

Distributed Micro-releases of Bioterror Pathogens: Threat Characterization and Epidemiology from Uncertain Patients Observables



Sandia National Laboratories

Jaideep Ray (PI), Brian Adams, Karen Devine, Youssef Marzouk, and Habib Najm.

Problem Definition

• Aim: To characterize and infer the genesis of epidemics from partial information

- Estimate the size of a bioattack (for medical response purposes)
- Estimate pathogenic characteristics (for tracking emerging infectious diseases)
- Uncertainty quantification (UQ), due to partial observations

• Technical challenges

- Stochastic model of disease spread
- Separating social and pathogenic contributions to disease propagation
- Inferring social parameters (social networks)
- Formulating a Bayesian inverse problem to do so
- MCMC methods for high-dimensional parameters spaces

Overall Approach

• Create a stochastic, individual-based epidemiological model separating social and pathogenic contributions

- Start with an individual-based dynamic social contact network model (Network Forward Model, NFM)
- Derive from it, an equivalent, but more-efficient, static network model

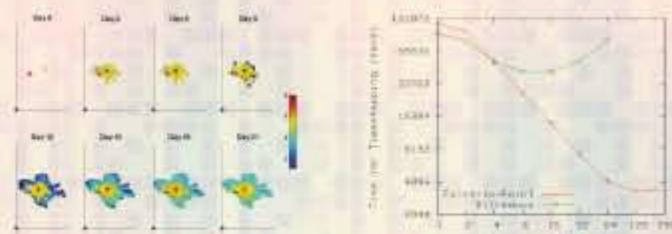
• Inverse problem: Bayesian; parameters estimated as PDFs

- Estimation of bioattack parameters from partial observations of the epidemic
- Estimation of pathogenic properties, e.g., transmissibility
- MCMC algorithms to infer graphs
- Prior beliefs of graph morphologies/parameters guided by previous item

Stochastic Epidemiological Model

- Dynamic model (EpiSims, Eubank, et al.) based on bipartite, time varying graph (transit network-based): people move among locations throughout a day; shed or absorb virus

- Each person or location has a disease "load"; when exceeds a threshold, progress through infection stages

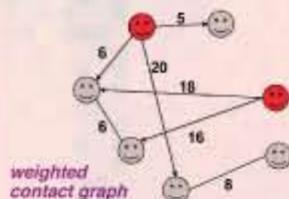


simulated spread of smallpox in an urban setting over 21 days

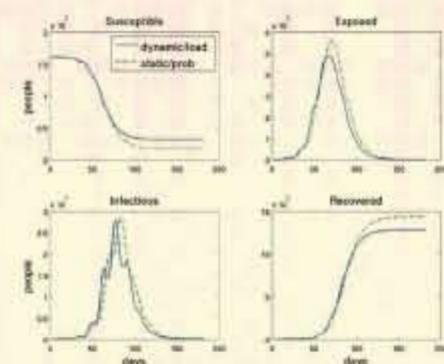
parallel scalability enables rapid scenario analysis

Epidemiological Model Reduction

- One reduced-order modeling approach: create static contact network based on person collocation during a 24-hour period
- Use a time-dependent probability of transmission model



weighted contact graph



- Similar epidemic prediction to dynamic, load-based model

- Also explored graph clustering and sampling techniques to reduce number of people/locations in simulation

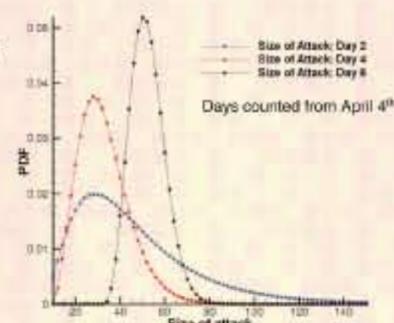
Estimation of Bioattacks (Anthrax)

• Approach:

- Disease model predicated on a dose-dependent incubation period distribution
- Analytical expression for the likelihood $\pi(N, \tau, DIS)$
 - N: number infected, τ : time of infection, D: average dose

Test/results: Sverdlovsk, 1979.

- Accidental release; 80 victims; 70 deaths
- Release: 2nd April
- First symptoms: 4th April
- Outbreak lasted 42 days
- Medical response starts: April 14th
- People affected: 50,000-60,000



It was quite clear by April 13th that the outbreak would be small (less than 100 infected)

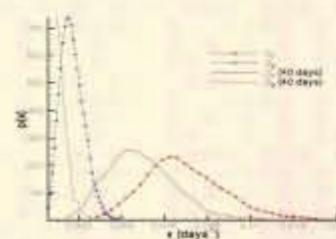
Estimation of Pathogenic Transmissibility

• Approach:

- Structured population, represented as a graph G , a collection of β -graphs
- Model disease transmission along links of G as a Poisson process, with rate β
- Differential transmission, inside and across groups
- MCMC to infer β , G and infection pathway P

Test/results: Smallpox outbreak, Abakaliki, 1967. WHO/SE/68.3

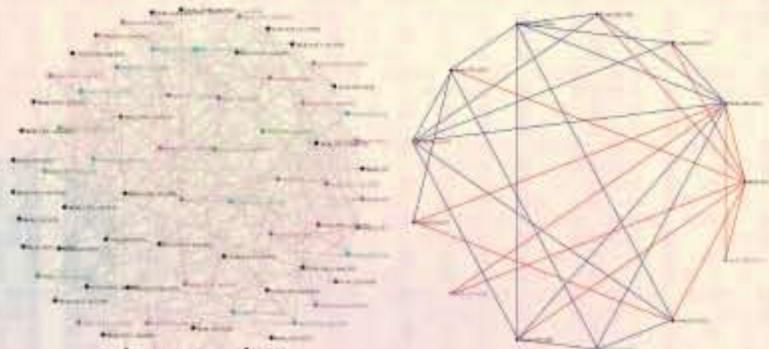
- Affected a closed population of 74, divided into 7 groups. 30 victims
- Differential rates of spread observed in data ("eyeball norm")
- Outbreak lasted 3 months
- Only dates of appearance of symptoms recorded; victims' fate unknown. No vaccinations.
- Inferences drawn from full data, and the first 40 days of data



Estimation of Social Characteristics

Expected social graph $\langle G \rangle$

Expected infection pathway $\langle P \rangle$



Results estimated from the first 40 days of the epidemic.

Significance

- One can derive simplified, static network models of disease spread from detailed individual-based models
- Partial observations can yield significant information about an epidemic's genesis and pathogenic characteristics
- Requires:
 - A good characterization of the social structure (to serve as a prior in the Bayesian inference method)
 - Powerful, multi-chain MCMC algorithms to traverse the parameter space
 - Mode-hopping MCMC to address multi-modality.
- Few previously published works on both topics
- Potential for largest impact
- More-realistic social networks, derived from individual-based models, used in the inference process
- Advanced MCMC schemes for inferring networks