

# **Early Detection of Bioterrorism: Monitoring Disease Spread Through a Multilayered Network**

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Presented at the 2012 INFORMS Annual Meeting in Phoenix, AZ

# Bioterrorism

*The intentional release of viruses, bacteria, or other toxic biological agents, to cause illness or death in people, animals, or plants*

Certain biological agents, such as anthrax or hemorrhagic fever, may present themselves as a more common illness that will not initially be detected by healthcare providers

Early detection is critical! Identifying the type of outbreak facilitates the implementation of the proper mitigation strategies and maximizes their effectiveness

**Objective:** Develop a technique for reliably and quickly differentiating between epidemic and bioterror disease scenarios

# Conceptual Model

Population is modeled using a **multilayered network**

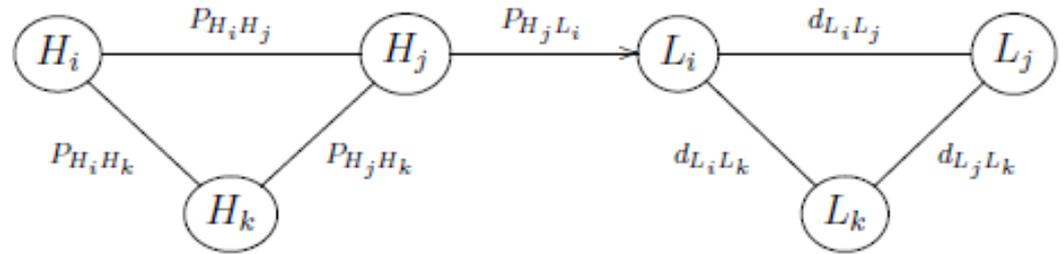
- Human social network
- Location network
- Human-location network

## **Disease scenarios**

1. Epidemic: Disease spreads through human interactions
2. Bioterrorism: Disease spreads through human-location interactions

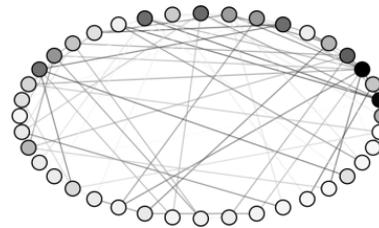
# Multilayered Network

Generalized  
Multilayered Network



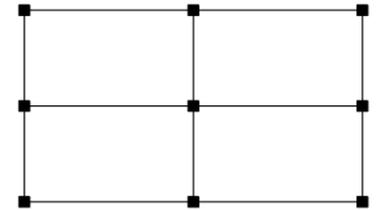
Human Network

(a)



Location Network

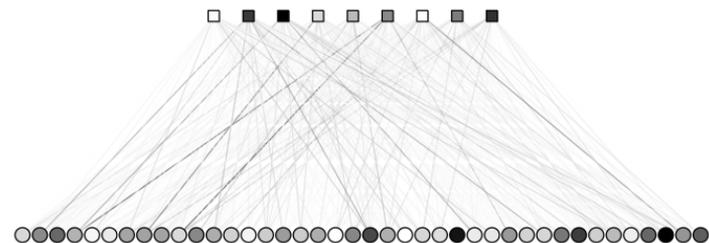
(b)



Sample Multilayered  
Network Instance

Human-Location Network

(c)



# Network Simulation Model

## Epidemic Scenario

1. Select humans to be initially infected
2. Each time step, only evaluate relevant network edges between susceptible and infected humans
3. Determine which edges lead to transmission
4. Simulate until all humans become infected

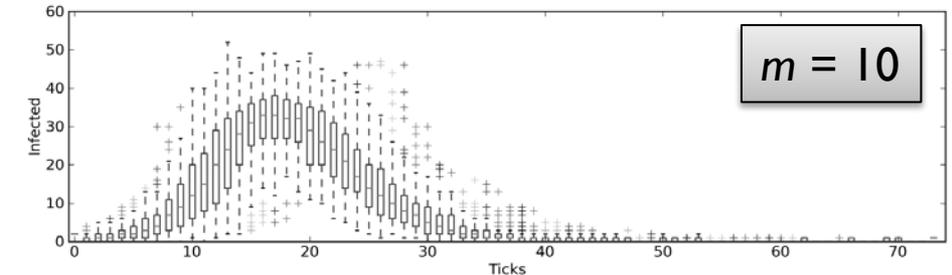
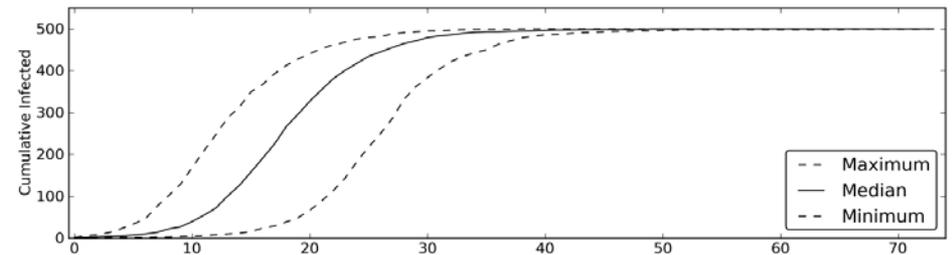
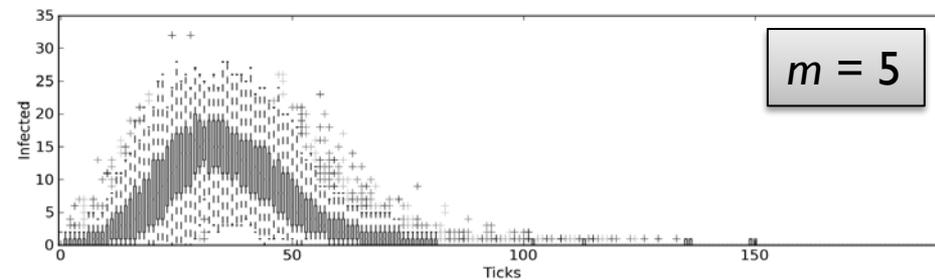
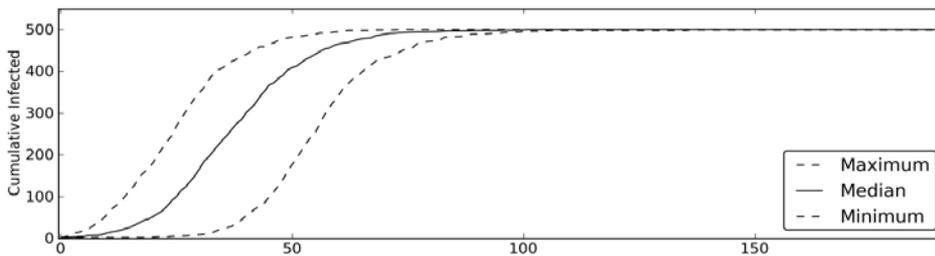
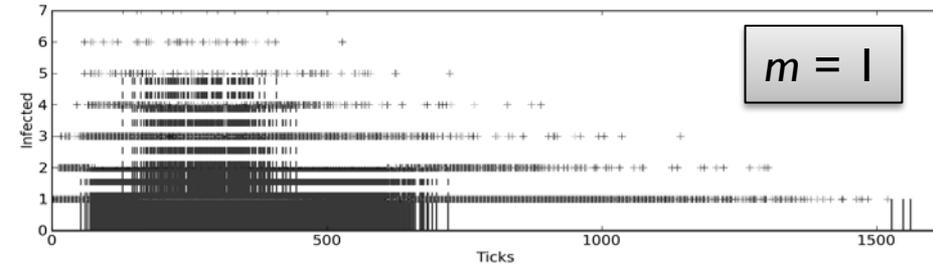
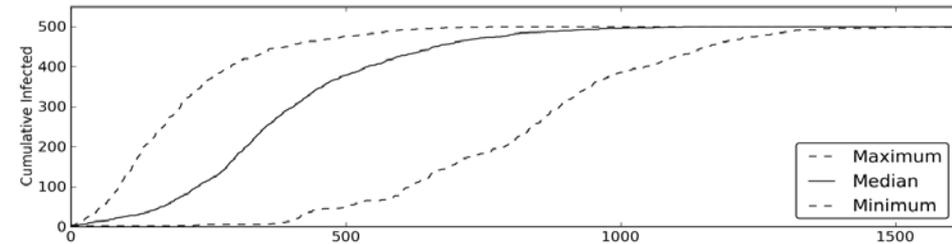
## Bioterrorism Scenario

1. Select a single location as the source of the attack
2. Each time step, evaluate relevant edges for location-location and human-location transmission
3. Determine which edges lead to transmission
4. Simulate until all humans become infected

# Epidemic Transmission Dynamics

The human social network density—defined by the Barabási-Albert algorithm parameter  $m$ —has a significant effect on the rate of transmission and the variance of the simulation replications

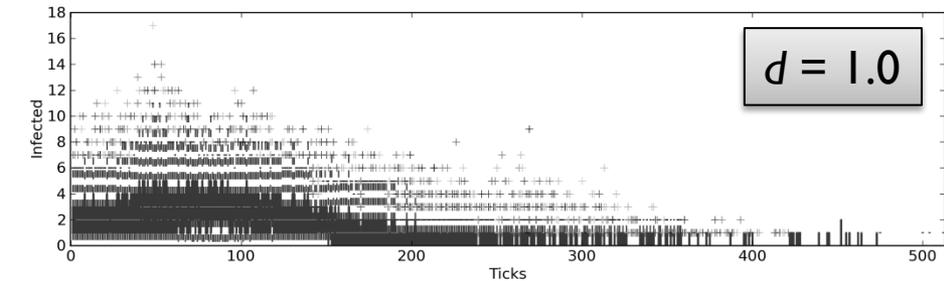
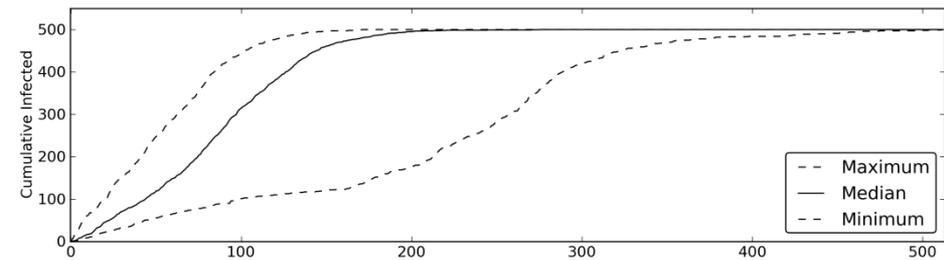
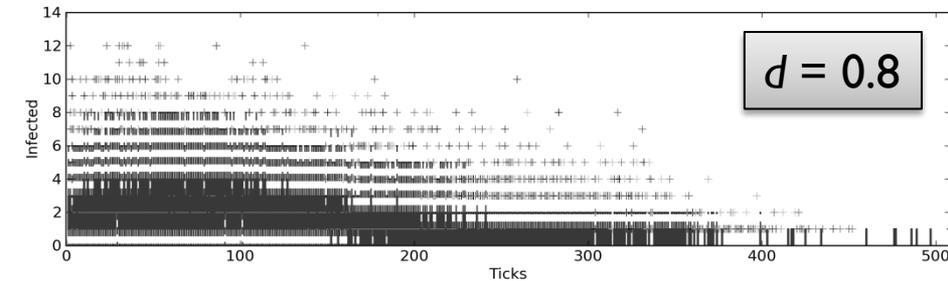
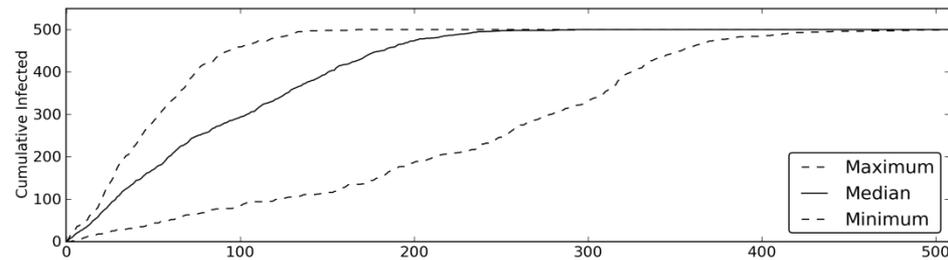
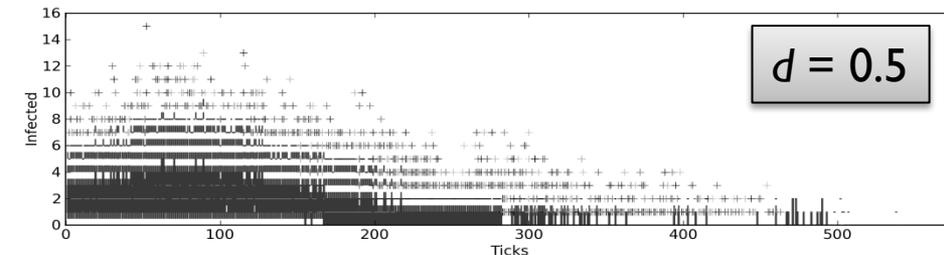
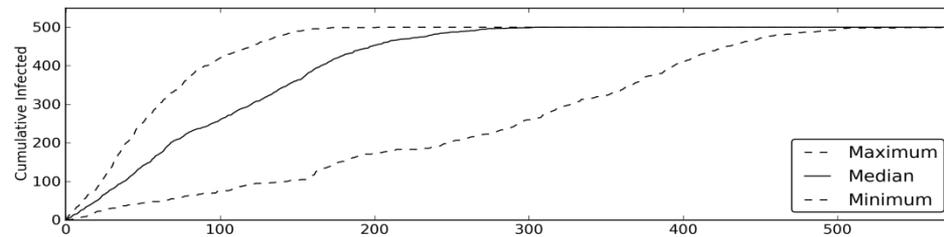
Transmission dynamics follows S-curve pattern, similar to SIR-type models



# Bioterrorism Transmission Dynamics

The human-location network density has a less significant effect on the rate of transmission, but the variance of the simulation replications is much larger

Transmission occurs immediately and continues at a nearly constant rate until the susceptible pool becomes small



# Detection Under Social Network Uncertainty

- In most cases, especially with large populations, we will not know enough information about the human social network
- We have to rely on available information, including the size of the population and reported infection cases

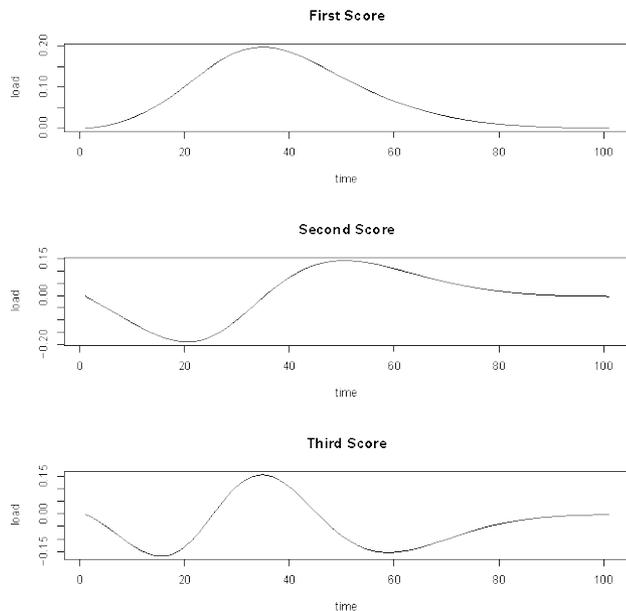
## Principal Component Analysis (PCA)

- Captures the dynamics of the transmission curves
- Coordinate transformation that aligns orthogonal axes in the directions of the largest variance → principal components (PCs)
- The first three PCs capture 99% of the transmission behavior

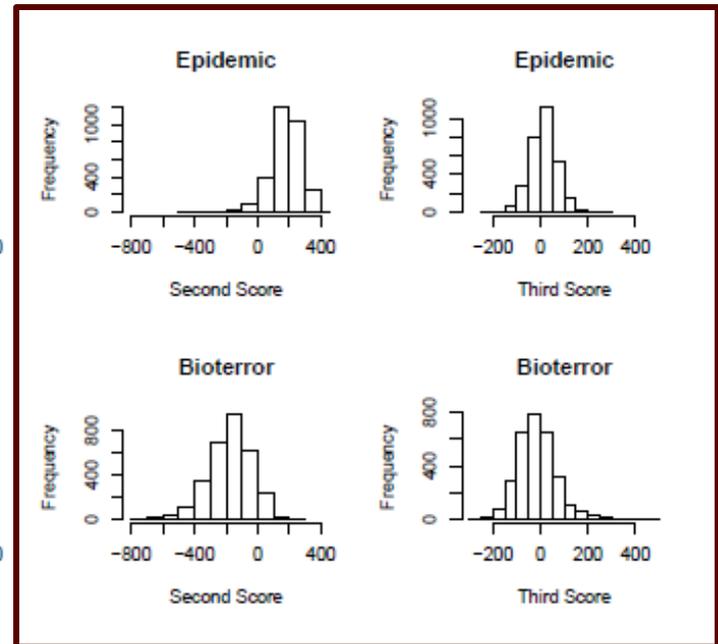
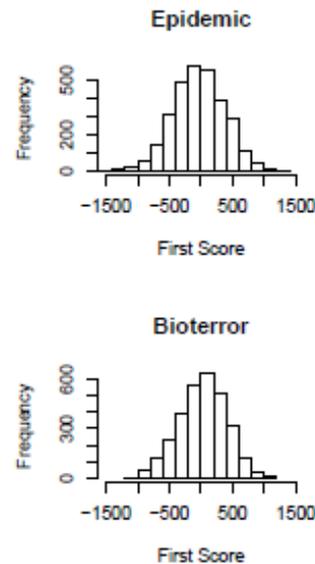
# PCA Results

Loads of the infection curves for each PC (i.e., how much information is captured by each PC)

$$Y^T = \int_t (X(t)^T - \bar{X}) W(t)$$



Infection curve score distribution for each PC and disease scenario (i.e., the projection of the infection curves onto the new PC space)



# Prediction Results

We calibrated a logistic regression model based on PC scores and evaluated its performance on predicting the disease scenarios

- The accuracy of the model was 95% for the training and validation data

The model was accurate when only a small fraction of the population was infected

- For  $f \geq 0.07$ , accuracy was  $\geq 95\%$
- For  $f = 0.05$ , accuracy was 93%
- For  $f = 0.02$ , accuracy was still 83%

$$\hat{Scenario} = \frac{1}{1 + \exp^{-(\beta_0 + \beta_1 PCS_1 + \beta_2 PCS_2 + \beta_3 PCS_3 + \epsilon)}}$$

Parameter	Estimate	Standard Deviation	<i>p</i> value
$\beta_0$	0.7309185	0.1147268	1.88e-10
$\beta_1$	0.0020193	0.0001709	< 2e-16
$\beta_2$	-0.0272249	0.0008508	< 2e-16
$\beta_3$	-0.0279236	0.0014694	< 2e-16

<i>Prediction</i>	Training		Validation	
	<i>Response</i>		<i>Response</i>	
	Epidemic	Bioterror	Epidemic	Bioterror
Epidemic	956	40	473	24
Bioterror	44	960	27	476

# Sensitivity Analyses

With the exception of the sparse human social network ( $m = 1$ ), the static model remained extremely accurate for varying multilayered network densities

The model can detect multiple simultaneous attacks, which are all distinguishable from epidemics

The model can differentiate bioterror attacks with different human-location probability distributions from epidemic outbreaks

<i>Prediction</i>	BA parameter=1		BA parameter=5	
	<i>Response</i>		<i>Response</i>	
	Epidemic	Bioterror	Epidemic	Bioterror
Epidemic	82	6	188	7
Bioterror	118	194	12	193

<i>Prediction</i>	Human-location density=0.5		Human-location density=0.8	
	<i>Response</i>		<i>Response</i>	
	Epidemic	Bioterror	Epidemic	Bioterror
Epidemic	190	13	190	6
Bioterror	10	187	10	194

Scenario	PC1	PC2	PC3
Single initial location	34.08 (378.26)	-180.31 (140.86)	-19.15 (83.01)
Two initial locations	377.13 (291.97)	-238.74 (102.43)	-75.52 (56.46)
Three initial location	559.59 (233.03)	-297.97 (90.91)	-113.96 ( 52.65)

Scenario	PC1	PC2	PC3
Epidemic	-37.36 (391.69)	177.17 (97.33)	14.47 (54.84)
Bioterror (Bimodal)	27.36 (379.71)	-177.17 (139.07)	-14.47 (83.58)
Bioterror (Uniform)	90.09 (341.64)	-174.17 (120.86)	-20.49 (67.55)

# Conclusions

- We developed a static model using PCA to ***quickly*** differentiate between epidemic and bioterrorism disease scenarios
- This model provided a highly reliable capability for differentiating the two scenarios with small error rates, except for very sparse networks
- This method could help ensure that the proper infection control strategy is implemented as soon as possible

# Questions and Comments

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