SAND2008-5199P

0. Information-only slide

- **Contents: Slides for the LDRD Day poster**
- **Title: Distributed micro-releases of bioterror pathogens: Threat characterization and epidemiology from uncertain patients observables**
  - Project: 93505
  - People: Jaideep Ray (PI), Brian Adams, Karen Devine, Youssef Marzouk, Habib Najm.
  - LDRD IA: Enabling Predictive Simulations
- **Constraints :**
  - 8 slides
  - 20 pt font and higher
  - Problem/Approach/Results/Significance structure
- ***To the artist in Creative Arts: Please play around with font sizes etc, as needed.***

Problem definition

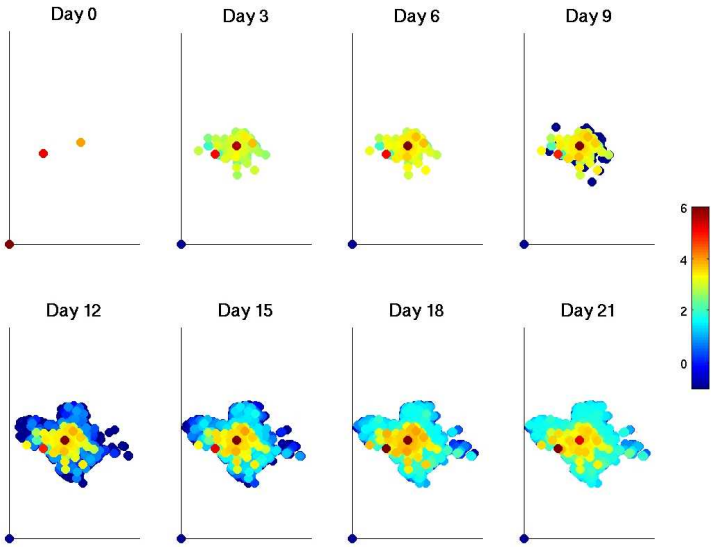
- **Aim: To characterize and infer the genesis of epidemics from partial information**
  - Estimate the size of a bioattack (for medical response purposes)
  - Estimate pathogenic characteristics (for tracking emerging infectious diseases)
  - Uncertainty quantification (UQ), due to partial observations
- **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

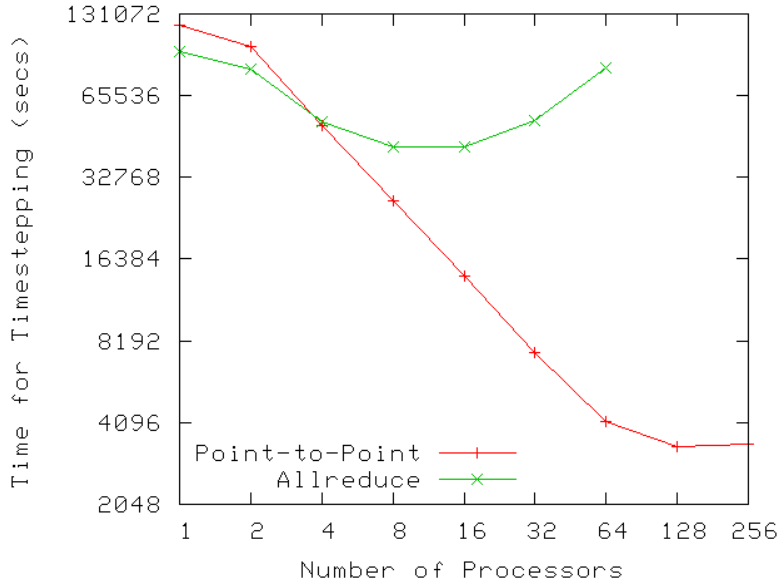
- **Create a stochastic, individual-based epidemiological model separating social and pathogenic contributions**
  - Start with an individual-based dynamic social contact network model (Network Forward Model, NFM)
  - Derive from it, an equivalent, but more efficient static network model
- **Inverse 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

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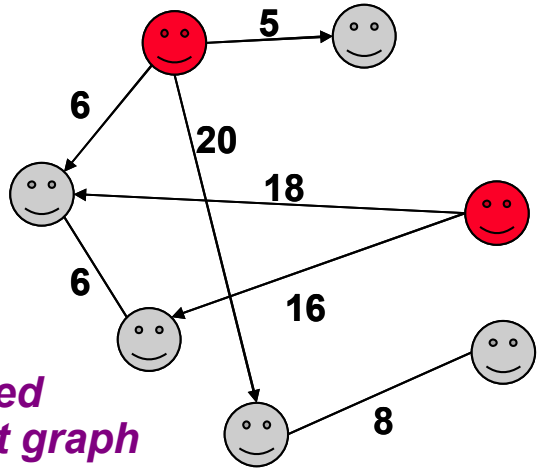
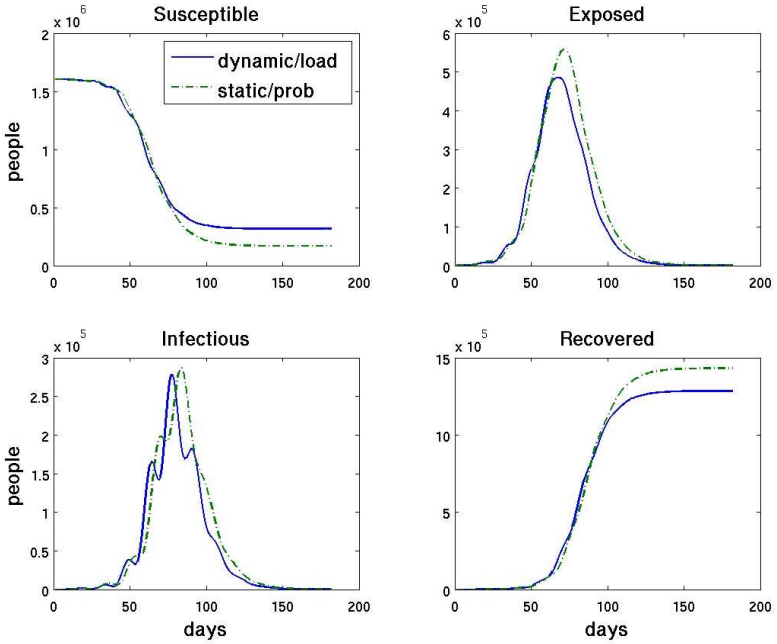
Epidemiological model reduction

- One reduced-order modeling approach: create static contact network based on person collocation in 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

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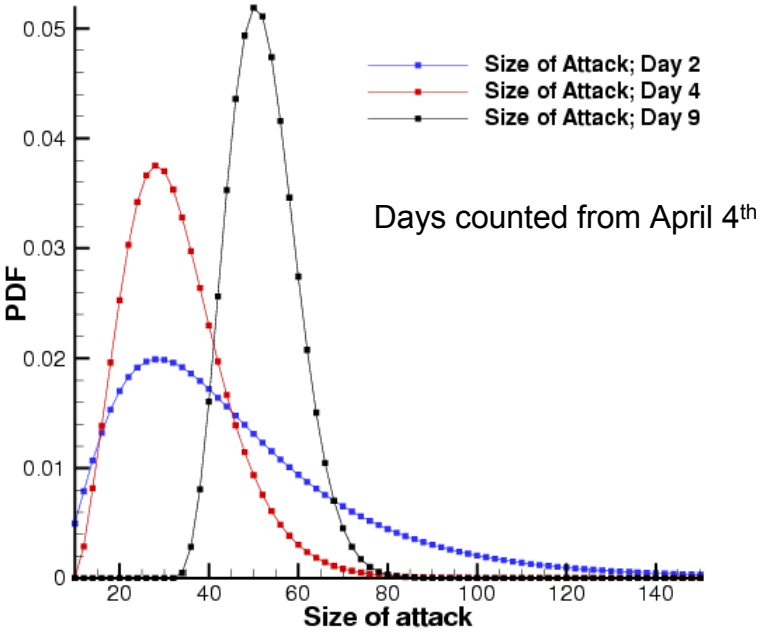
Estimation of bioattacks (anthrax)

- **Approach:**
  - Disease model predicated on a dose-dependent incubation period distribution
  - Analytical expression for the likelihood $\pi(N,\tau,D|S)$
    - 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)

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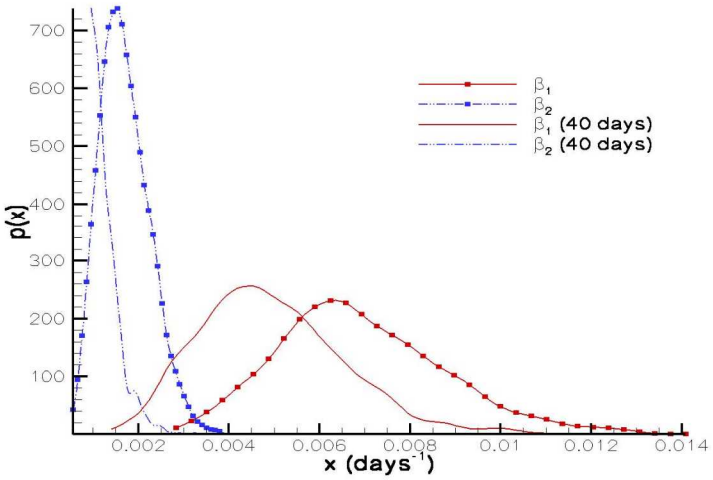
Estimation of pathogenic transmissibility

- **Approach:**
  - Structured population, represented as a graph $\mathcal{G}$, a collection of $\mathcal{B}$-graphs
  - Model disease transmission along links of $\mathcal{G}$ as a Poisson process, with rate β
  - Differential transmission, inside and across groups
  - MCMC to infer β, $\mathcal{G}$ and infection pathway $\mathcal{P}$



- **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

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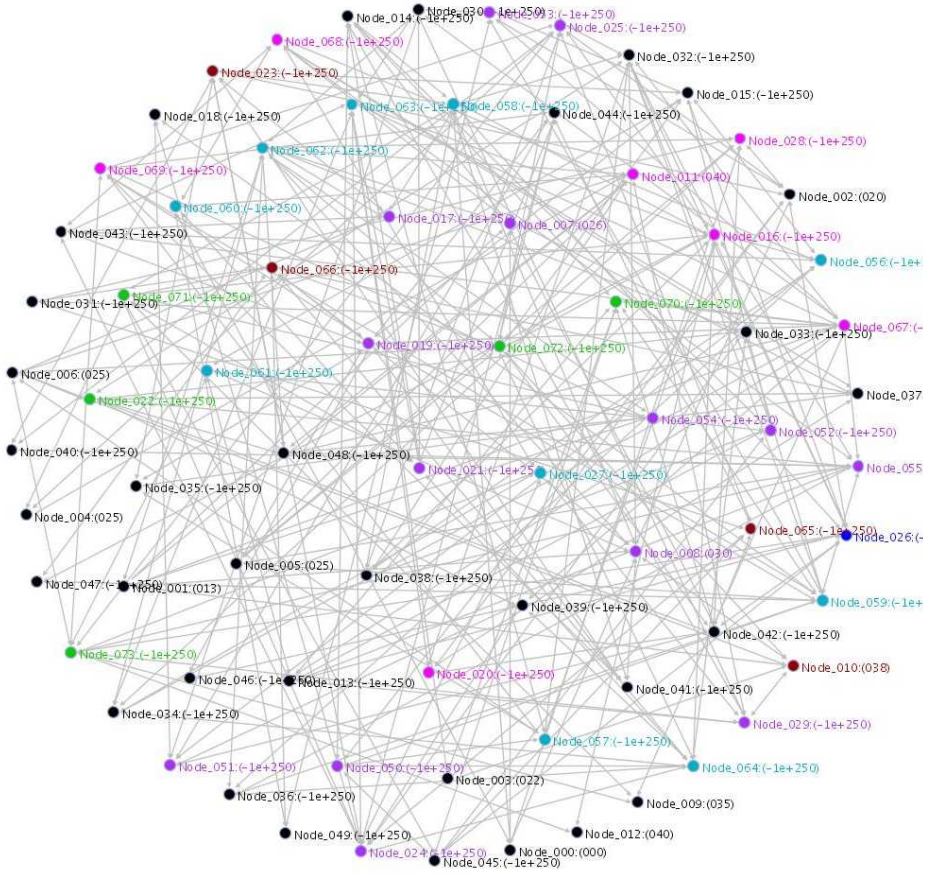
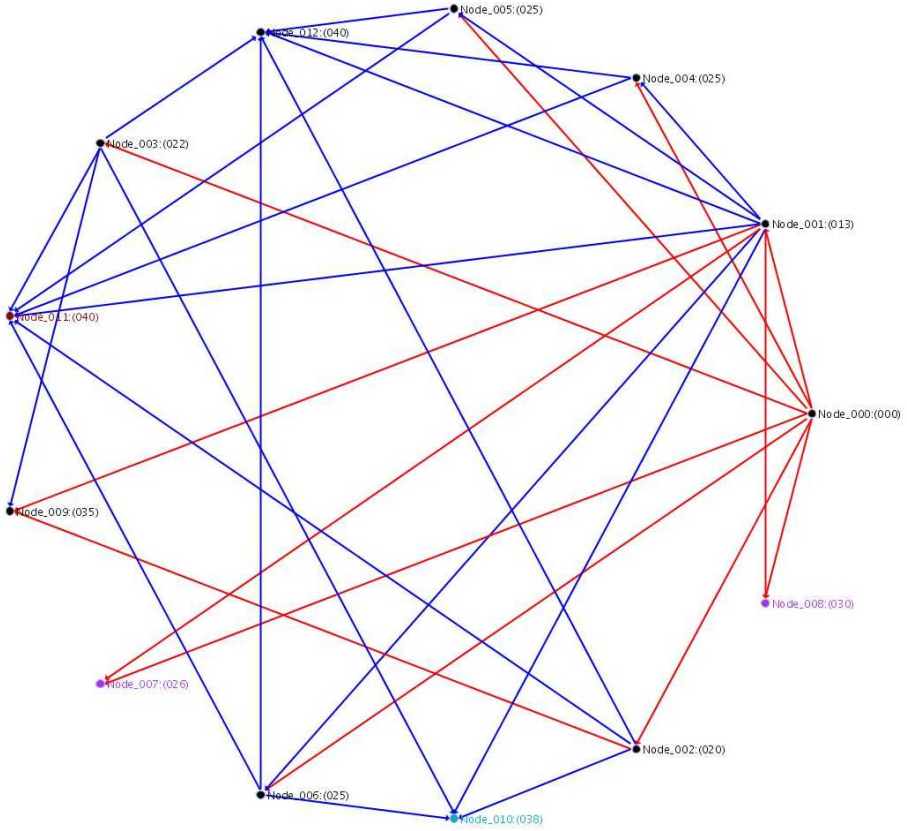
Estimation of social characteristics

Expected social graph <$\mathcal{G}$>



Expected infection pathway<$\mathcal{P}$>



Results estimated from the first 40 days of the epidemic.

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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