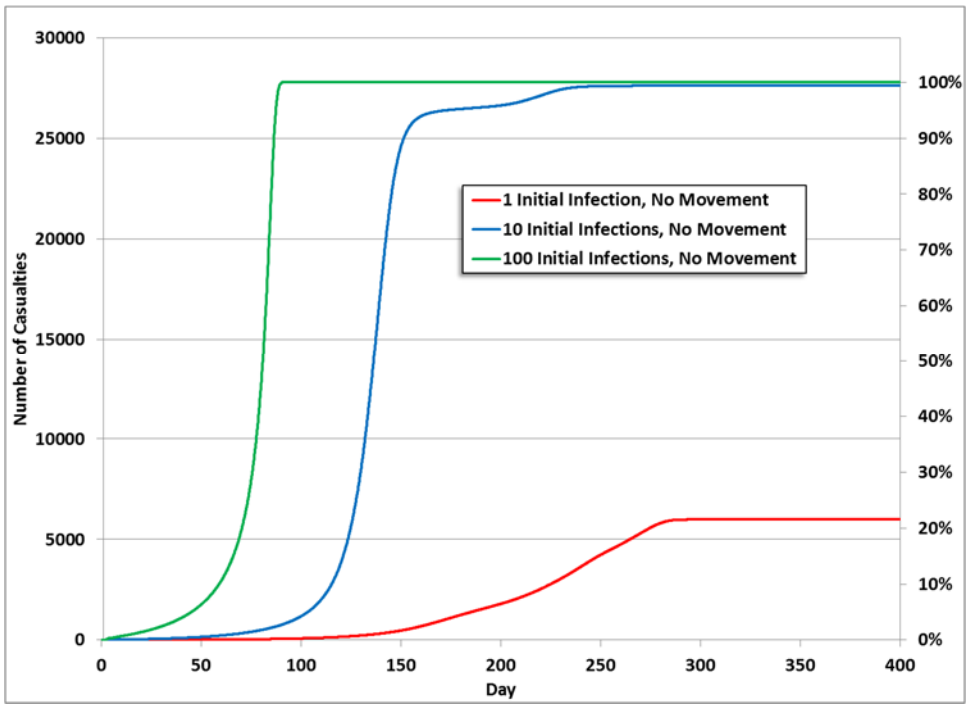


Figure 5. Baseline Estimates of Plague Casualties over Time

[14] Both of the diseases modeled for this paper have high morbidity and high mortality rates—in the case of plague, nearly 100% in the absence of prompt treatment. Because of the seriousness of the associated illness, it is reasonable to assume that individuals who become sick will not return to duty during the course of the outbreak. Of course, those who die are lost to the unit permanently. Individual and unit replacement are likely as long as an operation continues in this environment, but consideration of this response is complex and model results would then be highly sensitive to assumptions about the timing of personnel replacement. For simplicity, replacement of personnel is not considered in this analysis. Note, though, that within the model, augmentation of the S cohort at a rate equivalent to the movement of the population into the R cohort would in general lead to an increase in the overall number of casualties; this simplification, therefore, will tend to underestimate the number of expected casualties.

In the 10 initial infections case, the entire population becomes infected roughly 250 days after the start of the outbreak, and in the 100 initial infections case, the entire population becomes infected by 75 days. In the case of one initial infection, the total number of expected casualties is just under 6,000, reached at 275 days after the start of the outbreak.

Figure 6 shows expected casualties over time for all plague scenarios modeled. The results shown for the test scenarios (colored lines) correspond to the mean values from 100 statistical trials. As shown for 10 and 100 initial infections, the cases that considered structure and movement had fewer total numbers of casualties than the baseline had. For these same cases, the outbreak progressed more quickly than in the baseline at the beginning of the outbreak but had a longer duration. For one initial infection, the results were very similar in both baseline and structure and movement cases.

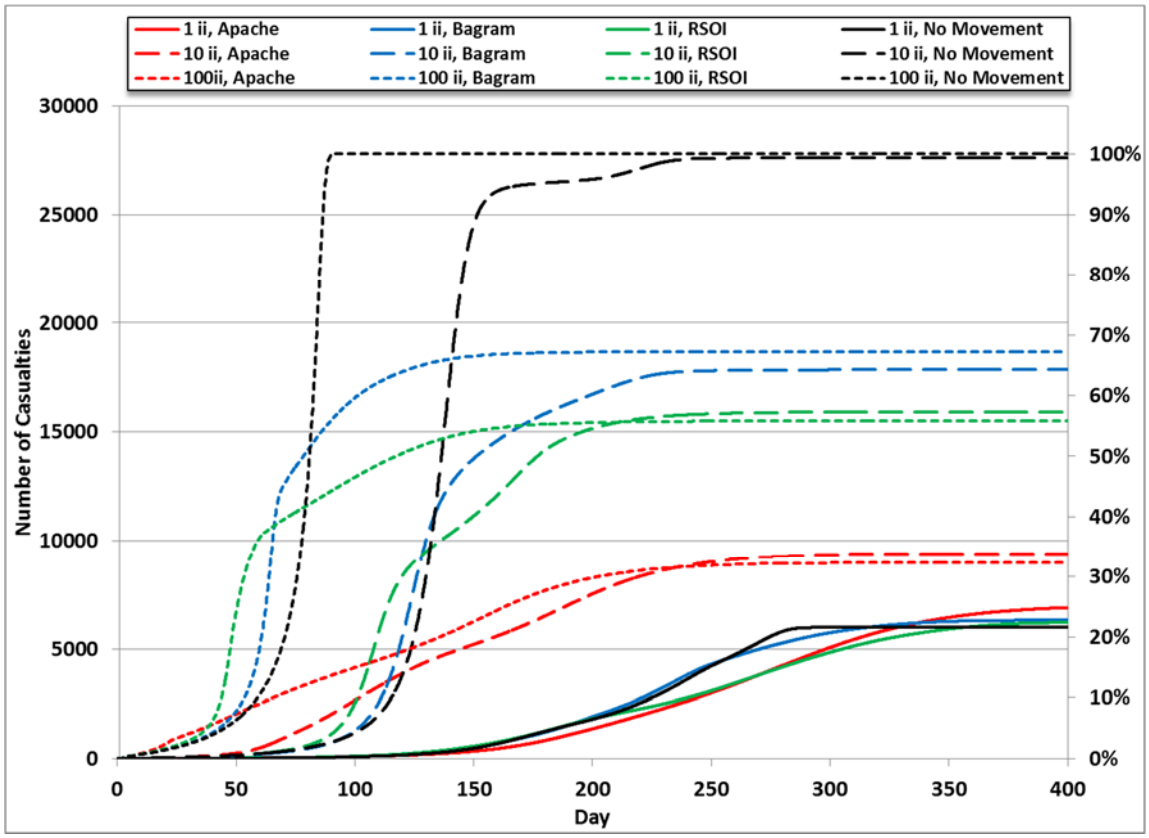


Figure 6. Expected Plague Casualties over Time for Baseline and Test Scenarios

Over the next two pages, Figures 7 through 9 show the three comparisons that were used to quantify the difference between the baseline and test cases.

- Figure 7 shows the total numbers of expected plague casualties.
- Figure 8 shows the duration of the modeled outbreak.
- Figure 9 shows the time to reach a casualty rate of 20%.

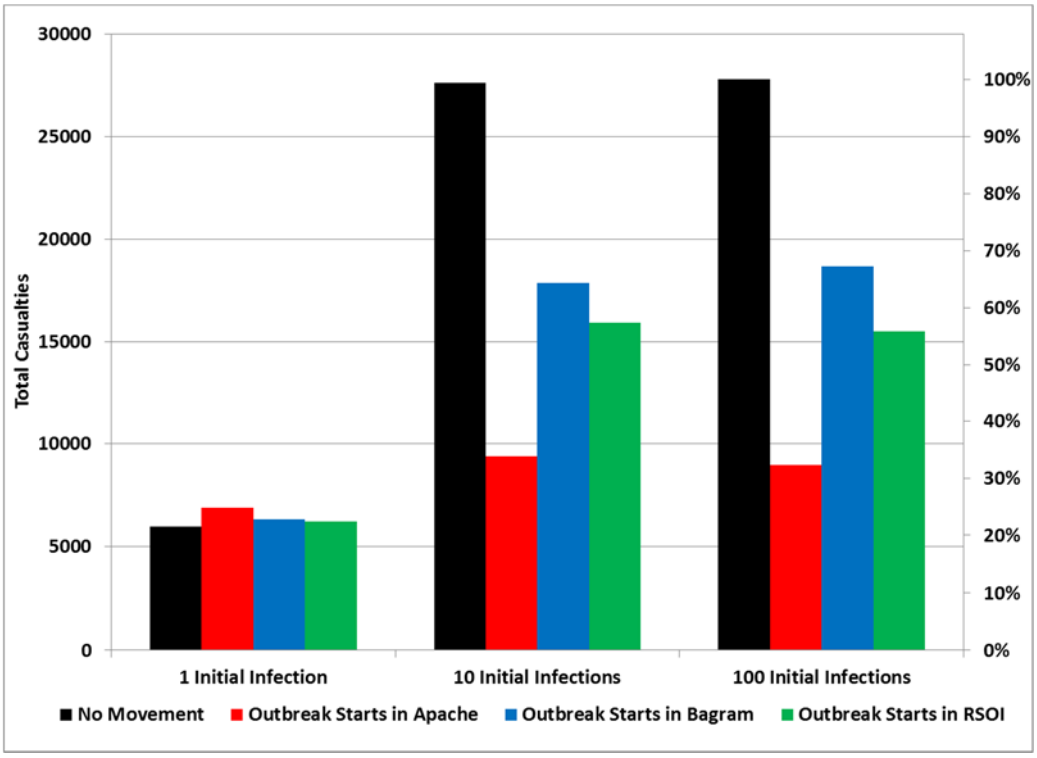


Figure 7. Total Number of Expected Plague Casualties

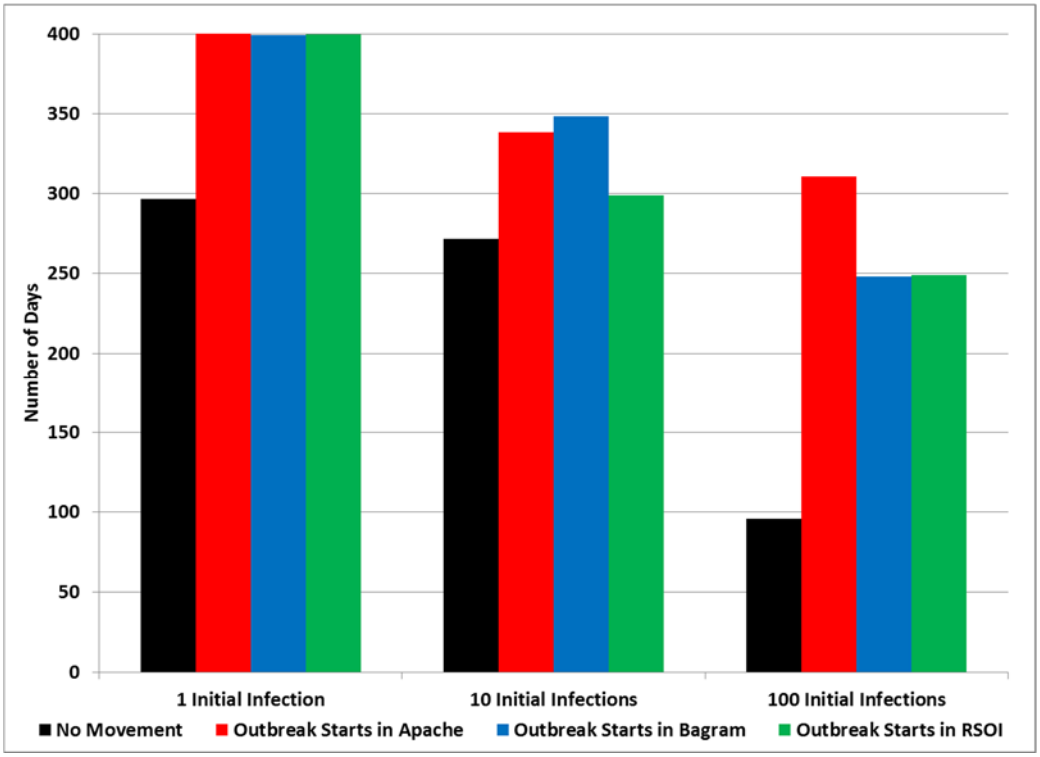


Figure 8. Duration of Plague Outbreak

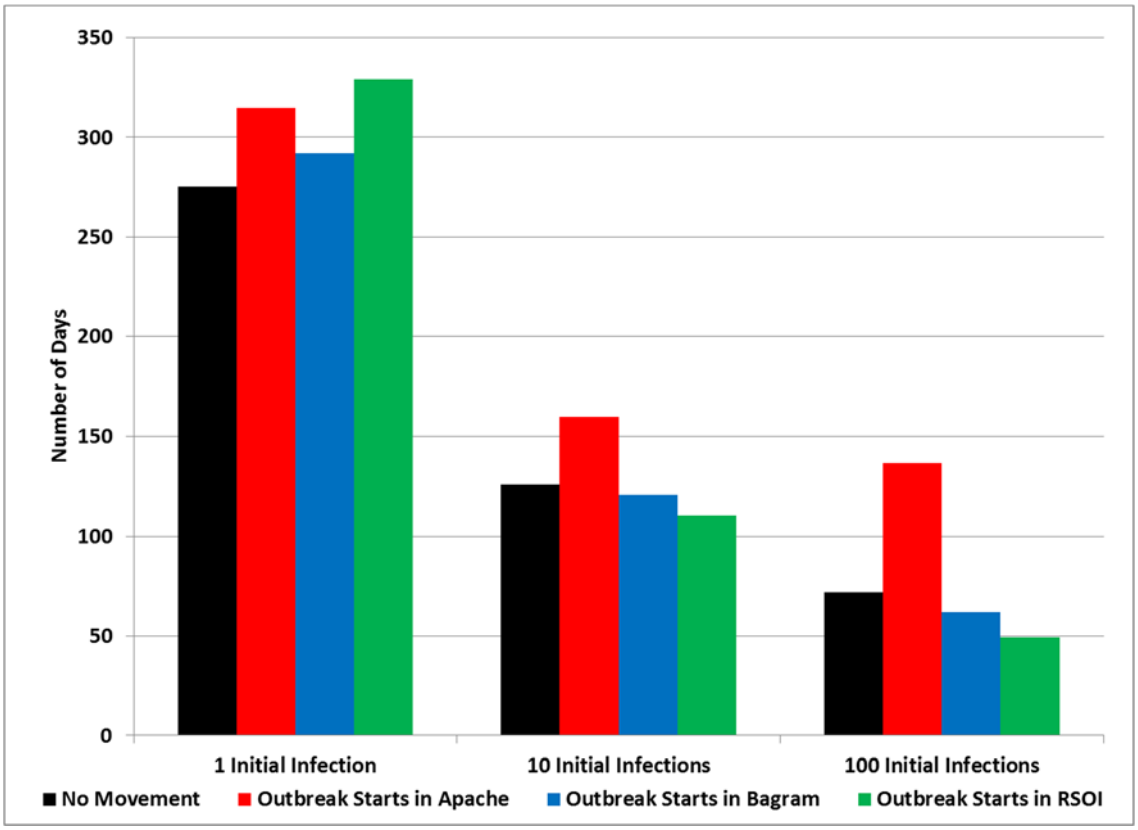


Figure 9. Time to Reach Combat Ineffectiveness (20% Plague Casualty)

B. Smallpox Results

The smallpox results are presented in the same manner as the plague results. The baseline casualty estimates for 1, 10, and 100 initial smallpox infections in a single population without considering structure and movement are shown in Figure 10. Without return to duty or replacement of personnel, the entire population of 27,800 personnel would be expected to eventually become casualties as a result of either 10 or 100 initial infections. In the 10 initial infections case, the entire population becomes infected roughly 300 days after the start of the outbreak, and in the 100 initial infections case, the entire population becomes infected by 200 days. In the case of one initial infection, the total number of expected casualties is just over 16,000, reached at 600 days after the start of the outbreak.

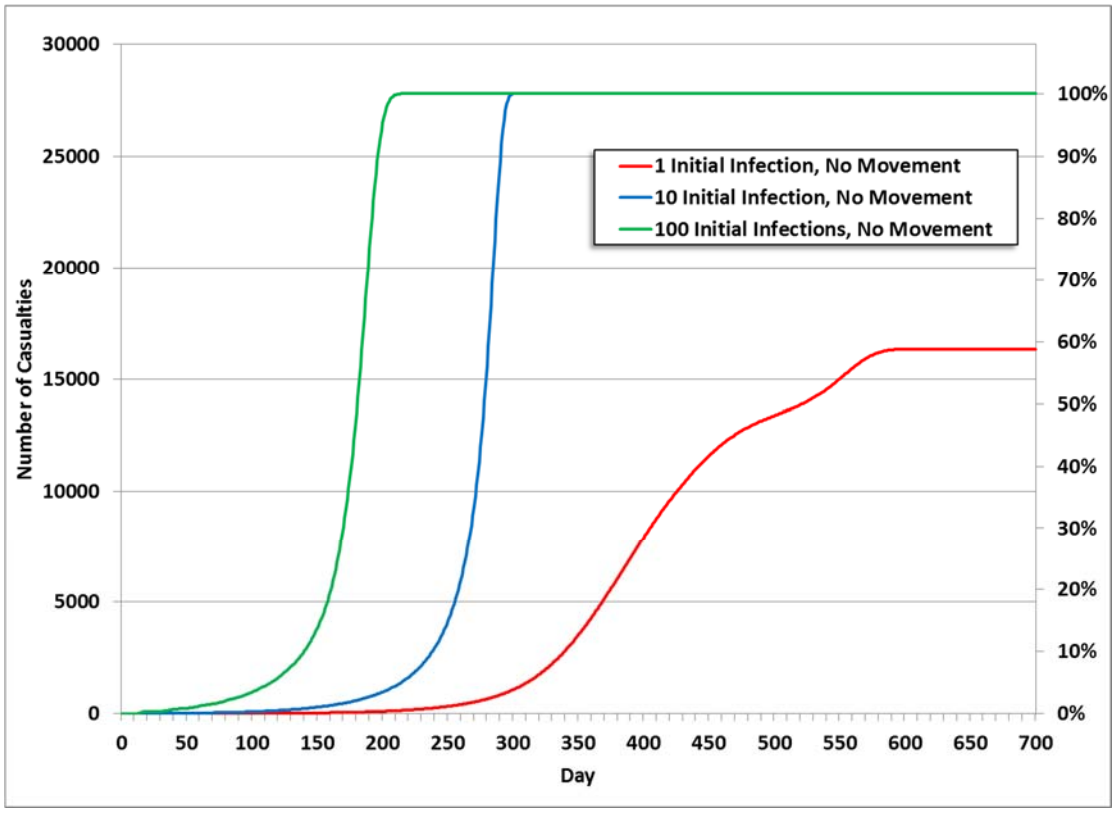


Figure 10. Baseline Estimates of Smallpox Casualties Over Time

Figure 11 shows expected casualties over time for all modeled smallpox scenarios. The results shown for the test scenarios (colored lines) correspond to the mean values from 100 statistical trials. As shown for 10 and 100 initial infections, the cases that considered structure and movement had fewer total numbers of casualties than the baseline. For these same cases, the outbreak progressed more quickly than in the baseline at the beginning of the outbreak but had a longer duration. For one initial infection, the results were very similar in both baseline and structure and movement cases.

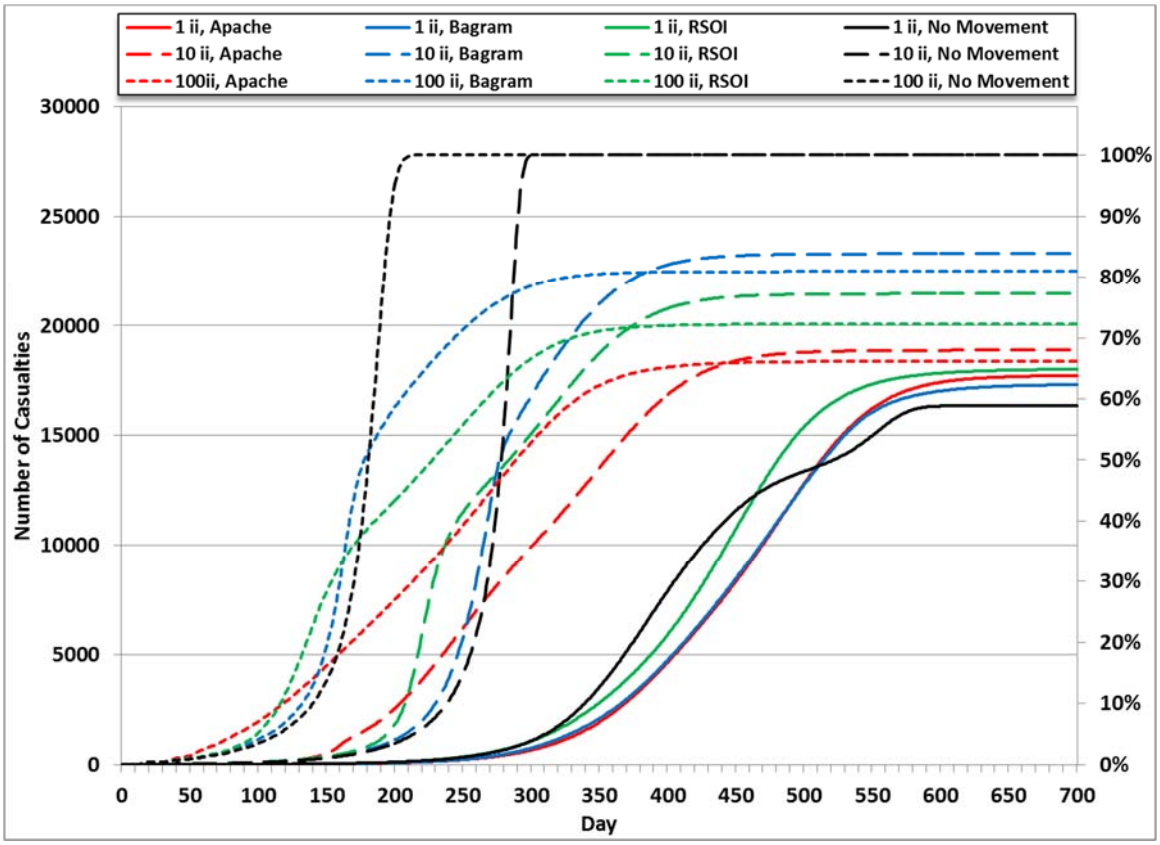


Figure 11. Expected Smallpox Casualties Over Time for Baseline and Test Scenarios

Figure 12 through Figure 14 show the three comparisons that were used to quantify the difference between the baseline and test cases. Figures 12 through 14 are baseline and test scenarios for 1, 10, and 100 initial infections at three locations.

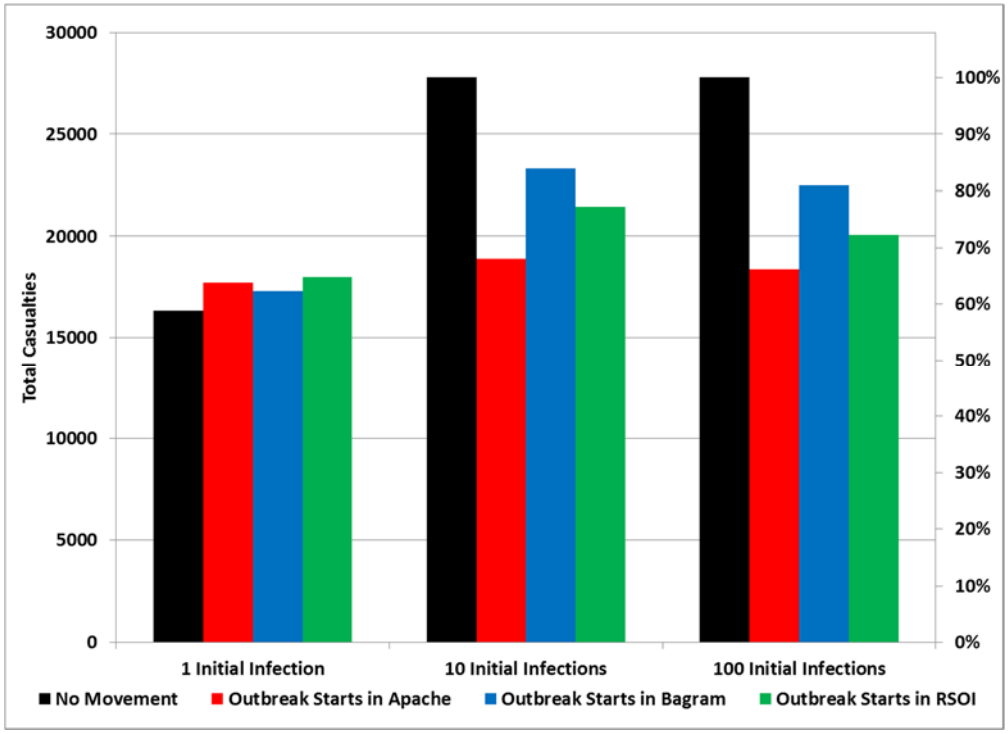


Figure 12. Total Number of Expected Smallpox Casualties

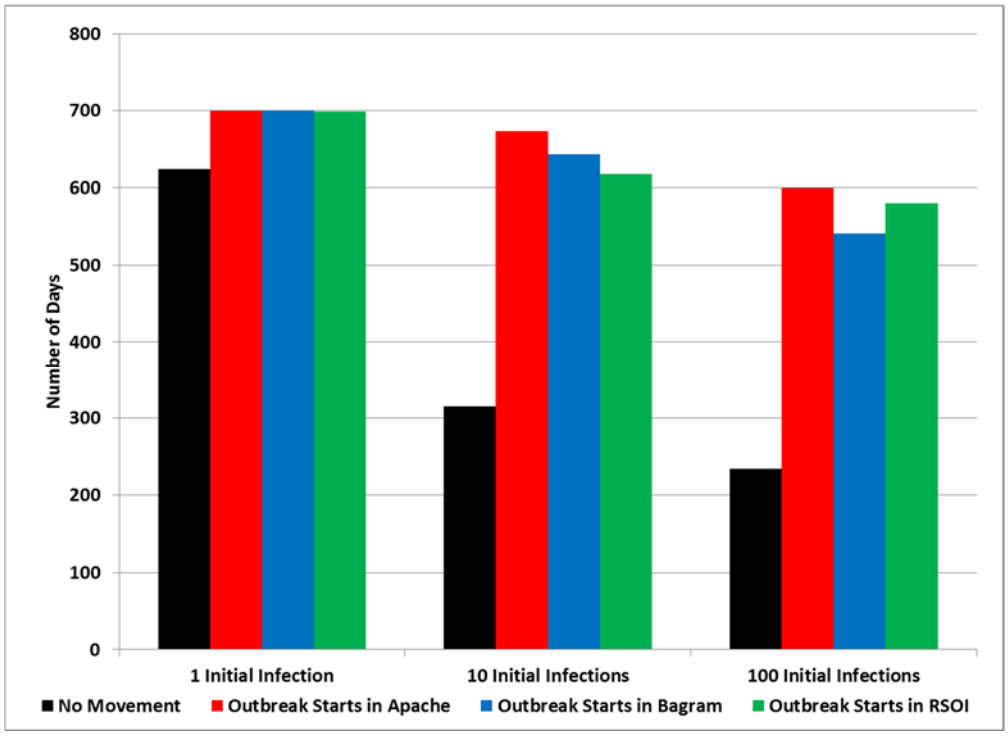


Figure 13. Duration of Smallpox Outbreak

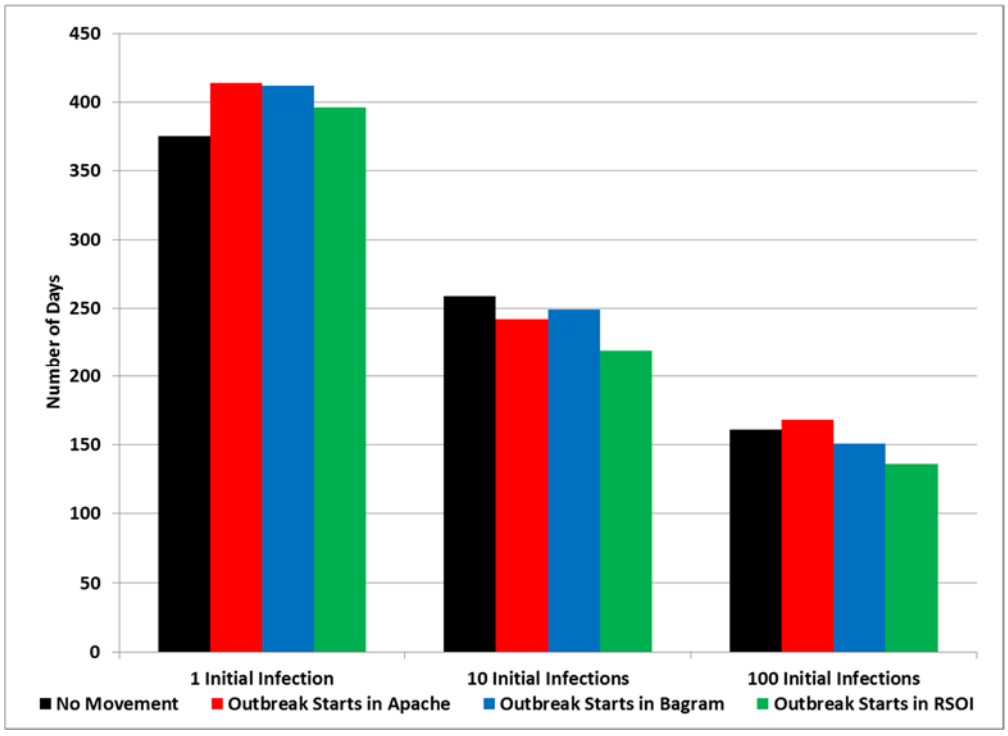


Figure 14. Time to Reach Combat Ineffectiveness (20% Smallpox Casualty)

C. Discussion of Results

To assess the effect of population structure and movement on casualty estimates from contagious diseases, the IDA team compared two scenarios:

- the results of the baseline scenarios, which did not include structure and movement,
- and the results of the scenarios that included structure and movement, hereafter referred to as the test scenarios, for both plague and smallpox.

Metrics used for these comparisons were

- total numbers of infections (see section 1 below),
- the overall duration of the modeled outbreak (see section 2 on the next page), and
- the time to reach an overall casualty rate of 20%, considered for the purposes of this analysis as a surrogate for the time to reach combat ineffectiveness (see section 3).

1. Comparing Total Numbers of Infections

The IDA team observed similar trends in the total numbers of infections in the results of the plague and smallpox scenarios. For scenarios involving 10 and 100 initial infections, more cases of disease occurred in the baseline scenarios than in the test scenarios, as shown previously in Figure 7 and Figure 12. Additionally, the number of total infections is correlated with the population of the PAR in which the 10 or 100 initial infections occurred. The larger the population of that PAR, the more total infections occurred.[15] These trends were not observed for the scenarios involving a single initial infection. The baseline and test scenarios had similar numbers of total infections for one initial infection, and there was no observable correlation between the population of the PAR in which the outbreak started and the total number of infections.

The total number of infections that occur in any PAR is dominated by the β values used for that location. As noted earlier in Chapter 2, in the test scenarios, the model calculated separate β values for each PAR, based on the number of initial infections. In the PAR where the outbreak begins, the number of initial infections will be either 1, 10, or 100, but in all other PARs the outbreak necessarily starts from a single initial infection, generated by the spread of the outbreak through movement. As observed in the baseline

[15] For example, for the smallpox 10 initial infections scenarios, the model estimated an average of 18,880 total infections when the outbreak started in Apache, with its population of 700; 21,458 total infections when the outbreak started in RSOI, with its population of 2,700; *and* 23,301 total infections when the outbreak started in Bagram, with its population of 10,900. In the baseline case, which considered the entire population as a single PAR with a population of 27,800, the model estimated that the entire population would become ill.

scenarios, 10 and 100 initial infections saturated the population, whereas 1 initial infection only infected a portion of the population. Therefore, the results of the test scenarios with one initial infection are similar to those of the corresponding baseline scenario, as all PARs were modeled with one initial infection. However, the test scenarios with 10 or 100 initial infections resulted in the entire population of the PAR in which the outbreak started becoming infected, but only a portion of the populations of the other PARs became infected, resulting in fewer casualties than the baseline scenarios.

2. Comparing Duration of the Outbreak

The test scenarios resulted in longer outbreaks than the baseline scenarios; see Figure 8 and Figure 13. The IDA team observed this trend across both diseases and all starting locations—Apache, Bagram, and RSOI. In general, the test scenarios with more initial infections resulted in longer outbreaks, relative to the corresponding baseline scenario, than test scenarios with fewer initial infections. For a given number of initial infections, the duration of the outbreak was relatively insensitive to the starting location of the outbreak.

In the baseline scenarios, the population is assumed to be evenly mixed, and therefore all of the susceptible individuals are in contact with the contagious individuals and are at risk of becoming infected. However, in the test scenarios only the susceptible individuals who are in PARs to which the disease has already spread can be infected. Since there is a delay in the time for the outbreak to reach each PAR, there is a delay in the time at which certain susceptible individuals can become infected, which results in longer outbreaks in the test scenarios compared to the baseline scenarios.

3. Comparing Time to Reach Combat Ineffectiveness

With the exception of 100 initial plague infections in Apache, the test scenarios generally reached combat ineffectiveness within 25% of the time of the baseline scenario, as shown previously in Figure 9 and Figure 14. The reason for this exception is unclear. Test scenarios involving one initial infection always reached combat ineffectiveness after the corresponding time from the baseline scenario. In comparison, test scenarios with 10 and 100 initial infections did not consistently result in combat ineffectiveness occurring either before or after the corresponding baseline scenario time.

The time at which combat ineffectiveness occurred in the test scenarios, relative to the baseline scenarios, is sensitive to the assumed combat ineffectiveness casualty level—20%. For many casualty levels lower than this value, combat ineffectiveness would occur in all test scenarios prior to the times from the corresponding baseline scenarios. However, for thresholds much greater than 20%, test scenarios would reach combat ineffectiveness after the times from the corresponding baseline scenarios. This observation is based on the test scenarios tending to result in a greater number of infections earlier in the outbreak and fewer infections later in the outbreak than the baseline scenarios, as shown previously in Figure 6 and Figure 11.

4. Conclusions

The IDA team ran the model twice with a given set of input parameters: once considering structure and movement (referred to as the *test scenario*) and once without (referred to as the *baseline scenario*). The team measured the difference between the two sets of casualty estimates using three metrics: (1) total numbers of expected casualties, (2) the overall duration of the modeled outbreak, and (3) the time to reach an overall casualty rate of 20%, considered for the purposes of this analysis as a surrogate for the time to reach combat ineffectiveness.

Based on a comparison of results, including structure and movement in the contagious disease methodology used in this analysis resulted in a significantly different casualty estimate than that generated when structure and movement were not included.

- The total number of infections resulting from the baseline scenarios (without structure and movement) were always greater than those resulting from the test scenarios (with structure and movement).
- The baseline scenarios resulted in shorter outbreaks. For some scenarios, the baseline scenario resulted in an outbreak that infected over three times as many individuals, but only lasted a third as long as the corresponding test scenarios.
- The observed differences in the time to reach combat ineffectiveness were not as apparent. Some of the test scenarios became combat ineffective earlier than the baseline scenarios, while other test scenarios became combat ineffective after. This comparison was highly sensitive to the assumed casualty threshold for combat ineffectiveness.
- Because of the large differences observed in the total number of infections and the duration of the outbreaks, including structure and movement, as conducted in the IDA analysis, will tend to produce a different, less conservative casualty estimate.
- This estimate will predict relatively longer outbreaks with fewer casualties and therefore, the outbreak response would require fewer resources.
- In addition, the ability to model structure and movement within a population allows planners to consider the operational impact of implementing restrictions of movement as a method of curtailing the outbreak.

The added benefits of a more situationally representative casualty estimate and the flexibility to model restrictions of movement associated with the model used in this analysis come at a cost of increased analytic and computational complexity.

- First, the enhanced model requires a user to create an analytic representation of structure and movement for the population at risk. The process of dividing a population of interest into evenly mixed subpopulations connected by specified movement rates is a challenging task. Even when data on populations and movements, such as the SPOT-JAMMS data for U.S. deployed forces in Afghanistan, are available, numerous simplifying assumptions must be made to incorporate the data into the model.
- Second, the implementation of movement between the PARs as a random process dramatically increases the computational complexity of the model. For each set of inputs, the model requires multiple executions to generate meaningful results. While the computational efficiencies of parallel processing were utilized, certain simulations required hours or days to complete.
- Finally, it is unclear how many runs are adequate to produce meaningful results for a given modeling scenario as well as how much variation is expected between individual trials. Both of these questions represent knowledge gaps that would require additional analysis to fill.

On balance, the IDA team believes that changes to the *AMedP-8(C)* methodology to account for the effects of structure and movement are not warranted now. The purposes of the methodology—to generate CBRN casualty estimates for planning—are adequately served by the relatively conservative estimates generated without structure and movement, especially for small numbers of initial infections. Moreover, right now the NATO casualty estimation methodology must be implemented manually, making the complexities of considering population structure and movement prohibitive. However, if casualty estimates are to reflect expected restrictions of movement in the population at risk, or if the casualties in a specific subpopulation are of a particular interest, *then the advantages of structure and movement outweigh the costs associated with the analytic complexities*.

Appendix A.
Past Contagious Disease Modeling at IDA

A. Evolution of Bombardt Contagious Disease Modeling

This appendix will briefly describe the development of contagious disease models at the Institute for Defense Analyses (IDA) and the point of divergence between the contagious disease model used in the current analysis and the model incorporated into *AMedP-8(C)*.[1] Both models are adapted from a set of models developed by Dr. John Bombardt, which are in general use at IDA for a variety of studies and analyses. Bombardt's models combine a traditional Susceptible-Exposed-Infectious-Removed (SEIR) approach with a time-varying disease transmission rate (colloquially referred to by its variable name, β).

In 1999, Bombardt developed a proof-of-concept contagious disease dynamics model of the Ebola infectious disease that introduced his concept of a time-varying disease transmission rate derived from historical outbreaks of disease. He subsequently published a series of papers, each of which calculated β for a new disease, again based on historical outbreaks, while simultaneously enhancing the model's functionality in various ways. The conceptual progression of the Bombardt methodology is depicted in Figure A-1.

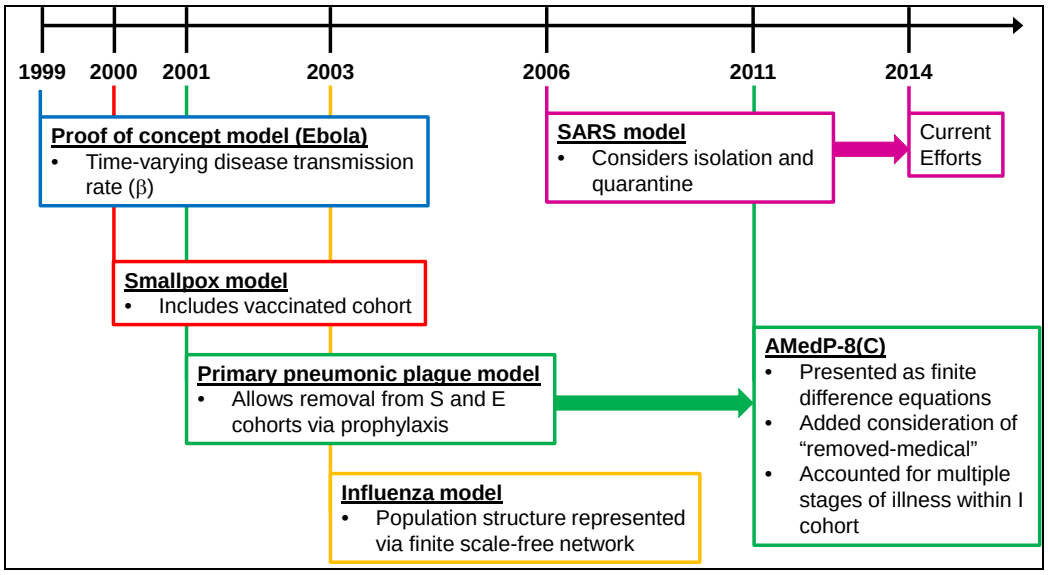


Figure A-1. Evolution of Bombardt Contagious Disease Models

[1] North Atlantic Treaty Organization (NATO), *Allied Medical Publication 8 (C) (AMedP-8(C)), NATO Planning Guide for the Estimation of CBRN Casualties*, STANAG 2553 (Brussels: NATO, 2011).

The proof-of-concept Ebola model[2] is the foundation for all subsequent contagious disease models shown in Figure A-1. This work introduced the concept of a time-varying disease transmission rate, demonstrated the derivation of β from historical outbreak data, and incorporated it within the SEIR framework for purposes of retrospective outbreak investigation and prediction of the dynamics of future outbreaks. The β parameter describes the number of new infections caused by each contagious person for each day of their contagious period and strongly influences the overall behavior of the outbreak. The parameter represents both the inherent infectivity of the disease as well as the "epidemiological circumstances" present during the course of any outbreak:

> Certain epidemiological circumstances surround any outbreak of a disease and these (along with disease characteristics) virtually determine the rate at which the disease is transmitted from person to person. These circumstances encompass factors such as physical profiles of the susceptible cohort, frequency and types of possible contacts between infectious and susceptible individuals, prevailing health care practices, health care system capacity, and disease awareness levels.[3]

Bombardt's smallpox model, published in 2000,[4] is almost identical to the Ebola model presented in his first paper on contagious disease dynamics. In addition to the derivation of smallpox-specific β values for two well-documented historical outbreaks, this model also introduces a vaccinated cohort, V. Individuals in the V cohort are considered to be removed from the population of susceptible individuals.

Bombardt's 2001 plague model[5] is the first model to include a cohort for individuals who have either received chemoprophylaxis and/or chemotherapy, termed the X cohort. Individuals who have received prophylaxis move from the S cohort to the X cohort for the duration of the effectiveness of the medication, then return to the S cohort. Individuals in the E cohort who are given prophylaxis remain in the X cohort indefinitely and are considered to be mitigated, non-fatal casualties. The paper discusses two non-homogenous population mixing methods, although these methods are only briefly introduced and are not fully incorporated into the model presented in the remainder of the paper.

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2 John N. Bombardt Jr., *Contagious Disease Dynamics for Biological Warfare and Bioterrorism Casualty Assessments*, Institute for Defense Analyses (IDA) Paper P-3488 (Alexandria, VA: IDA, February 2000).

3 Bombardt, 3.

4 John N. Bombardt Jr., *Smallpox Transmission and BW Casualty Assessments*, IDA Paper P-3550 (Alexandria, VA: IDA, October 2000).

5 John N. Bombardt Jr., *Primary Pneumonic Plague Transmission and BW Casualty Assessments*, IDA Paper P-3657 (Alexandria, VA: IDA, December 2001).

Bombardt's 2003 influenza model[6] uses a SEIRX[7] model similar to that presented in the plague paper; the primary innovation is the incorporation of structured populations. The subpopulations are modeled using scale-free networks (networks that grow in a predictable manner). Each subpopulation is capable of having a unique transmission rate vis-à-vis all other subpopulations. These subpopulation transmission rates are derived from and sum to the historical aggregate transmission rate.

The final model published in this series is the 2006 SARS (Severe Acute Respiratory Syndrome) model.[8] The SARS model is similar to the influenza model except that it incorporates a more sophisticated method of structuring the population. Like all previous methods, the SARS model is dependent on a disease transmission rate derived from historical outbreak data. The structured population model as presented allows for the incorporation of a number of different non-medical outbreak controls, such as quarantine, contact tracing, and patient isolation. These are accomplished via the removal and reinsertion of individuals in both the susceptible and infectious cohorts. Although not outlined explicitly in the published paper, medical outbreak controls such as prophylaxis and vaccination can theoretically be included in a similar fashion.

B. Principles of the Methodology of Bombardt Contagious Disease Models

All of the published Bombardt models share a common methodological flow, as shown in Figure A-2. The methodology begins with the collection and assessment of data from a historical outbreak of a contagious disease and information on the characteristics of that disease. The quality of such data can vary widely for the purposes of this methodology, but ideally would provide documentation of the time of onset, duration of illness, and outcome for every individual who became ill during the course of the outbreak. The methodology uses this data as input to the set of SEIR differential equations and to determine the number of new infections per day during the outbreak.

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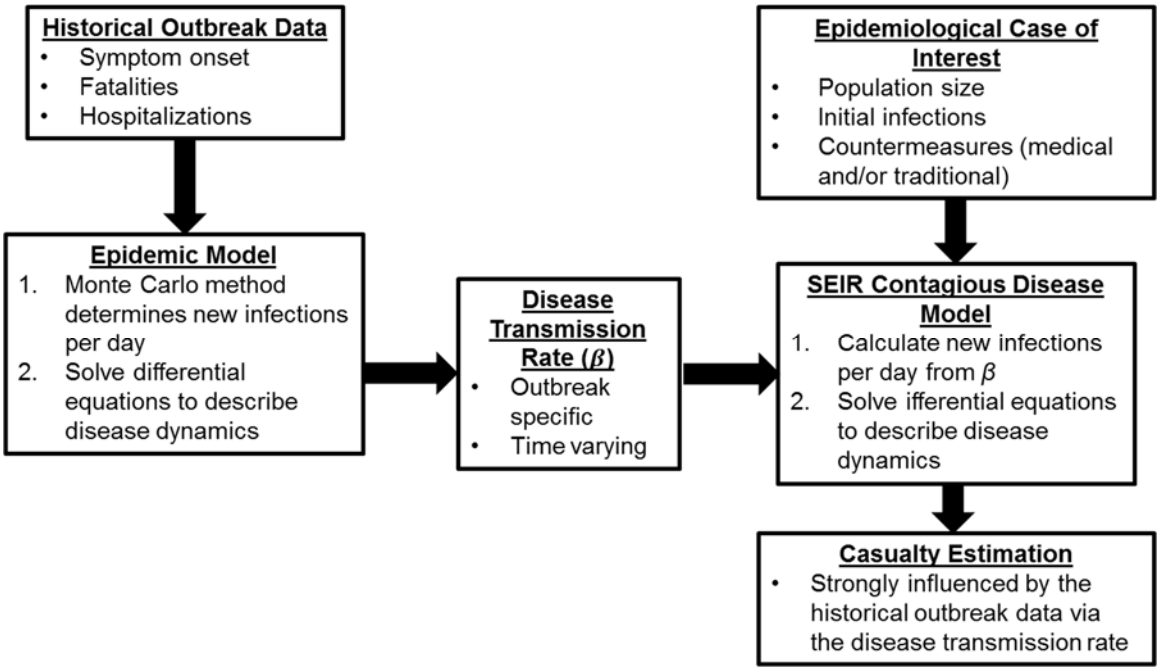
6 John N. Bombardt Jr. and Heidi E. Brown, *Potential Influenza Effects on Military Populations*, IDA Paper P-3786 (Alexandria, VA: IDA, December 2003).

7 SEIRX – S (susceptible to infection), E (exposed but non-contagious), I (infectious/contagious), R (removed as source of infection), X (individuals who have either received chemoprophylaxis and/or chemotherapy). Every member of the population at risk is in one of these cohorts at all times.

8 John N. Bombardt Jr., "Congruent Epidemic Models for Unstructured and Structured Populations: Analytical Reconstruction of a 2003 SARS Outbreak," *Mathematical Biosciences* 203 (2006): 171–203.



Note: Figure adapted from Bombardt, *Smallpox Transmission and BW Casualty Assessments*, IDA Paper P-3555 (Alexandria, VA: IDA, October 2000), Figure I-2, 8.

Figure A-2. Basic Contagious Disease Model

The next step in the methodology involves backtracking from fatality/recovery or symptom onset data to determine the average number of new infections per day. This calculation uses a Monte Carlo algorithm to account for random variation in incubation period and duration of illness; the output is a temporal profile of estimated new infections per day.

The resulting daily number of new infections is then combined with the SEIR model to reproduce the historical outbreak. The daily number of susceptible individuals, contagious individuals, and the daily number of new infections of the reproduced historical outbreak are used to derive the disease transmission rate β. The β values change over time, reflecting prevailing epidemiological circumstances and changes in population behavior during the course of the outbreak.

Once β has been calculated for the historical outbreak, it can be used analytically to address "what if" questions and to generate estimates of casualties over time for postulated scenarios. In this portion of the methodology, β serves as an input to the SEIR model, where values for other parameters, such as population size, number of initial infections, and control measures of various types, are selected to describe scenarios of interest.

C. Adapting Bombardt Models for Use in *AMedP-8(C)* and in IDA Analysis

The contagious disease model presented in *AMedP-8(C)* is loosely based on the 2001 plague model. Major features of the *AMedP-8(C)* model that differentiate it from the 2001 plague model include the following:

- The model is implemented in Microsoft Excel instead of Mathematica,
- The model uses mean values for relevant time periods, such as incubation period and contagious period, versus fully characterized probability density functions,
- The model adds a "removed-medical" cohort to distinguish between fatal and non-fatal removals, and
- The model can account for diseases with multiple stages of illness with varying levels of contagiousness.

As the beneficial features in the last two bullet points were unnecessary for the current analysis, the IDA team was not tied to the limitations associated with the *AMedP-8(C)* model (first two bullets), and the best available model could be used. As summarized in Chapter 2 of this document, the model used in the current analysis is based on Bombardt's 2006 "basic epidemic model for an unstructured population" model for SARS. Modifications were made to allow for a time-varying disease transmission rate that was less directly tied to the historic outbreak and multiple subpopulations with specifiable movement rates between each subpopulation.

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Appendix B.
Illustrations

Figures

Tables

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Appendix C.
References

Bombardt, John N., Jr. "Congruent Epidemic Models for Unstructured and Structured Populations: Analytical Reconstruction of a 2003 SARS Outbreak." *Mathematical Biosciences* 203 (2006): 171–203.

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Appendix D.
Abbreviations

AMedP-8(C)	*Allied Medical Publication 8(C)*
BW	Biological weapon
CBRN	chemical, biological, radiological, and nuclear
IDA	Institute for Defense Analyses
NATO	North Atlantic Treaty Organization
OTSG	Office of The Surgeon General
PAR	Population at Risk
PEP	Post-Exposure Prophylaxis
ROM	Restriction of Movement
RSOI	reception, staging, onward movement, and integration
SARS	Severe Acute Respiratory Syndrome
SEIR	S (susceptible to infection) E (exposed but non-contagious) I (infectious/contagious) R (removed as source of infection)
SEIRX	S (susceptible to infection) E (exposed but non-contagious) I (infectious/contagious) R (removed as source of infection) X (individual cohort who has received either chemoprophylaxis and/or chemotherapy)
SPOT-JAMMS	Synchronized Predeployment and Operational Tracker – Joint Asset Movement Management System
STANAG	Standardization Agreement
TRADOC	Training and Doctrine Command
U.S.	United States
V	vaccinated cohort

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14. ABSTRACT

As part of its efforts to update the NATO CBRN standard casualty estimation methodology, IDA wanted to better understand 1) whether casualty estimates would change if their calculation considered movement and structure, and 2) if estimates changed, whether the change was significant enough to warrant a change to the methodology. To answer this question, IDA adapted a contagious disease model to account for structure and movement and developed an analytic representation of a military population using troop location data from Afghanistan. Using these tools, IDA compared casualty estimates that considered structure and movement with those that did not, using three measures: total number of expected casualties; overall duration of the modeled outbreak, and time to reach an overall casualty rate of 20%. The results showed a significantly different casualty estimate when considering structure and movement. However, the added benefits of a more situationally representative casualty estimate come at a cost of increased analytic and computational complexity. On balance, the IDA team believes that the purpose of an updated version of the casualty estimation methodology—support for medical planning—would be adequately served by the relatively conservative estimates generated without structure and movement, especially for small numbers of initial infections.

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contagious disease modeling, casualty estimation

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