BioDefense through City Level Multi-Agent Modeling of Bio and Chemical Threats

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Objective

- Automated tools for
  - Evaluation of response policies, data efficacy, attack severity, and detection tools relating to weaponized biological attacks *in the presence of background diseases such as flu*
  - Generation of high fidelity virtual data for testing detection and fusion algorithms
- Systematically reason about:
  - The rate and spread of disease with high degree of realism
  - Early presentation of diseases, e.g., on secondary data streams
  - Potential inoculation and other response scenarios
  - Policy design with respect to BioWar response
    - What alert-level is appropriate
    - What to do given an alert level, patterns of outbreaks
- Push the frontier of social simulation models (fidelity, precision, speed, comprehensiveness, etc.)

Approach

- Realistic and Scalable Multi-Agent Dynamic-Network Model
  - Agent-based interactions allow the emergence of networks
- Flexible
  - 6 Cities (MSAs) - Hampton Roads, Norfolk, Pittsburgh, San Diego, San Francisco, Washington D.C.
  - 62 diseases – including Anthrax, Small Pox, Sars (currently working on Avian Flu)
  - 2 chemicals – Sarin, Chlorine
- Symptom Based
  - All diseases and illnesses are modeled at the symptom level
- Hybrid of many models: agent, network, geographic, weather, disease, diagnosis, treatment, recreation, etc.
- Utilizes real data streams
  - Census (population and economic)
  - School district, weather, geography, time-budget …
  - Sub-model of military bases
- Multiple outputs
  - OTC purchases, Dr and ER visits, web and phone calls, absenteeism …
  - Outputs at the population and sentinel group level (emergency responders, health care personnel)
- Validation by docking (alignment between models), input validation, and SME evaluation

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BioWar – conceptualization

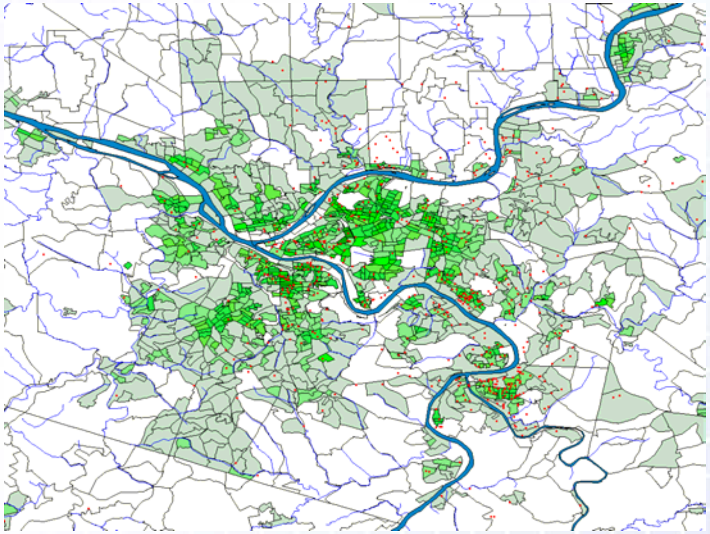
city scale multi-agent network model of weaponized attacks

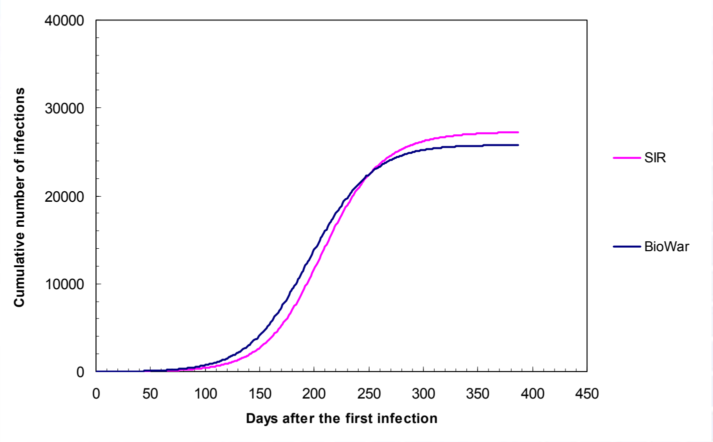
Support for Detection & Planning

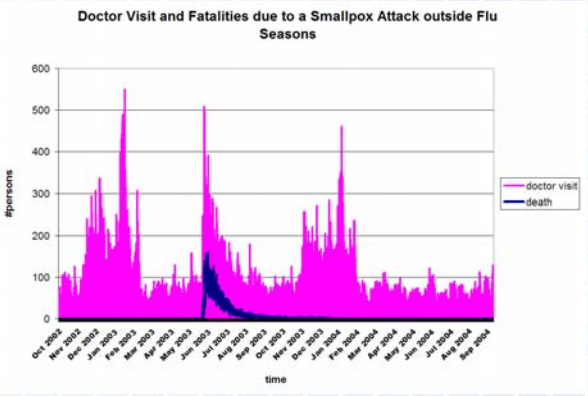
What if Analysis

Rapid Profile of Alternative Courses of Action

- Interventions
- Attack Profile
- City Profile
- Report Generation







BioWar IO

Agents move in networks which influence what they do, where, with whom, and what they know, what diseases they get, when, how they respond to them, etc.
Major difference in network and disease effects based on race, gender and age.

- Input
  - Census data – social&economic
  - School district data
  - Worksite and entertainment locations
  - Hospitals and clinics locations & size
  - Social Network characteristics
  - IT communication procedures
  - Wind characteristics
  - Spatial layout
  - Disease models
    - Influenza, small pox, anthrax, …
- Illustrative Output
  - Over the counter drug sales
  - Insurance claim reports (Dr. visits)
  - Emergency room reports
  - Absenteeism (school and work)
  - Infected
  - Contagious
  - Mortality

Overall or by sub-population
Military base
First responder

Input Sources

Origin	Source	Description
USGS	GNIS Database	Hospital, park locations
Census	Summary File 1	Demographics (population, race, age, sex)
	Economic Census	Work, medical, recreation location counts
	Geometry	Cartographic boundaries (region geometry)
NCES	CCD Database	School demographics, locations
	Publications	Student absenteeism statistics
GSS	GSS	Social network characteristics
EPA	www.epa.gov/scram001	Climate, wind data
Internist 1	QMR vocabulary QMR evoking strengths	Disease symptoms, diagnosis model
CDC	NCHS Surveys	Medical visit, mortality & morbidity statistics
CDC	Web sites	Disease timing, symptoms

City Features

	Pittsburgh	San Diego	Norfolk	Hampton
Doctor	1951	1776	841	75
Hospitals/ER	50	33	19	3
Pharmacy	479	274	199	16
Restaurant	4383	4886	2504	203
Stadium	200	143	97	10
Store	7540	8109	4944	374
Theater	551	516	307	30
Population	2,358,695	2,813,833	1,569,541	146,431

Respiratory and GI Diseases Modeled

Disease	ICD9Code	ICD9Name
ACUTE_NASOPHARYNGITIS	460	Acute nasopharyngitis [common cold]
INFLUENZA	487.1	FLU W RESP MANIFEST NEC
INFLUENZA_PNEUMONIA	480.2	PARINFLUENZA VIRAL PNEUM
SEVERE_ACUTE_RESPIRATORY_SYNDROME	480.9	Viral pneumonia, unspecified
BACTERIAL_PHARYNGITIS_ACUTE_NON_STREPTOCOCCAL_NON_GONO	462	ACUTE PHARYNGITIS
GRAM_NEGATIVE_PNEUMONIA_NON_KLEBSIELLA	482.1	PSEUDOMONAL PNEUMONIA
MYCOPLASMA_PNEUMONIA	31	PULMONARY MYCOBACTERIA
PNEUMOCOCCAL_PNEUMONIA	481	PNEUMOCOCCAL PNEUMONIA
PULMONARY_LEGIONELLOSIS	482.89	PNEUMONIA OTH SPCF BACT
STAPHYLOCOCCAL_PNEUMONIA	482.4	STAPHYLOCOCCAL PNEUMONIA
STREPTOCOCCAL_PHARYNGITIS_ACUTE	34	STREP SORE THROAT
STREPTOCOCCUS_PYOGENES_PNEUMONIA	482.3	STREPTOCOCCAL PNEUMONIA*
TUBERCULOSIS_CHRONIC_PULMONARY	11.9	PULMONARY TB NOS*
TUBERCULOSIS_DISSEMINATED	18.9	MILIARY TUBERCULOSIS NOS*
VARICELLA_PNEUMONIA	52.1	VARICELLA PNEUMONITIS
VIRAL_PHARYNGITIS_ACUTE_NON_HERPETIC	79.3	RHINOVIRUS INFECT NOS
BRONCHIAL_ASTHMA	493.1	INT ASTHMA W/O STAT ASTH
BRONCHITIS_CHRONIC_SIMPLE	491	SIMPLE CHR BRONCHITIS
PULMONARY_EMPHYSEMA	492	Emphysema, NOS
PLAGUE_PNEUMONIA	20.2	SEPTICEMIC PLAGUE
ANTHRAX_INHALATIONAL	22.1	Respiratory anthrax
Gastro-intestinal:		
STAPHYLOCOCCAL_GASTROENTERITIS_FOOD_POISONING	8.41	STAPHYLOCOCC ENTERITIS
BOTULISM	5.1	BOTULISM
CAMPYLOBACTER_ENTERITIS	8.43	Intestinal infection due to campylobacter
GIARDIASIS_INTESTINAL	7.1	Infection by Giardia lamblia
SALMONELLA_ENTEROCOLITIS_NON_TYPHI	3	SALMONELLA ENTERITIS
VIRAL_GASTROENTERITIS	8.8	VIRAL ENTERITIS NOS

Validation Over Time

Type	C1	C2	C3	C4	C5
Docking: Comparison against another model				✓	✓
Generic Pattern: Showing pattern for each generated data stream matches observed patterns	✓	✓	✓	✓	✓
Characteristic Matching: Showing for each generated output data stream that it has correct seasonal or daily pattern		✓	✓	✓	✓
Relative Timing of Peaks: Showing time between peaks for dif. data streams matches observed dif.		✓	✓	✓	✓
Empirical Pattern: Showing pattern for each generated data stream matches empirical pattern – best for input streams			✓	✓	✓
Within Bounds: Showing for each generated output data stream that the mean of simulated stream falls within min/max of that stream for real data			✓	✓	✓
First moments: Showing for each generated output data stream that mean is not statistically different than real data – yearly, monthly or daily				✓	✓

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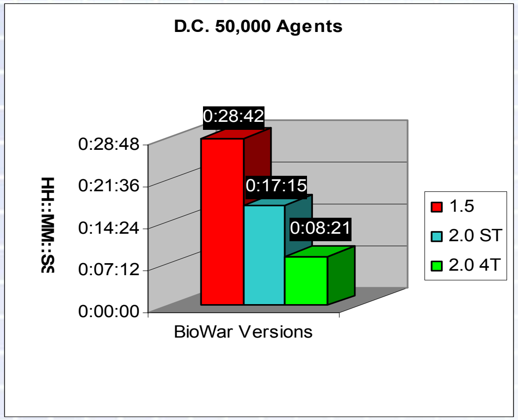
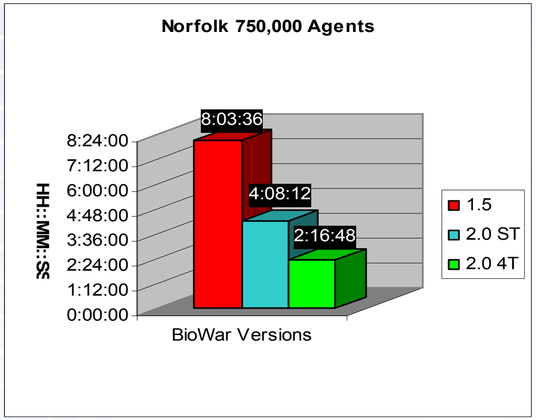
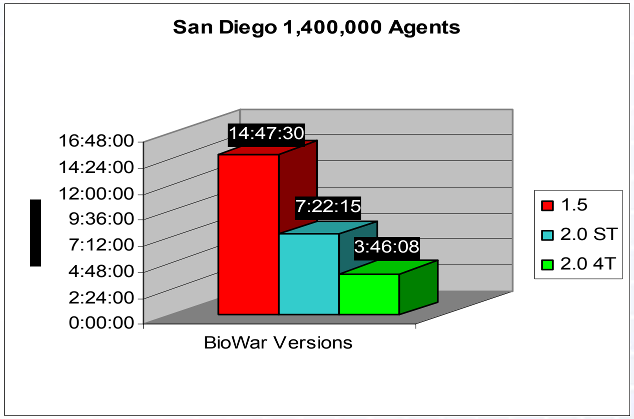
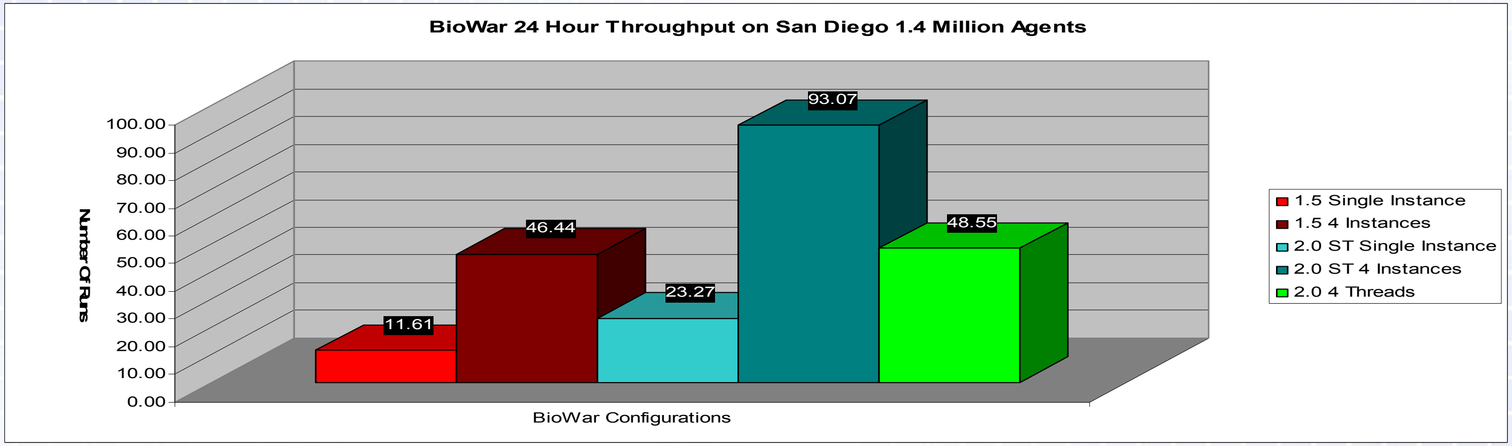
Performance Comparisons









Norfolk, VA. (1.5 million agents), completes 3 months in 2.3 hrs.
San Diego, CA (2.7 million agents) completes 3 month in 3.7 hours.

Anthrax Disease Model

- The dosage inhaled by the agent is calculated using the following equation:

$Dose = [QB][\pi u \sigma_y \sigma_z]^{-1} exp[-(1/2)(y/\sigma_y)^2]exp[-$

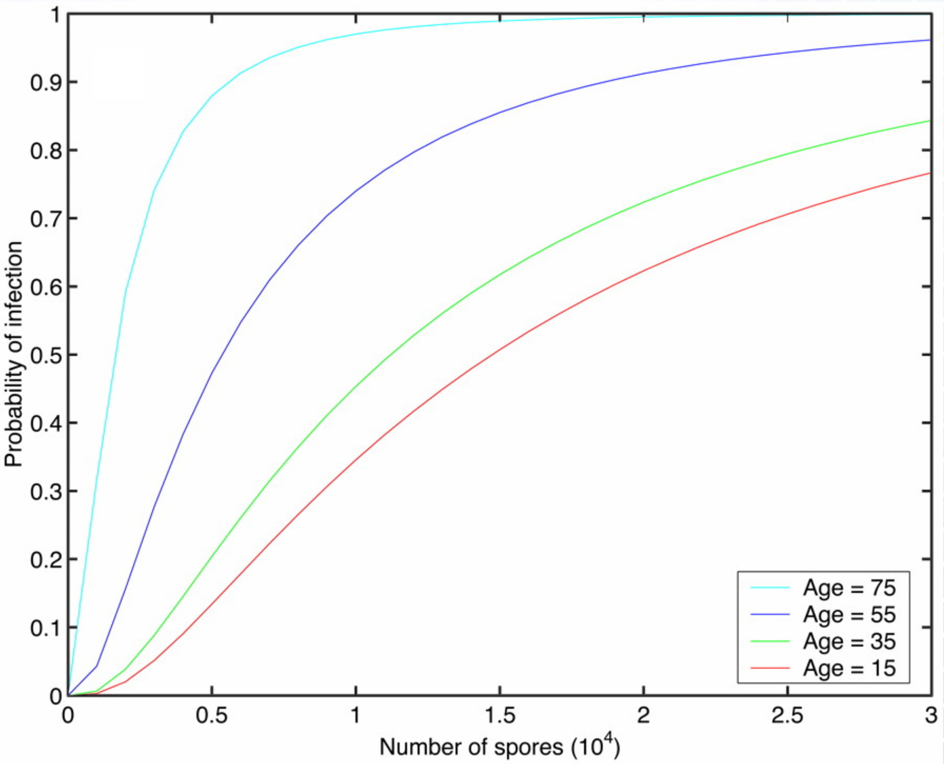
$(1/2)(H/\sigma_z)^2]$

where Q is the source strength (e.g., number of anthrax spores); B is breathing rate (usually for light work $B = 5 *10\text{-}4\ m3/sec$); u is wind speed in m/sec; σ_y and σ_z are dispersion parameters that are functions of downwind distance x; and H is height of the release in meters.

$\sigma_y = 0.08x/sqrt(1+0.0001x)$ $\sigma_z = 0.06x/sqrt(1+0.0015x)$

where x is the distance downstream of the realease point.

- Gaussian Puff model of wind dispersion
- Dose-age response relationship, shown on the side graph
- Lognormal distribution of duration of stages for anthrax (μ for incubation stage = 2.4 days, μ for prodromal stage = 0.85 days, μ for fulminant stage = 0.34 days)



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Dose-Age Response Equation

Probability of infection by age:

P[n](S) = b[n] (exp(S/a[n])-1)/(1+b[n](exp(S/a[n]) – 1)), n=1,2,3,4 (four age categories)

where the two parameters a[n] and b[n] are determined by the infectious doses that produce infections in 50% (ID_{50}) and 10% (ID_{10}) of exposed persons.

Age bracket (years)	ID_{50} infectious dose	ID_{10} infectious dose
<25	15,000	4,500
25-44	10,000	3,000
45-65	6,000	1,800
>65	1,500	450

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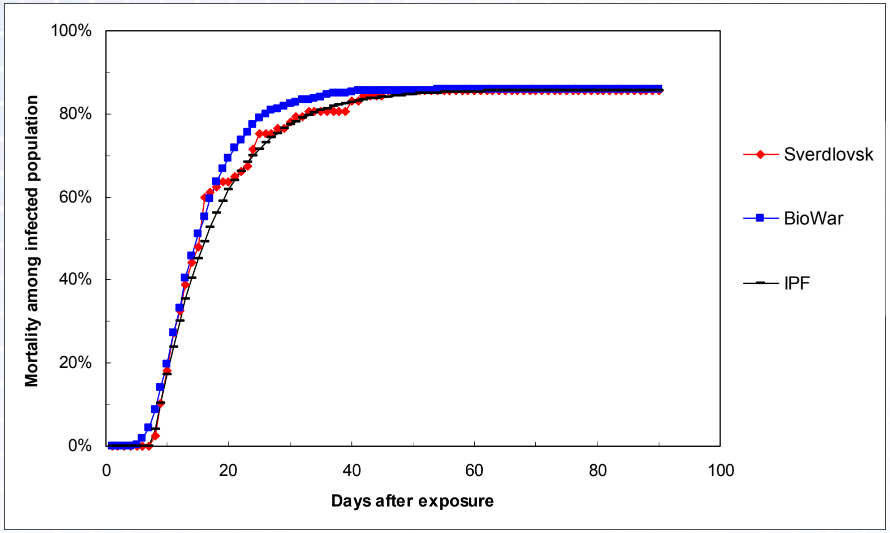
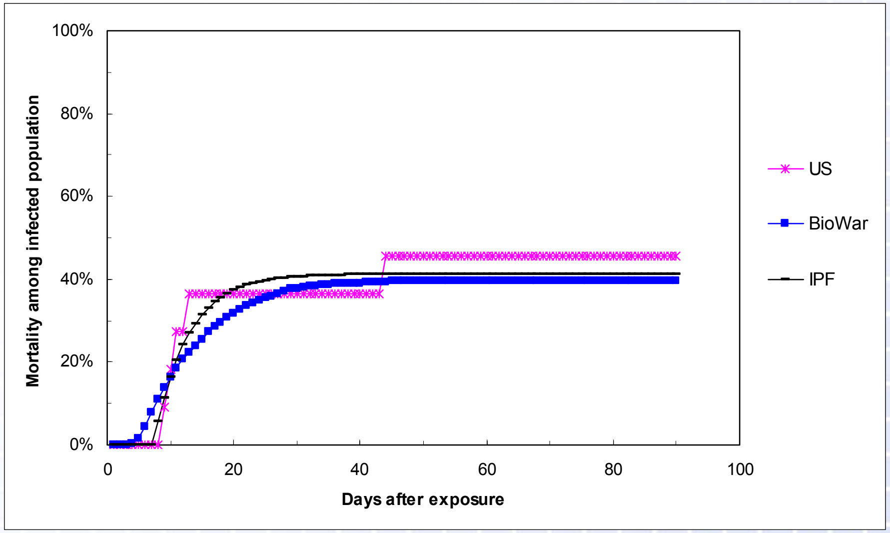
Anthrax: BioWar vs IPF based on Time to Death

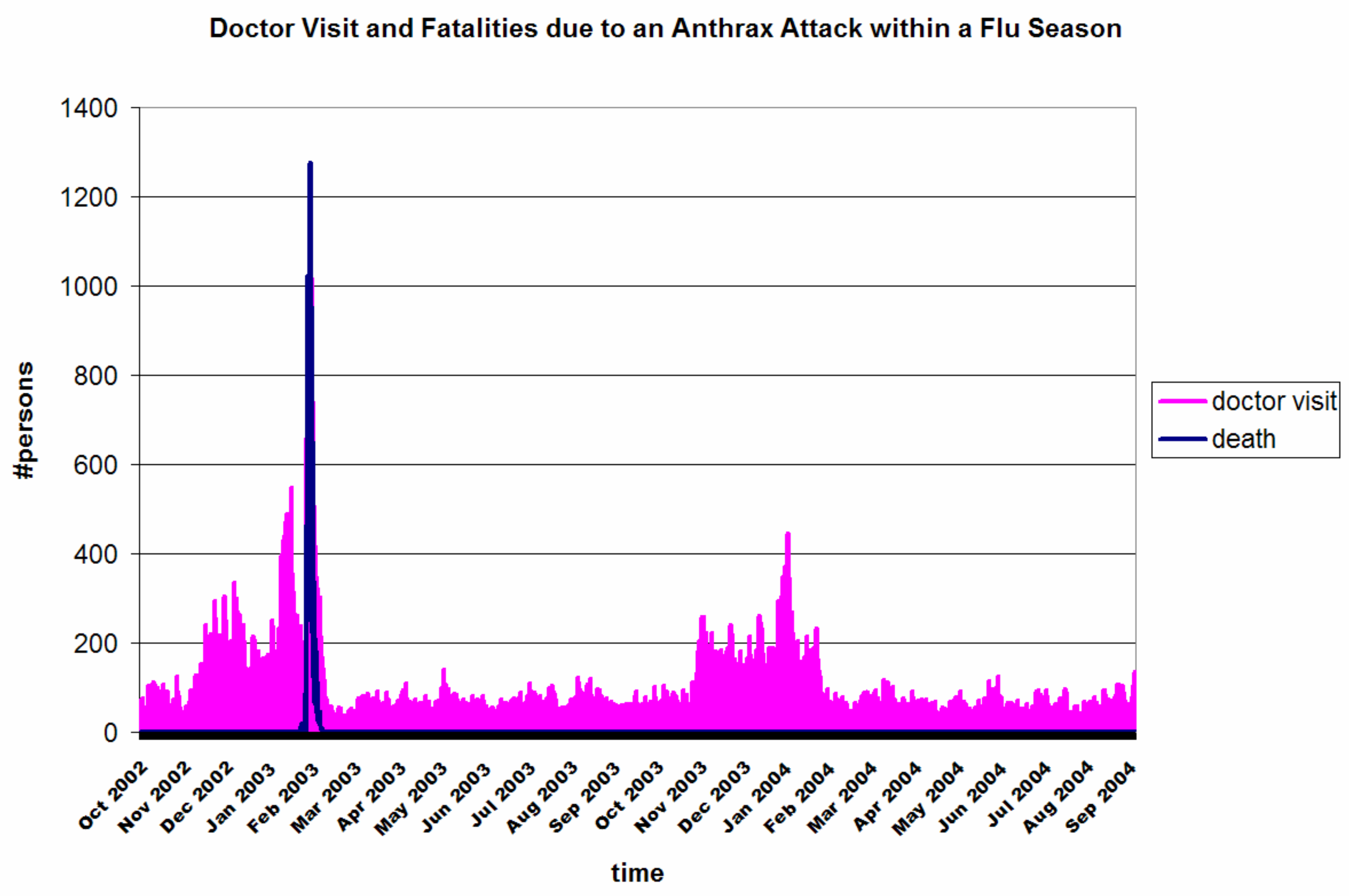
Sverdlovsk



US Mail



Anthrax Attack on Hampton

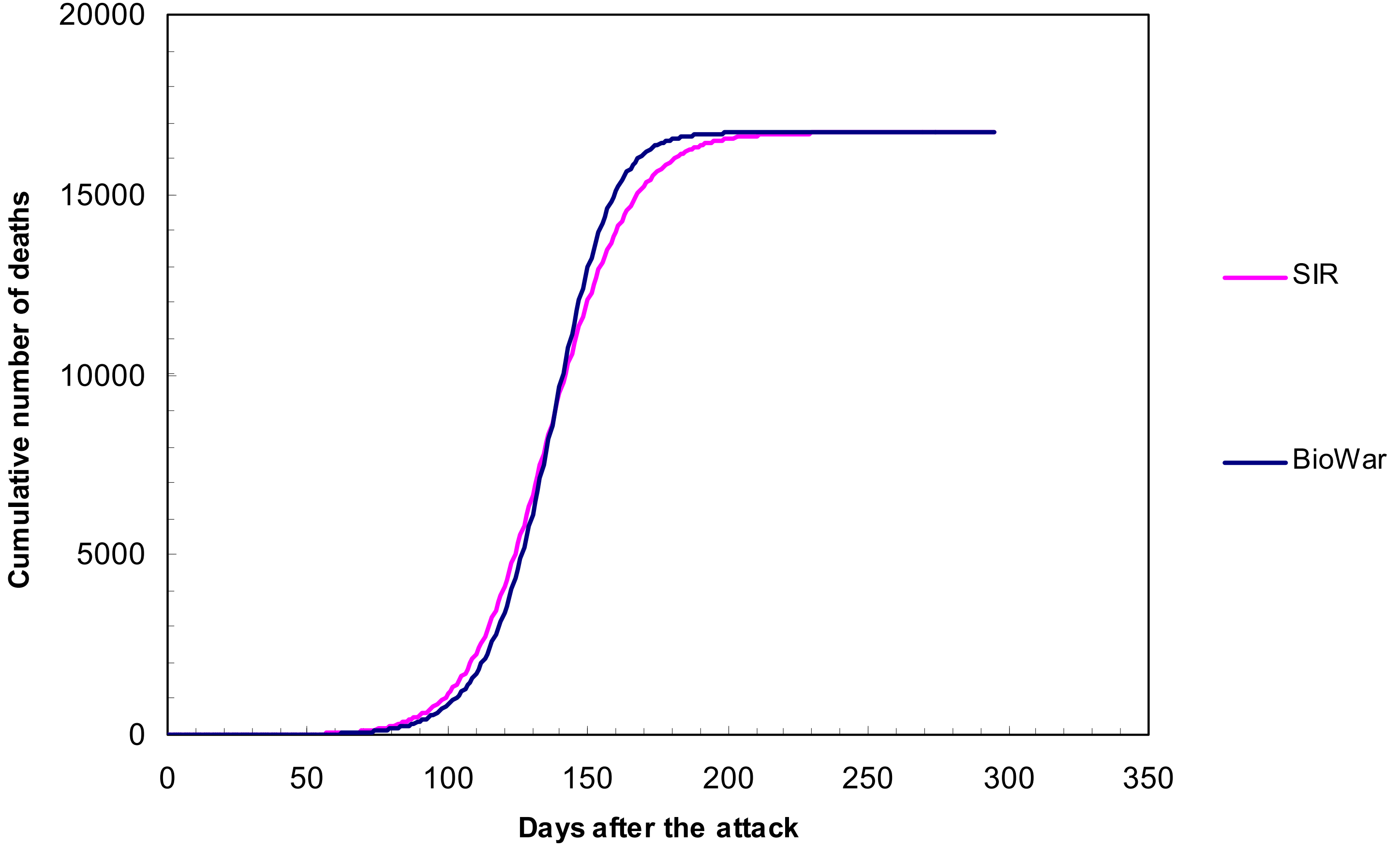


Contagious Diseases

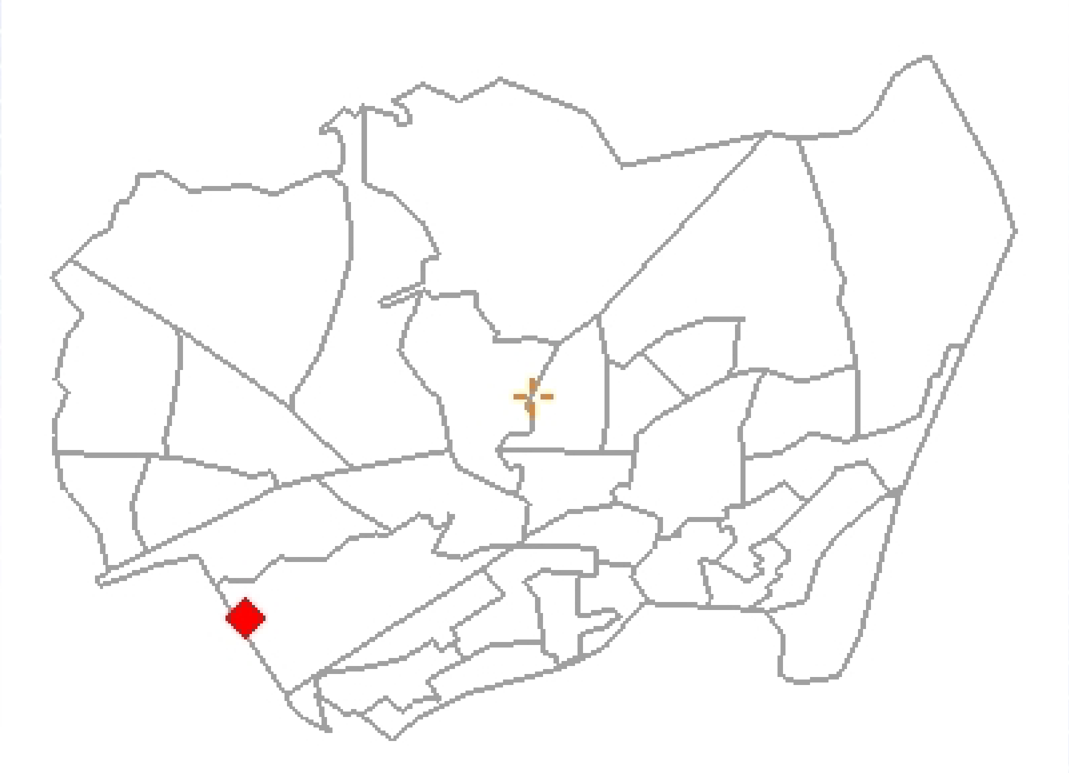
- Modeled as either attacks or outbreaks

Characteristic	Influenza	Avian Flu
Start tick	402	402
End tick	940	940
Scale	200	20
Number of locations	1	1
Number of strains	2	1
Low baserate	.0001, .0003	.0001
High baserate	.0004, .0008	.0012
Mean baserate	.000496, .000496	.00045
Low transmisivity	.02, .03	.01
High transmisivity	.03, .06	.08
Mean transmisivity	.033, .033	.063

Smallpox Death: SIR vs. BioWar



09/28/02 Simulated Attack! Smallpox introduced, infecting one agent



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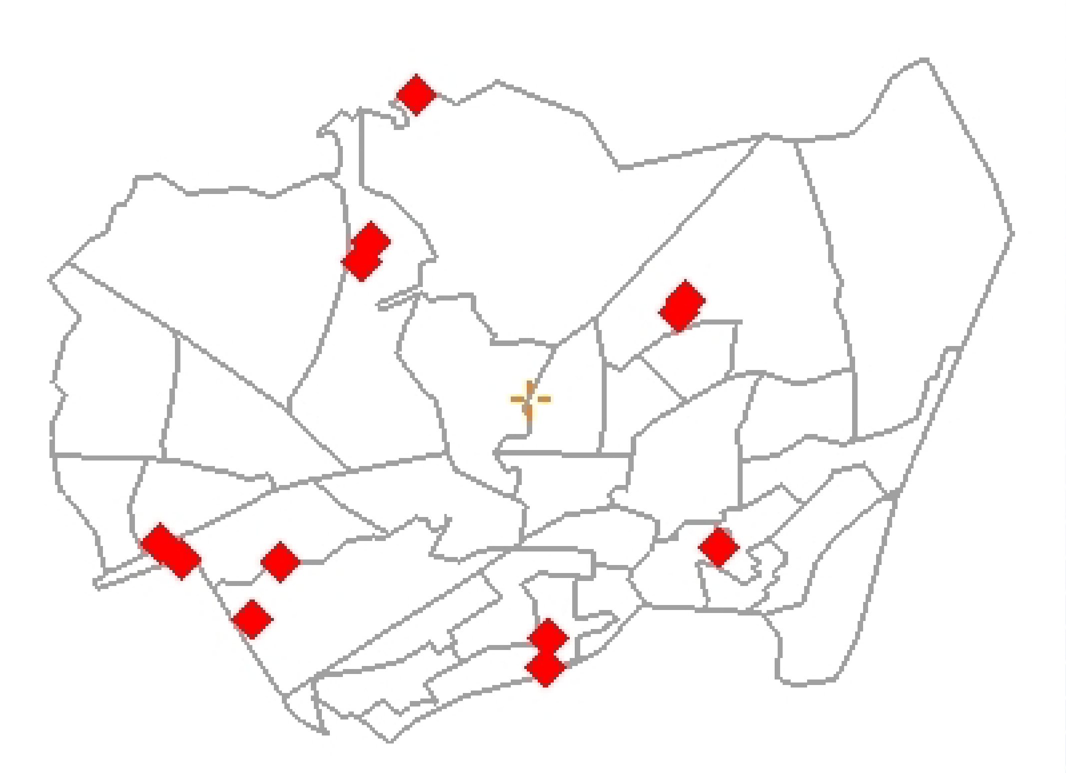
10/10/02 Simulated First transmission of smallpox to 11 agents



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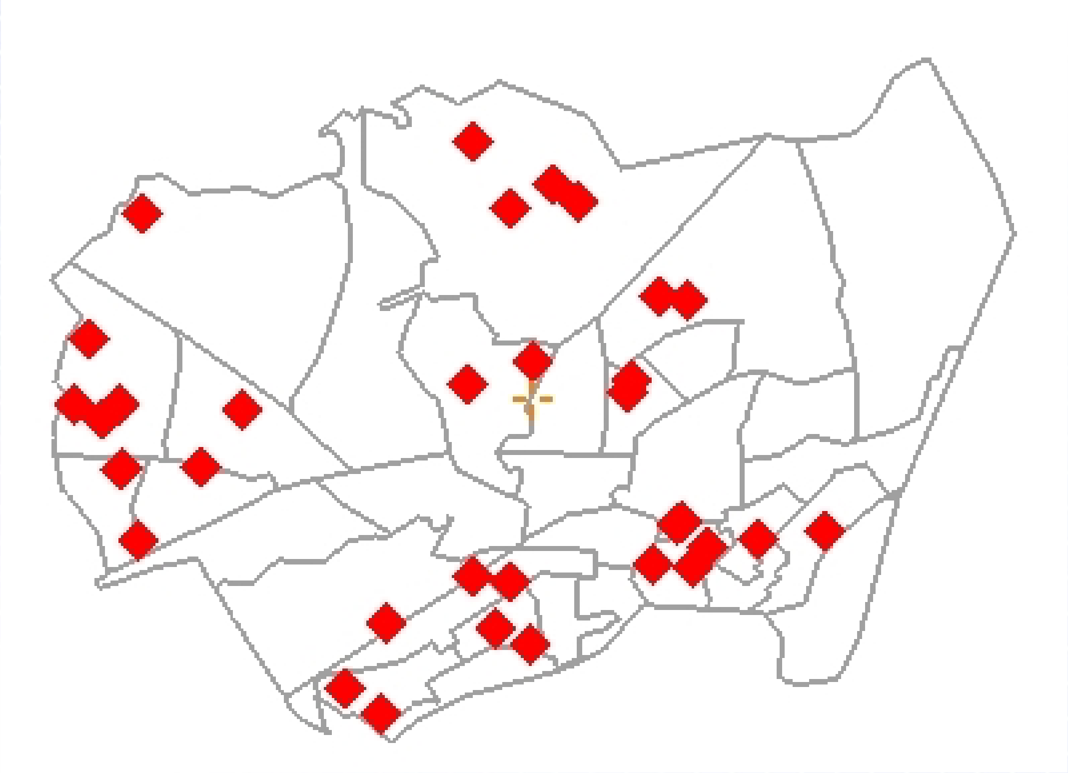
12/25/02 Simulated Prevalent Cases (45)



Scaling = apx 225 cases

CASOS Tools

- ORA – statistical toolkit for meta-network, identifies vulnerabilities, key actors (including emergent leaders), and network characteristics of groups, teams, organizations, C2 – used with army battle labs, risk estimation NASA
- DyNetML – XML based interchange language for relational data
- AutoMap – Semi-automated text mining
- Social Insight – network visualization

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CASOS
Complex Adaptive DNA Models

- Construct – MAS-DNA model for examining group change under diverse cultural, social and technological contexts
- DyNet – MAS-DNA model for examining change in networked systems under uncertainty
- NetWatch – impact of data integration, sharing and control on ability to detect evolving network
- BioWar – city scale MAS-DNA model of weaponized biological attacks
- OrgAhead – MAS-DNA model of evolving organizational forms
- RTE – MAS-DNA multi-level model for examining impact of blue and adversarial actions at the city, region, nation-state or inter-state level
  - Vista – estimating the evolving likelihood and impact of unanticipated events in urban settings
  - Acumen – state failure model