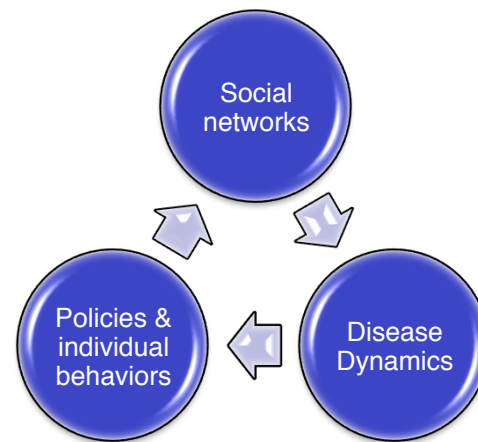

Studying the relationship between individual behavior, public policies, social networks and epidemic processes



Madhav Marathe

Dept. of Computer Science &
Network Dynamics and Simulation Science Laboratory
Virginia Bioinformatics Institute

Virginia Tech

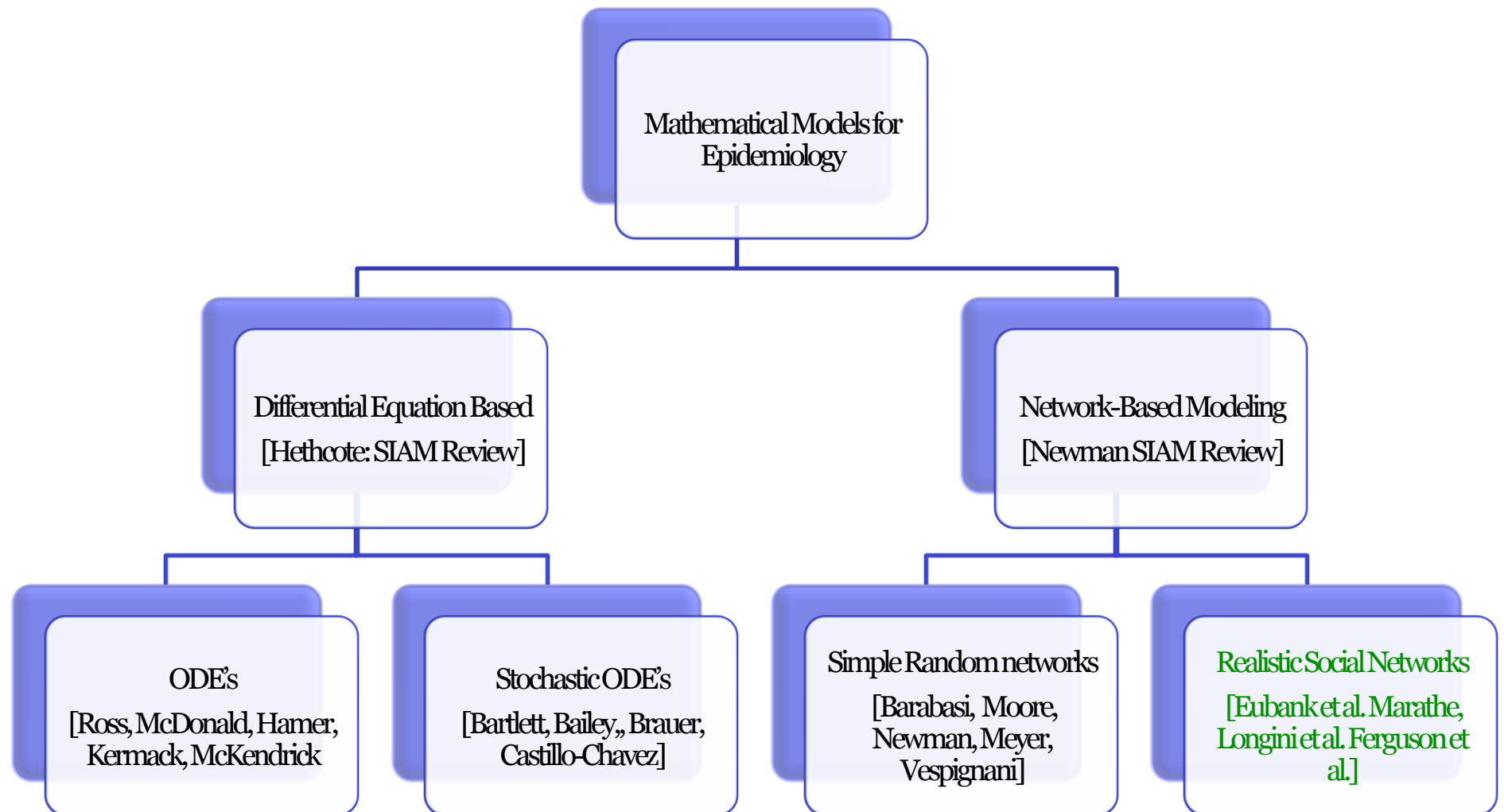
NDSSL TR-09-074

Acknowledgements: Virginia Tech: Network Dynamics & Simulation Science Laboratory, VBI and our external collaborators



Work funded in part by NIGMS, MIDAS program, CDC Center of Excellence in Medical Informatics, DTRA, NSF HSD, NECO, NETS and OCI programs

Models in Mathematical/Computational Epidemiology



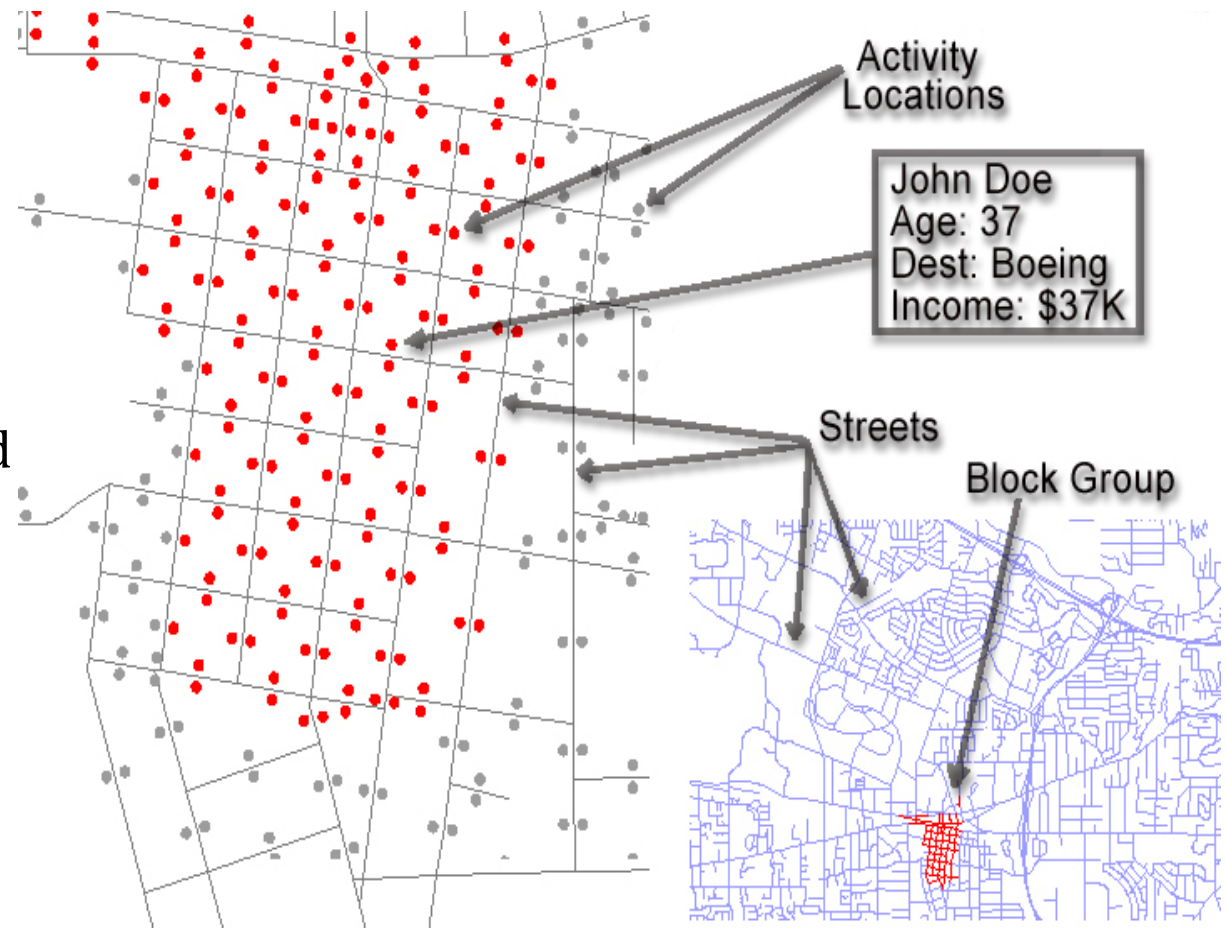
Simdemics: High resolution network-based modeling

1. Create a synthetic population
 - Sampling Contingency Tables, Assignment Problems
2. Derive a social contact network G
 - Assign activities (CART Trees), locations (Gravity models), Construction and analysis of large networks
3. Create a model of disease transmission
 - Design probabilistic timed finite state automata based on data
4. Simulate disease spreads over G
 - Simulation of a diffusion process
5. Study effect of interventions: co-evolution of G , behavior, policy and disease progression
 - Markov decision processes (MDP) and n -way games

Eubank, Marathe et al. Nature'04, SODA, Scientific American, DIMACS, Longini et al. PNAS 06, Science 05, Ferguson et al. Nature 05, 06.

Step 1: Synthetic populations

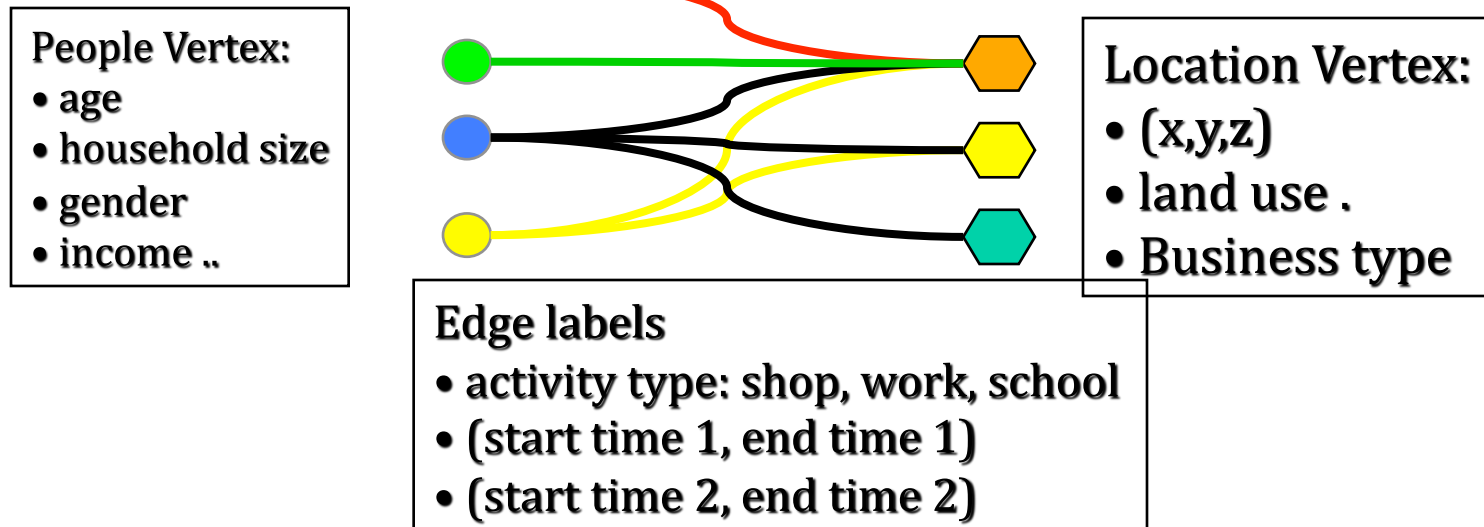
- Who, where, what, when: *People*
 - Individuals
 - Household structure
 - Statistically identical to U.S. Census
 - Assigned to Home and Activity Locations



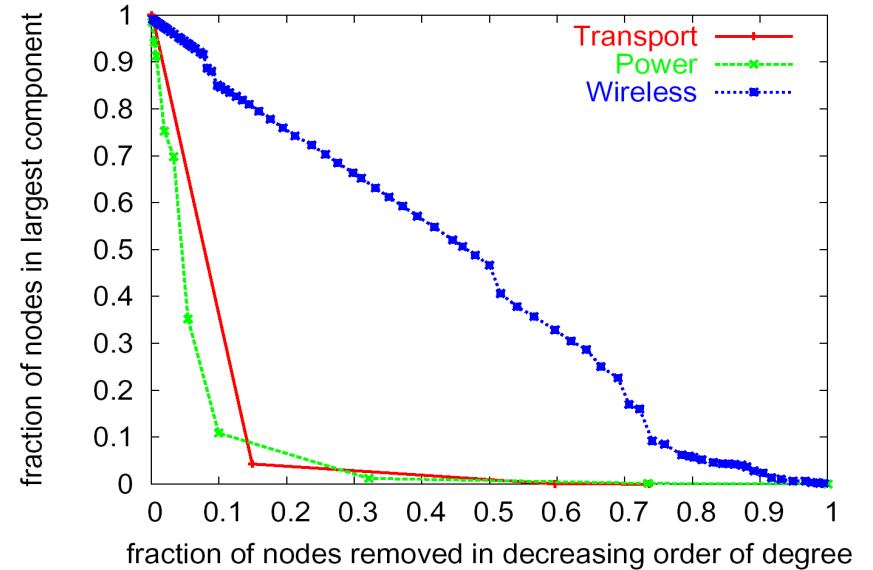
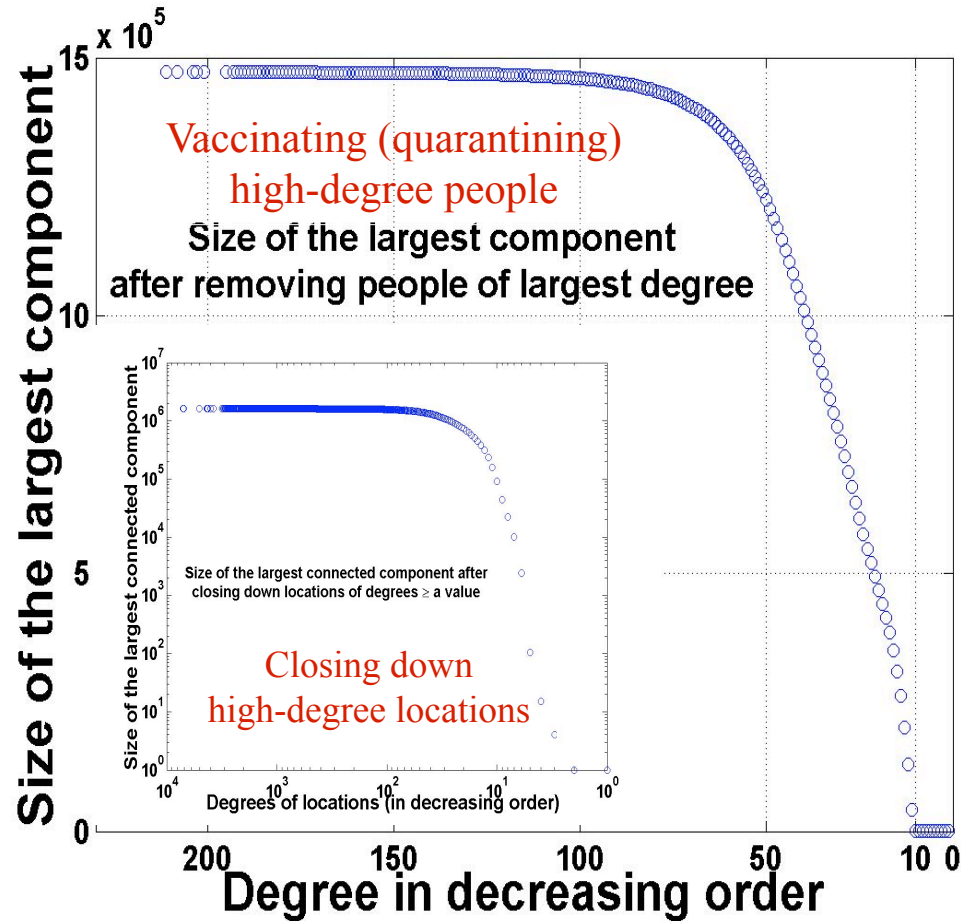
Beckman et al. Transportation Science, NISS technical reports, Barrett et al. TRANSIMS technical reports

Step 2: Urban dynamic social contact network

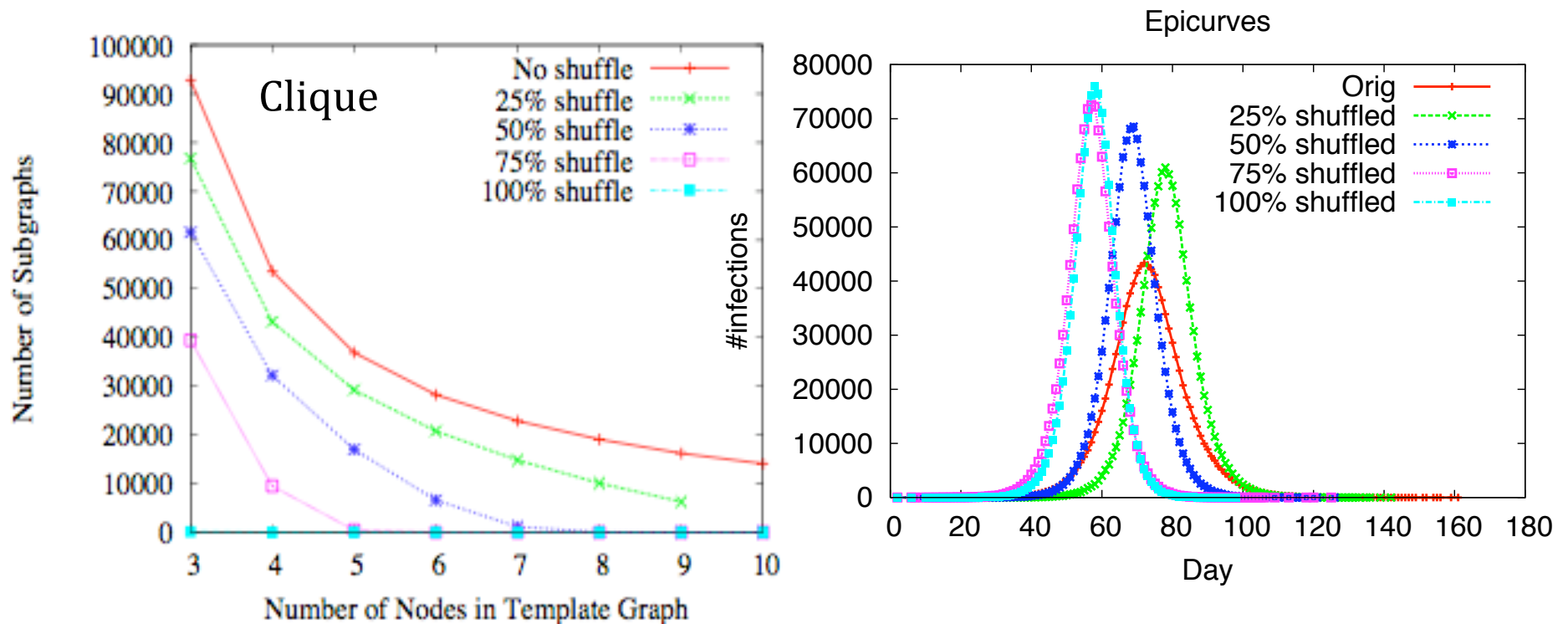
- Demographically match schedules
- Assign appropriate locations by activity and distance
- Determine duration of interaction
- Generate social network



Social Contact Networks are not easy to shatter



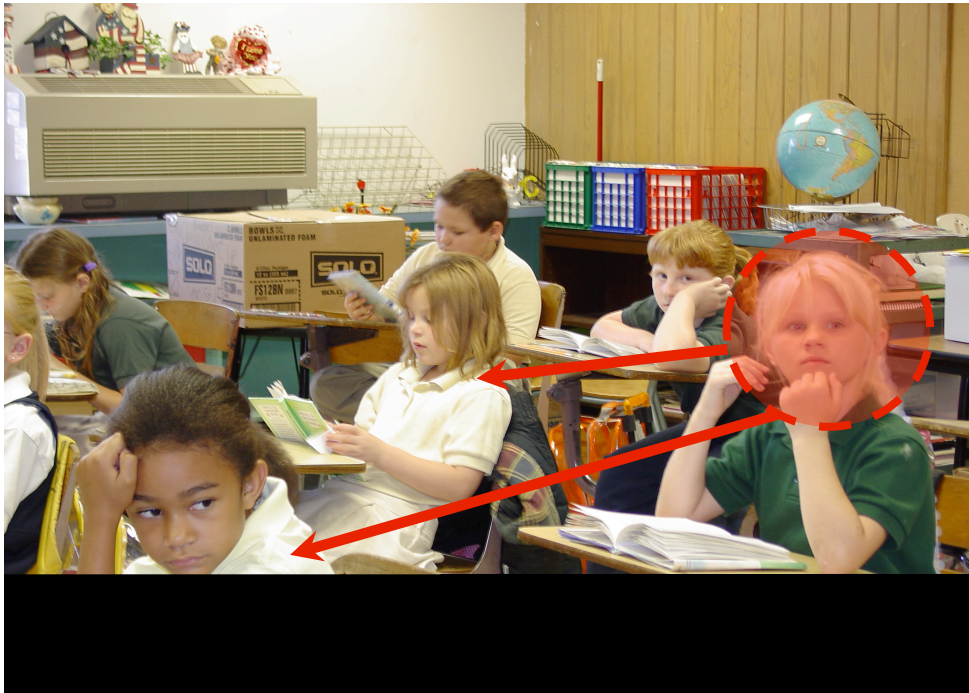
Realistic Social Contact network differ from “simple” random networks



Portland Network:

- Cliques within same age group (0-19).
- Simple random graph models cannot produce these structures

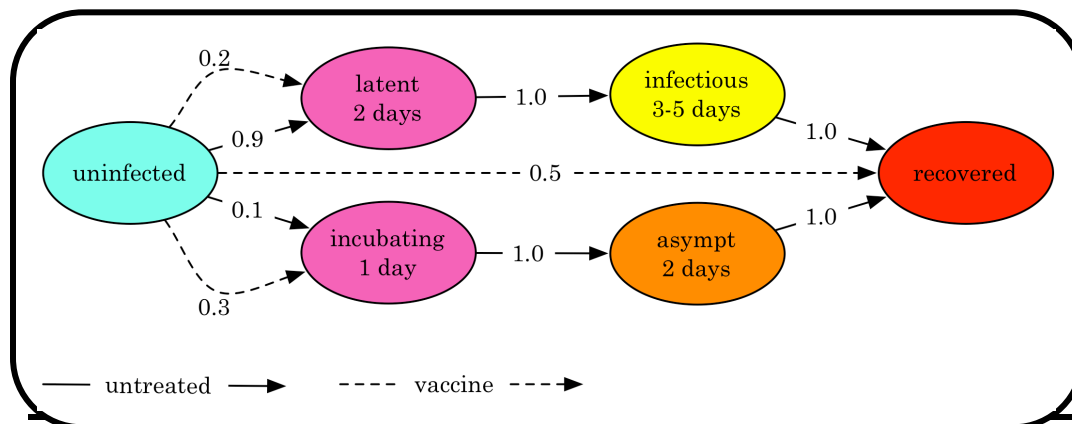
Step 3. Within Host Disease Models



Disease can be spread from one person to another.

The probability of transmission can depend on:

- type of disease
- duration and type of contact
- person's characteristics
 - age, health state, etc.



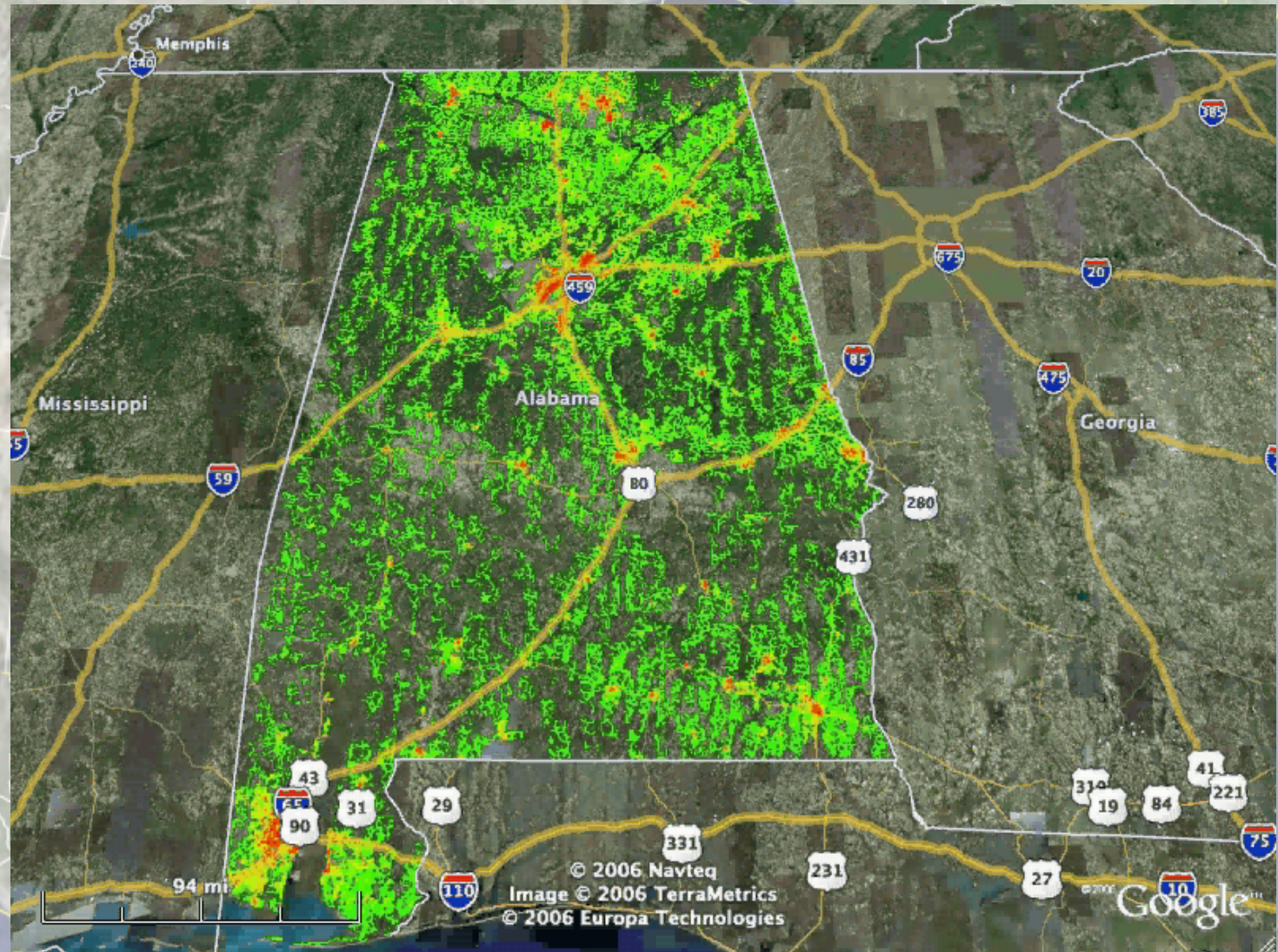
Within host model:
Probabilistic timed
transition systems (PTTS)

Step 4: Fast Simulations for Disease Spread

Distinguishing Features	EpiSims (Nature'04)	EpiSimdemics (SC'09)	EpiFast (ICS' 2009)
<i>Solution Method</i>	Discrete Event Simulation	Interaction-Based Simulation	Combinatorial +discrete time
<i>Performance 180 days 9M hosts & 40 proc.</i>	~40 hours	2 hours	Few minutes
<i>Co-evolving Social Network</i>	Can work	Works Well	Works <i>only</i> with restricted form
<i>Disease transmission model</i>	Edge as well as vertex based	Edge as well as vertex based (e.g. threshold functions)	Edge based, independence of infecting events

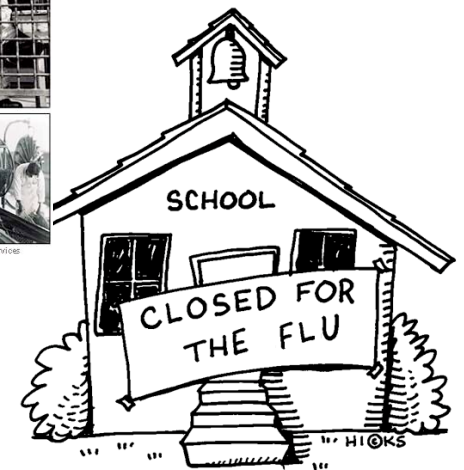
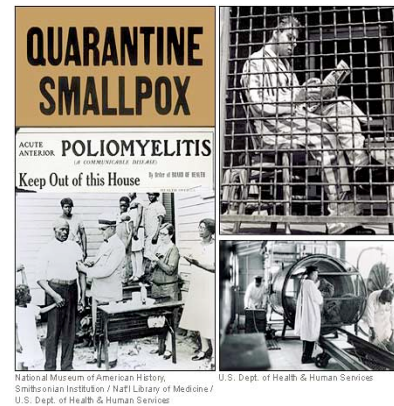
Visualizing the spatio-temporal diffusion

Spatial and Temporal details on spread of disease at this scale and fidelity



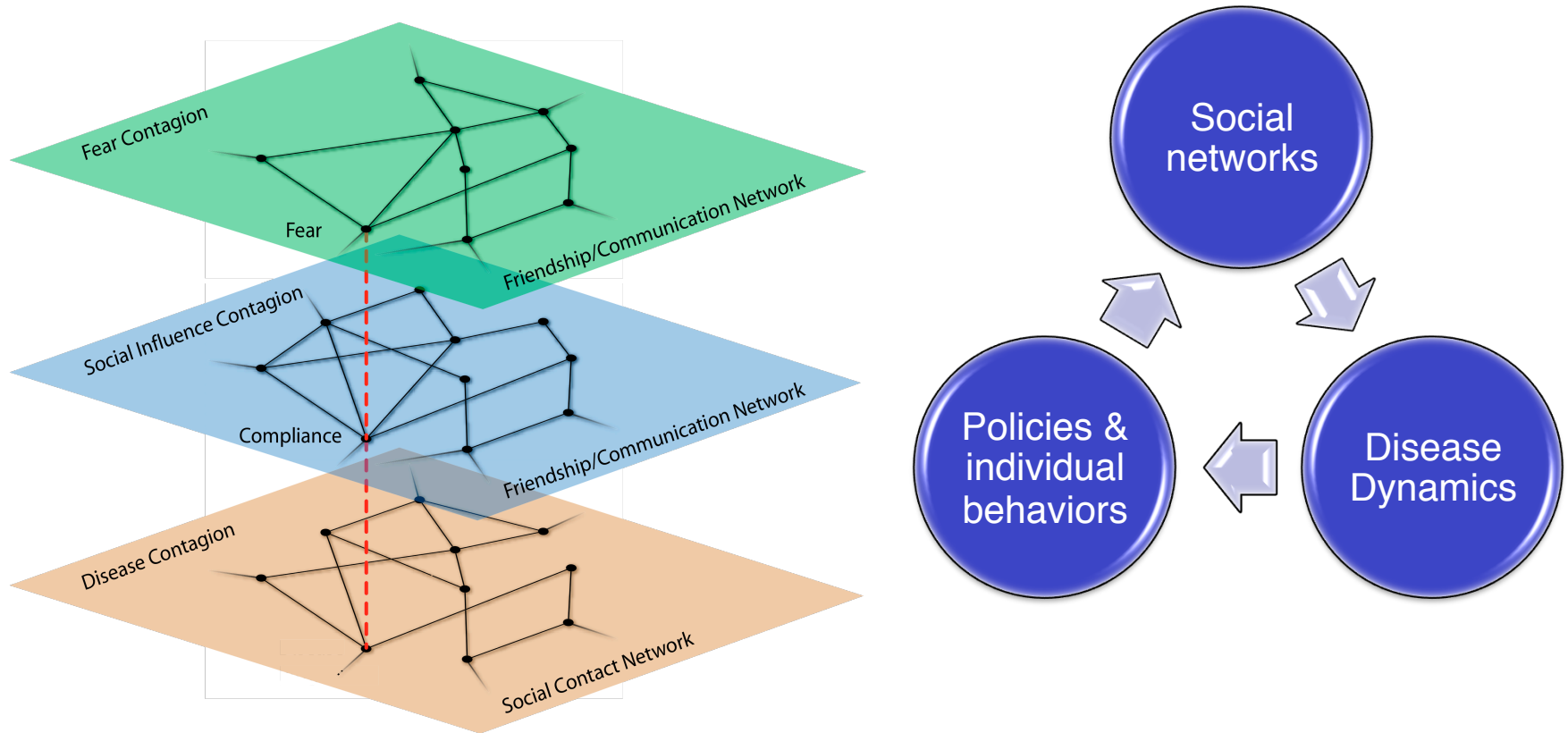
Step 5: Study Effects of Interventions

- Specifying a Situation (Scenario)
 - E.g. How to represent cascading failures?
- Kinds of Interventions
 - PI: Vaccines and Anti-viral, Anti-biotic
 - NPI: Social distancing, quarantining
- Specifying an Intervention
 - When, where, whom & how much
- Cost Functions
 - Human suffering averted
 - Time gained (delay of exponential growth)
 - Resource constraints



Mathematical Model: POMDP & n -way games

Interventions: Partially Observable Markov Decision Process (POMDP)

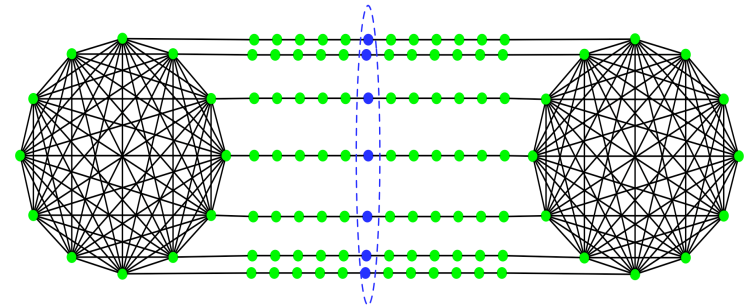
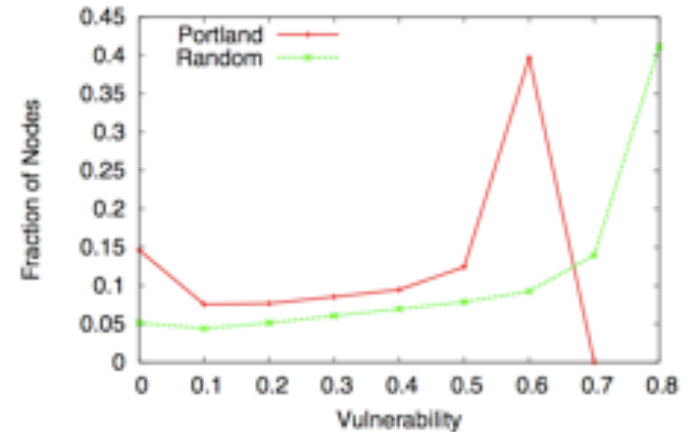


- Behaviors and Disease dynamics can be cast as generalized reaction diffusion: Leads to coupled networks
- Co-evolving dynamical systems

New Network Measures and an application to optimal allocation of PI

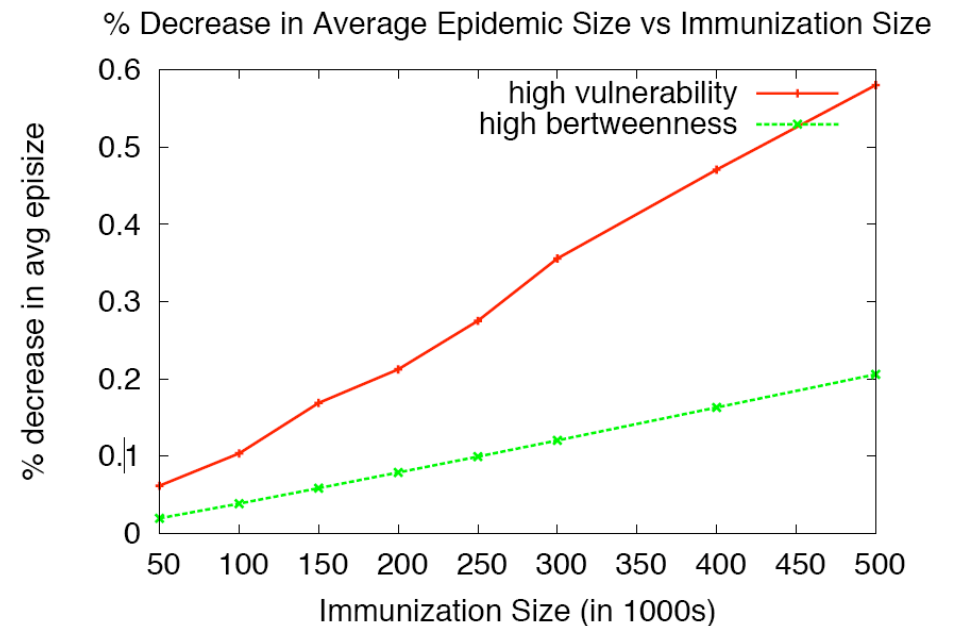
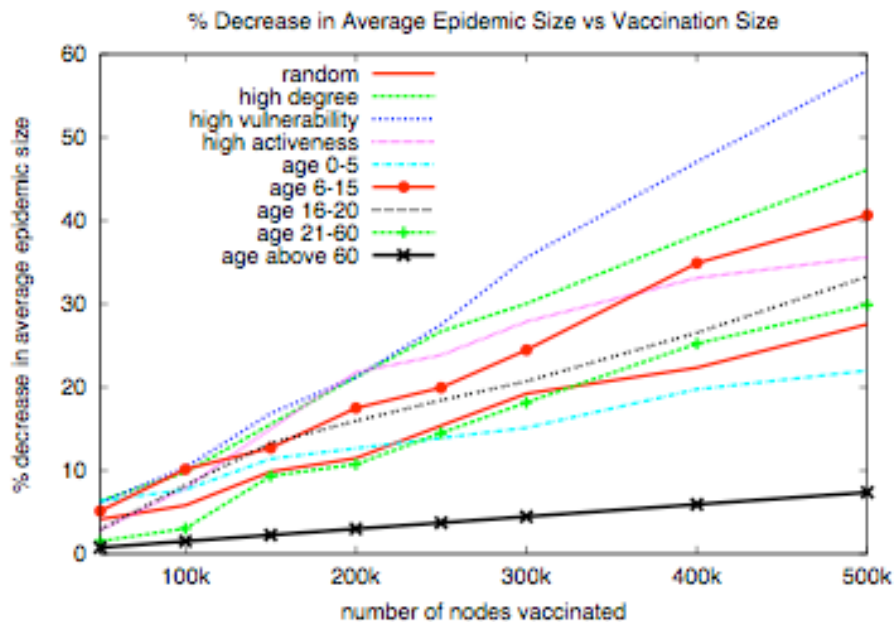
Vulnerability and Criticality of nodes

- $V(i)$ = Vulnerability of a node i = probability of getting infected, if the disease starts at a random node
- Criticality(v): reduction in epidemic size when the node is vaccinated
- $V(i, t)$ = Vulnerability of a node i at time t = probability of getting infected during the first t time steps
- Depends on
 - Initial conditions
 - Transmission probability
 - Network structure - not a first order property



Blue nodes are highly critical but not very vulnerable

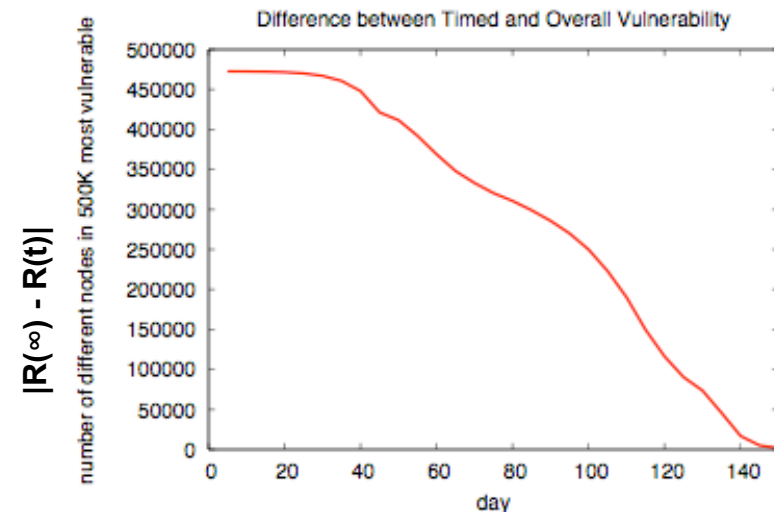
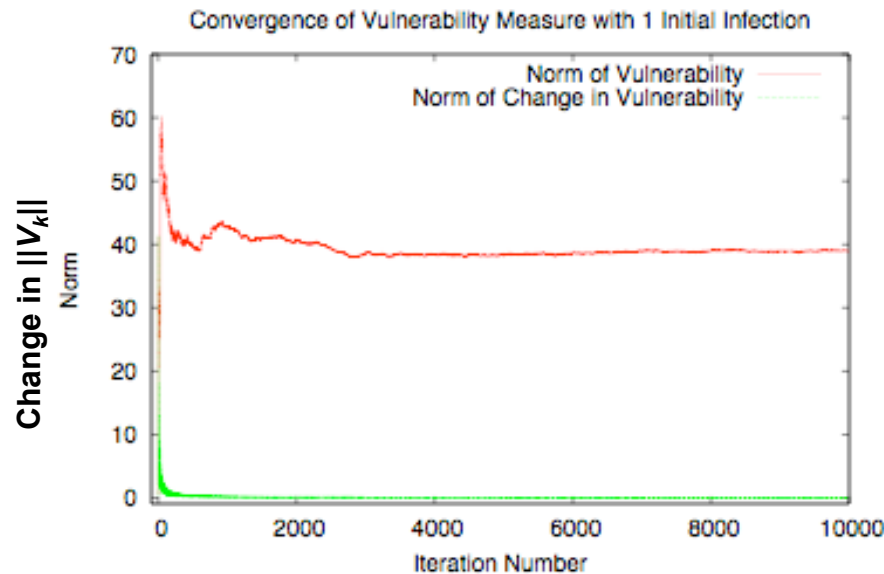
Vaccination based on vulnerability rank order



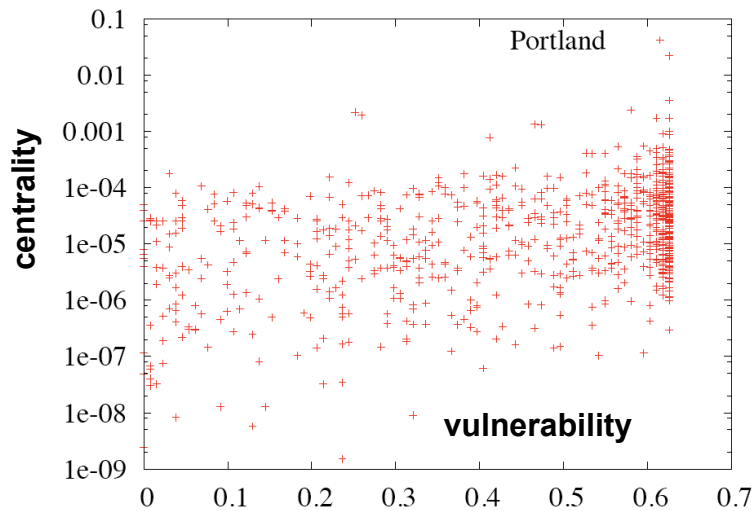
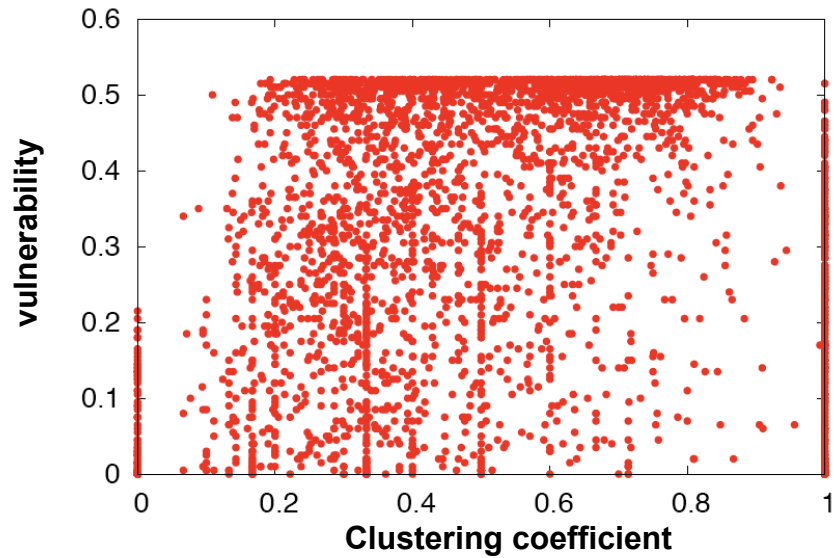
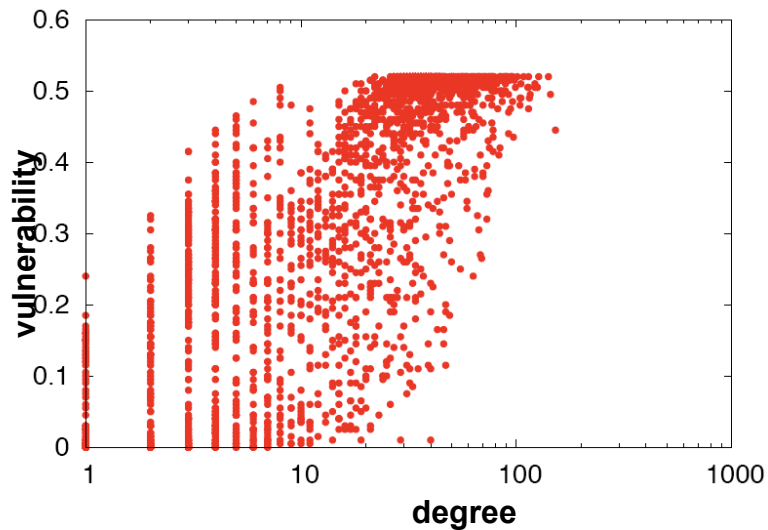
- Contact graph on Chicago, ~ 8 million people
- Highly vulnerable nodes are also most critical for this network

Computing vulnerability

- Monte-carlo samples: each sample by running EpiFast
- $V_k(i)$: probability node i gets infected in k iterations
- $R(\infty)$: top n nodes in vulnerability order, $V(i)$
- $R(t)$: top n nodes in temporal vulnerability order $V(i,t)$

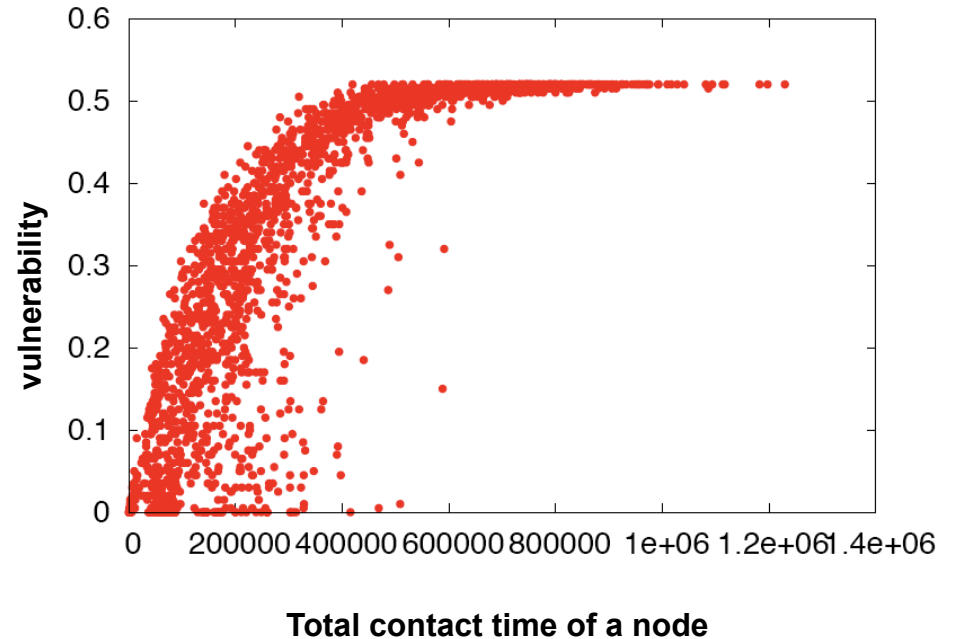
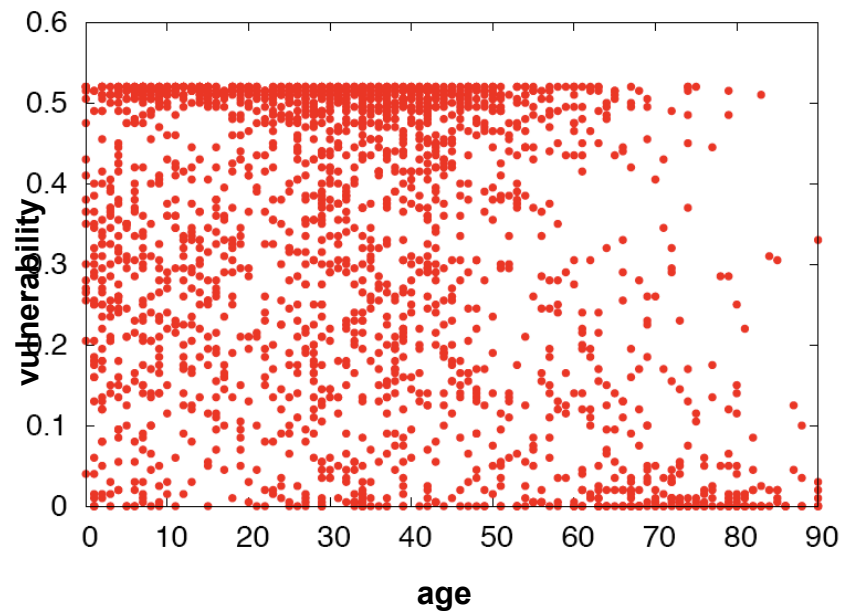


Correlation with static graph measures



Very little information from static graph measures

Correlations with labels



- ❑ Similar correlations at different transmission probabilities
- ❑ Need better models for individual activities and contact duration

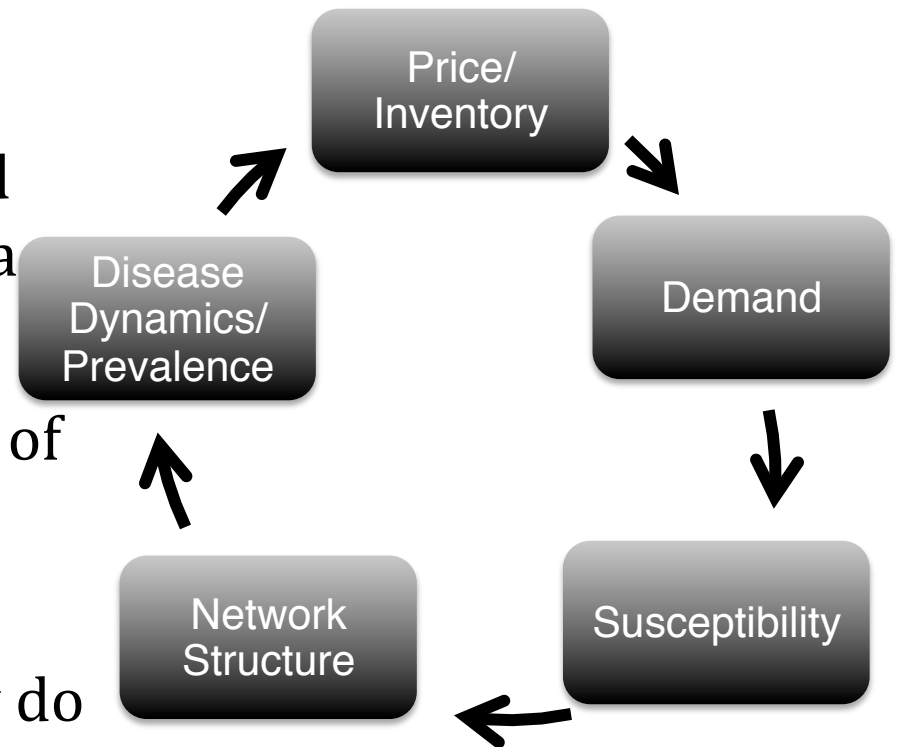
**An illustrative case study: allocating and
distributing A/Vs through public and private
stockpile
(Marathe et al.)**

The problem

Policy Problem: Is there an optimum strategy to partition the scarce AV doses between public stockpile administered through hospitals and private stockpile distributed using a market-mechanism

Measures of Effectiveness: Number of infected, peak infections, cost of recovery, equitable allocation

Additional Scientific Question: How do disease prevalence, individual behavior, network structure, disease dynamics and AV demand co-evolve?



The Setup

- Use Simdemics modeling framework
- All modeling assumptions used in this study are the same as were used for the “MIDAS medkit” study in June 2008
 - Exception 1: Market distribution replaces the pre-assignment of AV kits based on income
 - Exception 2: Self Isolation of households based on prevalence and sick member
 - Exception 3: Disease prevalence used as a mechanism for adaptation
 - Disease model, Reporting, Diagnosis and Distribution Models: Same
- New River Valley population size: 150K
- The total stockpile of AV is 15k (10% of the population size).
- The price of the AV kit can vary between \$50-\$150 (2008 study: 100\$).
- Total household budget for the AV is 1% of the income.
- The private stockpile can be purchased by anyone who can afford it.

Disease Models

- Disease Model:
 - SEIR model is used.
 - Transmissibility (prob. of transmission in every minute of contact between an infectious node and a susceptible node) = $3E-5$
 - Incubation and infectious period durations are chosen from distributions, mean = 1.9 and 4.1 days respectively.
 - A/V Efficacy: Susceptible nodes are 87% less likely to get infected; infectious nodes are 80% less likely to transmit the disease.
 - AV treatment and prophylaxis lasts 10 days.

Reporting, Diagnosing and Distribution of Public Stockpile

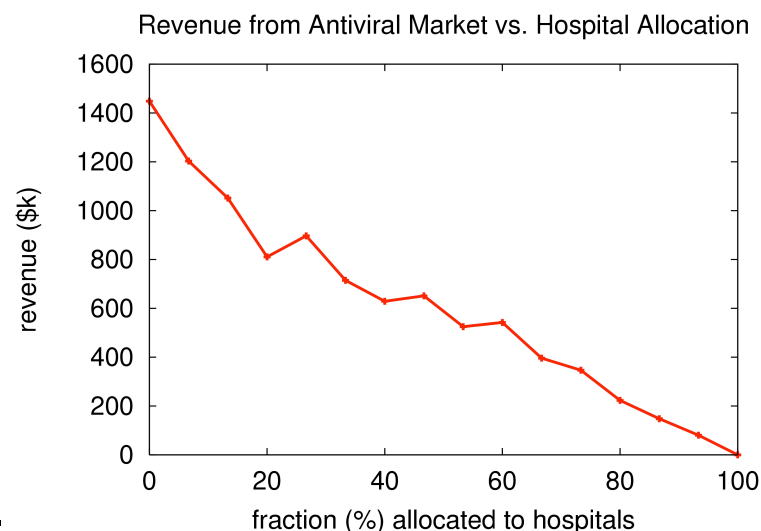
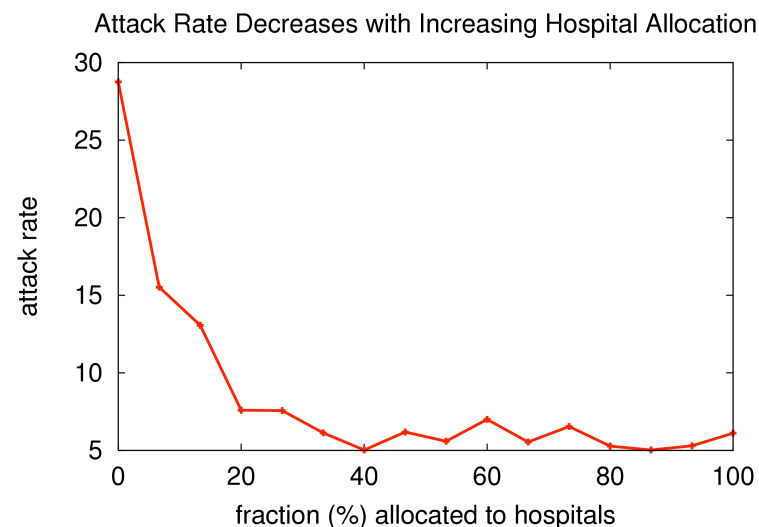
- Reporting and Diagnosis Model:
 - 2/3 of the infectious are symptomatic and report to the hospital.
 - Remaining 1/3 of the infectious are asymptomatic and 47% less likely to transmit.
 - Only 60% of those who report to the hospital get diagnosed.
 - Misdiagnosed: not sick but diagnosed as sick; In every 12 nodes diagnosed as sick 2 are not sick.
- Distribution
 - The hospital stockpile is distributed to only those diagnosed as infected.
 - There is no direct cost to the people for using the hospital stockpile.

Behavioral models

- **[Isolation based on Prevalence :]** Once the prevalence reaches 0.2%, for individuals diagnosed as infected, with compliance rate 40%, the entire household is isolated at home.
- **[Demand based on Prevalence:]** Total AV supply is 15k: allocated between hospitals and market
 - Hospitals: *give* to diagnosed as infected
 - Market: *sells* to households according to demand
- Household demand: $D_{t,h} = \frac{B_{t,h}}{P_t}(1 - e^{-\beta x_t})$
 - Increases with disease prevalence (x_t)
 - Increases with household budget ($B_{t,h}$); decreases with price (P_t)
 - price is linear in remaining supply
 - β reflects risk aversion or prevalence elastic demand to AV.

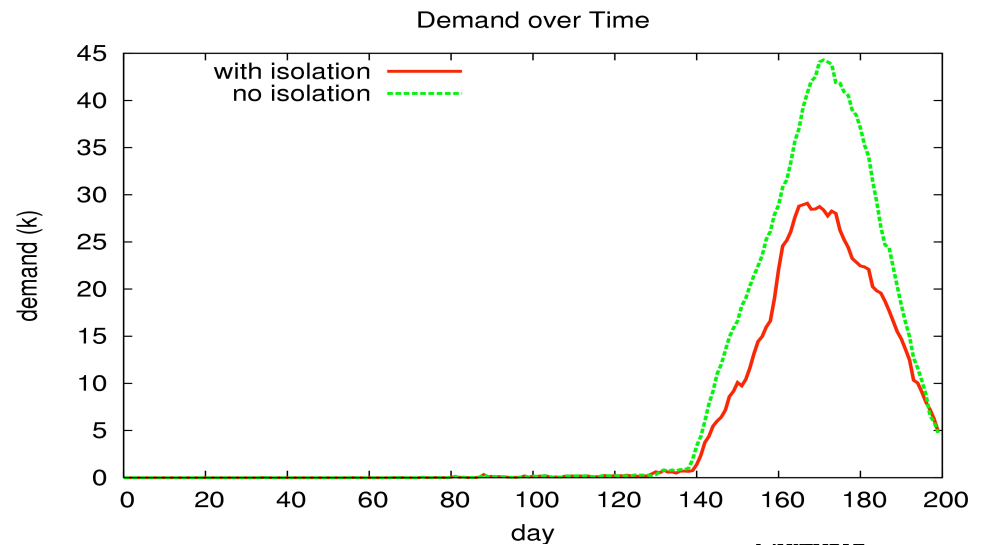
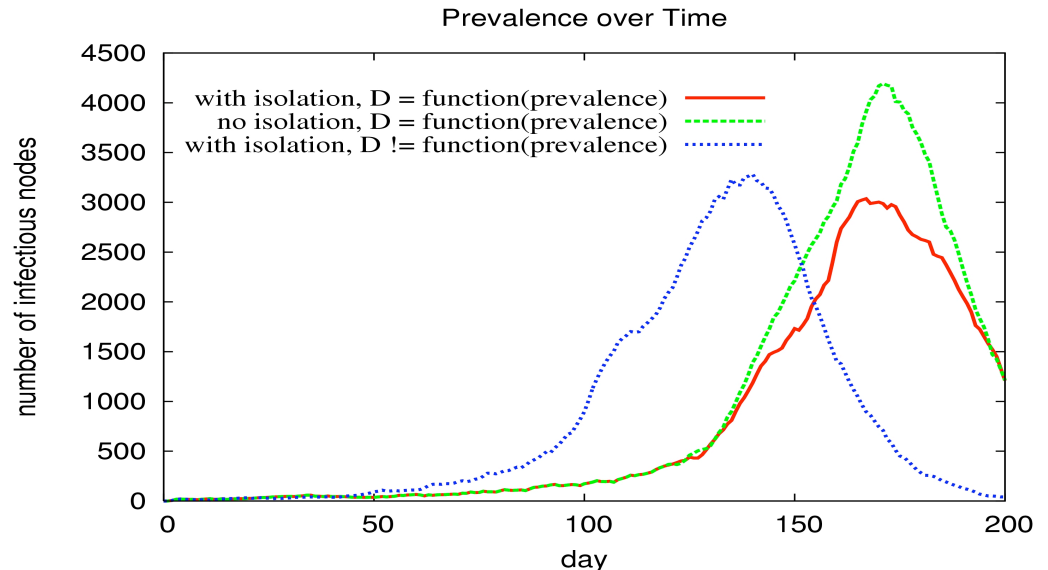
Suggests an optimal allocation strategy

- Suggests optimal allocation strategy of AVs between public and private stockpile
 - Hospitals (public sector) should be given priority
 - If $>$ threshold, the remaining stockpile be distributed via market.
 - Private stockpile useful for individuals who are infectious but not symptomatic
- Optimal split (40% to hospitals, 60% to the market) recovers the cost of antiviral manufacturing if the unit cost is $<$ \$42.



Importance of behavioral modeling

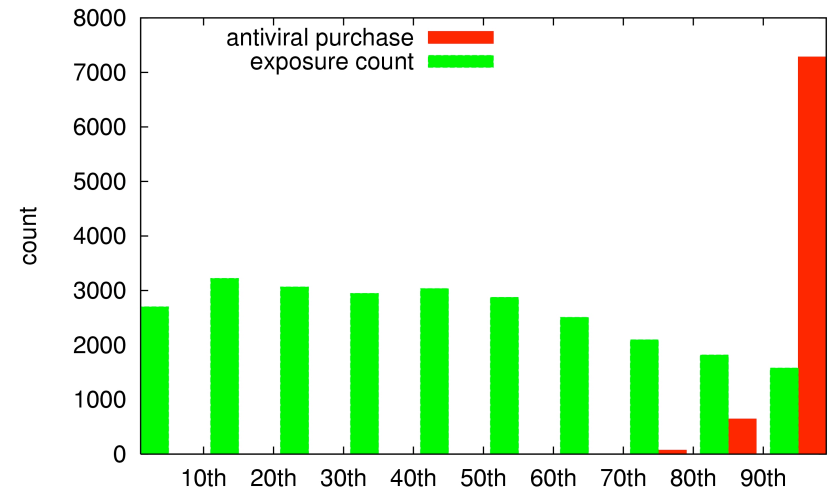
- *Prevalence elastic demand*: Delays the epidemic by about a month
- *Self Isolation triggered by Prevalence and sick member*: reduces the peak of the epidemic and reduces the overall demand



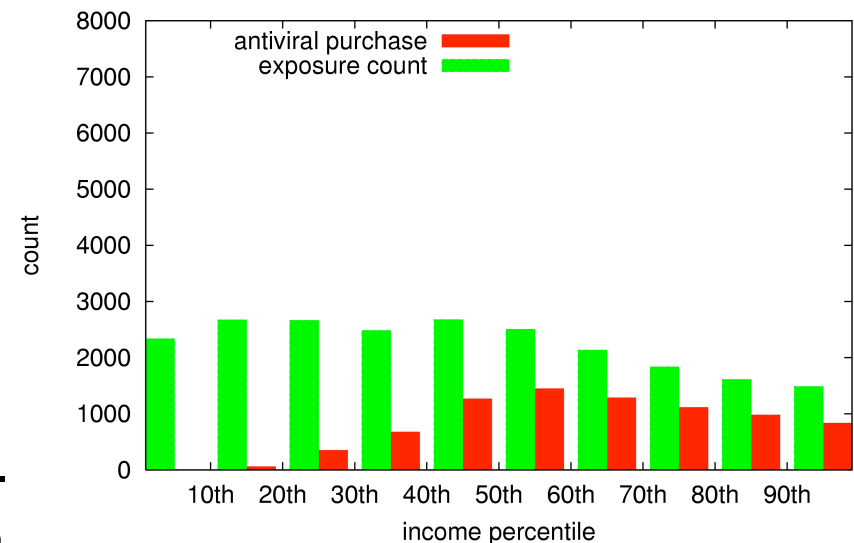
Inequitable allocation & role of government

- Market based distribution is inherently inequitable
 - Prevalence elastic demand creates more inequitable distribution (due to price increase)
- Provides a way for evaluating government subsidy or investment
 - More even distribution possible if price is capped or mechanisms are provided for reimbursing
 - The price range determines the investment needed by the government

Antiviral Purchase and Infection by Income Level
(demand depends on prevalence)



Antiviral Purchase and Infection by Income Level
(demand does not depend on prevalence)



A game theoretic view: AV purchase game

- Players: households
- Strategies: {buy antiviral, not to buy}
- Payoff: F (AV cost, expected number of infected household members)
- Information: AV supply (split between hospital and market stockpile) and price, disease prevalence, household budget.

Strategy	Payment	Infection count
buy	\$605.98	0.0769
not to buy	\$0	0.1692

DIDACTIC: HPC Services Based Epidemiological Planning Environment

Analyst can focus on delivering results rather than becoming a computing expert

Simple User Interface to Set up Experiments

Highly resolved parameters

Experiments Analyses Triggers User Manual Feedback About

bryan Logout

Name **i** Demo_Vax_SDS_50 Description: Vax = 0, 25,50 SDS=50 SDG=none Replicates **i** 25

Status **i** completed Total Cells **i** 3

Owner **i** sample Simulated Days **i** 200

Region **i** Alabama View

Disease Model **i** Catastrophic flu View

Initial Conditions **i** Saday View

Enabled Interventions **i** Vaccinate Antiviral Social Distance Close Work Close School

Vaccinate Antiviral Social Distance Close Work **Close School**

Close Schools **i**

Subpopulation **i**

- all
- preschool
- school-age
- adult
- senior
- Tier 1
- Tier 2
- Tier 3
- Critical Workers

View

Compliance **i**

% Value **i** 50

Sweep

Initial % Value **i**

Final % Value **i**

Increment **i**

Trigger **i**

0.5 percent

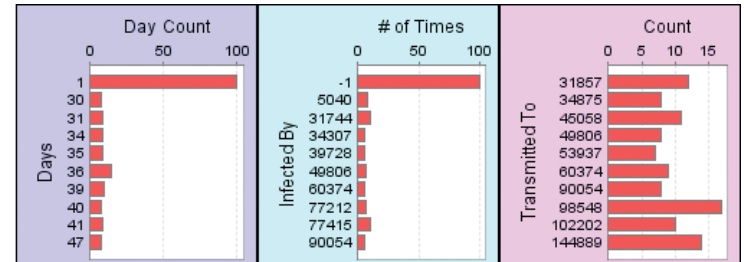
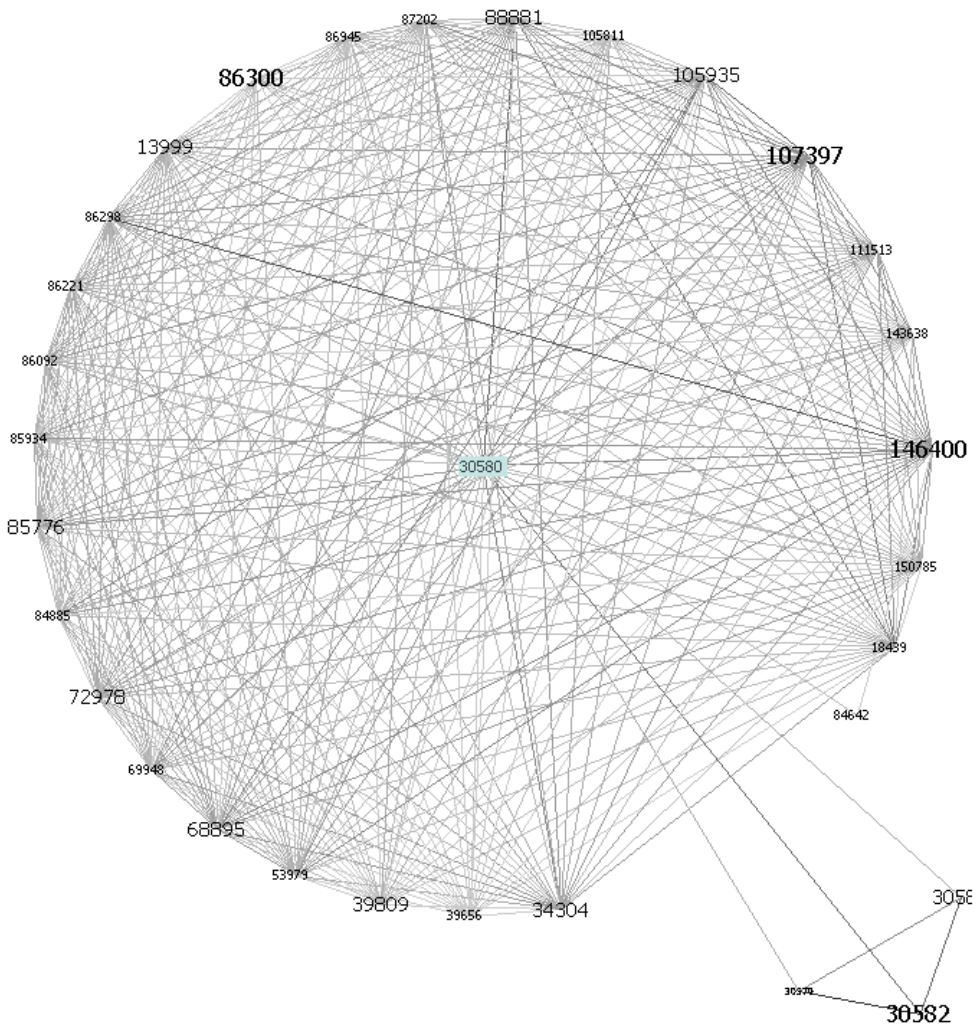
Sweep

Edit Triggers

Done Save Discard Unsaved Changes Show Cells

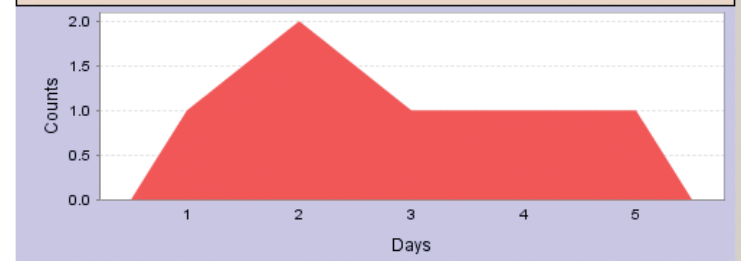
- Population
- Disease
- Initial conditions
- Interventions
 - Type
 - Efficacy
 - Compliance
 - Timing
 - Subpopulation

Visual Analytics Support



To clear the list of Ids above click here: [Clear List](#)

Select Epidemic Id:



Conclusions

- Start towards an integrated HPC-based policy informatics environment to support computational epidemiology that goes beyond simply agent-based disease modeling
 - Easy to use by SMEs, highly scalable and resolved
 - High performance computing grids & web-based services
 - Deployed and used successfully (e.g. during recent H1N1 response)
 - Flexible, realistic and efficient representation of individual behavior and public policy
- Presented a realistic case study to understand public health and economic consequences of AV allocations via public and market mechanisms
 - suggests a split between public and market-based stockpile that is optimal (in terms of the peak, time to peak and cost)
 - Individual behaviors play a crucial role – prevalence elastic demand and isolation is the key.

Summary: 3 take home points

- **Point 1:** Seamless access to powerful computational models for use by subject matter experts (SMEs) is *desirable and possible*.
 - Computing and modeling advances
 - Diversity of interests amongst various stakeholders
 - Yet a desire and need to share information and data during crisis: Social Computing
 - Leads to a qualitative change in the way public policies are supported
- **Point 2:** Models and data sources are increasingly complex and diverse: *Synthetic Information systems* provide a natural and scalable way for model composition and analysis
 - Unified view of models and data
 - Use of context based modeling and reasoning
 - Interactive simulations
- **Point 3:** In realistic situations, individual behavior, social networks, public policy & disease dynamics co-evolve
 - Representing multiple behavioral models & multiple network (MTML) *is now possible*: expressive, easy to use and computationally efficient