




## Small World Network Model for Contagious Diseases

Karen Cheng and David Crary  
Health Effects And Medical Response Group  
Applied Research Associates, Inc., Arlington, Virginia, USA

Jaideep Ray and Brian Adams  
Sandia National Laboratories  
Livermore, California, USA


Contact Info:  
Ms. Karen Cheng  
kcheng@ara.com  
703-816-8886 x 138



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## Benefits of Applying Small World Networks in Outbreak Modeling



- A large number of phenomena have been shown to be well described by small-world network structures
  - internet connections
  - world-wide-web structure
  - phone call networks
  - collaboration networks
  - cellular metabolic reaction networks
  - disease contact networks
- Simulation/Model is **Simple** and **Fast**
  - We are studying fitting a simple (two parameter) small-world network model of epidemic spread to epidemics created from complex, realistic, urban social network data.
  - Can simple, low dimensional models of epidemics accurately predict the structure of real-world epidemics?

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 **Potential Additional Benefits in a Biosurveillance Context** 

- Traditional epidemic models typically rely on fitting of historical datasets. However,
  - Historical outbreak profiles are specific to the conditions from which they were derived (population dynamics, disease, containment measures)
- Our small world network model incorporates population dynamics and disease-specific parameters intrinsically within the model. It holds the *potential to create* data sets for new scenarios.
  - Do the parameters of these models vary in a systematic way with population characteristics ?
    - Can fit parameters for numerous scenarios from realistic simulations
    - If we can derive a functional relationship between the two model parameters with scenario characteristics such as population density we can create new scenarios.

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 **Background** 

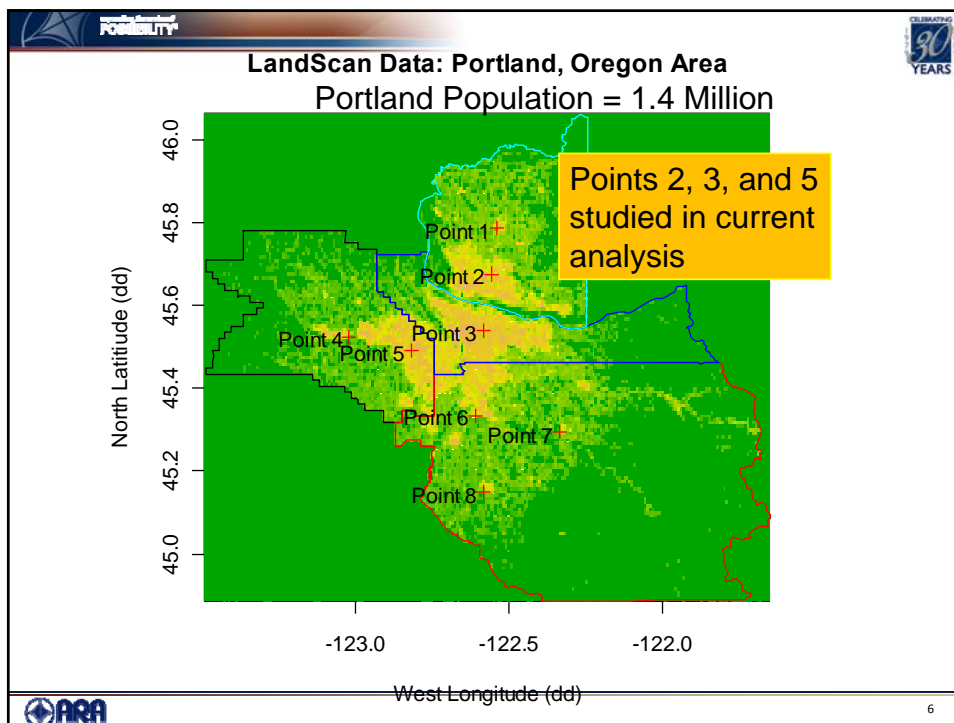
- Large-scale individual-based epidemic models have been developed by Sandia National Laboratories which do not depend on uniform or ad-hoc mixing assumptions (EpiSims, Eubank et al., 2004)
  - Uses dynamic bipartite graphs to model contact patterns
  - Graphs are generated by realistic urban traffic simulations based on census, land-use, and population data collected over a long period of time (over a decade) by Department of Transportation.
- Contact network shows a *small-world like structure* with short average distance between people (EpiSims, Eubank et al., 2004)
- Simulations have been developed (by Virginia Polytechnic Institute) for various cities and diseases. A contact network for Portland, Oregon has been published.

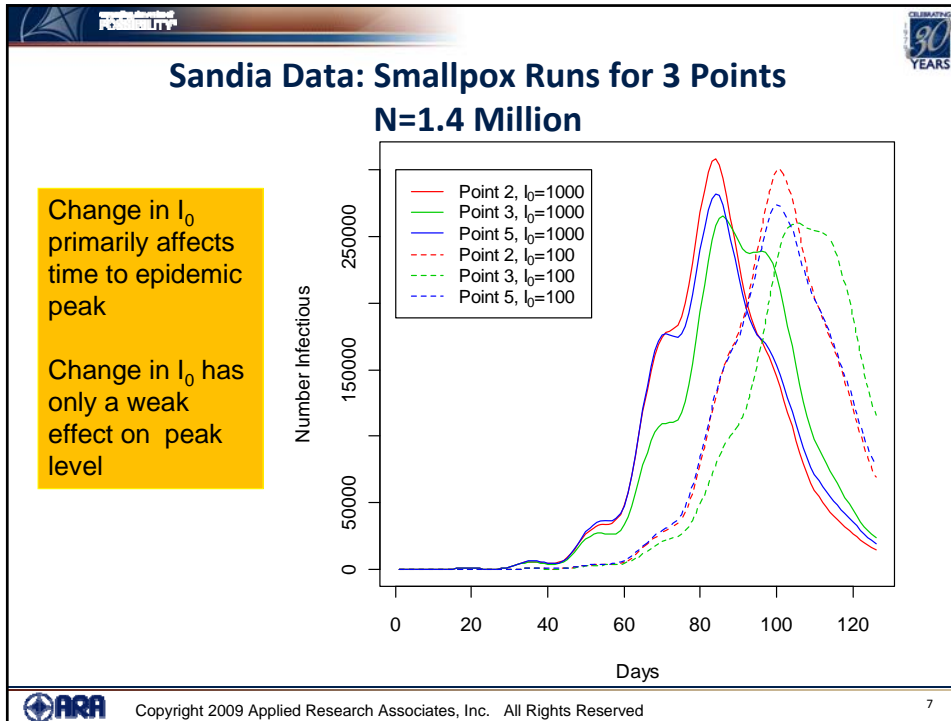
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**Simulation (Adams *et al.*, 2007)**

- We have done simulations using large scale model based based on the EpiSims contact network
  - Simulations take a couple of days to run
  - Simulation done for four counties in the Portland, Oregon region using SEIR models on a network for 126 days
  - Disease models used:
    - Smallpox
    - Pneumonic Plague
    - Influenza
  - Calculations performed for three values of initial number of infectious (10, 100, and 1000)
  - Calculations performed for three initial locations with varying population density.
  - Output consists of number of persons in each SEIR compartment for each day in simulation


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- Small World Model (Overview)**
- Discrete time simulation of SEIR model on network structure, where each node of the network represents a person in the simulation
  - Local network transmission is 2 dimensional, each node (representing a person) has 4 nearest neighbors (average family size in U.S. = 3.14 persons (U.S. Census Bureau factfinder.census.gov))
  - In addition, transmission can occur by 'jumps' to random 'non-local' locations in the network
  - Based on two parameters  $p_s$  and  $p_j$  which represent the probability/per day of local and non-local spreading
  - Output is number of persons in SEIR compartment for each day in the simulation
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**Small World Model**

Underlying network has 4 nearest neighbors, plus random long distance links


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**Small World Model (Details)**

- SEIR discrete time model for spread of an epidemic on a network with  $z$  nearest neighbors
- Depends on eight parameters
  - Population specific:  $N, I_0$ 
    - $N$ = total number in population
    - $I_0$ = number initially infected
  - Disease specific:  $\mu_{ei}, \sigma_{ei}, \mu_{ir}, \sigma_{ir}$ 
    - $\mu_{ei}, \sigma_{ei}$ = Mean and standard deviation of length of time exposed
    - $\mu_{ir}, \sigma_{ir}$ = Mean and standard deviation of length of time infectious
  - Network specific:  $p_s, p_j$ 
    - $p_s$ = Probability per day of spread to nearest neighbor
    - $p_j$ = Probability per day of 'jump' to non-neighbor
- Time development of an epidemic *for a specific disease* is known once  $z$  is specified (we use  $z = 4$ ), and  $I_0, p_s,$  and  $p_j$  are known


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**Fitting Small-World Network Parameters to Sandia Data**


- Because of the stochastic nature of the small world network simulation, direct search methods for the parameters do not converge efficiently (fit surface is noisy)
- We used exhaustive search in  $p_s$  and  $p_j$  space to calculate epidemic curves with the small world simulation, where range of  $p_s$  and  $p_j$  is  $[0,1]$ , and step size is 0.02 (50x50 grid)
- Values of  $I_0$  taken to be known, total population = 1.4M.
- Disease parameters taken from simulations
- For each curve generated using the small-world network model, we record
  - $p_s$  and  $p_j$  value
  - Peak value of I curve
  - Peak time (days)


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**Smallpox disease parameters (units = days)**


Period	Distribution/Value	Notes	SEIR Compartment
Susceptible	n/a		S
Incubation	$\sim N(12.0, 2.0)$		E
Prodromal	$\approx 3.0$	Symptomatic	E
Contagious Burst	$\approx 0.5$	Symptomatic, Infectious	I
Contagious Decline	$\sim N(6.5, 1.0)$	Symptomatic, Infectious	I
Recovery	$\sim U(6.0, 12.0)$	Not Infectious	R
<i>Recovered</i>	n/a		R

For SEIR Model used to fit Sandia data, we assume:  
 Time in E compartment  $\sim N(15.0, 2.0)$   
 Time in I compartment  $\sim N(7.0, 1.0)$


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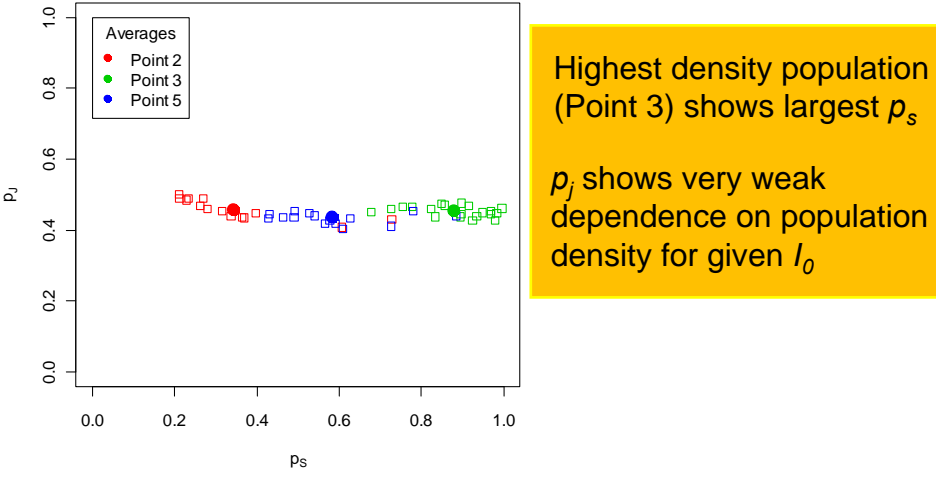
**Fitting Small-World Network Parameters to Sandia Data (Continued)**


- For each epidemic curve from the full simulation, the peak value and peak time in days is matched with values recorded in the table, according to specific filter
  - Peak value must be within certain percentage limits
  - Peak time must be with certain days
- All values of  $p_s$ ,  $p_j$  passing the filter are averaged to provide best estimate of small world parameters.

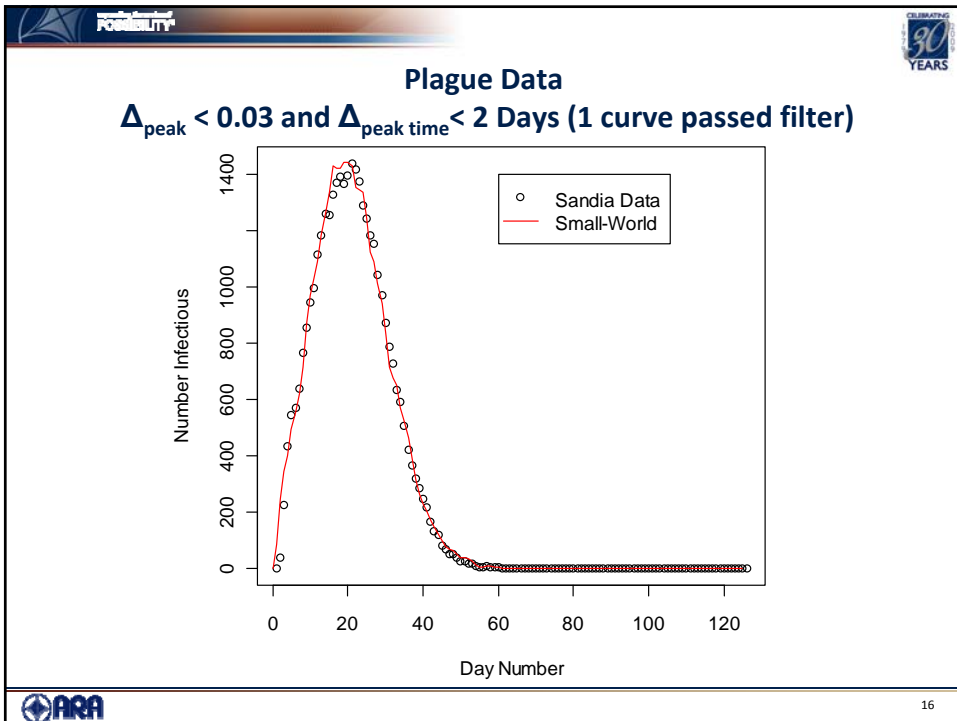
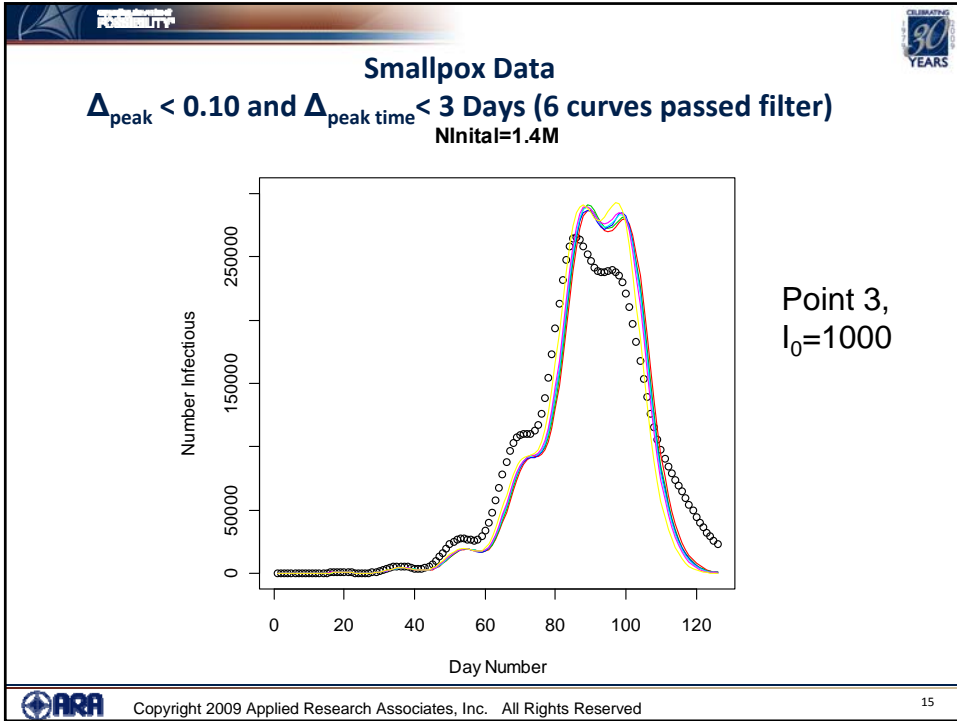

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**Example Fit: Smallpox, Points 2, 3, 5**


Smallpox 1000 Initial Infections




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## Conclusions

- Simple small world networks appear to provide promise in fitting realistic epidemic data
- Small world network models are attractive since they require significantly less data and computation times over complex simulations
- In smallpox study
  - $p_s$  shows linear dependence on population density of location of initial infection,  $p_j$  does not show this dependence
  - $p_j$  shows weak dependence on  $I_0$
- Further studies:
  - Investigate dependence of  $p_s$  with population density from Landsat data
  - Investigate dependence of fit parameters for different values of  $N$  (requires full scale simulation of different city)

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Dr. Christopher Kiley of DTRA is the S&T Manager  
Christopher.Kiley@dtra.mil

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