



# Spatial and Temporal Data Fusion for Biosurveillance

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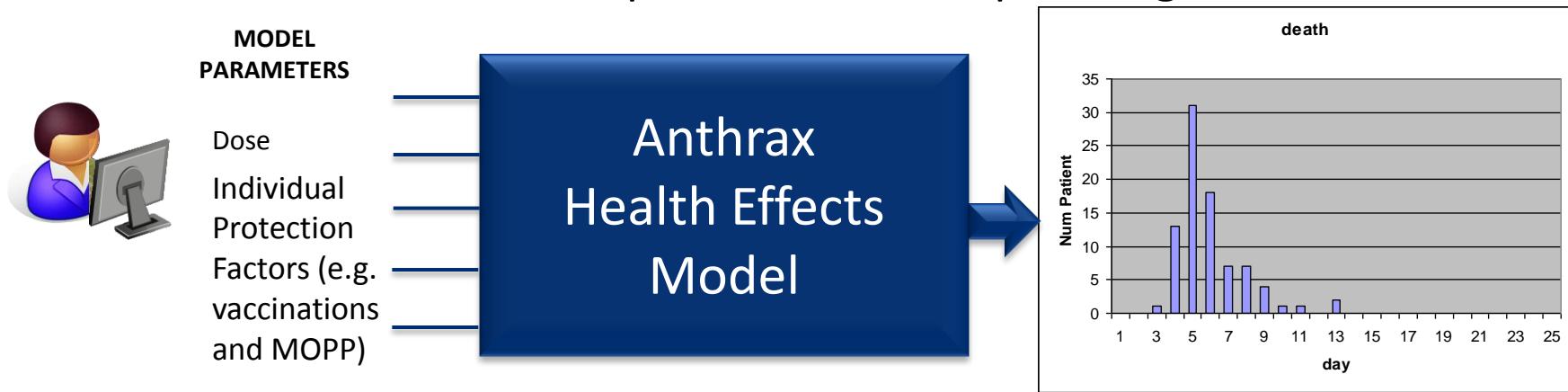
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# Early Event Detection and Characterization

- Early on in an outbreak (malicious or naturally-occurring) we will probably not know what the characteristics of the outbreak are
- What we do have today (e.g. hospital admission and discharge data) is:
  - Temporal data (e.g. number of hospital admissions on a daily basis)
  - Spatial data (e.g. the zip codes of the patients)
- We have focused on analyzing this data (available in hospitals or biosurveillance systems) to
  - **Characterize** the event
  - **Predict** the event
- My previous talk focused on **temporal** characterization. This talk emphasizes **spatial** characterization.

# Characterization

- Both **temporal** and **spatial** characterization rely on  
**INFERENCE**
- What is inference?
- In deliberate planning (what-if scenario analysis that assesses the damage of a theoretical event), analysts use **health effects/disease models**.
- The analyst sets the **parameters** of these **models** as he desires to assess worst case scenarios and perform medical planning



# What is Inference?

- In real-life situations (crisis response situations), early on, we have little understanding of what the event is.
  - All we have is data (usually can get spatial and temporal data) that represents some initial stage of the epidemic
- How can we do prediction?
- Answer: use the same models analysts use in **deliberate planning for crisis response planning**
- **Inference** is a technique that allows us to fit a particular model's (e.g. Plume Dispersion model's) parameters to the live data

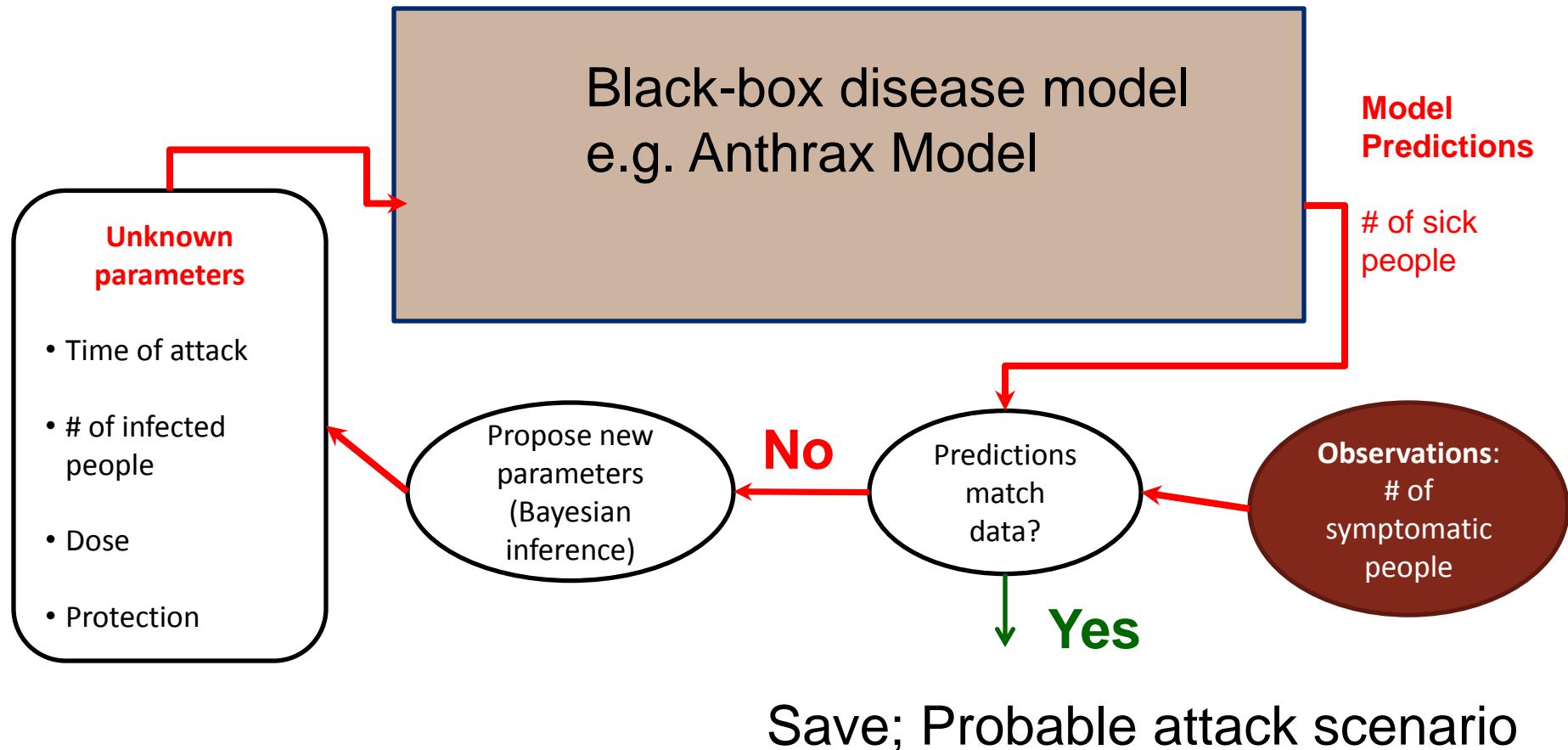
**Inference allows us to apply existing models to predict real-time crisis situations.**

**Prediction allows us to implement medical countermeasures and SAVE LIVES.**

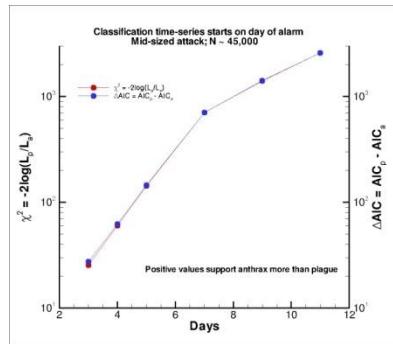
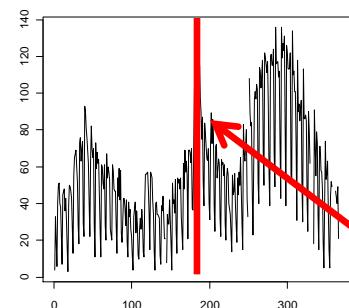
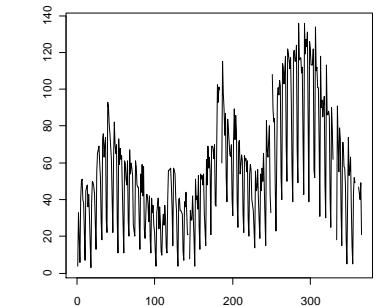
# We Use Bayesian Techniques to Perform Inference to Characterize the Outbreak

- From Dr. Nicole Rosenzweig's talk yesterday
  - "decision makers make unambiguous decisions on very ambiguous data". What do we do about this?
- Bayesian techniques allow us to provide **confidence intervals** around our inferences and predictions (e.g. on a daily basis)
- Bayesian techniques infer the parameters of an outbreak model from the outbreak data available.
  - We formulate the estimation as a statistical inverse problem
    - You are given the "answer", so what caused it?
- Solved using an adaptive Markov Chain Monte Carlo sampler
  - All parameters estimated as probability density functions (PDF)

# Inference – Fitting Models to Data: Disease Model



# Our Steps for Detecting, Characterizing, and Identifying an Outbreak from Syndromic Surveillance Data



Data Sources: Time Series Data

Kalman Filter Based Anomaly Detection and Epidemic Extraction

Trigger on anomaly

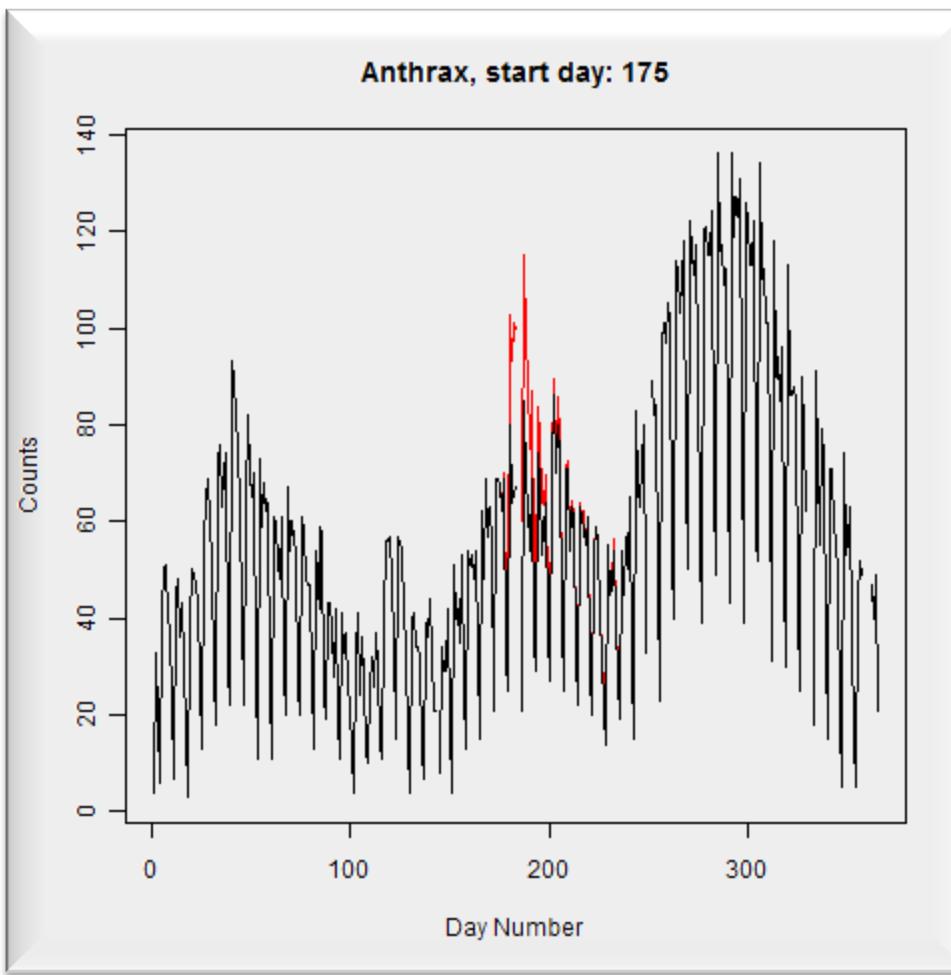
Bayesian Disease Classification Temporal and Spatial

Classification

Prediction

# Previous Analysis with Purely Temporal Information

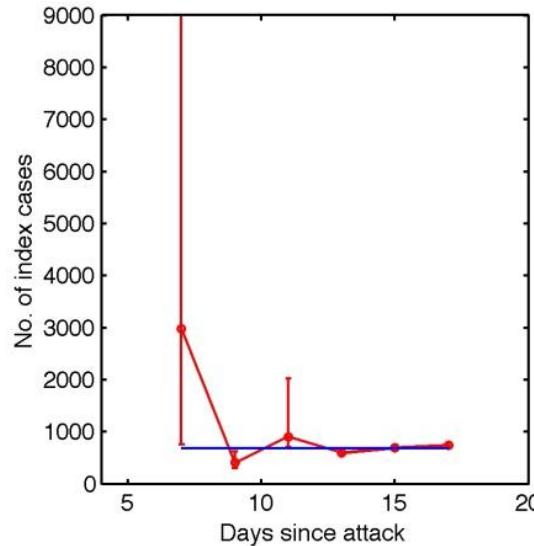
## Simulated Anthrax Attack on Day 175



- Background: ILI ICD-9 codes from Miami data
- Red Line: Calculated anthrax outbreak from Wilkening A2 model, plus visit delay; 500 index cases

We get an alarm on day 180.

# How Small An Outbreak Can We Characterize?



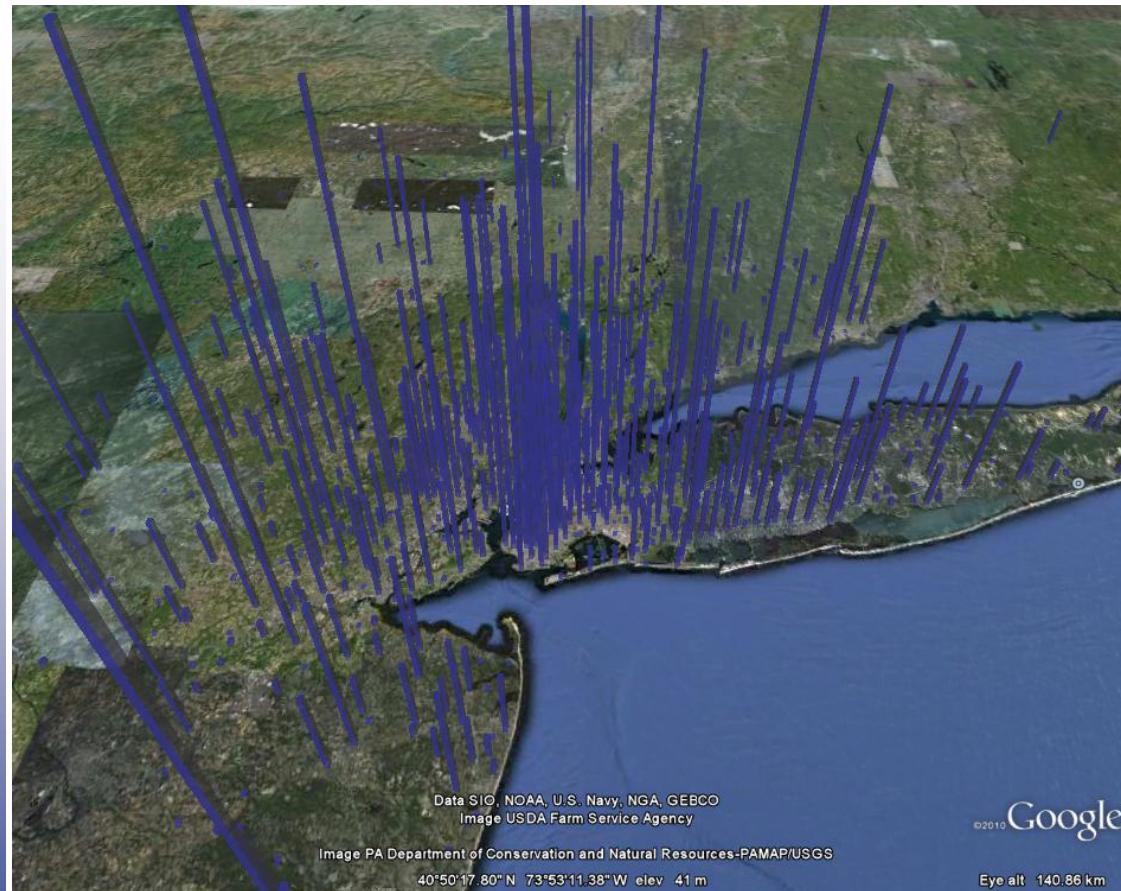
Number of index cases and time  
of attack for an anthrax outbreak  
with 680 index cases. True  
values indicated in blue

- Tested on simulated anthrax epidemic of various sizes
- Could estimate  $N_{index}$  and  $\tau$  for the attack  $\geq 680$  infected cases

# Initial Spatio-temporal Analysis - Introduction

- Syndromic surveillance data is spatio-temporal
  - We generally have the ZIP-codes of infected people
- Concept: Spatial data is a rich and very important source of information for disease prediction
  - one must know who/when/where people are infected or will become infected
  - Since diseases have an incubation period, there is a window of opportunity to save lives. Can also protect most susceptible population with prophylaxis measures.
- Contemporary Spatial Analysis Methods
  - Take the available data and cluster it; will provide a good region to concentrate resource allocation
  - As more data becomes available, and clusters widen / increase in number, widen your area of interest (evidence-based approach)
  - Limitation: lacks understanding of the source incident, timeliness for planning
- Conjecture : Can we infer the future region of infection (where others **will turn up sick**) with sparse data?

# New York Hospital Admission Data 2007 Count/Location Histogram



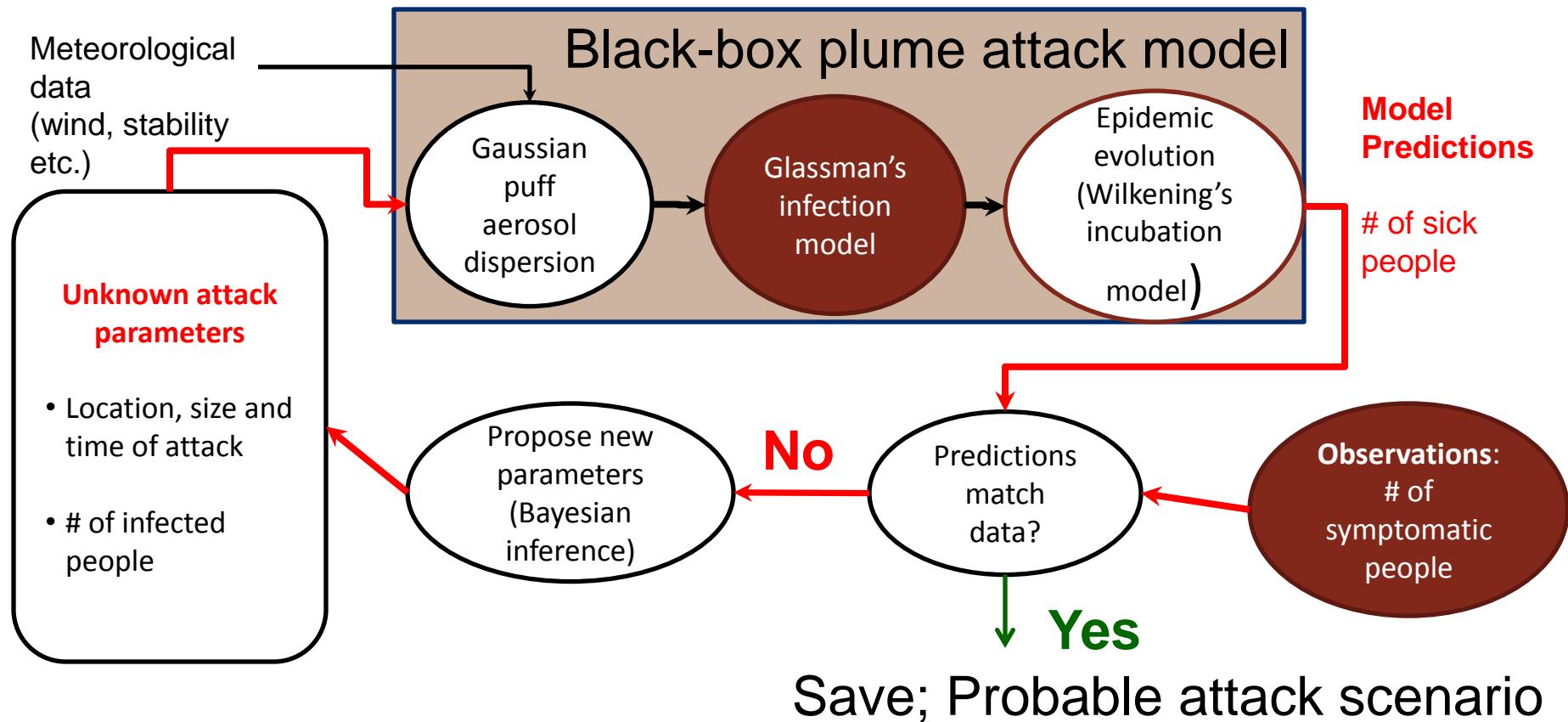
# Plume Estimation Approach

- The key to forecasting infected people is to characterize the attack probabilistically
  - Location, size and time
  - Use a dispersion model + epidemic model to identify where the incubating and imminently susceptible people are (we already know the symptomatic ones)
- How? The model
  - Use a dispersion model to “spread” an aerosol and infect people with different doses
    - Inputs: location of release, amount of release
  - Use an epidemic model (say, for anthrax) to predict the evolution of the disease, given infected people with varying doses
    - Inputs: time of infection, # of infected people and their dosages.

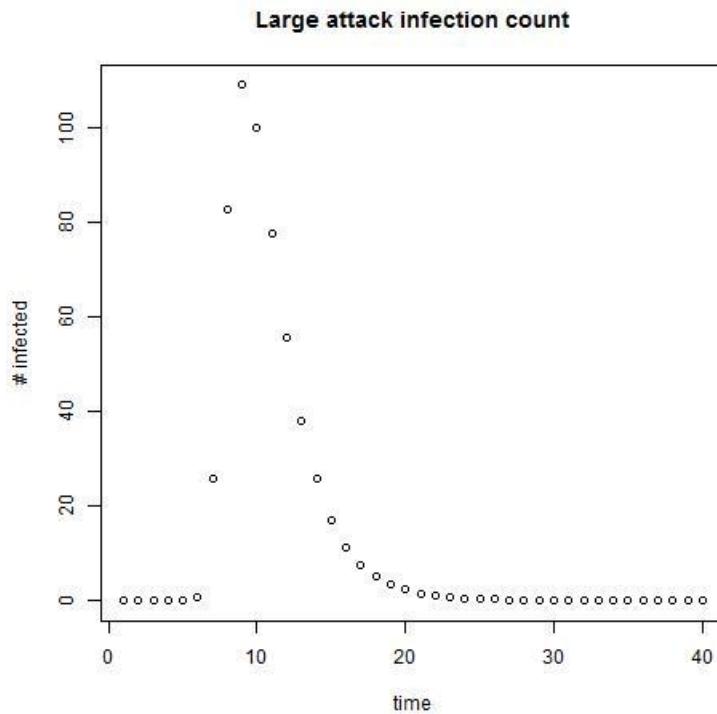
# Plume Estimation Approach (cont.)

- Inverse problem
  - Data: # of symptomatic people, per day, per zip-code (whose location is known)
  - To infer:  $(x, y, z)$  location of release point,  $Q$ , the # of spores released,  $t$  the number of days before 1<sup>st</sup> symptoms, when the people were infected
- Solution:
  - Use MCMC to create posterior distributions for  $(x, y, z, \log_{10}(Q), t)$
- Tests
  - Test with synthetic data, generated using Wilkening A1 model
    - With sufficient data, we should infer the true release point
  - Can small attacks be inferred? How well?
  - Test with synthetic data, generated using Wilkening's A2 model
    - Even with infinite data we will not infer back the true parameters
    - But will we come close? How close?

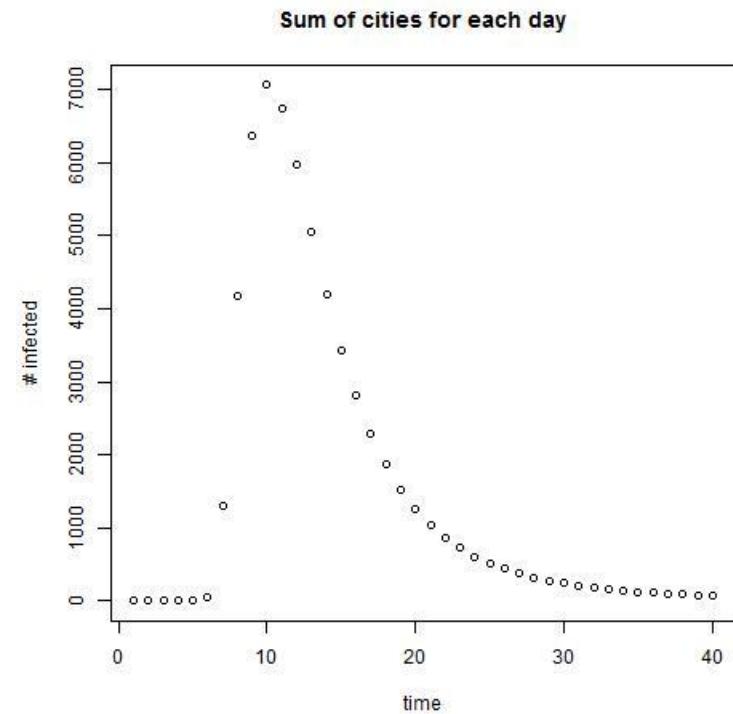
# Inference – Fitting Models to Data: Plume Model



# Case I –Attack with No Model Mismatch



Epidemic curve for a chosen zip-code

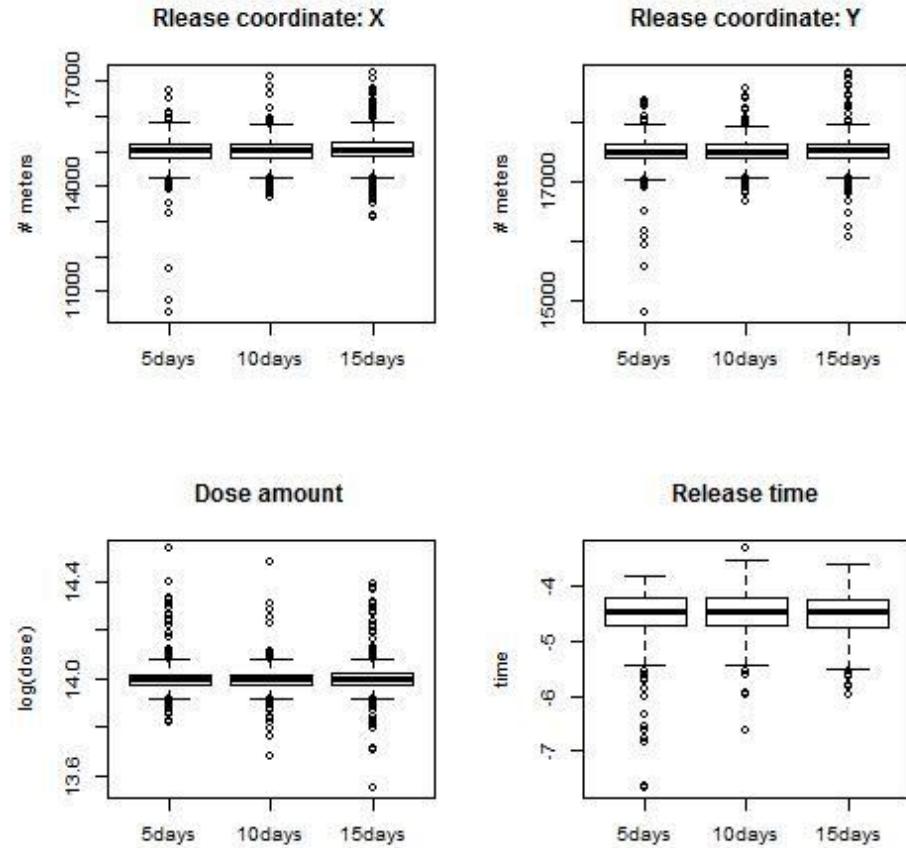


Epidemic curve for the entire city

- 50 km X 50 km city, divided into 1 km x 1km grid-cells
- Left – epidemic curve in a grid-cell
- Right – epidemic curve summed over all grid-cells

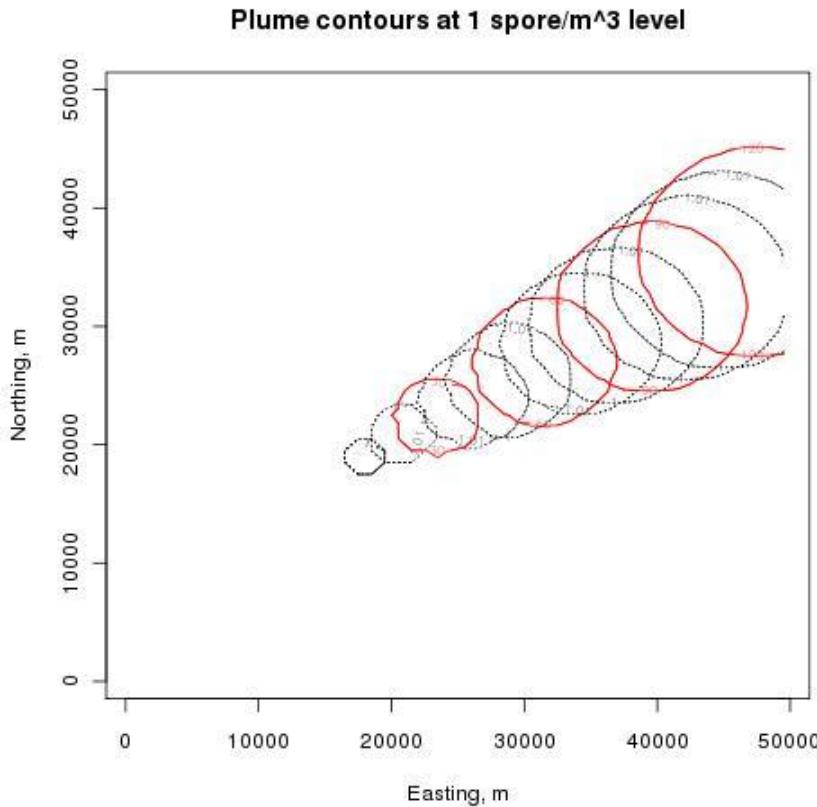
# Inferred Location, Quantity and Time of Release

- Even 5 days of data is good enough
- True values:
  - X : 15,000 m
  - Y : 17,500 m
  - $\log_{10}(\text{Dose}) = 14$
  - Time = -5 days

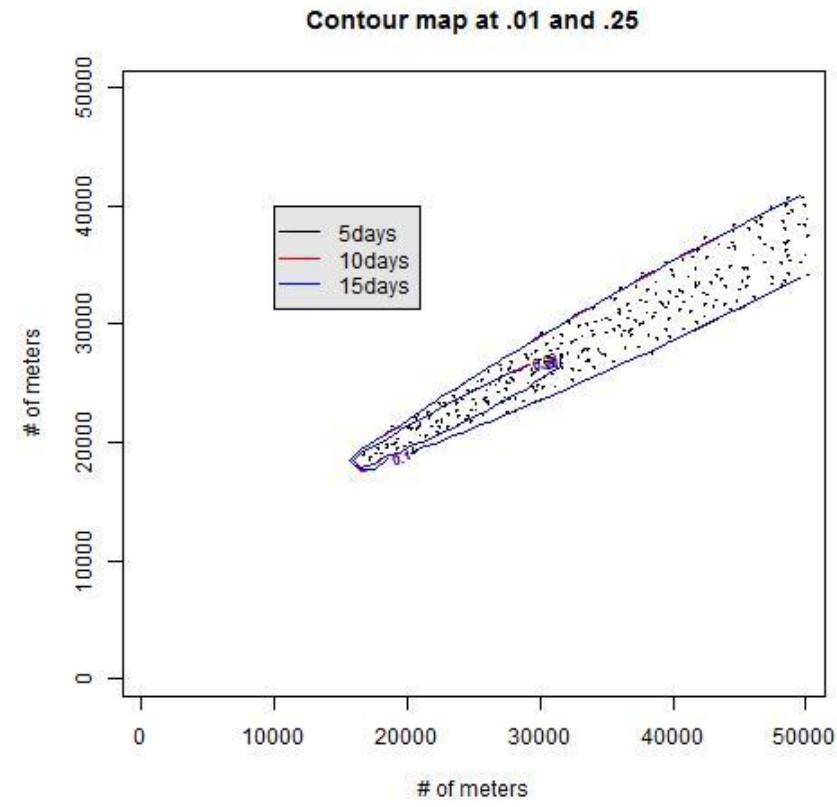


Inferred values of release location (X, Y), release size ( $\log_{10}(Q)$ ) and release time. True values [15,000; 17,500; 14, -5]

# Clusters – Observed and Predicted



Inferred contours of spore concentration. Red contours are at 30 min intervals.

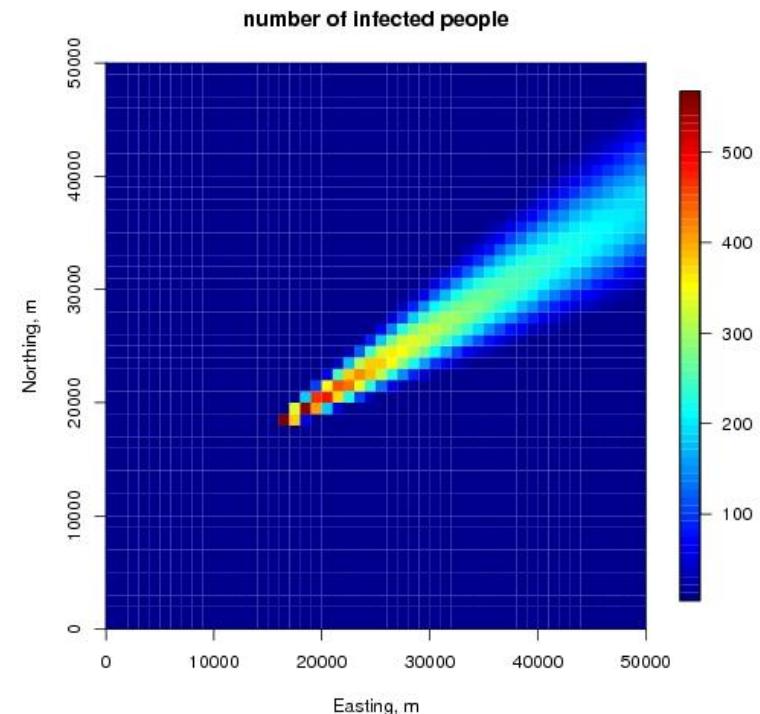
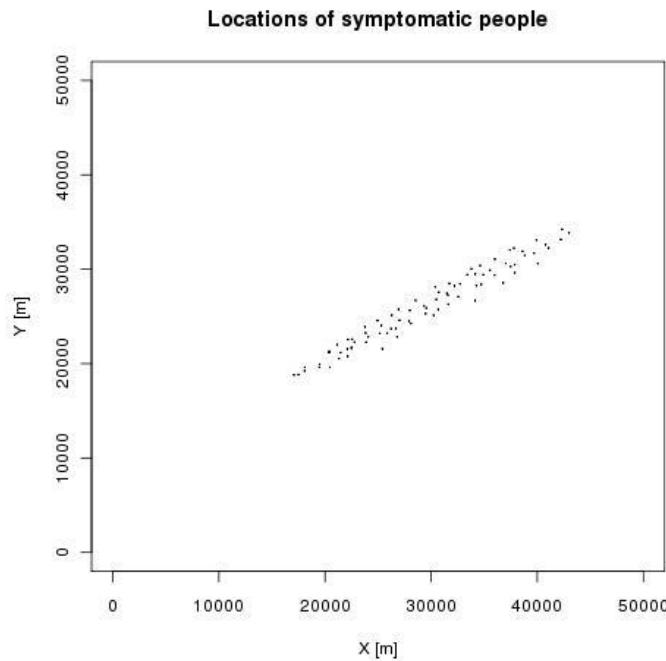


Contours show regions where 1% (outer) and 25% (inner) of the population are infected as a result of the release. Dots are individuals reporting.

# Estimated Distribution of Infected People

- Spatial dissemination over a distributed population
- Estimate affected area from sparse (early) data
- Data = # of sick people / day / zip code

Distribution of symptomatic people on Day 5

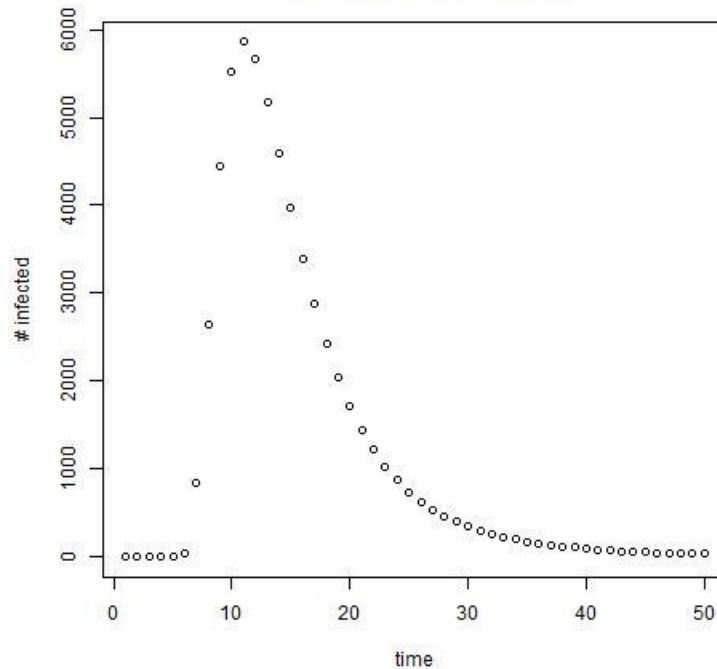


Estimated/true distribution of infected people

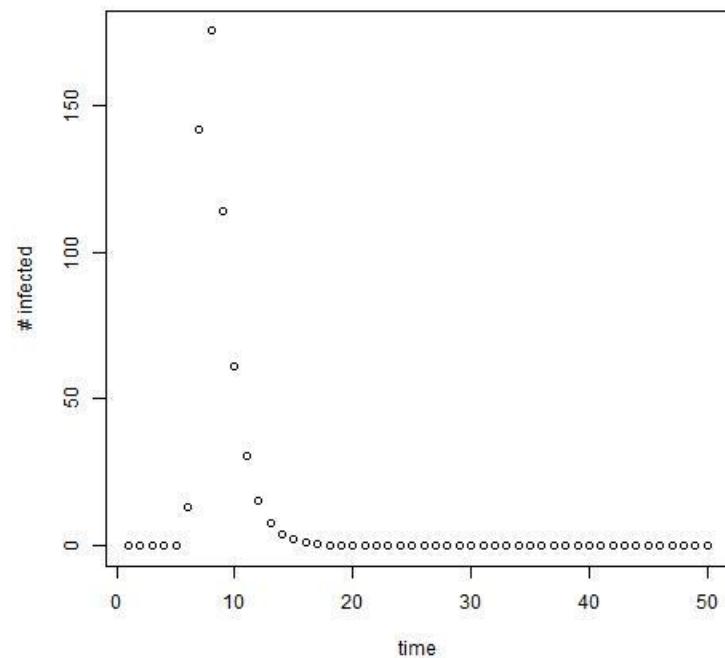
Naïve cluster analysis of the observations gives a wrong impression of true spatial distribution

## Case II – Inference under Model Mismatch

Epidemic curve for the entire city



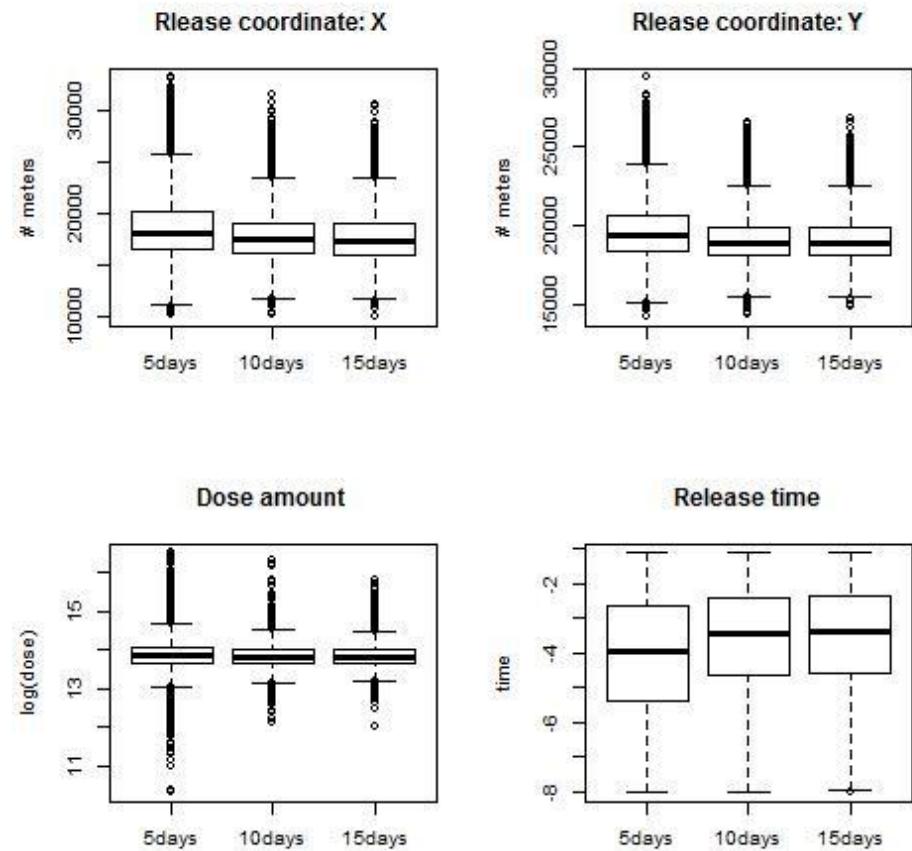
Epidemic curve for a chosen zip-code



- 50 km X 50 km city, divided into 1 km x 1km grid-cells
- Left – epidemic curve in a grid-cell
- Right – epidemic curve summed over all grid-cells

# Inference of Release Parameters

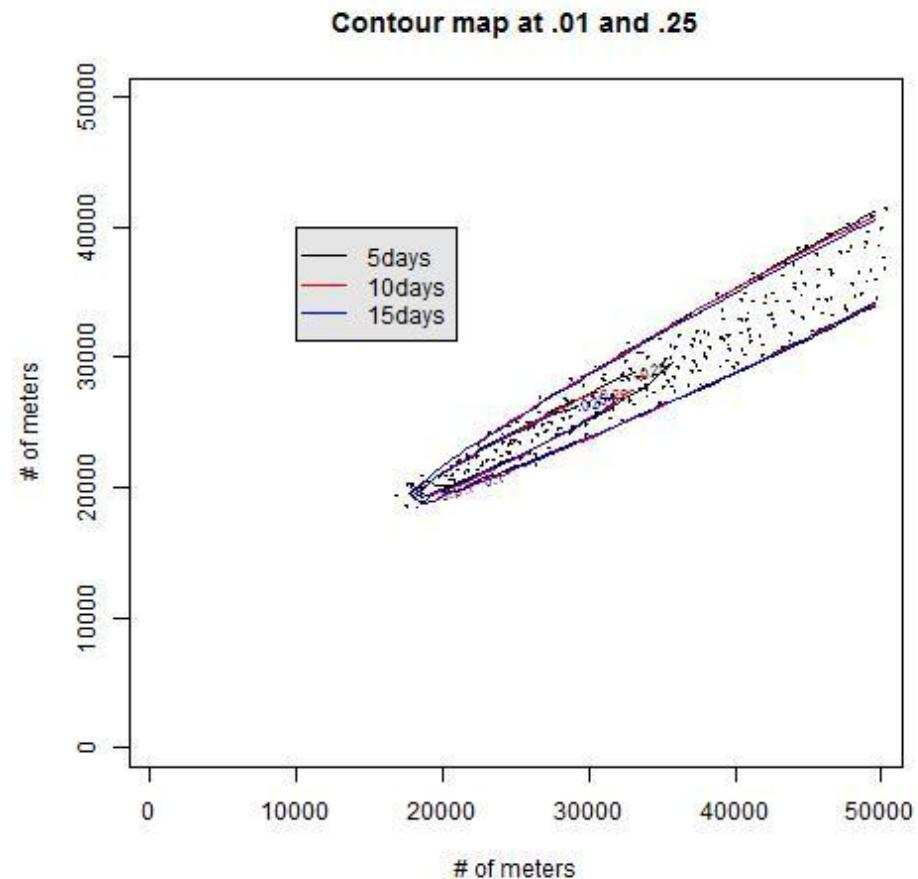
- Locations inferred wrongly – but by about 2 grid-cells (2 km)
- Underestimated release quantity
- Bigger uncertainties in time
- No improvement with addition of data (beyond 5 days)



Inferred values of release location (X, Y), release size ( $\log_{10}(Q)$ ) and release time. True values [15,000; 17,500; 14, -5]

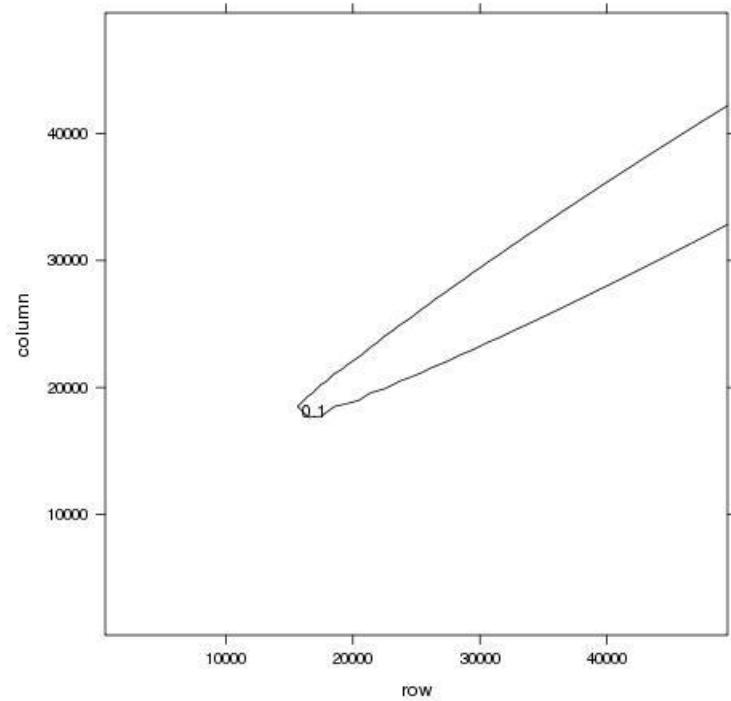
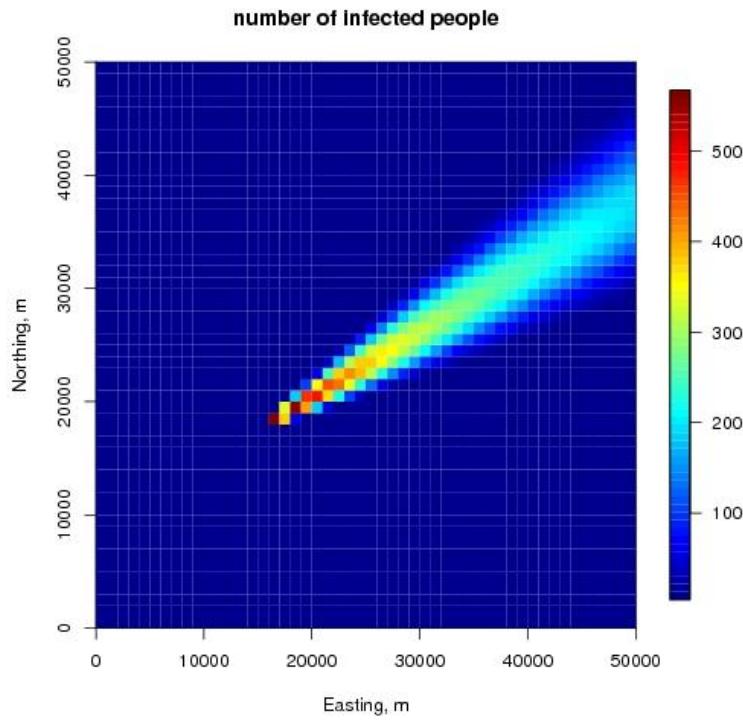
# Contours – Observed and Predicted

Clustering still OK even  
with model mismatch



Contours show regions where 1% (outer) and 25% (inner) of the population are infected as a result of the release. Dots are individuals reporting.

# Model-Informed Spatial Analysis

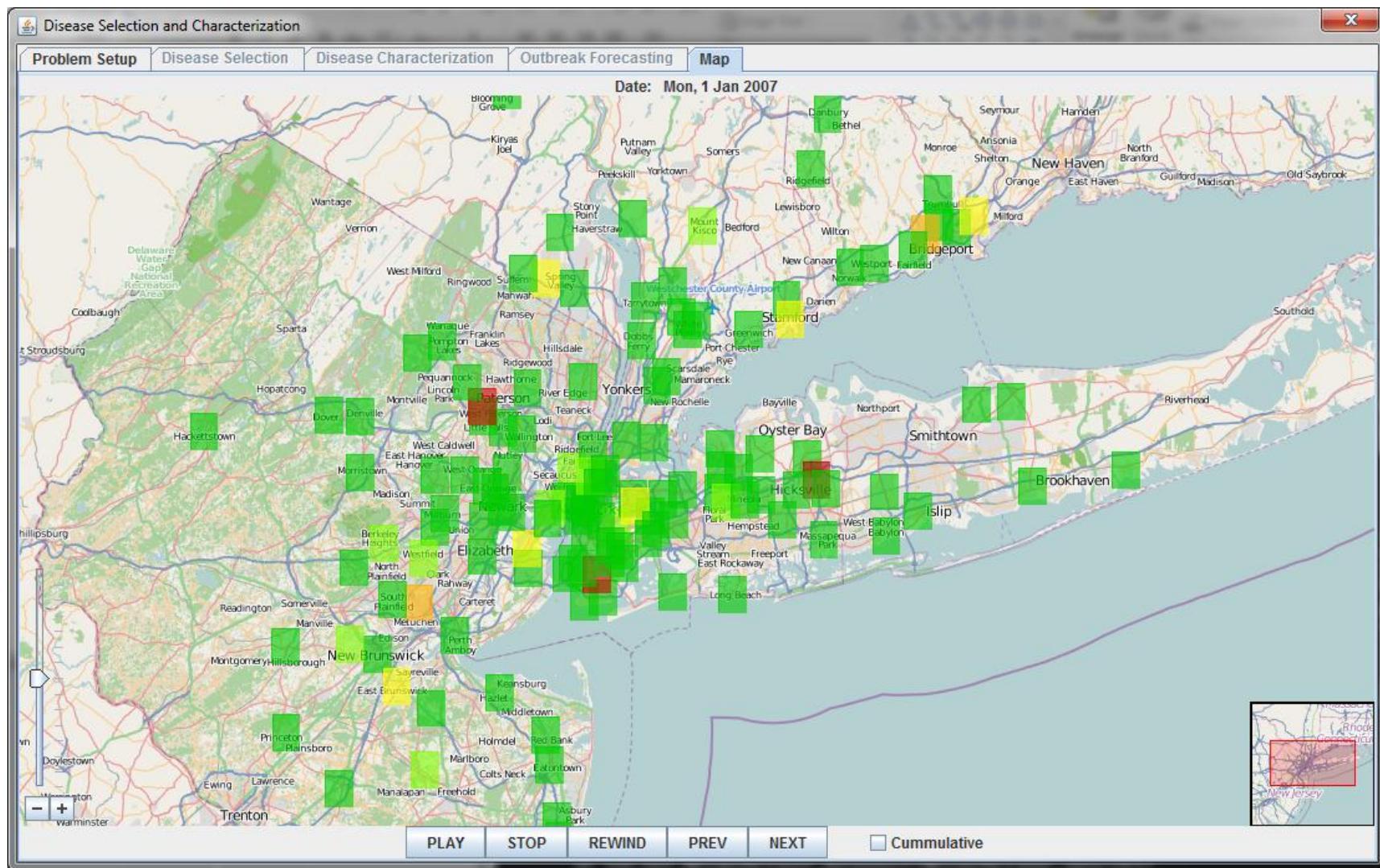


Model-enabled reconstruction provides a better starting point for clustering/analyzing spatial biosurveillance data

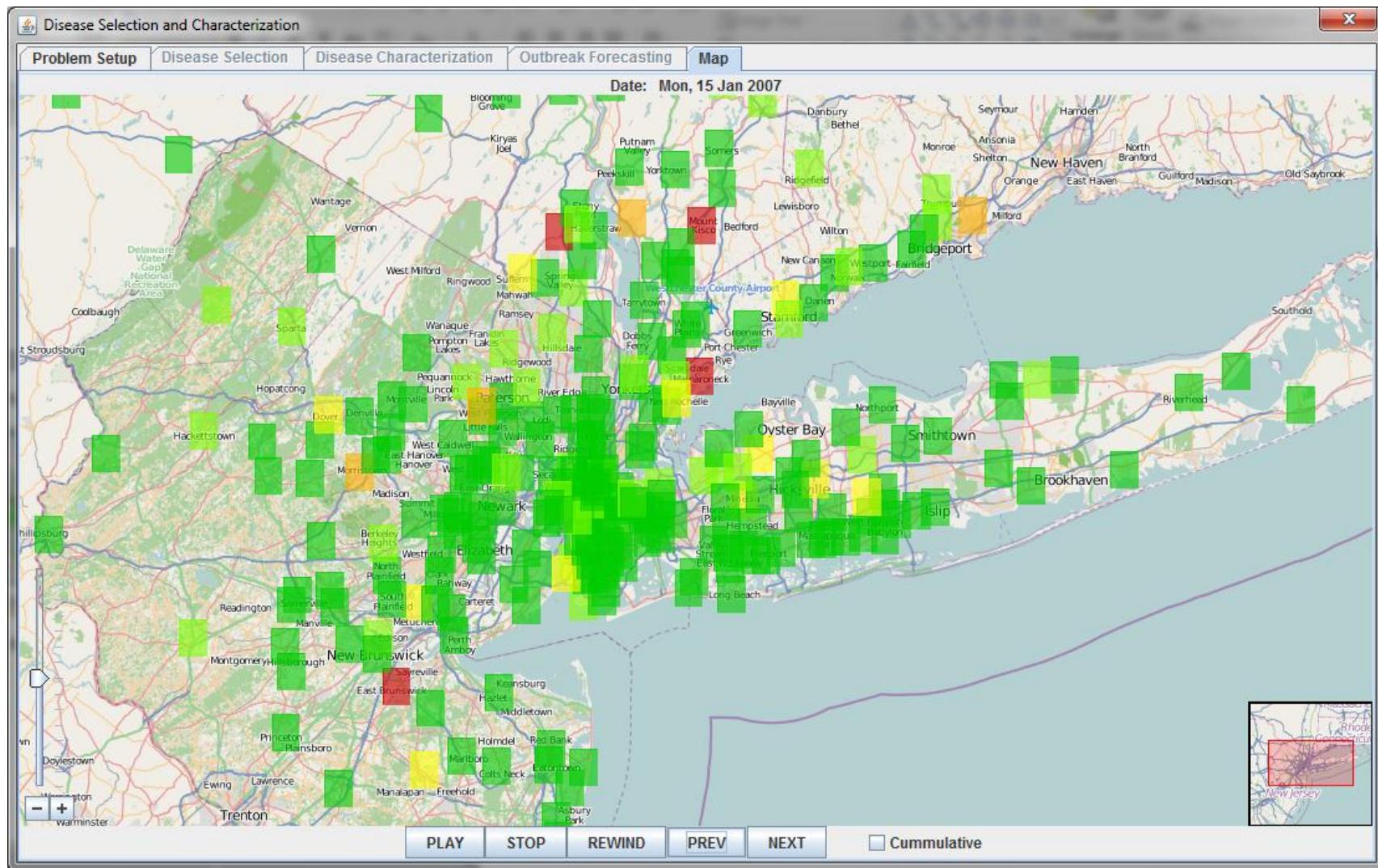
# Temporal-Spatio Visualization Prototype

- Pure visualization alone is very useful for understanding outbreaks
- Prototype “Heat Map” of reports by zip code
  - Color based on number of events
  - Current day or cumulative counts
  - Animates changes in “playback” mode through time
- Future Enhancements Possible
  - Add source term estimation, etc.
  - Medical Resource Planning, etc.

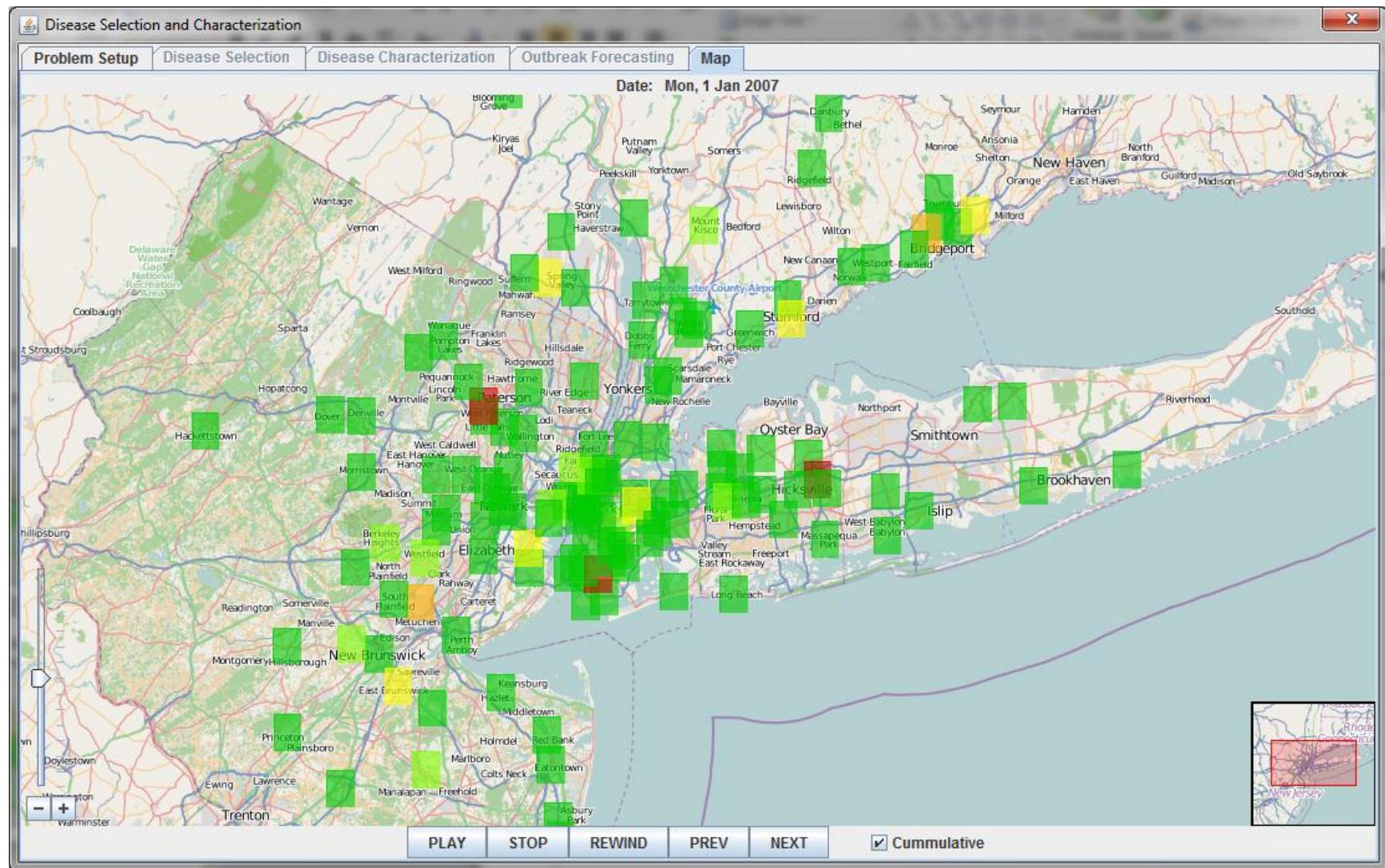
# Daily Report Heat Map



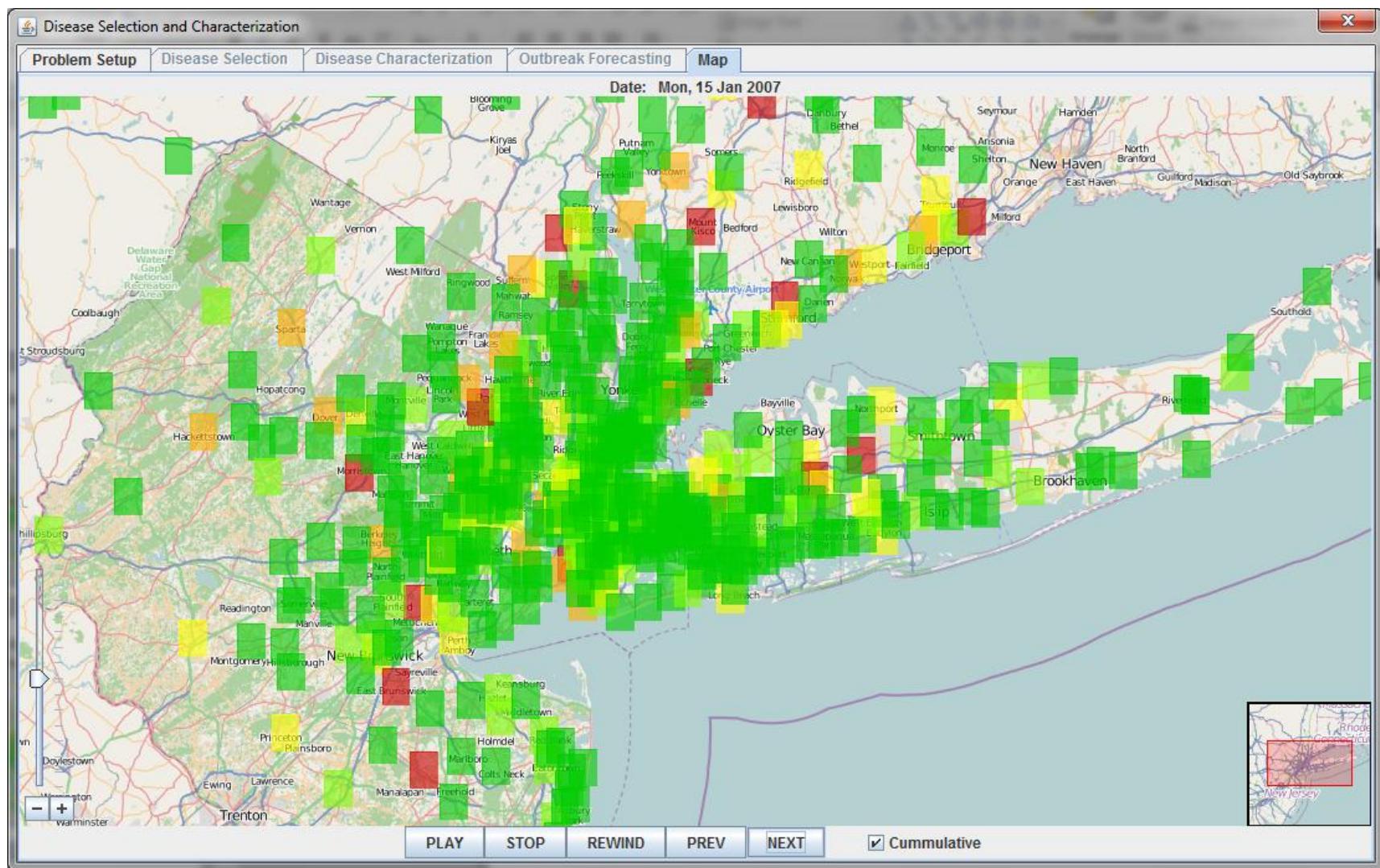
# Daily Report Heat Map



# Cumulative Report Heat Map



# Cumulative Report Heat Map



# Acknowledgements

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*Ms. Nancy Nurthen at DTRA is the Program Manager.*