THE BIOLOGICAL ATTACK MODEL (BAM)

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EXECUTIVE SUMMARY

The Biological Attack Model (BAM) is a disease containment model designed to assist emergency responders (ER) and emergencies planners (EP) with the selection of the optimal quarantine and/or containment strategies to use in the event of a biological terrorist attack. The disease containment model is an extension of existing generic disease behavior models and is designed to be used for viral pathogens such as Ebola, smallpox, or different strands of viral encephalitis that are typically transmitted from person to person. The model accepts inputs such as transmission rates, mortality rates, and treatment capability for these diseases and provides disease spread estimations to assist ER and EP to efficiently contain a disease outbreak. This project was developed using a waterfall model to produce prototypes in Microsoft Excel and MATLAB. Test engineers and the project sponsor evaluated the prototypes. The MATLAB prototype was used to simulate/model a biological attack involving smallpox. The results of this simulation were analyzed to provide recommendations on the use of the model to ER and EP.

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1. PROBLEM DEFINITION AND PROJECT OVERVIEW

1.1 Decision Problem

In the United States of America there is a significant risk of a biological attack. In October 2001, two envelopes containing the spores of *bacillus anthracis* (anthrax) were mailed to offices on Capitol Hill. Thousands of workers and business visitors were exposed to the virus at the processing and distribution center of the U.S. Postal Services located in Washington, DC. Historical evidence suggests that these types of biological attacks will continue, but as a nation are we fully prepared for a large-scale biological attack?

In considering the level of preparedness for a biological attack, it is important to identify potential exposure scenarios. One such scenario may be a biological attack on the National Mall in Washington, DC. Protests and rallies are often held on the National Mall and these types of events frequently draw crowds in the hundreds of thousands. A terrorist may target such an event because the conditions are ideal for the release of a biological agent and to maximize exposure to the public.

What are the optimal procedures to be used to contain the spread of an infectious substance in the event of such a biological attack? How can emergency responders (ER) and emergency planners (EP) best use existing/limited resources to treat and contain a potential epidemic? The objective of the BAM project is to address these questions.

1.2 High Level Conceptual Design

1.2.1 Overview

The Biological Attack Model (BAM) was developed to assist emergency responders (ER) and emergency planners (EP) with containment strategy selection in the event of a biological attack, to maximize the effectiveness of limited resources such as hospital beds and vaccines (if available), and to improve the time required to respond to and contain a potential epidemic. The BAM will include:

- a biological agent risk assessment,
- containment strategies,
- disease behavior modeling,
- emergency response recommendations, and
- emergency planning recommendations.

1.2.2 Project Context

The United States has a number of large cities that may be the target of a biological terrorist attack. For example, the Washington Metro Area (WMA) has more than 5 million residents and is home to over 45,000 business firms, 12 colleges and universities, and is the core location of the federal government. The historical city of Washington, DC is approximately 69 square miles with about 572,000 residents and has hundreds of museums, monuments, theaters, and events that attract 20 million visitors annually. These visitors are particularly susceptible to a biological terrorist attack because they hail from many different locations around the globe increasing the potential for an uncontrollable spread of an infectious disease.

The BAM is intended to work within the emergency planning and response framework outlined in the National Response Plan (NRP) and local emergency plans such as the District Response Plan (DRP) [DC EMA, 2007]. The BAM accepts disease parameters for a specific biological agent allowing ER and EP to customize containment strategies based on the availability of treatment facilities and/or vaccines. These inputs can be entered manually based on the outputs of an existing disease dispersion model. The BAM provides a disease behavior model to assist ER and EP select most appropriate disease containment strategy in the event of a high-risk biological terrorist attack. A visual representation of the project context is shown in the figure below.

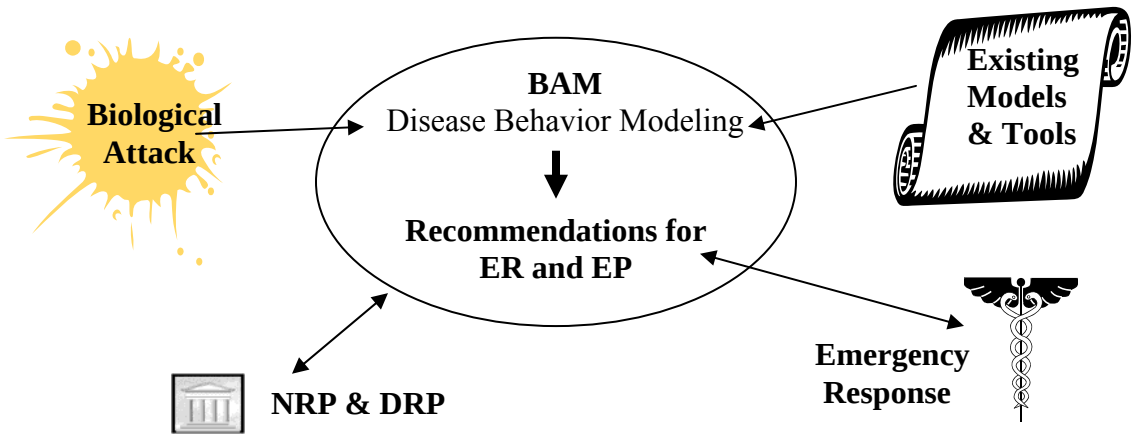

Figure 1 – Context Diagram

1.2.3 Assumptions and Constraints

The major assumptions for the BAM are as follows:

Attack Assumptions:

The BAM models a single or multiple source biological attack. A certain known number of people are initially exposed. This information may come from existing dispersion models. The BAM is designed to model diseases that are transmitted from person to person rather than air, water, or food borne transmissions.

Population Assumptions:

The BAM maintains a constant population with no immigration/emigration, births, or deaths that aren't related to the disease. People in the incubation stage (non-contagious) are considered susceptible in terms of quarantine and treatment since they are not yet known to be infected.

Quarantine Assumptions:

The BAM quarantine policy includes the quarantining of confirmed and suspected cases – contacts traced to confirmed cases are subject to the same actions. All other quarantine may be a form of voluntary confinement or movement restrictions. A percentage of the population cannot be quarantined.

Vaccination/Treatment Assumptions:

In the case of smallpox a percentage of the population is already vaccinated along with all emergency response and medical staff. The susceptible population in the BAM does not include these individuals. In addition, treatments are available for infected individuals. Those that receive treatment within a reasonable timeframe have a chance to survive. Furthermore, vaccination and treatment have no significant side effects compared to mortality and disability rate of the disease. Individuals in quarantine will receive vaccination or treatment.

1.2.4 Definitions and Acronyms

Definitions:

- Biological Attack – The intentional release of an infectious substance on a human population.
- Exposed – Individuals who are exposed to an infectious substance but do not display any outward symptoms. These individuals will become infected after the incubation phase of the disease.
- Infectious Substances – These are substances known or reasonably expected to contain pathogens.

- Pathogen – Microorganisms (including bacteria, viruses, rickettsiae, parasites, fungi) and other agents such as prions, which can cause disease in humans or animals.
- Recovered – Individuals that have either been vaccinated, treated, or survived the disease.
- Susceptible – Individuals within the general area (city) of a biological attack. This group does not include individuals that have been vaccinated if a vaccine is available.

Acronyms:

- ALOHA – Areal Locations of Hazardous Atmospheres
- BAM – Biological Attack Model
- BWIC – Biological Warning and Incident Characterization
- CAMEO – Computer-Aided Management of Emergency Operations
- CDC – Center for Disease Control
- DHS – Department of Homeland Security
- DRP – Washington, DC District Response Plan
- EMA – Emergency Management Agency
- EOC – Emergency Operations Center
- EP – Emergency Planners
- ER – Emergency Responders
- ESF – Emergency Support Function
- MARPLOT – Mapping Application for Response, Planning, and Local Operational Tasks
- NRP – National Response Plan
- ODEs – Ordinary Differential Equations
- SIR – Susceptible-Infected-Recovered
- UDM – Urban Dispersion Model
- WBS – Work Breakdown Structure
- WMA – Washington Metro Area

1.2.5 Requirements

This section presents the high-level requirements for the BAM and the associated institutional program necessary to achieve the needs and goals described by the high level conceptual design. These requirements describe the expected attributes and capabilities of the model as a whole and do not attempt to allocate capabilities to specific modules or equations within the BAM. This approach limits the high-level requirements in this document to those that can be derived from the context diagram (Figure 1.2.1) that pictures BAM as a single functional block with its interfaces. The types of requirements described in this section correspond roughly to these functions and interfaces. Functional requirements describe what happens inside the BAM itself: calculations, predictions, and results. Each interface to the BAM has its own requirements: on collection of data from providers as input; on the dissemination of data for output; on the controlling rules and

constraints under which the system operates; and on the means (primarily data management) by which it works. The table 1 includes the functional, non-functional, performance, and interface for the BAM.

Table 1 – Requirements Table

ID	Description
A-NNN	A Represents the classification of the requirements within the requirements document. The following classifications have been used for the high-level requirements: F-General Functional Requirements N-General Non-Functional Requirements P-Performance Requirements I-Interface Requirements NNN Provides unique identification. Numbering is not necessarily sequential; gaps in the sequence leave room to add additional related requirements when they are discovered.
F-100	The BAM shall be applicable to a class of phenomena (diseases, bio hazard) and shall not be restricted to a single event.
F-200	The BAM shall allow for at least 8 variables that can be used to perform sensitivity analyses of the various parameters and attributes that are inputs to the model. For example: Implicit attributes may be behavior of various pathogens (smallpox, bird flu…). Explicit input parameters may be: the efficacy of a vaccine, concentration of the pathogen, quantity of antidote available etc.
F-300	The BAM shall comprise of multiple states including: susceptible, exposed, infectious, dead, maimed, recovered, quarantined (non-symptomatic), and quarantined (symptomatic).
F-301	The BAM shall provide the total number of people in each state at time (t).
F-400	The mathematical formulation for BAM shall use ordinary differential equations to represent each state given time (t).
F-401	The mathematical formulation for BAM shall be solved using a common numerical method such as Forward Euler or Runge-Kutta.
F-600	The BAM shall leverage existing emergency response policies, procedures, and models to develop recommendations.
F-700	The BAM shall provide a disease behavioral model based on a single or multiple point of attack.
F-800	The BAM shall provide recommendations on the containment and control of a biological release based on the disease behavioral model.
F-900	The BAM shall provide recommendations on vaccination, if necessary, in the event of a biological release.
N-200	The BAM shall be usable by subject experts as end users and shall not mandate Operational Research skills for usage and interpretation of the results.
N-300	The components of the BAM shall be modular which will allow for the study to

	be extendable with the addition of additional modules or stages if necessary.
N-400	The outputs obtained from a simulation using BAM shall be traceable and repeatable for a given set of input parameters (precision).
N-500	The outputs of the BAM shall be logically consistent (i.e. there shall be no contradictions inherent in the model).
N-600	The mathematical formulation of the BAM shall be independently verifiable and recorded as part of the final report.
P-100	The BAM shall be implemented as a light solution solver versus being computer intensive. In short, it shall be possible to implement the model using standard personal computing hardware and software resources.
P-200	It shall be possible for the computerized implementation of the BAM to generate outputs for any valid input scenarios in less than 5 minutes.
P-300	It shall be possible to obtain an assessment of the accuracy and consistency of the outputs from multiple simulation runs in terms of confidence intervals, variances etc.
I-100	The BAM shall accept input parameters for the transmission rate, close contact identification rate, mortality rate, disability rate, treatment rate, quarantine rate, the incubation period, and the infection period.
I-200	The BAM shall accept input parameters for the initial size of the susceptible population and the initial size of the exposed populations.
I-201	The BAM shall accept emergency response capability information.
I-202	The BAM shall accept input parameters for the total amount of vaccine or hospital beds available to treat exposed and infectious patients.
I-300	The BAM shall output the number of people in each state at time (t). This can be accomplished by means of a graphical representation of the entire population over time.
I-400	The BAM shall be designed to work with existing dispersion models.

2. THE SYSTEM DEVELOPMENT PROCESS

This project produced a disease behavioral model that serves as a component of a complete biological attack model and can be used to generate recommendations to improve emergency preparedness and containment in the event of a biological terrorist attack. The BAM will be developed in four parts. Each part will be modular in design and developed in accordance with the preliminary requirements. The modular design will allow concurrent development. The four parts of the BAM project are as follows:

Part 1: Evaluate potential biological warfare agents to determine the threat potential

A risk analysis will be conducted to determine which pathogen has the greatest likelihood of use in a biological attack. This pathogen will be used to establish a baseline, evaluate, and analyze the model. A risk matrix will be developed and will assign a weight to each of the following parameters to calculate the treat potential:

- Spread: How does the agent spread (airborne, food, etc.)?
- Diagnosis: How easy/difficult is it to diagnose?
- Incubation: How long before symptoms appear?
- Vaccination: Does one exist? Is one in development?
- Deadliness: How toxic is it?

Part 2: Assess current policies, procedures, and model:

A survey of the Internet will be conducted to find information on current emergency response and management plans used by local, state, and national governments. This will also include a survey of existing models and software applications used by emergency responders (ER) and emergency planners (EP). The survey will be analyzed to determine modeling assumptions, constraints, and potential gaps in existing policies and procedures.

Part 3: Develop a disease behavior model

Existing disease behavioral models will be evaluated to determine their applicability to a biological attack. If an existing model lacks necessary capabilities, a new model will be produced to address those needs.

Part 4: Evaluate the effectiveness of various containment strategies

A sensitivity analysis will be conducted to evaluate the impact of variations in the input parameters to provide guidance on various containment strategies to ER and EP in the event of a biological attack. The analysis will use the disease behavioral model developed in part 3 to simulate the spread the disease selected in part 1 over a period of 200 days. This simulation will be produced in Microsoft Excel or MATLAB.

3. BIOLOGICAL RISK ASSESSMENT

A biological risk assessment was conducted in order to reduce the scope of the BAM to those biological agents that pose the greatest risk to susceptible populations. The BAM was designed and developed to fit the behavior of the highest risk biological agents.

3.1 Potential Biological Threats

According to the Center for Disease Control (CDC) there are 43 biological agents that have been identified as potential biological attack agents. The agents are as follows:

- Anthrax (Bacillus anthracis)
- Arenaviruses
- Bacillus anthracis (anthrax)
- Botulism (Clostridium botulinum toxin)
- Brucella species (brucellosis)
- Brucellosis (Brucella species)
- Burkholderia mallei (glanders)
- Burkholderia pseudomallei (melioidosis)
- Chlamydia psittaci (psittacosis)
- Cholera (Vibrio cholerae)
- Clostridium botulinum toxin (botulism)
- Clostridium perfringens (Epsilon toxin)
- Coxiella burnetii (Q fever)
- Ebola virus hemorrhagic fever
- E. coli O157:H7 (Escherichia coli)
- Emerging infectious diseases such as Nipah virus and hantavirus
- Epsilon toxin of Clostridium perfringens
- Escherichia coli O157:H7 (E. coli)
- Food safety threats (e.g., Salmonella species, Escherichia coli O157:H7, Shigella)
- Francisella tularensis (tularemia)
- Glanders (Burkholderia mallei)
- Lassa fever
- Marburg virus hemorrhagic fever
- Melioidosis (Burkholderia pseudomallei)
- Plague (Yersinia pestis)
- Psittacosis (Chlamydia psittaci)
- Q fever (Coxiella burnetii)
- Ricin toxin from Ricinus communis (castor beans)
- Rickettsia prowazekii (typhus fever)
- Salmonella species (salmonellosis)
- Salmonella Typhi (typhoid fever)
- Salmonellosis (Salmonella species)
- Shigella (shigellosis)

- Shigellosis (Shigella)
- Smallpox (variola major)
- Staphylococcal enterotoxin B
- Tularemia (Francisella tularensis)
- Typhoid fever (Salmonella Typhi)
- Typhus fever (Rickettsia prowazekii)
- Viral encephalitis (alphaviruses [e.g., Venezuelan equine encephalitis, eastern equine encephalitis, western equine encephalitis])
- Viral hemorrhagic fevers (filoviruses [e.g., Ebola, Marburg] and arenaviruses [e.g., Lassa, Machupo])
- Water safety threats (e.g., Vibrio cholerae, Cryptosporidium parvum)
- Yersinia pestis (plague)

3.2 High Risk Biological Agents

The list of 43 potential biological threats was reduced to a list of six high risk biological agents. This list reduction was based on "Category A" disease criteria established by the Center of Disease Control (CDC). "Category A" diseases are considered the "worst- of the - worst" in that they would have greatest impact on a susceptible population.

Category A Diseases/Agents

The U.S. public health system and primary healthcare providers must be prepared to address various biological agents, including pathogens that are rarely seen in the United States. High-priority agents include organisms that pose a risk to national security because they

- can be easily disseminated or transmitted from person to person,
- result in high mortality rates and have the potential for major public health impact,
- might cause public panic and social disruption, and
- require special action for public health preparedness.

High risk biological agents

The "Category A" biological agents identified by the CDC are as follows:

- Anthrax (Bacillus anthracis)
- Botulism (Clostridium botulinum toxin)
- Plague (Yersinia pestis)
- Smallpox (variola major)
- Tularemia (Francisella tularensis)
- Viral hemorrhagic fevers (filoviruses [e.g., Ebola, Marburg] and arenaviruses [e.g., Lassa, Machupo])

3.3 Risk Assessment

A risk assessment was conducted using the six "Category A" biological agents identified in the previous section. For each disease, a value was assigned to the following parameters: Spread, Diagnosis, Incubation, Vaccination/Antibiotic, and Deadliness. For each parameter a weight was assigned based on the relative importance of the parameter in a biological attack. Threat was calculated for each disease using the following equation: Threat = $\Sigma(\text{weight}_i * \text{parameter value}_i)$. The disease with the highest score for threat was selected for detailed parametric analysis.

Table 2 – Disease Risk Matrix

AGENT	Spread	Diagnosis	Incubation	Vaccination Antibiotic	Deadliness	***Threat***
Anthrax (Bacillus anthracis)	Air (3)	MEDIUM (3)	1-7 days (4)	Yes (1)	5	**3.1**
Botulism (Clostridium botulinum toxin)	Water (2)	MEDIUM (3)	12-36 hours (5)	No (5)	5	**3.2**
Plague (Yersinia pestis)	Human Animal (4)	MEDIUM (3)	2-6 days (4)	Yes (pre-exposure) (3)	5	**3.7**
Smallpox (variola major)	Human (5)	EASY (5)	12 days (3)	Yes (limited) (4)	5	**4.7**
Tularemia (Francisella tularensis)	Air (3)	HARD (1)	1-21 days (2)	No (5)	4	**2.6**
Viral hemorrhagic fevers (filoviruses [e.g., Ebola, Marburg] and arenaviruses [e.g., Lassa, Machupo])	Human (4)	EASY (5)	2-20 days (2)	No (5)	5	**4.3**
WEIGHTS	**.40**	**.30**	**.10**	**.10**	**.10**	**1.00**

Smallpox has the highest threat score (4.7). Therefore, smallpox was selected for detailed analysis.

Parameter Values for Risk Matrix

The parameter values for each disease were assigned a value between 1 and 5 based on the following criteria:

Spread – A terrorist is most likely to initiate a biological attack using air or water dispersion techniques. However, beyond the initial attack, a biological agent that can spread from human to human has the potential to affect more people. Thus agents with a high spread rate (person to person) were given a high score and those with a low spread rate (air or waterborne) were given a lower score.

Diagnosis – A disease that is easier to detect is ideal for a disease behavioral model and containment model. A disease that is harder to detect will likely effect the entire population before containment strategies can be initiated. Thus agents that are easier to detect were given higher scores and those that are difficult to detect were given low scores.

Incubation – A short incubation period is ideal in a biological attack. The sooner people begin to get sick the sooner mass hysteria will break which is the main objective of a terrorist. Thus agents with short incubation periods were given higher scores than those with long incubation periods.

Vaccination/Antibiotic – A biological agent that does not have a vaccination or an effective antibiotic treatment has a greater potential to cause mass hysteria. Thus agents without any available treatment were given higher scores than those with an effective vaccination.

Deadliness – A terrorist is more likely to use the deadliest or most toxic agents in an attack. Thus the deadlier agents were given the highest scores.

3.4 Detailed Background – Smallpox

Smallpox is a disease that has existed for thousands of years. The last case in the United States was in 1949 and the last natural occurrence was in 1977 in Somalia. Since then, smallpox has been eliminated by worldwide vaccination, except for two approved laboratory stockpiles in the United States and Russia. It remains a concern as a biological attack agent, so precautionary measures are still maintained to prevent a smallpox outbreak.

Smallpox is caused by the variola virus, which is highly contagious. There is no specific treatment after an infection and it can be fatal. The two clinical forms of smallpox are variola major and variola minor. The major form is the most common and severe. Symptoms include a rash with raised bumps on the face and body, along with a high fever. The four types of variola major are ordinary, modified, flat, and hemorrhagic. Ordinary variola major accounts for roughly 90% of the cases. Modified variola major is a milder case that occurs in previously vaccinated persons. Flat and hemorrhagic variola major are rare, extremely severe, and usually fatal. Overall, viriola major has a fatality rate of about 30%. Viriola minor is a less common and less severe strain, with historic death rates under 1%.

Smallpox is transmitted from person-to-person from direct and fairly prolonged face-to-face contact. It can also be transmitted through direct contact with infected bodily fluids or contaminated objects such as cloth. In some rare instances it has been spread through enclosed air settings. Laboratory experiments show that 90% of aerosolized variola virus dies within 24 hours, with even more dying in the presence of ultraviolet light. Humans are the only known natural host of the variola virus, so smallpox is not transmitted by insects or animals.

Once a person is exposed to smallpox, they enter a 7 to 17 day incubation period (averaging 12 to 14 days) where they may experience no symptoms and are not contagious. Initial symptoms occur during the prodrome phase, which can last for 2 to 4 days, and makes the person moderately contagious. These initial symptoms include high fever, malaise, head and body aches, and vomiting. A person is most contagious with the onset of rash. The rash emerges as small red spots on the tongue and inside the mouth that develop into sores. These sores break open and spread the virus into the throat. At this time a rash appears on the face and spreads to the arms, legs, hands, and feet. The rash will usually spread to all parts of the body within a 24 hour period. As the rash develops, the fever usually breaks and the person may start recovering. The rash becomes raised bumps by the third day of the rash. By the fourth day, the bumps fill with fluid and often have a depression in the center. The fever may rise again and stay high until scabs form over the bumps. Two weeks after the rash appears, most of the sores will have scabbed over and will fall off by the end of the third week. Scabs that fall off often leave pitted scars. Until the last scab falls off, an infected person remains contagious.

A proven treatment currently does not exist; however, some laboratory studies suggest that the drug cidofovir may fight the virus. Supportive therapy includes intravenous fluids, fever and pain control medications, and antibiotics for secondary bacterial infections. The only defense for smallpox is vaccination. After smallpox was eliminated worldwide, routine vaccination among the general public was no longer necessary for prevention and was stopped. It is currently not available to the general public unless an outbreak is taking place.

The smallpox vaccine is a live-virus vaccine. It is considered a safe vaccination; however, adverse post-vaccination events can occur. These events include inadvertent inoculation, generalized vaccinia, eczema vaccinatum, progressive vaccinia, and postvaccinial encephalitis. These lead to death in roughly one per million primary vaccinations.

The U.S. government has a detailed nationwide smallpox preparedness program for a biological attack using smallpox. This program includes preparedness teams that respond to a smallpox attack within the United States. These teams are already vaccinated in order to safely protect others. The U.S. government also stockpiles enough smallpox vaccine to vaccinate everyone who would need it in the event of an outbreak. Only one confirmed case of smallpox is required to be considered a public health emergency.

Smallpox preparedness teams will take immediate steps to control the spread of the disease. If there is an outbreak, public health officials will communicate with the public about what to do to protect themselves and their families. They will be told where to go for care if they think they have been exposed to smallpox. Patients will be isolated from others who could get sick from them and receive the best available treatment. Anyone who has had contact with a patient will be offered the smallpox vaccination as soon as possible. People who have had contact with those individuals will also be vaccinated and

monitored for symptoms. This is commonly referred to as a ring vaccination campaign. The vaccine may also be offered to those who have not been exposed, but would like to be vaccinated, but no one will be forced to have the vaccination, even if they have been exposed. To prevent spread, anyone who has been in contact with smallpox and decides to not get the vaccine may need to be isolated and monitored for at least 18 days.

Since smallpox does not spread as easily as measles or flu, ring vaccination and isolation are effective measures for wiping out the disease and are a preferred approach over indiscriminate mass vaccination. These measures were executed successfully in past eradication programs. Adverse events would be higher in an indiscriminate mass vaccination because of unrecognized contradictions to the vaccination. Also, mass vaccination of a large population would require a large number of health care workers to perform vaccinations and deal with adverse events. Mass vaccination could lead to improper reliance on the strategy and neglect of other essential outbreak control measures like surveillance, contact tracing, and case isolation. There may also be instances where there are inadequate supplies of vaccine for areas with the greatest need, which would prolong the epidemic rather than control it.

The ring vaccination concept should be the primary control tactic; however the size of the vaccinated ring of individuals surrounding a case or contact may vary. The ring size depends on the size of the outbreak, personnel resources, effectiveness of other outbreak control measures, and vaccine availability. The initial vaccination ring size, along with its expansion and contraction, will be determined jointly by federal and state health officials.

High-risk groups should be prioritized for vaccination in a smallpox outbreak. These include persons exposed to the initial release of the virus, face-to-face close contacts, household contacts, persons involved with direct medical care, laboratory personnel, and those involved in contact tracing, vaccination, quarantine/isolation enforcement, and law-enforcement interviews of suspected smallpox patients. Any other persons that have a high likelihood of exposure to infectious patients or materials, including all emergency response personnel, should also be prioritized as a high-risk group for vaccination [CDC, 2007].

4. THE PROJECT ASSESSMENT

4.1 Current Policies, Procedures, and Models

The federal, state, and local levels of the U.S. government have existing policies, procedures, and models that can be used in the event an emergency. The BAM must be designed to fit within the existing framework for emergency response and planning.

National Response Plan (NRP):

- Biological Agent Response (Non-sequential Order)
  - Rapid Detection of the outbreak
  - Swift agent identification and confirmation
  - Identification of the population at risk
  - Determine how agent is transmitted
  - Determine susceptibility of the pathogen to treatment
  - Control containment of the epidemic
  - Decontamination of individuals, if necessary
  - Identification of law enforcement implications/assessment of the threat
  - Augmentation and surging of local health and medical resources
  - Assessment of environmental contamination and cleanup requirements
  - Tracking and preventing secondary or additional disease outbreak [DHS, 2007]

Washington, DC District Response Plan (DRP):

- A Biological terrorist attack would trigger Operation Level 5
  - Requires full activation of the Consequence Management Team
  - All preliminary and support agencies under the DRP are notified
  - Likely to have regional implications and will likely require a request for regional or federal resources to support the District's response
  - The Emergency Operations Center (EOC) is on full activation with 24 hour staffing by EMA personnel and all necessary ESF Liaison Officers [DC EMA, 2007]

CDC Post-event Guidance for a Smallpox Outbreak:

The CDC has established guidelines for response in the event of a smallpox outbreak. These general activities are suggested to aid planners in developing a post-event smallpox plan that incorporates federal, state, and local agencies and organizations.

Public health personnel, healthcare response personnel, and first responders in affected communities need to be vaccinated as soon as possible after the first smallpox case is confirmed. This includes law enforcement and other public service personnel that are needed to control the outbreak.

The ring vaccination policy should be adhered to once enough vaccinated personnel are available. This involves identification of contacts of smallpox cases that are experiencing initial symptoms, household contacts of these contacts, and contacts that can be identified through the tracking of the past movements of each case. These patients need to be quickly moved to facilities that can provide appropriate health care and isolation to prevent additional spread of the disease. Contacts of cases should be vaccinated as soon as possible, since the smallpox vaccine can be effective after exposure. They need to be monitored for illness, so they can be isolated and given medical care if they become infectious.

The diagnosis of these cases needs to be executed rapidly and efficiently to ensure that the ring vaccination policy will effectively control the outbreak. This diagnosis should be based on the clinical characteristics of smallpox. It should be followed up with confirmation at regional laboratories and with the CDC. It may be necessary to conduct targeted vaccination within communities where a large number of cases are suspected. In some instances a large scale vaccination may be required. This decision to offer the vaccine to everyone within a city, county, or state would be made by public health officials or leaders.

During the outbreak, epidemiological investigations need to be conducted to identify potential linkages between the patients. Travel histories of a 2-3 week period prior to the onset of symptoms should be reviewed. This information can be used to determine if there is a common source for exposure, how large the initial source was, and to identify others that may require vaccination or treatment.

Detailed, real-time data will be required to keep policy makers, health officials, clinic managers, and the public informed about the status of the smallpox response activities. It is critical that proper communications are maintained to address public questions, minimize false rumors, and reassure the public that response measures are taking place and working effectively. Public health officials need to acknowledge the seriousness of a smallpox outbreak and efficiently communicate to the public through the media [CDC, 2007].

Existing Bio-Dispersion and Disease Behavior Models:

- Biological Warning and Incident Characterization (BWIC) – Developed by the Department of Homeland Security and provides integrated decision support to facilitate timely warning, attack assessment, communications, and effective response in the event of a biological attack.

- BioWar – A simulation tool that combines a computational model of social networks, communication media, disease models, spatial models, wind dispersion models, and a diagnostic model into a single integrated system that can simulate the impact of a bioterrorist attack on a city.

- Susceptible-Infected-Recovered (SIR) – Widely used basic to model the spread of epidemics and to study immunization strategies within a population.

- Urban Dispersion Model (UDM) – There are various modeling approaches for flow and dispersion in urban areas to estimate the effects of releasing chemical and biological agents [Carley, Altman, Kaminsky, Nave, and Yahja].

Software Applications Developed for Use by First Responders:

- Computer-Aided Management of Emergency Operations (CAMEO) – A database of over 6,000 hazardous materials with specific information on fire and explosive hazards, health issues, firefighting techniques, cleanup procedures, and protective clothing.

- Mapping Application for Response, Planning, and Local Operational Tasks (MARPLOT) – A mapping application to track contaminated areas for potential or actual scenarios.

- Areal Locations of Hazardous Atmospheres (ALOHA) – An atmospheric dispersion model used for evaluating a release of hazardous vapors. Outputs cloud footprint that can be plotted in MARPLOT to see hazards posed on vulnerable areas.

4.2 Existing Research

Much research has been done regarding the spread of disease among a population. One focus of this research is assessing the effects of control measures, such as mass vaccination, isolation of those infected, and ring vaccination around those infected. Ferguson et al. [15] reviewed and compared mathematical models of viral transmission and control policies that assess the threat posed by a deliberate release of smallpox.

Meltzer et al. [21] utilized a Markov chain model to evaluate the rates of mass vaccination and infected isolation. The goal of this study was to reduce the average transmissions per case (the reproductive number) to less than one. Contact tracing and ring vaccination were not considered. It concluded that intervention delays lead to more cases and that the use of both quarantine and vaccination would be an effective approach.

Kaplan et al. [18] used simulations of a deterministic model to compare the relative effectiveness of mass and ring vaccination in reducing the consequences of a smallpox release in a large population. The model assumed high infectivity in the prodrome phase. The study concluded that mass vaccination would lead to fewer deaths and faster eradication.

Halloran et al. [17] also compared mass and ring vaccination policies. The study used a stochastic simulation of smallpox within a small community. This model also assumed high infectivity during the prodrome phase. It discovered that timely mass vaccinations

would be more effective than targeted vaccinations, assuming there was no preexisting immunity. When preexisting immunity was present, targeted vaccination was a more reasonable option.

Bozzette et al. [1] used stochastic modeling to estimate smallpox deaths under various attack scenarios and track adverse vaccination effects. The conclusion was that prior vaccination of health care workers would be beneficial, unless there was a very low likelihood of an attack occurring.

With stochastic computer simulations, Eichner [13] showed that contact tracing and case isolation could control smallpox outbreaks. Using a stochastic branching process model, Kretzschmar et al. [19] showed that a policy of ring vaccination of contacts of infected people would sufficiently control a smallpox epidemic. The size and duration of the epidemic could be large depending on the average diagnosis time and average time for tracing and vaccinating contacts of those infected.

Castillo-Chavez et al. [3] developed a complex model that addressed the importance of transient populations on the transmission dynamics of smallpox. It incorporated a variety of environments, including mass transportation. The study concluded that control measures, like vaccination, need to be aimed at both local and transient populations. Delays in implementations of these control measures could be disastrous. A policy focusing only on local populations would not be sufficient and a global approach would be more appropriate.

Del Valle et al. [10] incorporated the effects of population behavioral changes into a smallpox release model. The purpose of this was to prevent the overestimation of the outbreak size and magnitude of interventions required to control it. It concluded that when affected individuals play an active role in diminishing the likelihood of transmission, the impact of standard control efforts are dramatically improved.

G. Chowell et al. [8] used a Susceptible-Exposed-Infectious-Removed (SEIR) epidemic model and data from two well-documented Ebola outbreaks to estimate a reproductive number in the absence of control interventions. These interventions included education, contact tracing, and quarantine. Using a 2-week delay for their implementation, the study showed that the interventions reduced the final epidemic size by a factor of 2 relative to the final size. P.E. Lekone et al. [20] used similar methods to develop a stochastic deterministic-time SEIR model for infectious diseases. This study estimated parameters from daily incidence and mortality time series for an outbreak of Ebola in the Democratic Republic of Congo.

4.3 Containment Strategies

Different infectious diseases need to be handled differently, in terms of epidemic control policies, based on their epidemic dynamics. Highly infectious diseases with short incubation periods, such as measles, need widespread childhood immunization to reduce the number of susceptible people in the long-term. Smallpox is less infectious and has a

much longer incubation period, so if an outbreak is detected in its early stages, there is sufficient time for localized control measures to be adopted. This is why smallpox was the first major viral pathogen to be eradicated worldwide.

Evaluating the effectiveness of a control policy requires a range of epidemiological and social processes. These can have significant effects on the success of a given intervention under different conditions. Various methods exist for controlling the spread of diseases. These range from different vaccination strategies to movement/contact restrictions placed on infectious cases and their contacts. The key goal of policies in epidemic modeling is to assess the adequacy of current policy and how it can be improved. In general, this involves minimizing mortality and morbidity, in the most rapid and efficient way possible.

Potential containment strategies:

The BAM can be used to evaluate the following six control policies individually and how they work in combinations:

Control Policy 1: Quarantine and isolation of suspected and confirmed cases is effective at reducing transmission from known cases. This is highly dependent on adequate isolation facilities and resources, population compliance, and rapid case detection.

Control Policy 2: Movement restrictions involve quarantine of neighborhoods or closure of schools, public gatherings, airports, and other transportation systems. This method is useful for containing a small outbreak where community transmission is occurring. It can be costly, difficult to enforce, and can be compromised by illegal movements.

Control Policy 3: Ring vaccination involves tracing and vaccinating contacts of suspected smallpox cases. It often also involves the isolation of the identified contacts. This method minimizes the use of vaccine, which reduces morbidity and mortality from adverse reactions to vaccination. Contact tracing needs to be well executed to adequately limit transmission. This is often more difficult to do in densely-populated urban environments. In order for the vaccine to be effective, contacts need to be found at an early stage before exposure.

Control Policy 4: Target vaccination would be vaccination of the entire population in an affected neighborhood or city. It is an eradication campaign for containing transmissions within a subpopulation. While it involves administering more vaccinations than ring vaccination, significantly less are administered compared to mass vaccination. Less vaccination means less adverse reactions. Targeted vaccination is also not dependent on contact tracing, but has a risk of the disease spreading beyond the targeted area.

Control Policy 5: Mass vaccination involves vaccinating the whole population of a country that is threatened by an outbreak, so contact tracing is not necessary. It is effective at stopping the spread of a virus across a large area and protecting the population from infection. A large number of people need to be vaccinated quickly. This

can lead to many cases of vaccine-related morbidity and mortality since there is little time to screen for potential adverse reactions.

Control Policy 6: Prophylactic vaccination is vaccination before an outbreak is detected. It is very useful for protecting essential emergency response personnel. When it is used for an entire population, it is very effective at preventing an outbreak. There is no rush to vaccinate, so there is time to screen for potential adverse reactions. If prophylactic vaccination is used on an ongoing basis for an entire population, the costs can be very high and many vaccine-associated adverse events are still possible. [Ferguson, Keeling, Edmunds, Gani, Grenfell, Anderson, and Leach]

4.4 Schedule Assessment

Based on the information collected about existing models, policies, and procedures the scope of the BAM was modified to provide only one model component of a biological attack: a disease behavioral model. This reduction of scope was further supported by the development of a detailed work breakdown structure (WBS). Upon detailed examination of the tasks and milestones within the WBS, it was determined that the BAM project would not include agent identification strategies, dispersion modeling, and evacuation strategies (other than quarantine recommendations).

The work breakdown structure is based on the 15-week semester allotted for development of the BAM. The BAM project team comprises 5 members, each of whom are available approximately 10 hours per week to work on the BAM development. The total amount of hours available to complete the BAM project was given as 750 hours (15 weeks * 5 members * 10 hours per week). The four primary tasks outlined in the development plan were divided into subtasks and then man-hours were allocated to each team member to complete the subtask. The initial WBS exceeded the 750-hour limitation (1237 hours) and need to be scoped down. Each task of the WBS was analyzed based on the following criteria:

Slip Risk – How likely is it that the task can be completed on time and not cause other critical tasks to be neglected or late? (LOW, MED, HIGH)

Importance – How important is the task in the context of existing policies, procedures and models? Would it be more advantageous to focus on other aspects of a biological attack that address critical gaps?

Compression – Can the time required to complete this task be reduced by assigning additional man-hours to the task? (YES, NO)

Eliminate/Reduce – Can this task be eliminated or can the time required to complete the task be reduced? (YES, NO, REDUCED) How many hours can we save?

Based this analysis, the total hours required to complete the BAM project was reduced to approximately 770 hours. The revised WBS and the results of the project assessment can be found in appendix 7.

5. THE MODEL

This section will describe the methodology for the development and implementation the disease behavioral model and describe its context within the BAM.

5.1 Overview

The disease behavioral model is the key component of the BAM and will be used to provide recommendations on containment strategies in the following section of this report. The first step in the development of a disease behavioral model is researching existing models. The simplest of these models is the SIR (Susceptible, Infected, Recovered) model. Although the SIR model offers easy to use inputs for an initial population size and transmission rates for diseases and provides a decent estimate of size of the population in each state, this model was found to be insufficient. The SIR model does not capture the possibility to implement containment strategies to change the outcome of the model to prevent a widespread epidemic.

The next existing model that was examined in detail was the SEIR (Susceptible, Exposed, Infected, Recovered) model. This model is significantly more robust than the SIR model in that it takes into account the fact that individuals in the susceptible population first become exposed and then become infectious (symptomatic and contagious). This transition is called the incubation period and can vary significantly depending on the specific pathogen. The additional capabilities of the SEIR are critical to accurately model a biological attack response. In the initial hours of a biological attack, many individuals will be exposed to the pathogen and will not necessarily be infectious. Secondary infections – especially in the case of smallpox – cannot occur during the incubation period. In most cases the best containment strategy is to quarantine everyone who has been initially exposed to prevent secondary infections. However, the SEIR model does not adequately address the quarantine concept. Nonetheless, it was chosen as the basis for the BAM.

5.2 Model Architecture

The SEIR comprises of four states: susceptible, exposed, infected, and recovered. This model was enhanced to include an additional four states: quarantined non-symptomatic, quarantined symptomatic, dead, and maimed (disabled). These additional states and their transitions are described below.

In the SEIR model, the susceptible population will become exposed at a certain transmission rate (β) and then infectious after a time period equal to the incubation period (μ_1). An infectious population will either die at a rate (d) or recover at rate (1-d). The BAM is a bit different in this regard; a susceptible person can transition to the exposed state at the transmission rate (β), quarantined at a rate (γ), or recovered state at a targeted vaccination rate (φ). These transitions are logical based on the availability of local treatment facilities and/or ability to conduct targeted or mass vaccinations. An exposed

individual will become infectious after the incubation period (μ_1); however, in the BAM, close contacts are traced at a rate (α) and are quarantined at a rate (γ). Infectious individuals will become dead at a rate (d), maimed (disabled) at rate (m), or recovered (1-d-m) after the infectious period (μ_2). However, infectious individuals may transition to quarantine at a rate (γ) before the pathogen runs its course to receive treatment. In quarantine, all individuals receive treatment or vaccination. Individuals that receive treatment and/or vaccination have an increased chance of survival and/or life without disabilities. The detailed BAM states, instantaneous transition rates, and input parameters are outlined in Appendix 1 of this report. In addition, a corresponding state transition diagram was developed and can be found in Appendix 3 of this report.

5.3 Solving the Model

The next goal of the BAM project team was to numerically solve the BAM. The first step in this process was to derive the ordinary differential equations (ODEs) for each of the eight states in the BAM. For example, consider the non-symptomatic quarantine state (Q_1). State (Q_1) has two inputs: people who are susceptible and are transitioned to quarantine ($Q_S(t)$) and people who are exposed and are transitioned to quarantine ($Q_E(t)$). State (Q_1) also has two outputs: people who transition to recovered after quarantine ($R_{Q1}(t)$) and people who become infectious and transition to symptomatic quarantine ($Q_Q(t)$). A graphical representation of state (Q_1) in figure 5.3 below:

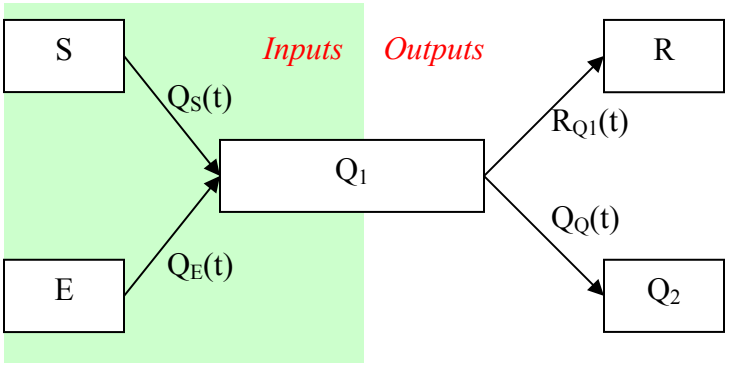

Figure 2 – Graphical representation of the non-symptomatic quarantine state

The ordinary differential equation for the state (Q_1) is represented by the difference between the inputs from the susceptible and exposed populations and the outputs to the recovered and quarantined symptomatic populations and can be written as follows:

$$\frac{dQ_1}{dt} = Q_S(t) + Q_E(t) - R_{Q1}(t) - Q_Q(t)$$

Each input and output transition must be further defined in the context of the input parameters. The transition $Q_S(t)$ is the product of the fraction people who have been identified as close contacts (α), the fraction of people that are quarantined (γ), the fraction

of the population who are infectious (i(t)), and the fraction of the population who are susceptible (s(t)). The transition $Q_S(t)$ can be written as follows:

$$Q_S(t) = \alpha \cdot \gamma \cdot i(t) \cdot s(t)$$

The transition $Q_E(t)$ is the product of the fraction of people who have been identified as close contacts (α), the fraction of people that are quarantined (γ), the fraction of the population who are infectious (i(t)), and the fraction of the population who are exposed (e(t)). The transition $Q_E(t)$ can be written as follows:

$$Q_E(t) = \alpha \cdot \gamma \cdot i(t) \cdot e(t)$$

The transition $R_{Q1}(t)$ is the product of the fraction of people who are non-symptomatic and in quarantine ($q_1(t)$), one over the incubation period (μ_1), and the fraction of the population who are susceptible (s(t)) over the total fraction of people who are susceptible or exposed (s(t)+e(t)). The transition $R_{Q1}(t)$ can be written as follows:

$$R_{Q1}(t) = q_1(t) \cdot \frac{1}{\mu_1} \cdot \frac{s(t)}{s(t) + e(t)}$$

Note: The s(t) / (s(t) + e(t)) term in this transition equation is necessary to capture the fraction of those in quarantine who are susceptible. Susceptible individuals who receive treatment and/or vaccination will go to the recovered state whereas the exposed individuals will not.

The transition $Q_Q(t)$ is the product of the fraction of people who are non-symptomatic and in quarantine ($q_1(t)$), one over the incubation period (μ_1), and the fraction of the population who are exposed (e(t)) over the total fraction of people who are susceptible or exposed (s(t)+e(t)). The transition $Q_Q(t)$ can be written as follows:

$$Q_Q(t) = q_1(t) \cdot \frac{1}{\mu_1} \cdot \frac{e(t)}{s(t) + e(t)}$$

Note: The e(t) / (s(t) + e(t)) term in this transition equation is necessary to capture the fraction of those in quarantine who are exposed. Exposed individuals who receive treatment and/or vaccination will remain in quarantine until the incubation period has expired. At that time they will be transferred to the symptomatic quarantine state.

The complete transition equation for the non-symptomatic quarantine state (Q_1) is as follows:

$$\frac{dq_1}{dt} = \alpha \cdot \gamma \cdot i(t) \cdot s(t) + \alpha \cdot \gamma \cdot i(t) \cdot e(t) - q_1(t) \cdot \frac{1}{\mu_1} \cdot \frac{s(t)}{s(t) + e(t)} - q_1(t) \cdot \frac{1}{\mu_1} \cdot \frac{e(t)}{s(t) + e(t)}$$

This process was repeated to derive each of the eight transition equations. The equations can be found in Appendix 2 of this report.

5.4 Implementation

In order to solve the ordinary differential equations numerically, two methods were considered: the Forward Euler method and the Runge-Kutta method. The Forward Euler method is a first-order method that uses a small time step to solve ODEs. The Runge-Kutta method is a fourth-order numerical method.

Initially, the ODEs were implemented in Microsoft Excel using the Forward Euler numerical method. This Excel implementation proved to be valuable when troubleshooting problems with equations and state transitions during the early stages of our model development. This implementation also validated the integrity of our model architecture. However, the Forward Euler approximation, while less time-consuming and resource-intensive than other numerical methods, is prone to the most error. Therefore, after the Excel model was completed and validated, we transferred the model implementation into MATLAB and utilized its ODE45 solver. The MATLAB ODE45 solver uses a fourth-order Runge-Kutta numerical method and a much smaller variable time-step to solve systems of ODEs. This reduces the errors in the numeric approximations. The code for the MATLAB implementation can be found in Appendix 4 of this report.

5.5 Baseline Model

In order to implement the BAM in MATLAB, the initial input parameters were ascertained from existing research on smallpox (see references). In addition, detailed information regarding the disease can be found at the following CDC website: http://www.bt.cdc.gov/agent/smallpox/overview/disease-facts.asp

Table 3 – Initial Input Parameters

Parameter	Definition	Small Pox Values
E(0)	Initially exposed	300
β	transmission rate	3 / day
α	close contacts identification rate	5 / day
d	mortality rate of the disease	0.3
m	disability rate of the disease	0.05
φ	treatment rate	5000 / day
γ	quarantine rate	0.3
μ1	incubation period	13 days
μ2	infectious period	20 days

Using the baseline input parameters described above, the BAM was simulated for 200 days after the initial biological attack in a region where the susceptible population is roughly 1 million. This population does not include individuals who have already been vaccinated by smallpox. The results of this initial run are shown in Figure 3 and Table 4 as follows:

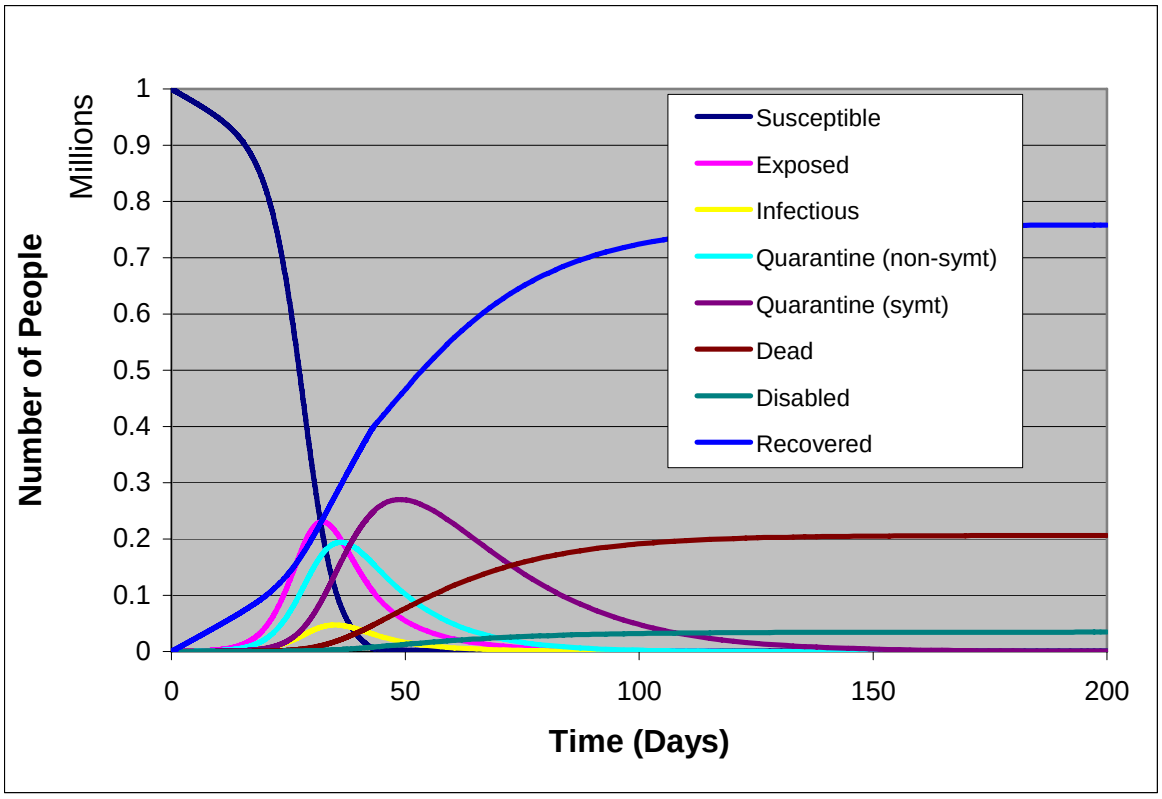

Figure 3 – Baseline Results of the BAM

Table 4 – Final Totals for the Number of People in Each State

State	Definition	Final # People in Each State
S	Susceptible	1025
E	Exposed	1
I	Infectious	0
Q1	Quarantined (Non-symptomatic)	1
Q2	Quarantined (Symptomatic)	352
D	Dead	206,297
M	Maimed (disabled)	34,383
R	Recovered (immune)	757,942

6. SYSTEM EVALUATION

It is important to evaluate and validate the BAM before using the model to make recommendations.

6.1 Evaluation Plan

The results of the BAM are compared against both historical outbreaks of smallpox and prior research done in the epidemic modeling of smallpox. Although the BAM is not designed to only model smallpox, this particular disease has the most historical information available for comparison purposes. However, many of the historical occurrences of smallpox happened prior to the existence of a vaccine and knowledge of proper control measures.

A great deal of epidemic modeling and research has been done for assessing various control strategies of a smallpox outbreak. This evaluation compares the results of the BAM to the results of other studies. When making such comparisons it is important to recognize that inputs, outputs, and assumptions for each model vary. Still, comparing the results of the BAM to prior studies does provide some insight into the validity of the study conducted. Four studies that model control strategies for a smallpox epidemic were selected to compare to the BAM. These models were selected based on their similarities to the BAM when considering modeling methods, goals, or both.

The main method of this evaluation process is to compare the time it takes to control the epidemic. This is a critical factor when assessing the effectiveness of control tactics. The control of the outbreak can be judged by the effective reproductive number, $R_{eff}(t)$, which measures the average number of secondary cases per infectious case t time units after the introduction of the initial infections. It is a common comparative parameter used in epidemic modeling, but there are different approaches to calculating it. The method used by Chowell et al. [8] fits the modeling structure of the BAM appropriately. This method uses the equation $R_{eff}(t) = \beta(t)*\mu_2*(S(t)/N)$. In a closed population, $R_{eff}(t)$ is non-increasing as the size of the susceptible population, S(t), decreases. When $R_{eff}(t)$ gets below 1 over time, the outbreak is considered under control. Once this occurs, the number of infectious people will gradually decrease to zero and the disease will be eradicated, as long as the control measures are continued. If data is not available to calculate the effective reproductive number, the time to control the outbreak can be roughly estimated when the number of infected people levels off and starts to decrease over time.

It may seem more intuitive to compare the time it takes to completely eradicate the disease or the number of deaths when comparing the BAM to other models. The time to eradicate involves a larger amount of variability and doesn't work well for comparison purposes. The number of deaths is heavily dependent on the size of the population and the initial number of people infected. This is also true for the time it takes to control the outbreak, but to a lesser degree. Overall, since getting an outbreak under control as

quickly as possible leads to faster eradication and fewer deaths or disabilities, it can be considered an ideal parameter for evaluation.

6.2 Prototype Evaluation Results

The baseline results for the BAM show that a smallpox outbreak would take approximately 42 days after detection to get to a controlled state. This is the time that $R_{eff}(t)$ drops below 1 and continues to decrease. This result from the BAM involves a specific set of assumptions and baseline inputs. These need to be considered when comparing the model to historical occurrences and other models. The initial population was 1 million people, including 300 initially infected. Other assumptions and baseline inputs for the BAM can be found in sections 5 and 7, respectively, of this report.

Gani et al. [16] provide a collection of historical data that shows that a typical outbreak, prior to the existence of vaccination and modern control techniques, will last anywhere from 5 months to a full year before getting controlled. Documented case fatality rates where as high as 25%. Some smallpox epidemics in history appear to have gone on without control even longer, but are difficult to track due to poor record keeping. Vaccination was available when London experienced frequent epidemics during the 19th century; however records of its use and effectiveness are limited. Between 1836 and 1890, epidemics occurred in London roughly every 4 years, taking 2 to 3 years to eradicate. The large disparity between the baseline results of the BAM and these cases are expected since the BAM takes into account control procedures that were either not in place or not available at the time of these historical events.

Gani et al. [16] also discuss one of the best documented smallpox epidemics, which occurred in Kosovo in 1972. Vaccination and quarantine of contacts was initiated and followed by the vaccination of roughly 95% of the population. It should be noted that a large part of the population (possibly 50%) may have been protected by vaccinations before the outbreak occurred. Considering these factors, data indicates that the outbreak was controlled in about 40 days, which is comparable to the baseline results from the BAM.

The model by Meltzer et al. [21] examined the separate effects of quarantining the infectious, mass vaccination, and the effects of combining the two strategies. The study assumed an unlimited susceptible population and a range of 100 to 1,000 initially infected. The outbreak took roughly 90 days to control using the infectious quarantine strategy, roughly 75 days with mass vaccination alone, and approximately 55 days combining both strategies. The model did not incorporate the effects of contact tracing and ring vaccination. These results are comparable to the baseline results from the BAM. However, one important difference between the two models is that the BAM incorporates the effects of contact tracing and the Meltzer model does not. This accounts for the short time to control the outbreak using the BAM.

Eichner [13] focused his study on how the spread of smallpox is influenced by infectious case isolation and close surveillance of contacts for a 3-week period. It also incorporated

vaccination of the close contacts under surveillance. Conclusions showed that with this method a smallpox outbreak could be controlled anywhere from 40 to 60 days depending on the level of close contact investigation and surveillance, which is comparable to the baseline results from the BAM.

Kaplan et al. [18] studied the effects of ring vaccination compared to mass vaccination in reducing the consequences of a smallpox release in a population of 10 million people, with 1,000 initially infected. Results of the study estimate 100 days to control an outbreak using targeted vaccination and 15 days using an aggressive mass vaccination policy. The BAM baseline results fall between the two cases examined in the Kaplan study, which is reasonable considering the differences in the two models. The study also included quarantine and isolation tactics as a means on containment.

In summary, the prototype evaluation shows that the results from the BAM are consistent with similar studies as well as historical data on smallpox outbreaks.

7. ANALYSIS

7.1 Analysis Plan

This section describes the methodology used to analyze the various "known" and "controllable" parameters that can be used in the BAM to simulate a biological terrorist attack. The objective of this analysis is to demonstrate the effectiveness of the six containment strategies described in section 3.3 of this report.

7.1.1 Pathogen

Although the BAM can be used for any pathogen that spreads from human to human, smallpox will be used for this analysis as the baseline disease agent to demonstrate the effectiveness of the BAM. Smallpox has the most readily available information for baseline input parameters. A number of researchers have studied smallpox. Many of these studies include disease spread and disease containment analyses that can be used as a benchmark for the BAM. Some of these studies are discussed in section 6.2 while others are listed as references in section 9 of this report.

7.1.2 Parameters / Containment Strategy Correlation

The BAM has eight parameters that dictate the number of individuals who ultimately enter, leave, or pass though each state as described in Appendix 1 of this report. Of these parameters, five are "known" and are typically determined by the specific pathogen used in the biological attack. The "known" parameters include: the incubation period (μ_1), the infectious period (μ_2), the mortality rate (d), the disability or maimed rate (m), the transmission rate (β), and the number of individuals initially exposed to the pathogen. The remaining three parameters are considered "controllable" parameters and include: the close contacts identification rate (α), the quarantine rate (γ), and the treatment rate (φ). Emergency responders (ER) and emergency planners (EP) can manipulate the "controllable" parameters to simulate various containment strategies in order to minimize the impact of a biological attack on a susceptible population. On the other hand, the "known" parameters are inherent to the disease and cannot be controlled by ER or EP. The "controllable" parameters correlate to the containment strategies as follows:

Quarantine and isolation – The quarantine rate (γ) can be raised or lowered based on the availability of treatment/containment facilities.

Movement restrictions – The quarantine rate (γ) can be raised or lowered based on implementation of a voluntary quarantine policy. This may include requesting susceptible individuals to stay at home until the attack can be controlled.

Ring vaccination – The close contacts identification rate (α) can be raised or lowered to make optimal use of limited resources such as vaccination.

Target vaccination – The treatment rate (φ) can be raised or lowered to reflect vaccination (if available) of the susceptible population in the area of the attack.

Mass vaccination – The treatment rate (φ) can be raised or lowered to reflect vaccination (if available) of the susceptible population inside and outside of the area of the attack.

Prophylactic vaccination – This containment strategy is beyond the scope of the BAM. Prior knowledge of an outbreak and/or terrorist biological attack is not likely. The BAM is designed to assist ER and EP in the event of a biological attack, not prior to the event.

7.1.3 Sensitivity Analysis – Smallpox

The input parameters listed in 7.1.3 will varied in the cases listed below. One parameter will be varied while the rest are held constant to observe the effect on the BAM. Determination of necessary runs will be continually evaluated as the results of each new case are analyzed.

Case 1:

The quarantine rate (γ) will be varied between its minimum value and its maximum value based on the availability of treatment/containment facilities. The baseline, minimum, and maximum values for γ are as follows:

Quarantine rate (γ)	
Baseline	0.3
Minimum	0.1
Maximum	0.5

Case 2:

The transmission rate (β) will be varied between its minimum value and its maximum value based on the "known" properties of smallpox. The value for this parameter varies in literature. The baseline, minimum, and maximum values for β are as follows:

Transmission rate (β)	
Baseline	3
Minimum	1
Maximum	5

Case 3:

The Incubation Period (μ_1) will be varied between its minimum value and its maximum value based on the "known" properties of smallpox. The value for this parameter varies in literature. The baseline, minimum, and maximum values for μ_1 are as follows:

Incubation period (μ_1)	
Baseline	13
Minimum	7
Maximum	17

Case 4:

The Infectious Period (μ_2) will be varied between its minimum value and its maximum value based on the "known" properties of smallpox. The value for this parameter varies in literature. The baseline, minimum, and maximum values for μ_2 are as follows:

Incubation period (μ_2)	
Baseline	20
Minimum	16
Maximum	24

Case 5:

The mortality rate (d) will be varied between its minimum value and its maximum value based on the "known" properties of smallpox. The value for this parameter varies in literature. The baseline, minimum, and maximum values for d are as follows:

Mortality rate (d)	
Baseline	0.3
Minimum	0.2
Maximum	0.4

Case 6:

The disability (maimed) rate (m) will be varied between its minimum value and its maximum value based on the "known" properties of smallpox. The value for this parameter varies in literature. The baseline, minimum, and maximum values for m are as follows:

Disability rate (m)	
Baseline	0.05
Minimum	0.01
Maximum	0.2

Case 7:

The close contact identification rate (α) will be varied between its minimum value and its maximum value based on the ability of emergency responders to identify individuals exposed to the pathogen. The value for this parameter varies depending on the capabilities of the local community. The baseline, minimum, and maximum values for α are as follows:

Close contact identification rate (α)	
Baseline	5
Minimum	1
Maximum	10

Case 8:

The treatment (vaccination) rate (φ) will be varied between its minimum value and its maximum value based on the ability of emergency responders to vaccinate the susceptible population. The value for this parameter varies depending on the capabilities of the local community. The baseline, minimum and maximum values for φ are as follows:

Treatment (vaccination) rate (φ)	
Baseline	0.005
Minimum	0
Maximum	0.025

7.2 Analysis Results

This section reports the results of the sensitivity analysis outlined in section 7.1.5. The details of the sensitivity analysis can be found in Appendix 5.

7.2.1 Case 1 – Quarantine rate

When the quarantine rate is varied, the entire BAM is changed. In general, a larger quarantine rate will yield less dead and disabled individuals. An increased quarantine rate may reflect the availability of treatment facilities (hospital beds) and points of distribution for vaccinations. Another important aspect of the quarantine rate is that it reduces the impact of uncertainties with the infectious period length, as further described in Section 7.2.4. The analysis indicates that quarantine, isolation, and movement restrictions are effective means for containment of an epidemic.

7.2.2 Case 2 – Transmission rate

The transmission rate is by far the most sensitive input parameter in the BAM. However, emergency responders and planners have limited ability to manipulate this parameter. The transmission rate is estimated from data of previous disease outbreaks. It should be noted that this rate is difficult to quantify and data errors can cause significant uncertainty in the estimated transmission rate. This uncertainty can have a significant impact on the model's final results.

7.2.3 Case 3 – Incubation period

Manipulation of the length of time (days) required for a disease to incubate in an individual's body had little to no affect on the BAM because contact tracing often transfers exposed individuals into the quarantine state before their incubation period ends and subsequently cannot cause secondary infections. Thus, tracing close contacts of infectious individuals negates potential consequences arising from uncertainty with the incubation period length. A similar effect was noted with the infectious period, shown in the next section. The use of the mean incubation period value is therefore sufficient for our model.

7.2.4 Case 4 – Infectious period

Manipulation of the length time (days) required for a disease to run its course after the individual has become symptomatic has almost no affect on the final results of the BAM. This is due to the model having a sufficiently high quarantine rate for infections individuals. For example, the baseline quarantine rate used is 0.3. This translates to 30% of the infectious population being quarantined per day, or from another vantage point, an infectious individual has a 30% probability of being quarantined each day he/she is infectious. Therefore, an infectious person has about a 99.5% probability of being quarantined before the minimum infectious length of 16 days has passed. Thus increasing the infectious length to an extremely large number has a negligible effect on the final results since nearly all infectious are quarantined before the minimum infectious period had ended. In essence, a sufficiently high quarantine rate nullifies possible uncertainty with the length of the infectious period. The use of a mean value for the incubation period will yield sufficient results.

7.2.5 Case 5 – Mortality rate

Variations in the mortality rate only affects the dead and recovered populations and does not affect the susceptible, exposed, infected, quarantine, or maimed (disabled) populations. Since these are two populations that ER and EP are particularly concerned with, reducing uncertainty in the expected mortality rate is important for obtaining accurate results. However, the results from the runs in Case 5 show a linear relationship between the mortality rate and the total number of deaths. Thus the results are easily scalable as new information emerges.

7.2.6 Case 6 – Disability rate

Variations in the disability rate only affects the maimed (disabled) and recovered populations and does not affect the susceptible, exposed, infected, quarantine, or dead populations. The disability rate is typically not known and varies considerably depending on the disease. Due to this, the sensitivity of the BAM to the disability rate is acceptable since the variations are isolated to the maimed (disabled) and recovered states, which

means that the primary populations of interest to ER and EP (dead and quarantine) are not adversely impacted.

7.2.7 Case 7 – Close contact identification rate

Variations in the close contact identification rate have a small affect on the BAM. An increased value for the close contact identification rate will yield less dead and disabled individuals. The close contact identification rate does not have a larger affect mainly due to the size of the initial susceptible and exposed populations. However, a sufficiently high close contact identification rate reduces the impact of uncertainties with the incubation period length, as described in Section 7.2.3. The analysis indicates that ring vaccination is a moderately effective containment strategy.

7.2.8 Case 8 – Treatment (Vaccination) rate

The treatment rate reflects the capability of the local community to treat (vaccinate) the susceptible population prior to pathogen exposure. In other words, susceptible individuals will move directly to the recovered state. These individuals cannot become exposed and are essentially removed from the BAM. More individuals removed form the susceptible population will yield fewer dead and disabled. The analysis indicates that target and mass vaccination are effective containment strategies.

8. CONCLUSIONS

8.1 Summary

The BAM was found to be a good approximation of what can be expected in the aftermath of a biological terrorist attack. The BAM was designed with the flexibility to be used for various "Category A" pathogens and to interface with existing biological attack models. For example, the BAM assumes that an initial number of individuals are exposed in a biological attack. Emergency responders can use a discrete value or use an existing dispersion model to initialize the BAM and then predict the outcome of the outbreak. However, the BAM is dependent on prior knowledge of the pathogen used in the attack and prior knowledge of the emergency response capabilities for such an attack. The BAM is highly sensitive to parameters such as the pathogen transmission rate (β), the mortality rate (d), the quarantine rate (γ), and the treatment rate (φ). Poor predictions of these parameters may reduce the overall accuracy of the BAM. Furthermore, it is critically important to accurately predict the characteristics of a biological attack in order to ensure that local communities are adequately prepared and equipped with proper treatment facilities and/or vaccinations to handle a potential epidemic.

8.2 Lessons Learned

Throughout the BAM development process the project team found a number of best practices to manage the time as well as the scope of the project. From the onset of the BAM development, it was not clear how much could be accomplished in one semester, especially since all members of the project team also work full-time professional jobs. It was found that the best approach to such a problem is to develop an initial work breakdown structure (WBS). For each week in the WBS, team members perform tasks while limiting their overall workload to less than 10 hours per week on average. This process revealed a number of time-consuming tasks that were overly optimistic and not critical to the end objective of the project. These tasks were eliminated or reduced to make the project manageable.

In addition, hours required to complete the BAM were dramatically reduced through the use of online meetings. One team member would serve as the moderator, and another would serve as the scribe. However, the responsibilities of the scribe were reduced by utilizing the capability to copy/paste full discussions directly in to an electronic document. This document was uploaded on a shared website and could be easily retrieved at a later date.

During the model development phase of the BAM, the project team found it useful to create a model that would be more adaptable and not spend as much time on details such as the exact input parameters for a particular disease. However, to establish a baseline model for evaluation and analysis purposes, research was conducted on smallpox. In addition, the project team found assigning one member to manage the model equations was preferred to limit duplicity in efforts.

8.3 Recommendations

In the event of a biological attack, the BAM is a quick and easy way to simulate the potential impact of a biological attack and select optimal strategies for containment. Based on the simulations, the most effective containment strategies include target vaccination, if available, and quarantine / isolation of those individuals that have been initially exposed and their close contacts.

The rate at which vaccinations are dispersed drastically reduces that number of individuals exposed to the pathogens. For example, the baseline BAM for smallpox assumes that 0.005% of the susceptible population can be vaccinated per unit time. Realistically, this number can be increased through the use points of dispersion or by simply mailing the vaccination thorough the U.S. Postal system to reduce the size of the susceptible population. By doubling this percentage to 1 % roughly 5 times as many people can be spared from the horrific ordeal known as smallpox.

Quarantine and isolation of confirmed and suspected cases is absolutely critical in order to contain a disease outbreak in a reasonable amount of time. These individuals need to be kept clear of the susceptible population to prevent additional exposures. This may include the use hospitals, schools, and other public facilities to remove individuals from the population. In addition, local television news programs should be utilized to spread the word about an outbreak; to recommend that individuals not in the immediate biological attack region remain at home; and avoid high density areas such as the mass transit system, concerts, or other events.

8.4 Future Work

Based on the results of the project assessment, the scope of the BAM project was reduced to create a manageable 15-week project. Although the BAM is a complete disease behavioral model, certain aspects can be expanded upon to include the following artifacts:

- The BAM is a deterministic model in that the input parameters are fixed values and do not change over time. In order to incorporate the uncertainty that exists in the real world the model could be converted to a stochastic one. Elements that contain significant uncertainty or, with slight perturbations, have large impact on the final results, can be modeled with stochastic variables.

- The model could be modified to include a decay variable for the transmission rate (β). This would be a way to account for the public reaction to the dissemination of information regarding the outbreak (such as an increase in the number of people who reduce their outside activities as the outbreak spreads).

- The BAM has a total of eight states. Additional states can be added to reflect the difference between quarantine facilities such as hospitals, schools and points of treatment / vaccine distribution.

- The model can be enhanced to incorporate optimal strategies for the allocation of fixed resources to tackle an epidemic such as available vaccinations dosages, quarantine facilities, hospital beds and emergency responders.

- The BAM assumes that there are no entries, exits, births, or deaths during the aftermath of the biological attack. In other words, the total population does not change over time. The BAM could be modified to work with a dynamic population.

- The model assumes that individuals in the recovered population do not become susceptible again. This may not be reasonable for diseases for which there are no effective vaccinations. The model could be enhanced to address this variation.

- The BAM is only relevant for pathogens that spread from human to human. The BAM could be expanded to account for other "Category A" pathogens that may be transmitted by other means (i.e. animal to human, waterborne, airborne).

- The BAM model could be expanded to address other classes of events such as the containment and spread of computer viruses over the internet by ascertaining the right parameters for such an event.

- The BAM was implemented in MATLAB. Although this implementation is very fast and accurate for simulations runs, it is not particularly user friendly. The BAM could be implemented with a graphical user interface in the form of a 'dash board' to improve ease of use by emergency responders and emergency planners.

- BAM project included basic sensitivity analysis and parametric analysis. Further analysis can be conducted. For example, additional runs could include cases where multiple "controllable" parameters (quarantine rate (γ), contact identification rate (α), and treatment rate (φ)) are varied simultaneously. This would allow for detailed analysis to be performed that would result in more specific recommendations for ER and EP when responding to a specific attack.

9. REFERENCES

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A. APPENDICES

A.1 Model Variables

States (sum up to the whole population)

S(t) = # of susceptible people at time t
E(t) = # of exposed people at time t (incubation state)
I(t) = # of infectious people at time t
$Q_1(t)$ = # of non-symptomatic people in quarantine at time t
$Q_2(t)$ = # of symptomatic (infectious) people in quarantine at time t
Q(t) = # of people in quarantine at time t = $Q_1(t) + Q_2(t)$
D(t) = # of people dead at time t
M(t) = # of people disabled/maimed at time t
R(t) = # of people recovered at time t

s(t) = fraction of total population susceptible at time t
e(t) = fraction of total population exposed at time t (incubation state)
i(t) = fraction of total population infectious at time t
$q_1(t)$ = fraction of total population who are non-symptomatic & in quarantine at time t
$q_2(t)$ = fraction of total population e who are symptomatic (infectious) & in quarantine at time t
q(t) = fraction of total population in quarantine at time t = $q_1(t) + q_2(t)$
d(t) = fraction of total population dead at time t
m(t) = fraction of total population disabled/maimed at time t
r(t) = fraction of total population recovered at time t

Transition Rates (instantaneous rates … # per unit time)

B(t) = # of susceptible people who become infected (exposed)
C(t) = # of exposed people who develop symptoms
$Q_S(t)$ = # of susceptible people who are quarantined
$Q_E(t)$ = # of exposed people who are quarantined
$Q_I(t)$ = # of infectious people who are quarantined
$Q_Q(t)$ = # of quarantined exposed people who develop symptoms
$D_I(t)$ = # of infectious people who die
$M_I(t)$ = # of infectious people who become disabled/maimed
$D_Q(t)$ = # of quarantined people who die
$M_Q(t)$ = # of quarantined people who become disabled/maimed
$R_I(t)$ = # of infectious people who recover
$R_S(t)$ = # of susceptible people who recover
$R_{Q1}(t)$ = # of quarantined non-symptomatic people who recover
$R_{Q2}(t)$ = # of quarantined infectious people who recover

Input Parameters (all are instantaneous rates)

β = transmission rate (# of new people exposed per infectious person per time period)
α = close contacts identification rate (# of non-symptomatic persons that have been identified as a close contact of an infectious person who was quarantined within the last time period)
d = mortality rate of the disease (fraction of the infected people who will die)
m=disability rate of the disease (fraction of the infected people who end up disabled/maimed)
φ = treatment rate (fraction of total people treated/vaccinated)
γ = quarantine rate (fraction of infectious people who get quarantined during each time period)
μ_1 = incubation period (mean length of time)
μ_2 = infectious period (mean length of time)

A.2 Model Equations

ODEs

$$\frac{dS}{dt} = -Q_S(t) - B(t) - R_S(t) \quad (1)$$

$$\frac{dE}{dt} = B(t) - C(t) - Q_E(t) \quad (2)$$

$$\frac{dI}{dt} = C(t) - D_I(t) - M_I(t) - R_I(t) - Q_I(t) \quad (3)$$

$$\frac{dQ_1}{dt} = Q_S(t) + Q_E(t) - R_{Q1}(t) - Q_Q(t) \quad (4)$$

$$\frac{dQ_2}{dt} = Q_I(t) - D_Q(t) - M_Q(t) - R_{Q2}(t) + Q_Q(t) \quad (5)$$

$$\frac{dD}{dt} = D_I(t) + D_Q(t) \quad (6)$$

$$\frac{dM}{dt} = M_I(t) + M_Q(t) \quad (7)$$

$$\frac{dR}{dt} = R_I(t) + R_{Q1}(t) + R_{Q2}(t) + R_S(t) \quad (8)$$

ODE with detailed Transition Equations

$$\frac{ds}{dt} = -\alpha \cdot \gamma \cdot i(t) \cdot s(t) - \beta \cdot i(t) \cdot s(t) - \varphi \quad (1a)$$

S to Q_1 S to E S to R

- The S to Q_1 transition is α * (I to Q_2) * s(t) which is also α * Q_I(t) * s(t)
- The S to R transition is just a fixed (constant) treatment rate of the susceptible population (for simulating mass vaccination)

$$\frac{de}{dt} = \beta \cdot i(t) \cdot s(t) - e(t) \cdot \frac{1}{\mu_1} - \alpha \cdot \gamma \cdot i(t) \cdot e(t) \quad (2a)$$

S to E E to I E to Q_1

- The E to Q_1 transition is α * (I to Q_2) * e(t) which is also α * Q_I(t) * e(t)

$$\frac{di}{dt} = e(t) \cdot \frac{1}{\mu_1} - d \cdot i(t) \cdot \frac{1}{\mu_2} - m \cdot i(t) \cdot \frac{1}{\mu_2} - (1 - d - m) \cdot i(t) \cdot \frac{1}{\mu_2} - \gamma \cdot i(t)$$

E to I I to D I to M I to R I to Q_2

$$\frac{di}{dt} = e(t) \cdot \frac{1}{\mu_1} - i(t) \cdot \frac{1}{\mu_2} - \gamma \cdot i(t) \tag{3a}$$

$$\frac{dq_1}{dt} = \alpha \cdot \gamma \cdot i(t) \cdot s(t) + \alpha \cdot \gamma \cdot i(t) \cdot e(t) - q_1(t) \cdot \frac{1}{\mu_1} \cdot \frac{s(t)}{s(t)+e(t)} - q_1(t) \cdot \frac{1}{\mu_1} \cdot \frac{e(t)}{s(t)+e(t)}$$

S to Q_1 **E to Q_1** **Q_1 to R** **Q_1 to Q_2**

- People moving out of Q_1 can go to either Q_2 or to R. We use $1/\mu_2$ to capture the delay between states (will not know that an individual has actually recovered until they make it through an incubation period without getting sick). The ratios with s(t)+e(t) in the denominator use used to differentiate between the people in Q_1 who have the disease and those who don't (all are non-symptomatic). The assumption is that the fraction of people that fall into the two categories (exposed, but not yet showing symptoms, and non-exposed) are the same in Q_1 as they are in the general population.

$$\frac{dq_1}{dt} = \alpha \cdot \gamma \cdot i(t) \cdot s(t) + \alpha \cdot \gamma \cdot i(t) \cdot e(t) - q_1(t) \cdot \frac{1}{\mu_1} \tag{4a}$$

$$\frac{dq_2}{dt} = \gamma \cdot i(t) - d \cdot q_2(t) \cdot \frac{1}{\mu_2} - m \cdot q_2(t) \cdot \frac{1}{\mu_2} - (1-d-m) \cdot q_2(t) \cdot \frac{1}{\mu_2} + q_1(t) \cdot \frac{1}{\mu_1} \cdot \frac{e(t)}{s(t)+e(t)}$$

I to Q_2 **Q_2 to D** **Q_2 to M** **Q_2 to R** **Q_1 to Q_2**

$$\frac{dq_2}{dt} = \gamma \cdot i(t) - q_2(t) \cdot \frac{1}{\mu_2} + q_1(t) \cdot \frac{1}{\mu_1} \frac{e(t)}{s(t)+e(t)} \tag{5a}$$

$$\frac{dd}{dt} = d \cdot i(t) \cdot \frac{1}{\mu_2} + d \cdot q_2(t) \cdot \frac{1}{\mu_2} \tag{6a}$$

I to D **Q_2 to D**

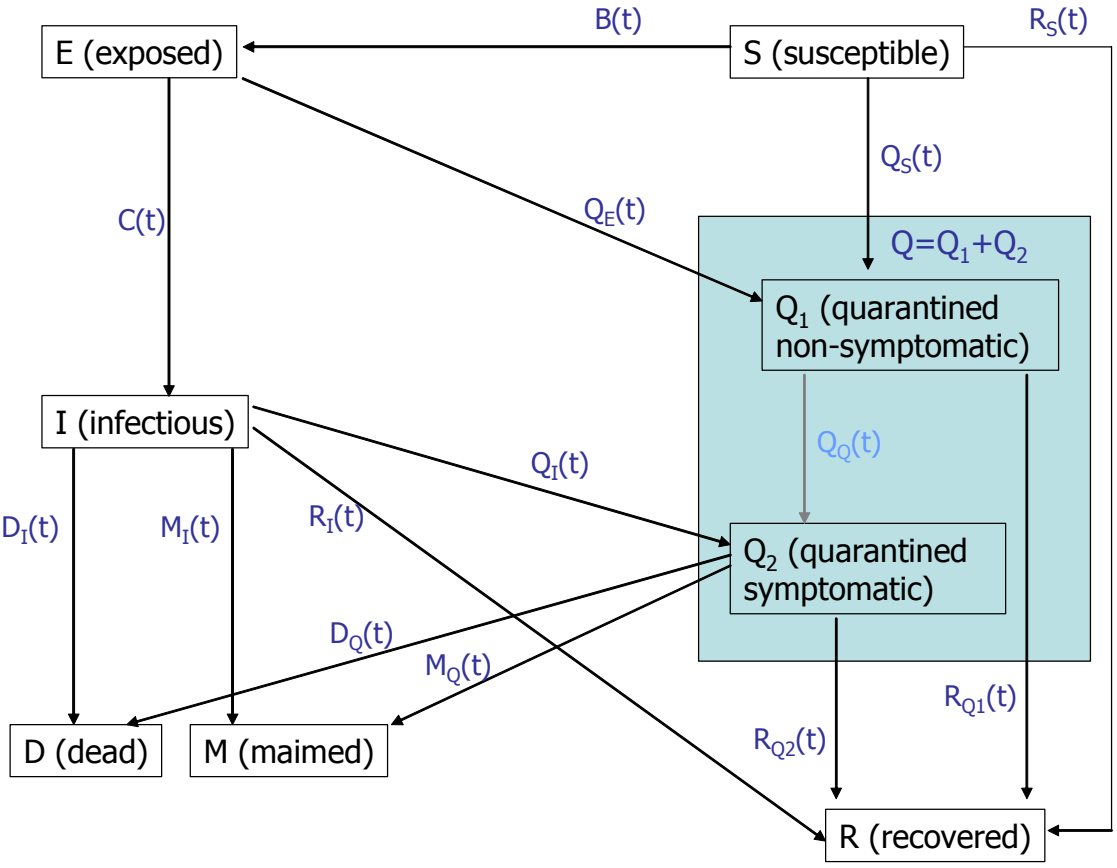
$$\frac{dm}{dt} = m \cdot i(t) \cdot \frac{1}{\mu_2} + m \cdot q_2(t) \cdot \frac{1}{\mu_2} \tag{7a}$$

I to M **Q_2 to M**

$$\frac{dr}{dt} = (1-d-m)\cdot i(t)\cdot\frac{1}{\mu_2} + q_1(t)\cdot\frac{1}{\mu_1}\cdot\frac{s(t)}{s(t)+e(t)} + (1-d-m)\cdot q_2(t)\cdot\frac{1}{\mu_2} + \varphi \qquad (8a)$$

Q_2 to R **Q_1 to R** **Q_2 to R** **S to R**

A.3 System Architecture



A.4 MATLAB Model

Base MATLAB Model:

```
%s(t) = total population susceptible at time t
%e(t) = total population exposed at time t (incubation state)
%i(t) = total population infectious at time t
%q1(t) = total population who are non-symptomatic & in quarantine at
time t
%q2(t) = total population e who are symptomatic (infectious) & in
quarantine at time t
%d(t) = total population dead at time t
%m(t) = total population disabled/maimed at time t
%r(t) = total population recovered at time t
```

```
%   where
%       s = w(1)
%       e = w(2)
%       i = w(3)
%       q1 = w(4)
%       q2 = w(5)
%       d  = w(6)
%       m  = w(7)
%       r  = w(8)

function wBAM = BAM (t,w,params)
% Right hand sides of system of O.D.E.'s as per BAM_ModelEquations_v10
%global alpha beta gamma mu1 mu2 mu3 x phi

persistent tprev  tstep steps

if (nargin < 3)
    params = [5 3 0.3 0.3 13 20 0.05 0.005];
end

if steps == 0
    tstep = 0;
    tprev = 0;
else
    tstep  = t - tprev;  % compute the time period in this step
end

steps = steps + 1; % iteration number
tprev = t;         % store the current time

if or(tstep == 0 , w(1) < params(8))
   phi     = 0;
else phi   = params(8);
end

alpha   = params(1);
beta    = params(2);
gamma   = params(3);
dead    = params(4);
mu1     = params(5);
mu2     = params(6);
maimed  = params(7);

SE = beta*w(3)*w(1);
SQ1 = alpha*gamma*w(3)*w(1);
SR = phi;
EI = w(2)/mu1;
EQ1 = w(3)*w(2);
ID = dead*w(3)/mu2;
IM = maimed*w(3)/mu2;
IR = (1-dead-maimed)*w(3)/mu2;
IQ2 = gamma*w(3);
Q1R = w(4)*w(1)/(mu1*(w(1)+w(2)));
Q1Q2 = w(4)*w(2)/(mu1*(w(1)+w(2)));
Q2D = dead*w(5)/mu2;
Q2M = maimed*w(5)/mu2;
Q2R = (1-dead-maimed)*w(5)/mu2;
```

```
 s  =  -SQ1-SE-SR;
 e  =  SE-EI-EQ1;
 i  =  EI-ID-IM-IR-IQ2;
 q1 =  SQ1+EQ1-Q1R-Q1Q2;
 q2 =  IQ2-Q2D-Q2M-Q2R+Q1Q2;
 d  =  ID+Q2D;
 m  =  IM+Q2M;
 r  =  IR+Q1R+Q2R+SR;

 wBAM = [ s ; e ; i ; q1 ;q2; d ;m ;r; SE; SQ1; SR; EI; EQ1; ID; IM;
IR; IQ2; Q1R; Q1Q2; Q2D; Q2M; Q2R];
```

MATLAB Run Setup:

File runBAM.m

```
% Runs the BAM SIRQ disease & quarantine model
%
% Definitions used by this implementation
% s(t) = total population susceptible at time t
% e(t) = total population exposed at time t (incubation state)
% i(t) = total population infectious at time t
% q1(t) = total population who are non-symptomatic & in quarantine at
time t
% q2(t) = total population e who are symptomatic (infectious) & in
quarantine at time t
% d(t) = total population dead at time t
% m(t) = total population disabled/maimed at time t
% r(t) = total population recovered at time t
% Right hand sides of system of  O.D.E.'s
%  dw(1)/dt=...
%  dw(2)/dt=...
%  dw(3)/dt=...
%  ....
%
%   where
%       s = w(1)
%       e = w(2)
%       i = w(3)
%       q1 = w(4)
%       q2 = w(5)
%       d  = w(6)
%       m  = w(7)
%       r  = w(8)
function RunBAM (filenam,plist)

totalpopulation = 1000000

initExposed = 300

Sinit   = (totalpopulation-initExposed)/totalpopulation  % initial
number of susceptible a very large city
Einit   = initExposed/totalpopulation   % initial number of exposed due
to the attack
```

```
Iinit   = 0.0000   % initial number of infected at the time of the
attack
Q1init  = 0       % initial number of people in Q1
Q2init  = 0       % initial number of people in Q2
xinit   = 0       % initial number of Dead because of attack
minit   = 0       % initial number of Maimed because of attack
Rinit   = 0       % initial number of Recovered at the time of attack

SEinit = 0.0;
SQ1init = 0.0;
SRinit = 0.0;
EIinit = 0.0;
EQ1init = 0.0;
IDinit = 0.0;
IMinit = 0.0;
IRinit = 0.0;
IQ2init = 0.0;
Q1Rinit = 0.0;
Q1Q2init = 0.0;
Q2Dinit = 0.0;
Q2Minit = 0.0;
Q2Rinit = 0.0;

tmax    = 200 % amount of time to run the model

% Setup Intial values for all states

%w0 = [Sinit; Einit; Iinit; Q1init; Q2init; xinit; minit ;Rinit];

w0 =
[Sinit;Einit;Iinit;Q1init;Q2init;xinit;minit;Rinit;SEinit;SQ1init;SRini
t;EIinit;EQ1init;IDinit;IMinit;IRinit;IQ2init;Q1Rinit;Q1Q2init;Q2Dinit;
Q2Minit;Q2Rinit];

%Setup the time range for the simulation
tlim = [0 tmax];

options =
odeset('RelTol',.0000000000001,'AbsTol',.00000000000001,'Stats','on');

% run the model
[t, w, stats ] = ode45(@BAM, tlim, w0,[], plist);

wcopy = w;
tempw = w;

tempw (:,[1 2 3 4 5 6 7 8]) =[];    % Discard columnes 1-8

temptransit = tempw;

temptransit = [ 0 0 0 0 0 0 0 0 0 0 0 0 0 0; temptransit];  % Add a row
to the beginining

temptransit(end,:) = [];                                    % Delete
the last row

transit = tempw - temptransit;
```

```
w(:,[9 10 11 12 13 14 15 16 17 18 19 20 21 22]) = [];         % Delete
columns from w

% write output to excel

par = {'alpha','beta','gamma','dead','mu1','mu2','maimed','phi' };

filenam = strcat(filenam, '.xls');

delete(filenam);

hdr  = {'t' , 'S' , 'E' , 'I' , 'Q1' ,'Q2', 'd','m', 'r','SE', 'SQ1',
'SR', 'EI', 'EQ1', 'ID', 'IM', 'IR', 'IQ2', 'Q1R', 'Q1Q2', 'Q2D',
'Q2M', 'Q2R'};

wtemp = [t wcopy];
xlswrite(filenam, hdr,   'Debug','A3');
xlswrite(filenam, wtemp, 'Debug', 'A4');
wtemp = []; % Deallocate

wtemp = [t w  transit];
xlswrite(filenam,par,'Percentage','A1');
xlswrite(filenam,plist,'Percentage','A2');
xlswrite(filenam, hdr,   'Percentage','A3');           % Creates a
sheet called Output and writes a header row for all data items
xlswrite(filenam, wtemp, 'Percentage','A4');           % Writes the
output of the wtemp vector to sheet outputs starting at cell A2
wtemp   = []; % Deallocate


w       = w*totalpopulation;
transit = transit* totalpopulation;
wtemp = [t w transit];

xlswrite(filenam,par,'Counts','A1');
xlswrite(filenam,plist,'Counts','A2');
xlswrite(filenam, hdr,   'Counts','A3');           % Creates a sheet
called Counts and writes a header row for all data items
xlswrite(filenam, wtemp, 'Counts','A4');
wtemp = []; % Deallocate

 %make a plot
plot(t, w, 'LineWidth', 2)
title(filenam)
xlabel('time')
ylabel('Individuals in Each State')
legend('S', 'E', 'I','Q1', 'Q2', 'D','M','R')
```

A.5 Analysis Details

The following analysis corresponds with section 7 of this report. For this analysis the BAM project team focused on the effects of varying one parameter while all other parameters are held constant. In particular, the BAM project team was most interested in the number of individuals in the dead state D(t) after the outbreak has been reasonably contained (200 days). For each case the BAM was simulated two times: once at a minimum value for the parameter in question and once at a maximum value for the parameter. These minimum and maximum values for each parameter were selected based on variations apparent in existing research.

Case 1 – Quarantine rate (γ)

Final totals in each state of the BAM after 200 days of simulation are as follows:

State	Definition	Minimum (γ=0.1)	Baseline (γ=0.3)	Maximum (γ=0.5)
S	Susceptible	50	1,025	2,587
E	Exposed	0	1	1
I	Infectious	0	0	0
Q1	Quarantined (Non-symptomatic)	1	1	2
Q2	Quarantined (Symptomatic)	309	352	428
D	Dead	240,655	206,297	164,497
M	Maimed (disabled)	40,109	34,383	27,416
R	Recovered (immune)	718,875	757,942	805,069

Results – The variation between the minimum and maximum values for the quarantine rate results in a difference in the number of individuals who reach the dead state. The results are as follows:

	TOTAL DEAD
MIN	34,358
BASELINE	-
MAX	-41,799

When the quarantine rate is higher more people will survive the disease outbreak. This parameter has a noticeable effect on the output of the BAM. It is critical to have an accurate estimate of this parameter to accurately simulate the capability of the region where the outbreak occurred to handle a large-scale quarantine.

Case 2 – transmission rate (β)

Final totals in each state of the BAM after 200 days of simulation are as follows:

State	Definition	Minimum (β=1)	Baseline (β=3)	Maximum (β=5)
S	Susceptible	4,859	1,025	88
E	Exposed	28	1	0
I	Infectious	8	0	0
Q1	Quarantined (Non-symptomatic)	50	1	1
Q2	Quarantined (Symptomatic)	1,226	352	274
D	Dead	44,528	206,297	246,266
M	Maimed (disabled)	7,421	34,383	41,044
R	Recovered (immune)	941,880	757,942	712,328

Results – The variation between the minimum and maximum values for the transmission rate results in a significant difference in the number of individuals who reach the dead state. The results are as follows:

	TOTAL DEAD
MIN	-161,769
BASELINE	-
MAX	39,969

When the transmission rate is lower more people will survive the disease outbreak. This parameter has a noticeable effect on the output of the BAM. Although the transmission rate is a function of the pathogen used in the biological attack, it is critical to have an accurate estimate of this parameter to get an accurate prediction from the BAM.

Case 3 – Incubation period (μ_1)

Final totals in each state of the BAM after 200 days of simulation are as follows:

State	Definition	Minimum (μ_1=7)	Baseline (μ_1=13)	Maximum (μ_1=17)
S	Susceptible	993	1,025	1,018
E	Exposed	0	1	15
I	Infectious	0	0	3
Q1	Quarantined (Non-symptomatic)	0	1	32
Q2	Quarantined (Symptomatic)	135	352	746
D	Dead	217,609	206,297	197,789
M	Maimed (disabled)	36,268	34,383	32,965
R	Recovered (immune)	744,995	757,942	767,432

Results – The variation between the minimum and maximum values for the incubation period results in a slight difference in the number of individuals who reach the dead state. The results are as follows:

	TOTAL DEAD
MIN	12,584
BASELINE	-
MAX	-11,150

When the incubation period is longer more people will survive the disease outbreak. Although the incubation period is a function of the pathogen used in the biological attack, it is not critical to have an accurate estimate for this parameter. Use of the mean value for the incubation period is sufficient to get decent estimates out of the BAM.

Case 4 – Infectious period (μ_2)

Final totals in each state of the BAM after 200 days of simulation are as follows:

State	Definition	Minimum (μ_2=16)	Baseline (μ_2=20)	Maximum (μ_2=24)
S	Susceptible	1,131	1,025	956

E	Exposed	1	1	0
I	Infectious	0	0	0
Q1	Quarantined (Non-symptomatic)	1	1	1
Q2	Quarantined (Symptomatic)	66	352	1,154
D	Dead	204,534	206,297	207,281
M	Maimed (disabled)	34,089	34,383	34,547
R	Recovered (immune)	760,177	757,942	756,061

Results – The variation between the minimum and maximum values for the infectious period results in a slight difference in the number of individuals who reach the dead state. The results are as follows:

	TOTAL DEAD
MIN	-1,762
BASELINE	-
MAX	984

When the infectious period is shorter more people will survive the disease outbreak. Although the infectious period is a function of the pathogen used in the biological attack, it is not critical to have an accurate estimate for this parameter. Use of the mean value for the infectious period is sufficient to get decent estimates out of the BAM.

Case 5 – Mortality rate (d)

Final totals in each state of the BAM after 200 days of simulation are as follows:

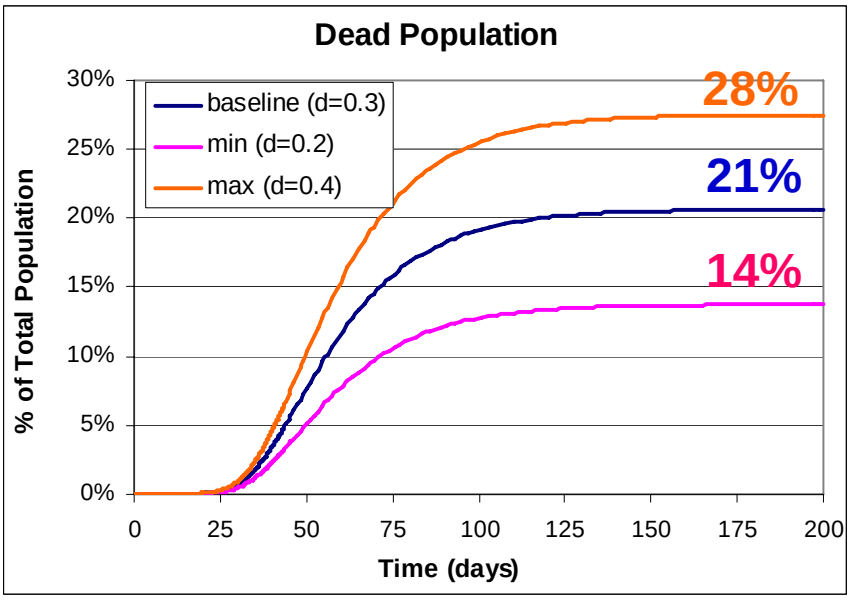
State	Definition	Minimum (d=0.2)	Baseline (d=0.3)	Maximum (d=0.4)
S	Susceptible	1,025	1,025	1,025
E	Exposed	1	1	1
I	Infectious	0	0	0
Q1	Quarantined (Non-symptomatic)	1	1	1

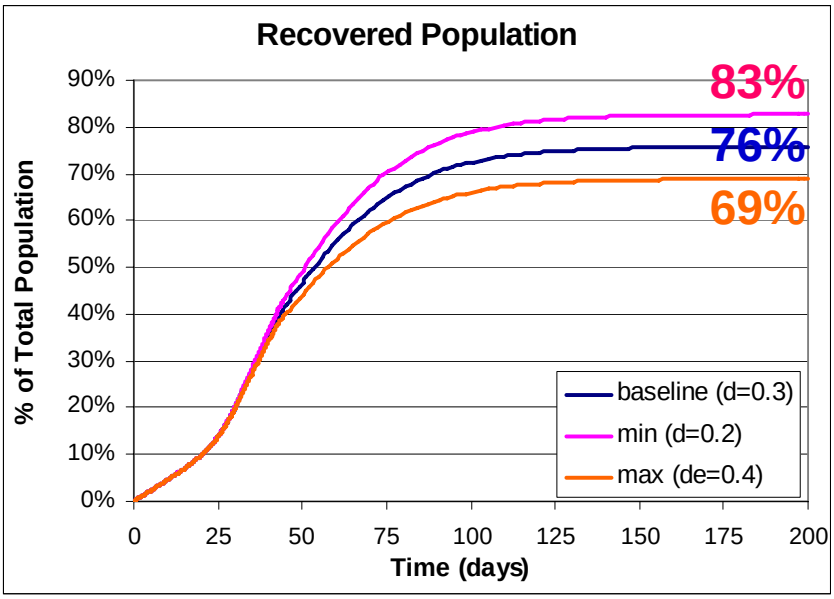
Q2	Quarantined (Symptomatic)	352	352	352
D	Dead	137,531	206,297	275,063
M	Maimed (disabled)	34,383	34,383	34,383
R	Recovered (immune)	826,707	757,942	689,176

Results – The variation between the minimum and maximum values for the mortality rate results in a significant difference in the number of individuals who reach the dead state. The results are as follows:

	TOTAL DEAD	TOTAL DISABLED
MIN	-68,766	0
BASELINE	-	-
MAX	68,766	0

Triplots for the dead and recovered states are as follows:





When the mortality rate is lower more people will survive the disease outbreak. This parameter has a noticeable effect on the output of the BAM. Although the mortality rate is a function of the pathogen used in the biological attack, it is critical to have an accurate estimate of this parameter to get an accurate prediction from the BAM.

Case 6 – Disability rate (m)

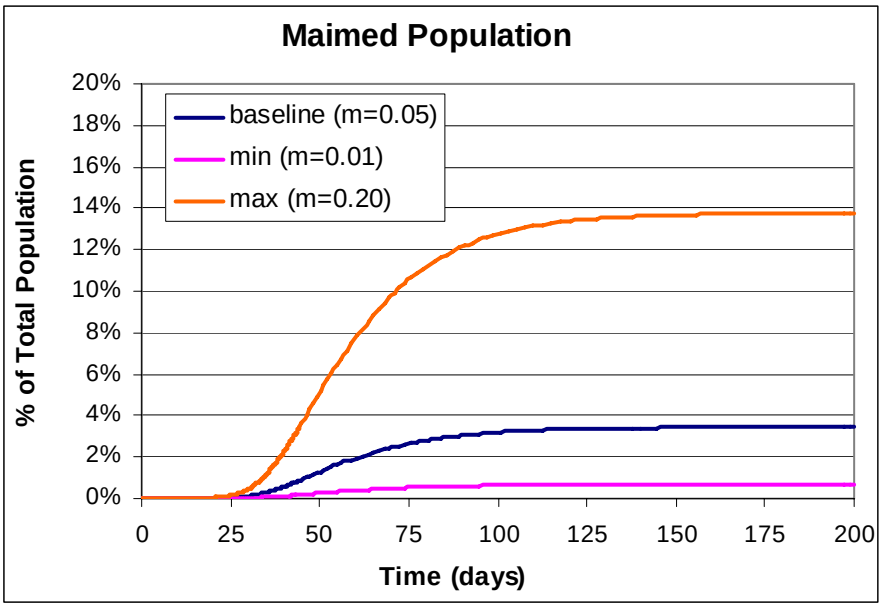
Final totals in each state of the BAM after 200 days of simulation are as follows:

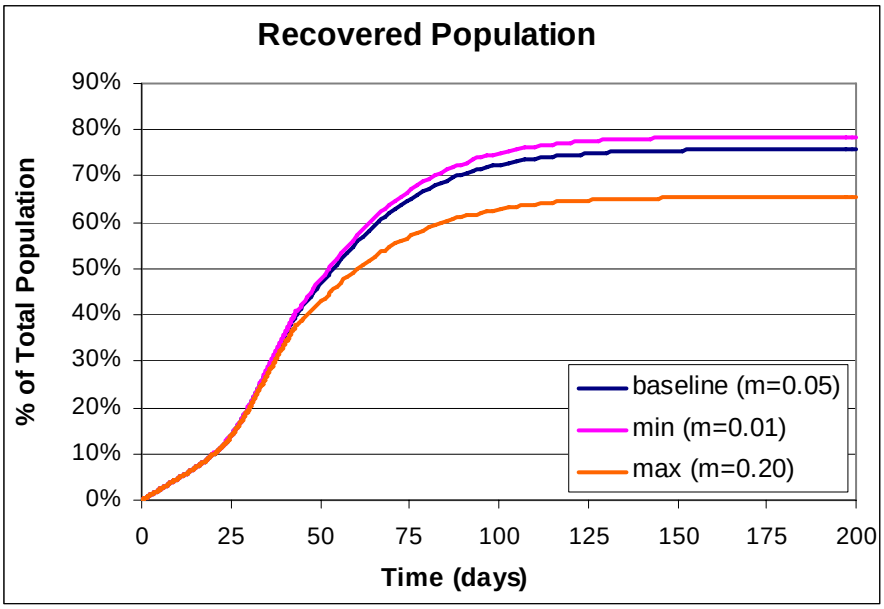
State	Definition	Minimum (m=0.01)	Baseline (m=0.05)	Maximum (m=0.2)
S	Susceptible	1,025	1,025	1,025
E	Exposed	1	1	1
I	Infectious	0	0	0
Q1	Quarantined (Non-symptomatic)	1	1	1
Q2	Quarantined (Symptomatic)	352	352	352
D	Dead	206,297	206,297	206,297
M	Maimed (disabled)	6,877	34,383	137,531
R	Recovered (immune)	785,448	757,942	654,793

Results – The variation between the minimum and maximum values for the disability rate results in a no difference in the number of individuals who reach the dead state. However, the variation does directly affect the number of individuals who reach the maimed (disabled) stated. The results are as follows:

	TOTAL DEAD	TOTAL DISABLED
MIN	0	-27,506
BASELINE	-	-
MAX	0	103,148

Triplots for the maimed (disabled) and recovered states are as follows:





When the disability rate is lower more people will survive the disease outbreak without serious disabilities. This parameter has a noticeable effect on the output of the BAM. Although the disability rate is a function of the pathogen used in the biological attack and in many cases it is impossible to predict, it is important to have an accurate estimate of this parameter to predict the amount of out patient care that is necessary after the biological attack is contained.

Case 7 – Close contact identification rate (α)

Final totals in each state of the BAM after 200 days of simulation are as follows:

State	Definition	Minimum (α=1)	Baseline (α=5)	Maximum (α=10)
S	Susceptible	1,393	1,025	768
E	Exposed	1	1	0
I	Infectious	0	0	0
Q1	Quarantined (Non-symptomatic)	1	1	1
Q2	Quarantined (Symptomatic)	382	352	326
D	Dead	218,881	206,297	195,146
M	Maimed (disabled)	36,480	34,383	32,524

R	Recovered (immune)	742,861	757,942	771,234

Results – The variation between the minimum and maximum values for the close contact identification rate results in a slight difference in the number of individuals who reach the dead state. The results are as follows:

	TOTAL DEAD
MIN	12,584
BASELINE	-
MAX	-11,150

When the close contact identification rate is higher more people will survive the disease outbreak. This parameter had a small effect on the output of the BAM. It is not critical to have an accurate estimate for this parameter. Use of the mean value for the close contact identification is sufficient to get decent estimates out of the BAM.

Case 8 – Treatment rate (φ)

Final totals in each state of the BAM after 200 days of simulation are as follows:

State	Definition	Minimum (φ=0)	Baseline (φ=0.005)	Maximum (φ=0.025)
S	Susceptible	2,886	1,025	12,805
E	Exposed	1	1	1
I	Infectious	0	0	0
Q1	Quarantined (Non-symptomatic)	2	1	0
Q2	Quarantined (Symptomatic)	409	352	64
D	Dead	251,061	206,297	34,010
M	Maimed (disabled)	41,843	34,383	5,668
R	Recovered (immune)	703,799	757,942	947,451

Results - The variation between the minimum and maximum values for the treatment rate results in a significant difference in the number of individuals who reach the dead state. The results are as follows:

	TOTAL DEAD
MIN	44,764
BASELINE	-
MAX	-172,287

When the treatment rate is higher more people will survive the disease outbreak. This parameter has a noticeable effect on the output of the BAM. It is critical to have an accurate estimate of this parameter to accurately simulate the capability of the region where the outbreak occurred to handle a large-scale treatment campaign.

A.6 Project Management Plan

Project deliverables:

The project deliverables will be an assessment of current capabilities, a risk assessment, a disease behavior model, and recommendations for emergency planners and responders.

Project organization:

The waterfall model will be used for project planning and execution. If necessary several iterations of the final testing and rework phase will be conducted.

Organizational structure:

The project team will be a hierarchical structure. Richard Bornhorst will serve as the project lead and Kathryn Poole will serve as the technical lead. Robert Grillo, Deepak Janardhanan, and Shubh Krishna will be used to assist the project lead or technical lead as needed.

Management:

- Objectives – The objective of the management team is to produce a useful product on time and on budget. A tradeoff analysis will be conducted to determine the relative importance of each requirement.

- Risk management – The risk of project over run will be assessed initially and then revisited at the midway point of the project.

- Monitoring and controlling mechanisms – Project management will monitor the progress of the project team during meetings as well as through the inspection of activity logs. The progress will be reported during formal progress reports. Changes to system requirements will be controlled through configuration management.

Communication and documentation:

- Work sites – The project team will communicate and exchange information using the project site on a Google Groups website.

- Online meetings – Online meeting will be held on WebCT at designated times.

- Project Planning – The project plan will be developed using Microsoft Project will a detailed schedule for meetings, status briefings, and due dates.

- Documentation – Revisions will be posted on the Google Groups website. Older revisions will not be deleted for configuration management purposes.

- Activity Log – Each member of the project team will keep an activity log detailing the work completed each week and the time spent to complete the task.

Deliverables, briefings, and schedule:

- Deliverables – Development work is broken into the following tasks:
  - Assess current policies, procedures, and models.
  - Evaluate potential biological warfare agents to determine the threat potential.
  - Develop a disease a behavior model.
  - Evaluate the effectiveness of various emergency response strategies.

- Briefings – For status briefings or formal presentations, each project team member is expected to contribute to the presentation and speak his or her fair share.

- Schedule – Initial project milestones are listed below. The work breakdown structure and schedule will be finalized after an initial project assessment.

Event	**Description**	**Completion Time (wks)**	**Start Date**	**Completion Date**
Task	Project Evaluation	1	01/25/2007	02/01/2007
Milestone	Team Formulation	-	02/01/2007	02/01/2007
Task	Project Proposal Drafting	2	02/01/2007	02/15/2007
Milestone	Project Proposal Due	-	02/15/2007	02/15/2007
Task	Research Biological Agents	3	02/15/2007	03/29/2007
Task	Research Existing Models	3	02/15/2007	03/29/2007
Task	Finalize Project Plan and Schedule	1	02/15/2007	02/22/2007
Task	Risk Assessment	1	02/15/2007	02/22/2007
Milestone	Status Report # 1	-	02/22/2007	02/22/2007
Task	Detailed Design and Model Development	5	02/22/2007	03/29/2007
Milestone	Progress Presentation	-	03/08/2007	03/08/2007
Milestone	Status Report # 2	-	03/22/2007	03/22/2007
Milestone	Progress Discussion	-	03/29/2007	03/29/2007
Task	Testing, Evaluation, and Recommendations	2	03/29/2007	04/12/2007

Event	Description	Completion Time (wks)	Start Date	Completion Date
Milestone	Formal Progress Presentation	-	04/05/2007	04/05/2007
Task	Final Report Drafting	3	04/12/2007	05/03/2007
Milestone	Final Report Due	-	05/03/2007	05/03/2007
Task	Presentation Preparation	1	05/03/2007	05/11/2007
Milestone	Final Presentation	-	05/11/2007	05/11/2007

A.7 Work Breakdown Structure

Project Task	Week 1					Week 2					Week 3				
Units---->	**RB**	**RG**	**DJ**	**SK**	**KP**	**RB**	**RG**	**DJ**	**SK**	**KP**	**RB**	**RG**	**DJ**	**SK**	**KP**
Project Evaluation	2	2	2	2	2										
Project Management						1					1				
Project Proposal						5.5	4	4	4	4	5.5	4	4	4	4
Project Planning															
Configuration Management						1					1				
Group Meetings						2	2	2	2	2	2	2	2	2	2
Online Discussions						0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5
Status/Progress Brief Preparation												2			2
Assess current policies and procedures															
Assess existing models															
Research/Assess biological agents															
Develop a dispersion model.															
Develop a disease behavioral model															
Develop containment model															
Testing and Evaluation of models															
Evaluate the effectiveness of various emergency response strategies.															
· Containment strategies,															
· Agent identification strategies,															
· Emergency response procedures,															
· Check point recommendations,															
· Emergency response positioning															
· Evacuation strategies (time permitting).															
Final Report Drafting															
Final Presentation Preparation															
TOTALS	**2**	**2**	**2**	**2**	**2**	**10**	**6.5**	**6.5**	**6.5**	**6.5**	**10**	**8.5**	**6.5**	**6.5**	**8.5**

Project Task	Week 4					Week 5					Week 6				
Units---->	**RB**	**RG**	**DJ**	**SK**	**KP**	**RB**	**RG**	**DJ**	**SK**	**KP**	**RB**	**RG**	**DJ**	**SK**	**KP**
Project Evaluation															
Project Management	1					1					1				
Project Proposal															
Project Planning	5														
Configuration Management	1					1					1				
Group Meetings	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
Online Discussions	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5
Status/Progress Brief Preparation	0.5	0.5	0.5	0.5	2							2			2
Assess current policies and procedures		2	2	2	0.5		2	2				2	2		
Assess existing models		2	2	2	0.5			2	2				2	2	
Research/Assess biological agents					4										
Develop a dispersion model.						5	10	10	10	10	5	10	10	10	10
Develop a disease behavioral model						5	10	10	10	10	5	10	10	10	10
Develop containment model						5	10	10	10	10	5	10	10	10	10
Testing and Evaluation of models															
Evaluate the effectiveness of various emergency response strategies.															
· Containment strategies,															
· Agent identification strategies,															
· Emergency response procedures,															
· Check point recommendations,															
· Emergency response positioning															
· Evacuation strategies (time permitting).															
Final Report Drafting															
Final Presentation Preparation															
TOTALS	**10**	**7**	**7**	**7**	**9.5**	**19.5**	**35**	**36.5**	**34.5**	**32.5**	**19.5**	**37**	**36.5**	**34.5**	**34.5**

Project Task	Week 7					Week 8					Week 9				
Units---->	**RB**	**RG**	**DJ**	**SK**	**KP**	**RB**	**RG**	**DJ**	**SK**	**KP**	**RB**	**RG**	**DJ**	**SK**	**KP**
Project Evaluation															
Project Management	1					1					1				
Project Proposal															
Project Planning															
Configuration Management	1					1					1				
Group Meetings	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
Online Discussions	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5
Status/Progress Brief Preparation							1			1		2			2
Assess current policies and procedures															
Assess existing models															
Research/Assess biological agents															
Develop a dispersion model.	5	10	10	10	10	5	10	10	10	10	5	10	10	10	10
Develop a disease behavioral model	5	10	10	10	10	5	10	10	10	10	5	10	10	10	10
Develop containment model	5	10	10	10	10	5	10	10	10	10	5	10	10	10	10
Testing and Evaluation of models															
Evaluate the effectiveness of various emergency response strategies.															
· Containment strategies,															
· Agent identification strategies,															
· Emergency response procedures,															
· Check point recommendations,															
· Emergency response positioning															
· Evacuation strategies (time permitting).															
Final Report Drafting															
Final Presentation Preparation															
TOTALS	**19.5**	**33**	**32.5**	**32.5**	**32.5**	**19.5**	**34**	**32.5**	**32.5**	**33.5**	**19.5**	**35**	**32.5**	**32.5**	**34.5**

Project Task	Week 10					Week 11					Week 12				
Units---->	**RB**	**RG**	**DJ**	**SK**	**KP**	**RB**	**RG**	**DJ**	**SK**	**KP**	**RB**	**RG**	**DJ**	**SK**	**KP**
Project Evaluation															
Project Management	1					1					1				
Project Proposal															
Project Planning															
Configuration Management	1					1					1				
Group Meetings	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
Online Discussions	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5
Status/Progress Brief Preparation		2			2	◆									
Assess current policies and procedures															
Assess existing models															
Research/Assess biological agents															
Develop a dispersion model.															
Develop a disease behavioral model															
Develop containment model															
Testing and Evaluation of models			8	8				8	8						
Evaluate the effectiveness of various emergency response strategies.															
· Containment strategies,	2	2				2	2								
· Agent identification strategies,		2	2				2	2							
· Emergency response procedures,				2	2				2	2					
· Check point recommendations,	2			2		2			2						
· Emergency response positioning			2		2			2		2					
· Evacuation strategies (time permitting).															
Final Report Drafting											7.5	7.5	7.5	7.5	7.5
Final Presentation Preparation															
TOTALS	**8.5**	**15**	**14.5**	**14.5**	**14.5**	**8.5**	**13**	**14.5**	**14.5**	**12.5**	**12**	**10**	**10**	**10**	**10**

Project Task	Week 13					Week 14					Week 15				
Units---->	**RB**	**RG**	**DJ**	**SK**	**KP**	**RB**	**RG**	**DJ**	**SK**	**KP**	**RB**	**RG**	**DJ**	**SK**	**KP**
Project Evaluation															
Project Management	1					1					1				
Project Proposal															
Project Planning															
Configuration Management	1					1					1				
Group Meetings	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
Online Discussions	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5
Status/Progress Brief Preparation															
Assess current policies and procedures															
Assess existing models															
Research/Assess biological agents															
Develop a dispersion model.															
Develop a disease behavioral model															
Develop containment model															
Testing and Evaluation of models															
Evaluate the effectiveness of various emergency response strategies.															
· Containment strategies,															
· Agent identification strategies,															
· Emergency response procedures,															
· Check point recommendations,															
· Emergency response positioning															
· Evacuation strategies (time permitting).															
Final Report Drafting	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5					
Final Presentation Preparation											7.5	7.5	7.5	7.5	7.5
TOTALS	**12**	**10**	**10**	**10**	**10**	**12**	**10**	**10**	**10**	**10**	**12**	**10**	**10**	**10**	**10**

Project Task	Duration	Completion Time	Total Time	Slip Risk?	Importance?	Compress?		Eliminate or Reduce?		Adjusted Total Time
Units---->	**Wk**	**hr/wk**	**hrs**			**Y/N**	**hrs**	**Y/N/R**	**hrs**	**hrs**
Project Evaluation	1	10.00	10.00	MED		N		N		10
Project Management	15	0.93	14.00	LOW		N		N		14
Project Proposal	2	21.50	43.00	LOW		N		N		43
Project Planning	1	5.00	5.00	LOW		N		N		5
Configuration Management	15	0.93	14.00	LOW		N		N		14
Group Meetings	15	9.33	140.0	LOW	Efficient Meetings (25% reduction)	N		R	35	105
Online Discussions	15	2.33	35.00	LOW		N		N		35
Status/Progress Brief Preparation	6	3.67	22.00			N		N		22
Assess current policies and procedures	6	2.42	14.50	LOW		Y	12	N		26.5
Assess existing models	6	2.42	14.50	LOW		Y	12	N		26.5
Research/Assess biological agents	1	4.00	4.00	LOW	High Importance	N		N		4
Develop a dispersion model.	5	45.00	225.0	HIGH	Existing Models	N		Y	225	0
Develop a disease behavioral model	5	45.00	225.0	HIGH	Existing Models can modified (75% reduction)	N		R	168.7	56.25
Develop containment model	5	45.00	225.0	HIGH		N		N		225
Testing and Evaluation of models	2	16.00	32.00	MED		N		N		32
Evaluate the effectiveness of various emergency response strategies.										
· Containment strategies,	2	4.00	8.00	MED	High	N		N		8
· Agent identification strategies,	2	4.00	8.00	LOW	Low	N		Y	8	0
· Emergency response procedures,	2	4.00	8.00	MED		N		N		8
· Check point recommendations,	2	4.00	8.00	MED		N		N		8
· Emergency response positioning	2	4.00	8.00	MED		N		Y	8	0
· Evacuation strategies (time permit)	2	12.00	24.00	HIGH	low	N		Y	24	0
Final Report Drafting	3	37.50	112.5	MED	Reduce 10	N		R	10	102.5
Final Presentation Preparation	1	37.50	37.5	MED	Reduce 10	N		R	10	27.5
TOTALS			**1237**				**24**		**488**	**772.25**

A.8 Management Report

Project Assignments:

The development of the BAM prototype, the presentation, and this final report was broken down into tasks and were assigned as follows:

Project Task	**Responsible Engineer**
Project Manger	Richard Bornhorst
Technical Lead	Kathryn Poole
Research/Scribe	Robert Grillo
Modeling and Simulation Design	Deepak Janardhanan, Shubh Krishna
Brainstorming	All
Project Proposal	Richard Bornhorst (LEAD) developed by All
Project Assessment	Robert Grillo, Richard Bornhorst
Biological Risk Assessment	Richard Bornhorst, Robert Grillo
The Model	Kathryn Poole, Deepak Janardhanan, Shubh Krishna
Model Implementation	Deepak Janardhanan
Evaluation Plan	Robert Grillo, Deepak Janardhanan
Analysis Plan	Richard Bornhorst, Kathryn Poole
Prototype Evaluation	Robert Grillo
Parametric Analysis	Kathryn Poole, Shubh Krishna
Final Report Development	Richard Bornhorst (LEAD) reviewed by All
Website Development	Deepak Janardhanan
Final Presentation Development	Kathryn Poole -(LEAD) reviewed by All

Weekly Progress Summary:

Group interaction to produce the BAM primarily took place over the internet with online meetings, roughly twice a week, and thorough posting on the BAM "Google Group" site. In person communications generally took place during or around OR 680 class time. The following is a summary of the weekly progress from these group interactions.

Week 1 (1/25/07 – 1/31/07)

Project groups were not formed during the first week of the OR 680 course. Operations research students were given the option of building upon projects sponsored by Fairfax County Public Schools or brainstorming a unique project idea with a sponsor to be determined at a later time.

Week 2 (2/1/07 – 2/7/07)

Students exchanged background information and interests to determine ideal groups. Operations research students began reviewing prior work done by students for Fairfax County Public Schools to determine what additional work could be done. Other project ideas proposed by operations research students included studies in the areas of public health or hazardous material routing.

Based on student background and project interests, the five person BAM team was formed. Because the project to be tackled was unknown, the group was temporarily named the Opt-o-mizers. The project "Google Group" was created and online meetings began. The majority of team discussions during this week involved determining what the group project would be about and how it would be approached. After further researching the prior work done for Fairfax County Public Schools, the group came to a consensus that it would be more interesting to take on a project that has not already been studied by George Mason University students.

The group discussed project ideas in the areas hazmat routing and public health issues. It was decided that the group project would involve analyzing a biological terrorist attack in Washington, DC. Project management was structured, group roles were established, and potential project sponsors were considered.

Week 3 (2/8/07 – 2/14/07)

Much of week 3 involved research for scoping the project and proposal preparation. Two types of biological attack responses were initially considered. They were evacuation of the city following an attack or containing the spread of the pathogen through the population. The later was chosen since it was discovered that a detailed routing model for evacuating Washington, DC after a disastrous event had recently been completed. In addition, it was agreed that an epidemic containment model would be more interesting. The group decided to conduct a brief risk assessment pertaining to various pathogens that could be used in an attack.

Dr. Yifan Liu agreed to sponsor the project and joined into group correspondence. A written proposal was created, along with a presentation. Proposal deliverables included discussion of management approach, emergency response background, fundamental requirements, the types of modeling that may be appropriate, and possible resources.

Week 4 (2/15/07 – 2/21/07)

After presenting the proposal, it became a priority for the group to scope the project down to a size where it could be completed in one semester. Ideas included simplifying the problem to analyzing points of distribution for administering vaccines or modeling a scenario for a specific type of biological attack. The later could involve modeling a disease that spread through the air, person-to-person, or through poisoning a food supply.

It was decided that the scope would be limited to analyzing the human to human spread of highly contagious diseases. It would build upon an existing model for person-to-person disease spread. Research indicated that a variation of the Susceptible-Infected-Recovered (SIR) disease spread model would be appropriate for the project.

The project and team name was changed to the Biological Attack Model (BAM). The disease assessment was completed and narrowed the project to include modeling smallpox, Ebola, and viral encephalitis. Preliminary assumptions were documented and presentation materials were prepared for a status briefing.

Week 5 (2/22/07 – 2/28/07)

Week 5 involved extensive research of modeling approaches and review of prior studies performed that had similar goals as the BAM. Resources were posted to the "Google Group" for all to review. Once a significant amount of resources were gathered, the group began discussing a modeling approach would make the BAM a unique operations research study.

Week 6 (3/1/07 – 3/7/07)

The group came across a number of issues that would need to be addressed in the BAM. These included availability of inputs, time dependence in parameters, managing treated/untreated people, and quarantining individuals. There were also caregiver issues and the availability of treatment resources. It was clear that a significant amount of parametric studies would be involved. Various modeling approach ideas were debated including whether the model would be stochastic or deterministic, how to track the different states of the model, and incorporating time lag for emergency response and vaccination. Without resolving all issues to the modeling approach, a preliminary 10 state model was developed.

Modeling programs were considered and included C++, Microsoft Excel, Arena, and MATLAB as candidates. The initial model was created in Microsoft Excel knowing it would later be brought into a more complex modeling platform as the project matured. A progress presentation was prepared that included project management, refined model assumptions, schematics, preliminary input parameters, and the modeling approach as topics.

Week 7 (3/8/07 – 3/14/07)

After presenting the progress of the project, sponsor and instructor feedback suggested that a deterministic model with ordinary differential equations (ODEs) would be appropriate for the BAM before attempting a stochastic model. At this point, the group realized creating a generic model for various diseases would be difficult. A generic model would still be attempted, but the focus of the analysis would likely be on smallpox. An evaluation of Ebola in the BAM would be considered if time permitted.

The BAM state diagram was modified into 8 states to better structure it for using ODEs. The group needed to account for the time it takes to transition between states before writing out equations. The ODE system would be solved numerically using MATLAB and concurrently modeled in Microsoft Excel using the Forward Euler method for comparison and verification.

Week 8 (3/15/07 – 3/21/07)

Much of week 8 involved developing the ODEs to be used in the BAM. This involved continued research since no one in the group had expertise in developing ODEs. A numerical method for solving the ODEs still needed to be determined. At this point the majority of the disease background information and input parameter information had been gathered. The new state model, modeling approach, and background information were summarized into a status presentation. A rough draft of the final report was also developed with certain sections to be filled in as the project progressed.

Week 9 (3/22/07 – 3/28/07)

The equations required further refining at this point since the model was experiencing computational issues. Some of these issues were resolved by making slight changes to the definitions of some of the input parameters. Other issues lead the group to realize areas where the equations didn't make sense. An analysis plan was drafted for use once the ODEs were finalized. The analysis would focus on comparing the effectiveness of various epidemic control strategies. Additions were made to the final report.

Week 10 (3/29/07 – 4/4/07)

Since only minor modifications to the ODEs would be required, the group began to program the BAM in MATLAB. Debugging the equations continued. For the analysis plan, inputs parameters were separated into controllable and uncontrollable parameters for parametric and sensitivity analysis.

A progress presentation was developed and including further discussion of input parameters, an update of the model (including equations), an introduction to our analysis plan, and the course of action for completing the remainder of the project.

Week 11 (4/5/07 – 4/11/07)

Both a functional MATLAB and Microsoft Excel model were completed. The model equations were finalized, so a set of baseline input parameters for smallpox were selected for initial analysis runs. MATLAB and Microsoft Excel model results were comparable. A set of parameter values were determined for use in the sensitivity and parametric analysis stage of the project.

Week 12 (4/12/07 – 4/18/07)

A baseline analysis was done. Results were used to evaluate the BAM by comparing results to historical smallpox outbreak data and results of prior models created for the spread of smallpox. Since the results of the BAM appeared valid, further analysis runs could be conducted. More additions were made to the final report.

Week 13 (4/19/07 – 4/25/07)

At this point a large portion of the final report was completed. The MATLAB model code was modified to run more efficiently for the sensitivity and parametric runs. These runs were executed. With these results, the last significant portion of the final report was completed. It was now ready for final editing. With the final report nearly complete, a draft of the final presentation was made.

Week 14 (4/26/07 – 5/2/07)

With the modeling and analysis for the BAM complete, week 14 was spent editing the final report and completing the draft presentation to be used in the dry run of the final presentation.

Week 15 (5/3/07 – 5/10/07)

The final report was completed and handed in. Refinements were made to the draft presentation to create a final version. The BAM project team conducted practice runs and made personal preparations for the final presentation of the BAM on Friday, May 11, 2007.

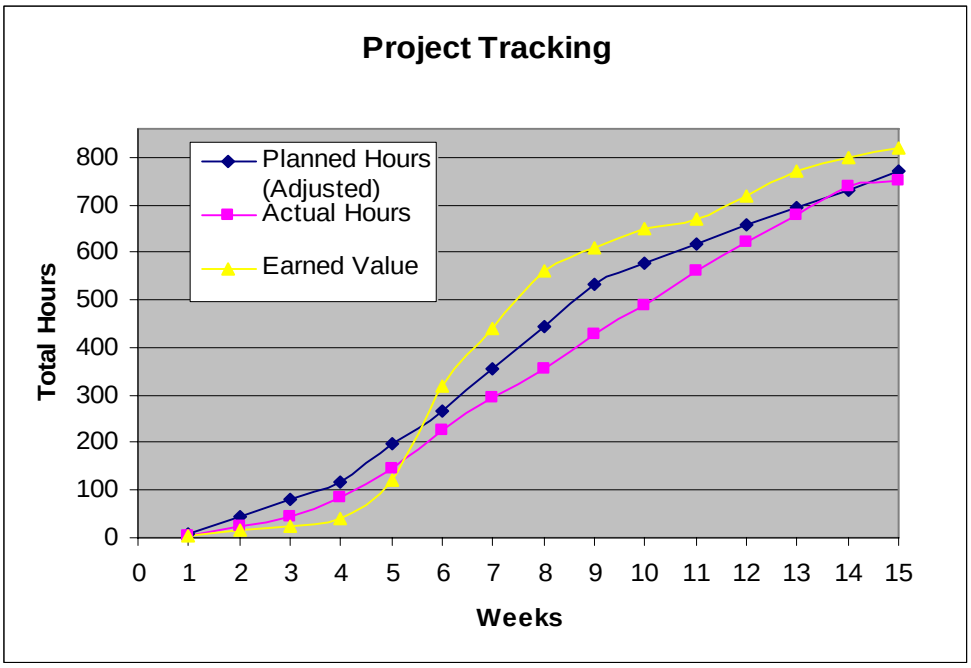
Project tracking:

The progress of the BAM project was tracked throughout the semester. Planned hours were tracked against actual hours spent working on the project. Earned Value (EV) was assessed and tracked based on the amount and quality of work completed at a given time. The tracked hours are as follows:

Weekly Breakdown	Planned Hours	Planned Hours (Adjusted)	Actual Hours	Earned Value
Week1	10	10	5	5
Week2	36	33.5	20	10
Week3	40	36	20	10
Week4	40.5	38	40	15
Week5	157.5	80	60	80
Week6	161.5	70	80	200
Week7	149.5	87	70	120
Week8	151.5	90	60	120
Week9	153.5	90	75	50
Week10	66.5	44	60	40
Week11	62.5	40	70	20

Week12	52	38.5	60	50
Week13	52	36	60	50
Week14	52	37.5	60	30
Week15	52	39.5	10	20
Total	1237	770	750	820
Average		**51.33**	**50.00**	**54.67**

The figure below illustrates the progress of the BAM project team throughout the semester.



Team member participation:

The BAM project team equally distributed the tasks described above to individual team members. Team members had the responsibility to complete work in a timely fashion in order to facilitate subsequent work. Team members were evaluated throughout the semester and individual ratings are as follows:

Engineer	**Rating (Scale: 1-10)**
Richard Bornhorst	10
Robert Grillo	10
Deepak Janardhanan	10
Shubh Krishna	10
Kathryn Poole	10