The Structure of Social Contact Graphs and their impact on Epidemics

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Understanding disease dynamics: key questions

- New outbreak
  - Characteristics of total outbreak size and peak
  - Will it become an epidemic?
- Who is likely to get infected?
- Design effective interventions to detect and control epidemics

Effect of graph structure

- Graph structure matters!
  - Disease dynamics depend on properties of graph structure
- Common *local* measures (e.g., degree, clustering distributions) or *global* but *static* measures (e.g., centrality) not very effective
  - Graphs with same properties w.r.t. these measures but varying disease dynamics
  - Individual epidemic characteristics not captured by these measures
- Main challenges
  - Lack of good social contact network models at large scale
  - Computational issues: efficient simulations

This talk

- *Vulnerability* measure for characterizing disease dynamics
  - Form of stochastic centrality
  - Better insights about disease spread
- Computationally difficult
  - efficient sequential and parallel methods to compute it on large social contact graphs
- No correlations with *static* graph measures

- Applications:
  - Effective strategy for vaccination: use high vulnerability nodes
  - Understanding likelihood of an epidemic

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- Synthetic social contact graphs
- SIR model for epidemics
- Vulnerability: definition and basic properties
- Fast algorithms for disease simulation and computing vulnerability
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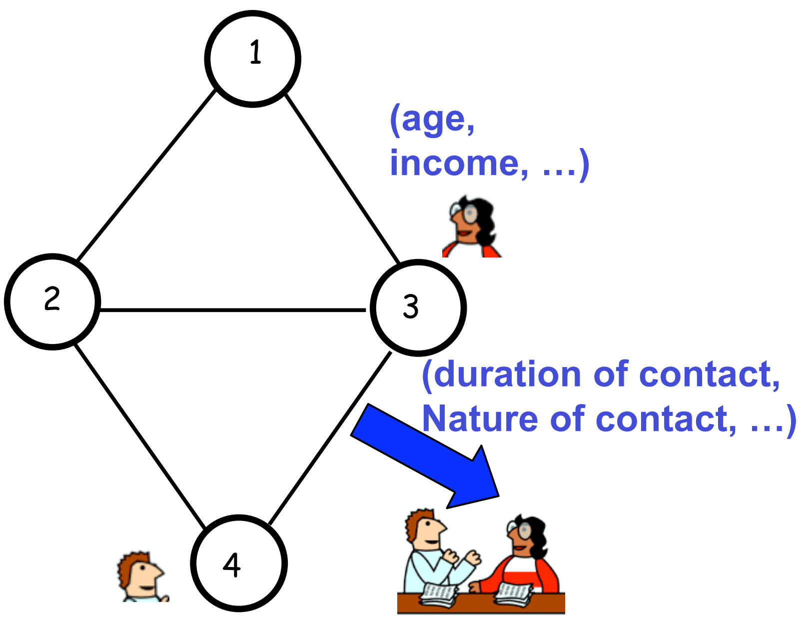
Focus: social contact graphs



- Difficult to construct real contact graphs
  - Privacy/security issues
  - Dynamic networks
  - Data sets for small populations, e.g., [Meyers et al., 2006]

- Our focus: synthetic social contact graphs
  - Constructed by integrating a number of public and commercial data sets
  - Statistically similar to realistic contact networks
  - significantly different from other complex networks

Synthetic Contact Graphs

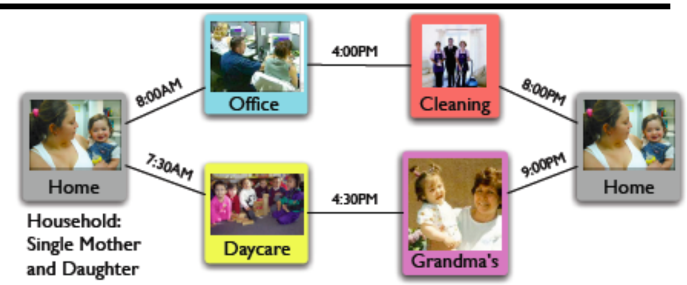
Census

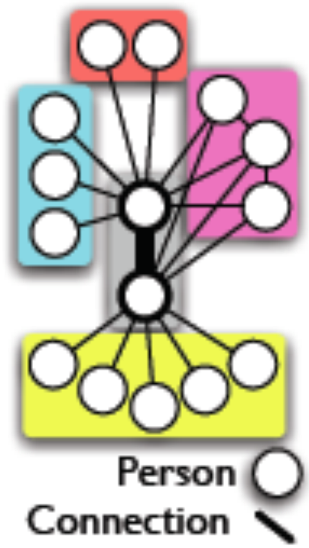
Road Network

Activity surveys

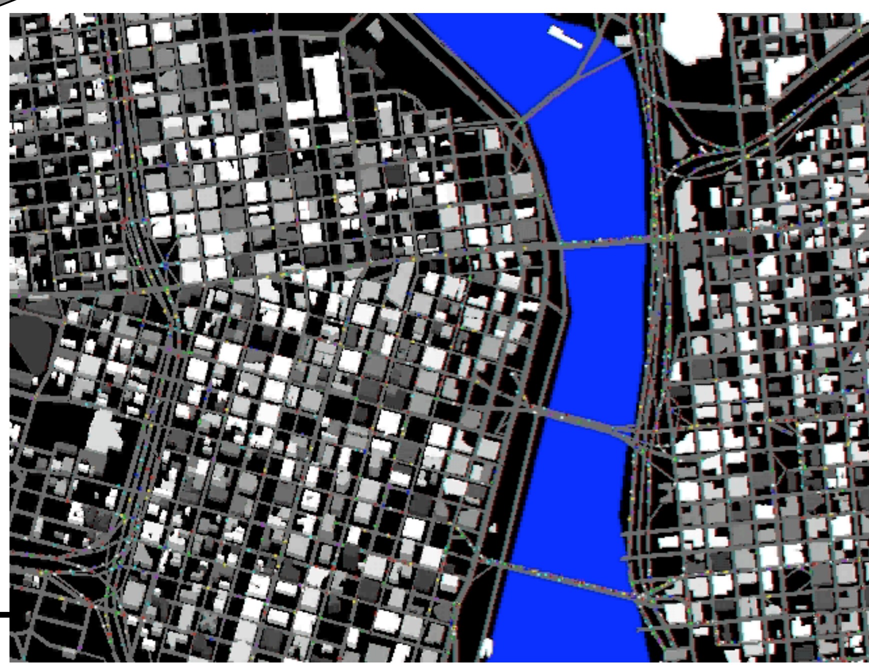
Urban Mobility Model

Synthetic social Contact graphs



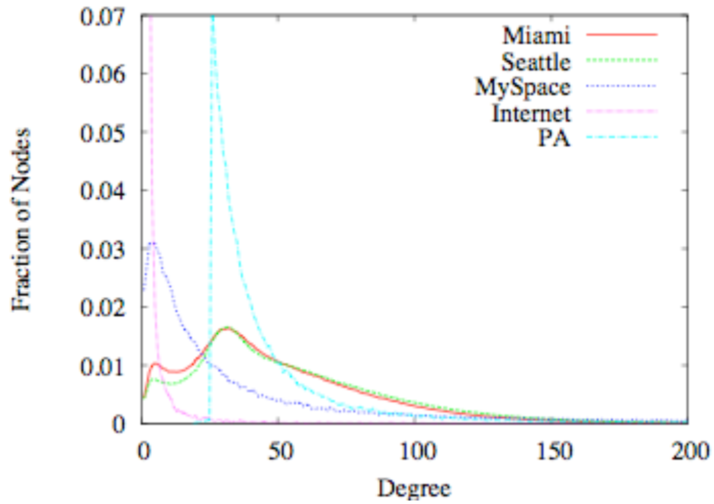


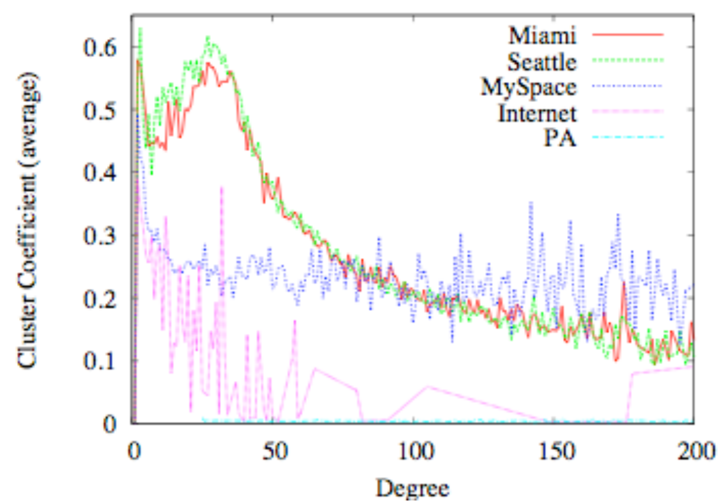
More than 12 public and commercial data sets

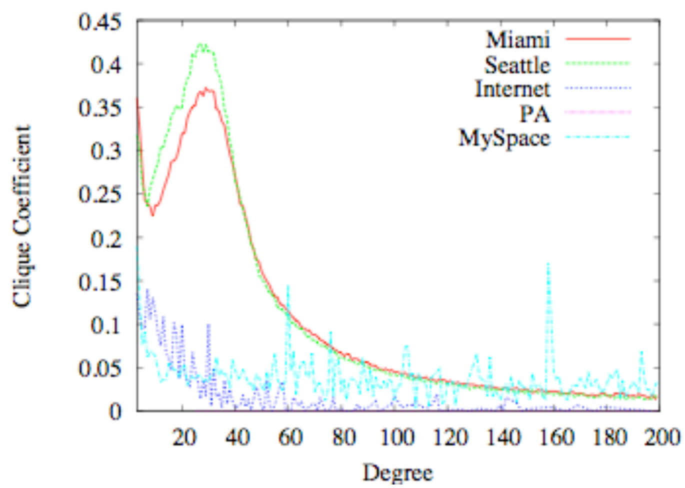


Data sets, documentation at:
ndssl.vbi.vt.edu

Some structural properties of these graphs

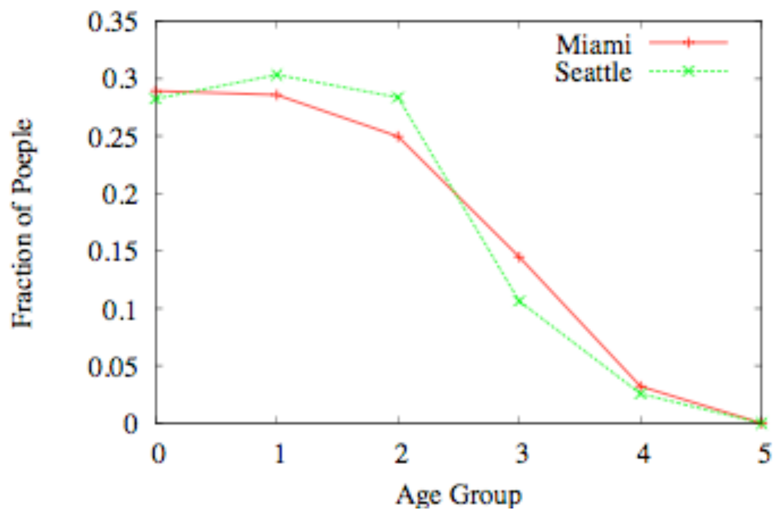


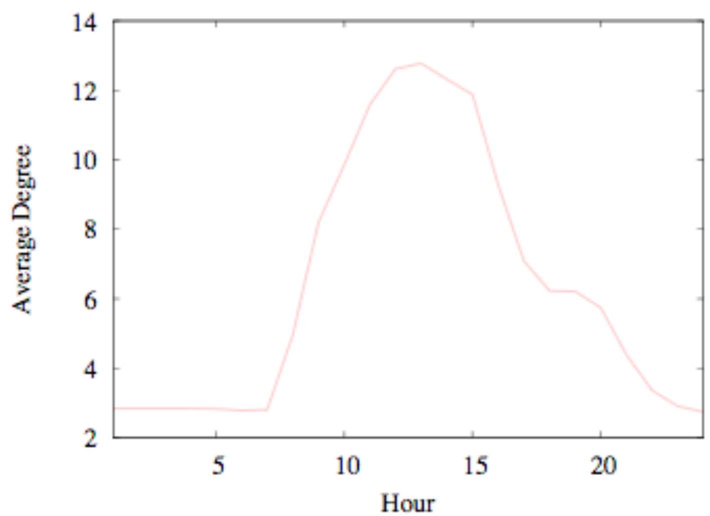




- Different from other complex networks
- Clique coefficient

Labeled graph properties

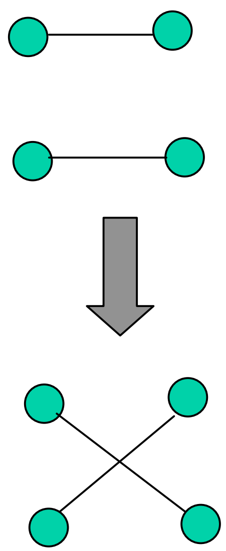




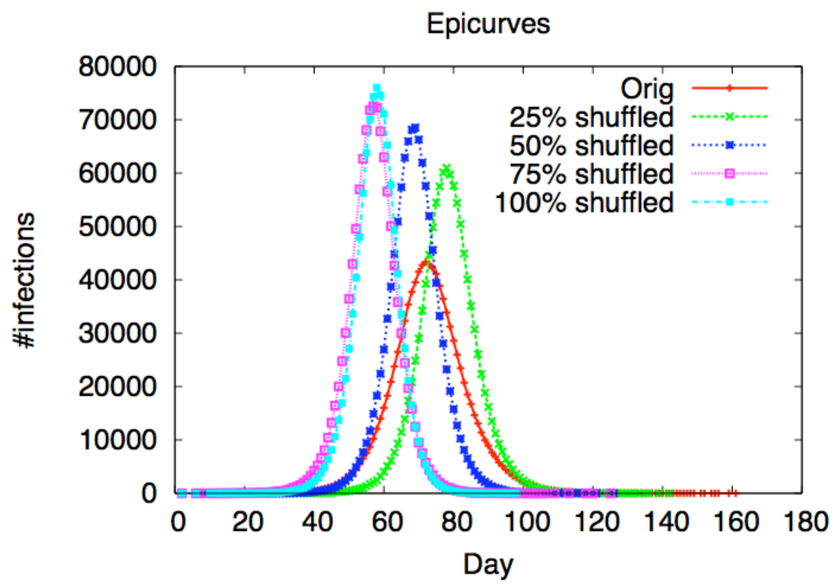
- ❑ Rich node and edge labeled structure
- ❑ Significant variation in individual properties with node/edge labels

Beyond degree distributions

Edge flip chain



Preserves degree distribution



Edge flips change disease dynamics

Outline

- Synthetic social contact graphs
- SIR model for epidemics
- Vulnerability: definition and basic properties
- Fast algorithms for disease simulation and computing vulnerability
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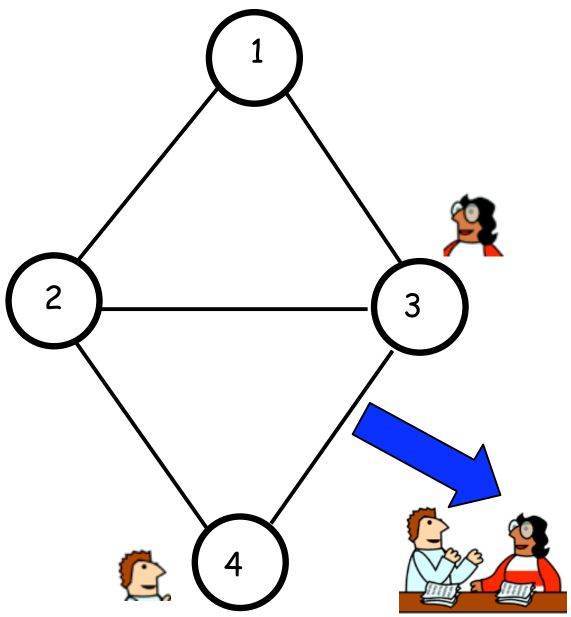
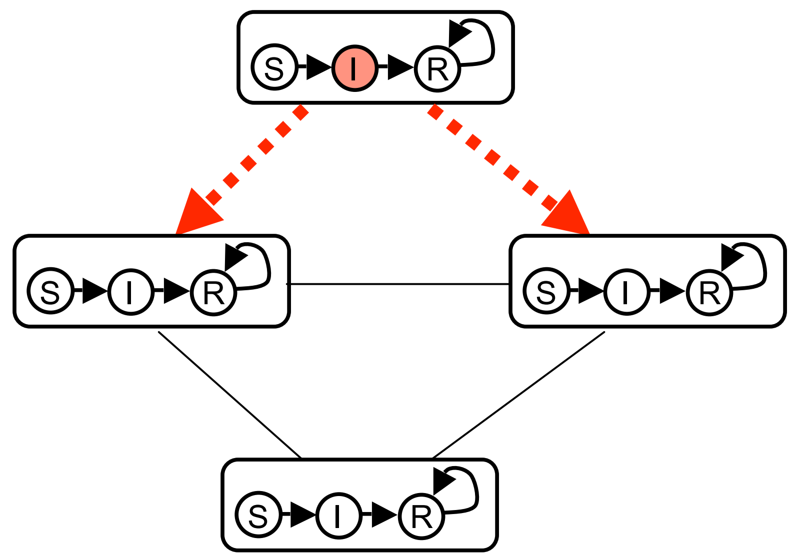
Epidemics on networks

Nodes: people
Properties: demographics, immunity

Edges: contacts between people
Properties: duration, nature of
contact

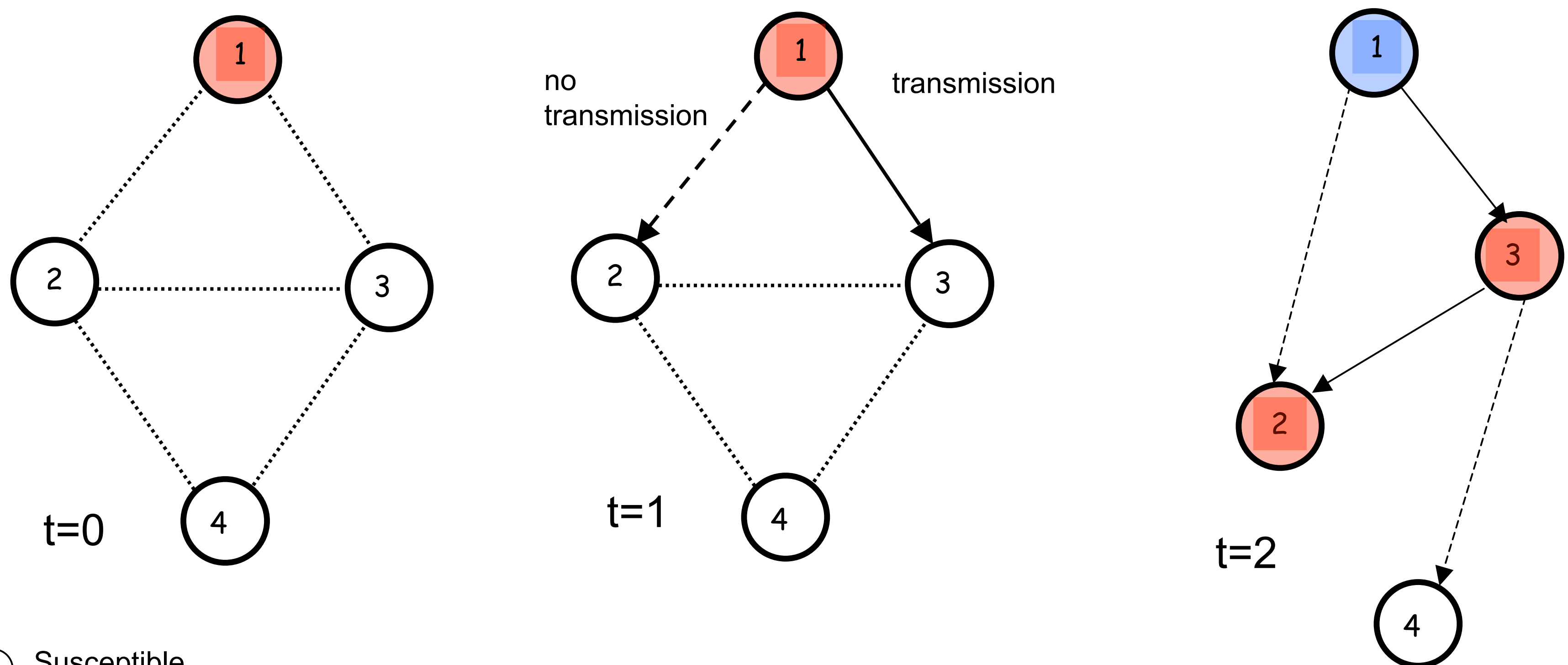


<u>Communicating FSM model</u>
Transmission probabilities depend on states of neighbors



p(u,v): transmission prob. on edge (u,v)

Example: SIR process on a network



Susceptible

Infected

Recovered

transmission

No transmission

Probability =
p(1,3)(1-p(1,2))

Probability =
(1-p(1,2))p(3,2)(1-p(3,4))

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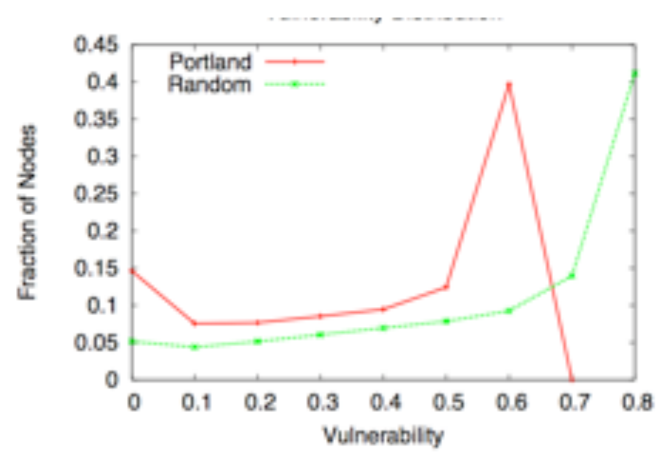
The *Vulnerability* measure

V(i) = Vulnerability of a node *i* = probability of getting infected, if the disease starts at a random node



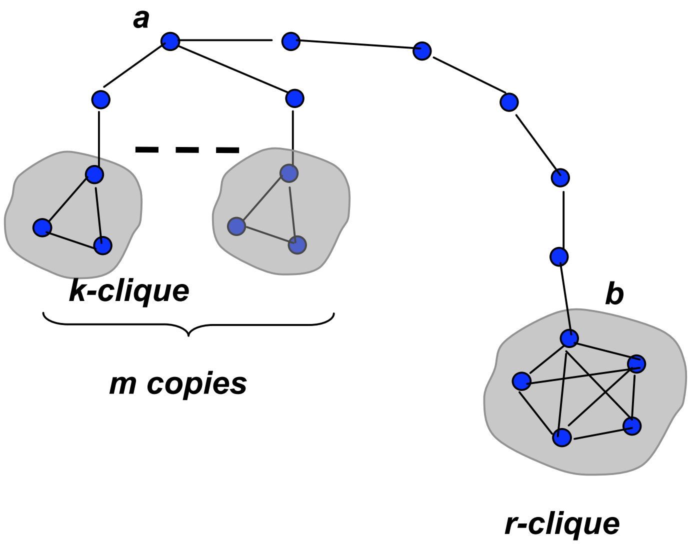
Depends on

- Initial conditions
- Transmission probability
- Network structure - not a first order property

Temporal version: probability of infection in specific duration

V(i, t) = Vulnerability of a node *i* at time *t*= probability of getting infected during the first *t* time steps

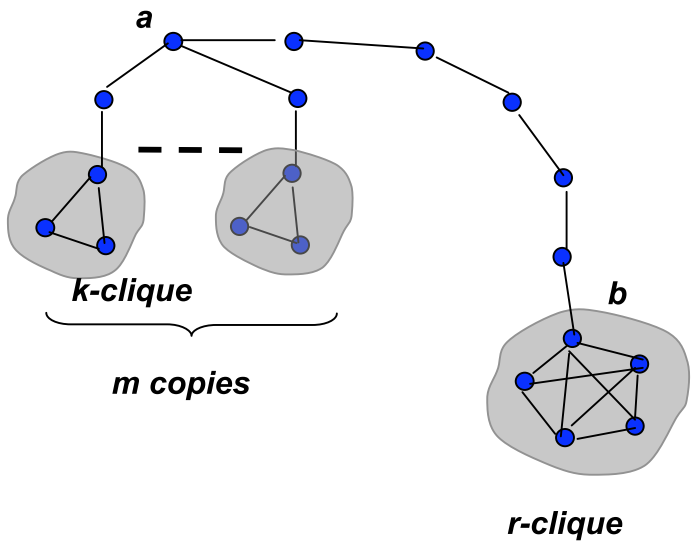
Vulnerability based rank order: Dependence on transmission probability



Ordering can change in specific graphs

- *small p*: *V(a)<V(b)*
- *large p*: *V(a)>V(b)*

Vulnerability based rank order: Dependence on transmission probability



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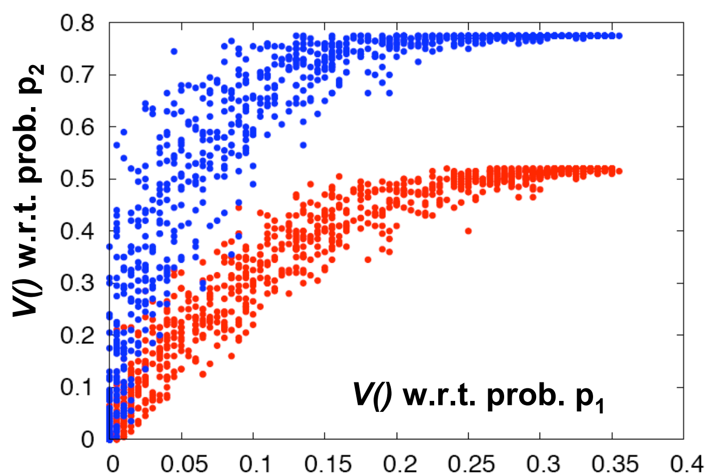
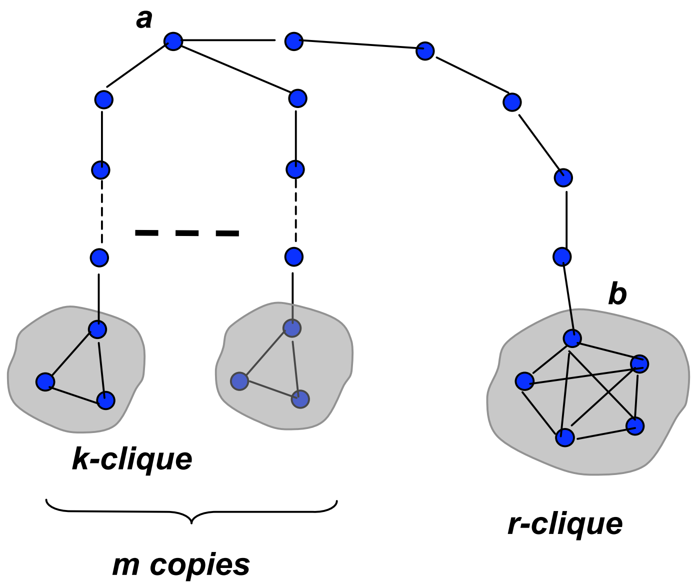


Ordering relatively stable in Portland social contact network for different transmission probabilities

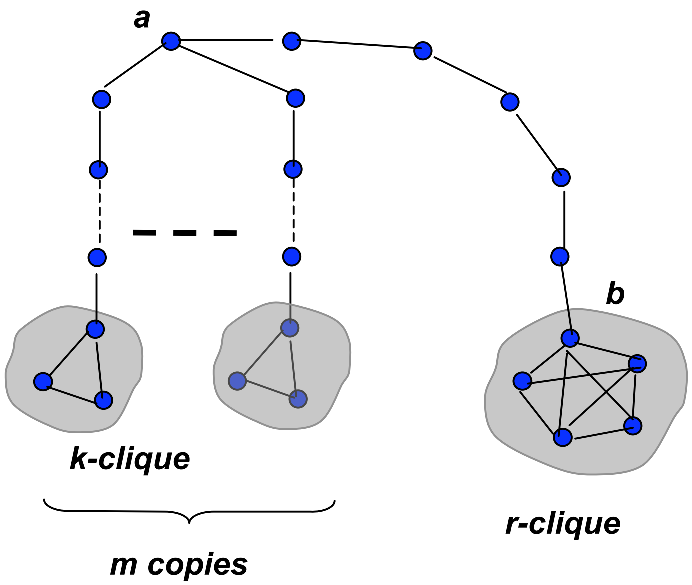
Vulnerability based rank order: Dependence on initial conditions



Low transmission probability

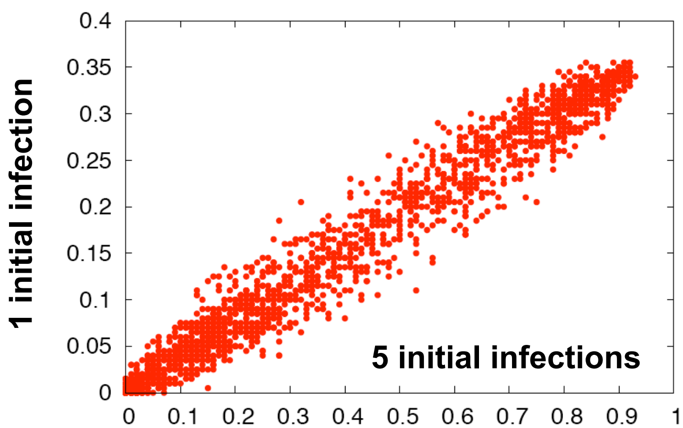
- *few initial infections*: *V(a)<V(b)*
- *many initial infections*: *V(a)>V(b)*

Vulnerability based rank order: Dependence on initial conditions



Low transmission probability

- *few initial infections*: *V(a)<V(b)*
- *many initial infections*: *V(a)>V(b)*



Ordering relatively stable in Portland contact graph with different initial infections

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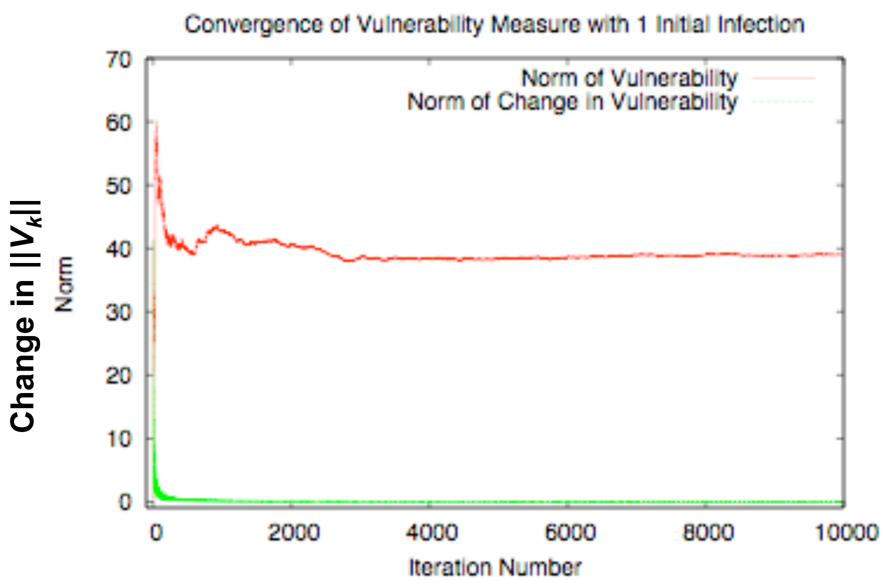
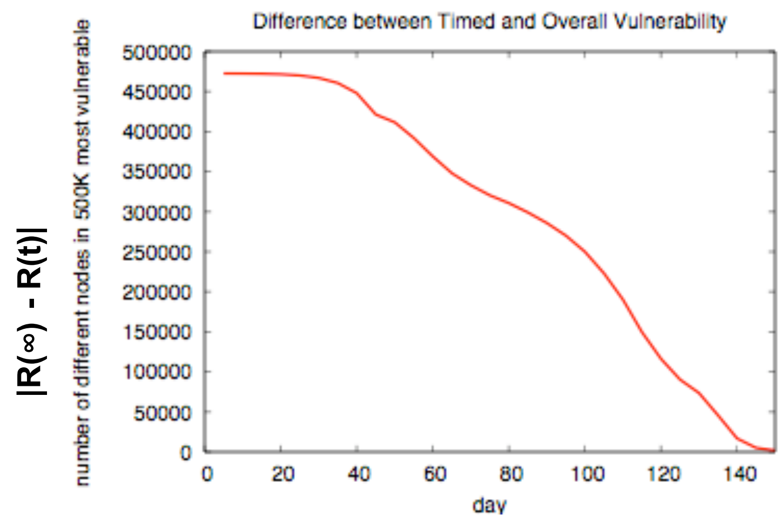
Computing vulnerability

- Monte-carlo samples: each sample by an epidemic simulation tool
- $V_k(i)$: 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 $V(i,t)$





EpiFast: sequential version

Graph *G* and disease model → Choose random length *l(e)* of each edge e of *G* → Compute distances from *s* in w.r.t. length function *l()* → One random run of simulation

random length for edge e=(u,v):

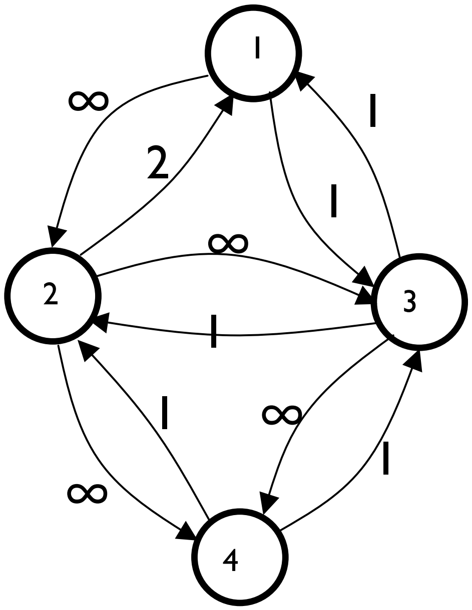
p(e)= transmission prob. on edge e
S(u) = infectious duration of node *u*

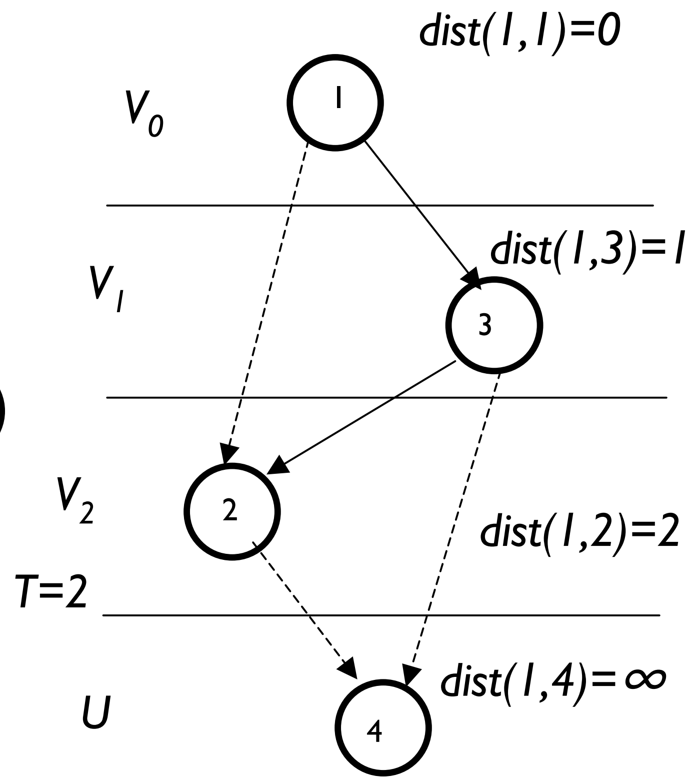
$$\ell(e) = \begin{cases} i \in \{1, \ldots, S(u)\}, & \text{with probability } (1-p(e))^{i-1}p(e); \\ \infty, & \text{with probability } (1-p(e))^{S(u)}. \end{cases}$$

$$V_t = \{v : dist_\ell(s, v) = t\}$$

$$I = \{e = (u, v) : \ell(e) = dist_\ell(s, v) - dist_\ell(s, u)\}$$

Example





dist(1,3)-dist(1,1)=1
dist(1,2)-dist(1,3)=1

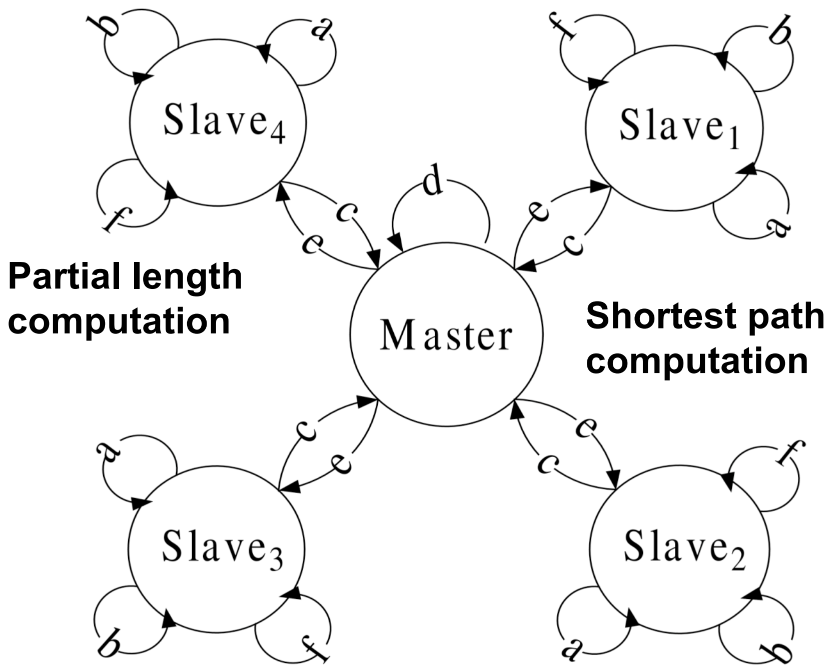
$I = \{(1,3), (3,2)\}$

Produce output
$R = ((V_0, V_1, V_2, U), I)$

$P_S[R] = p^2 (1-p)^6$

Theorem EpiFast produces each possible random disease trajectory *R* with the same probability.

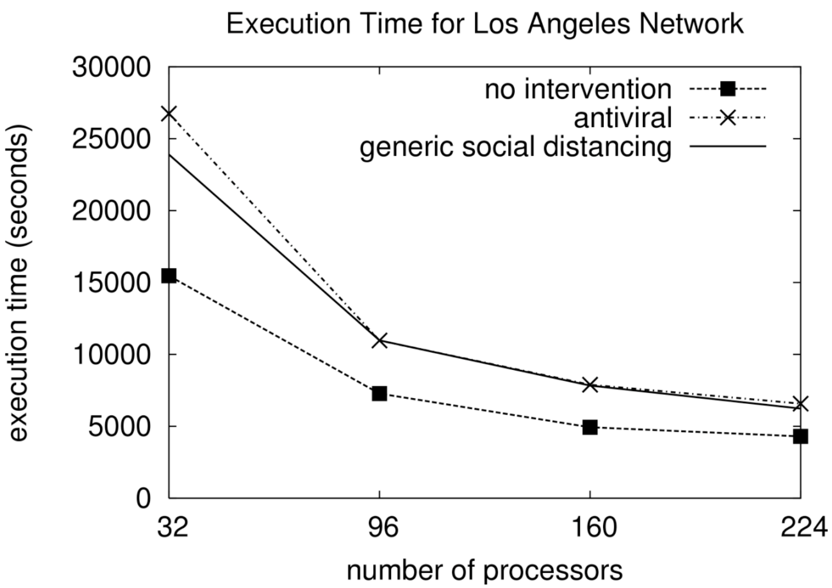
EpiFast: parallel version

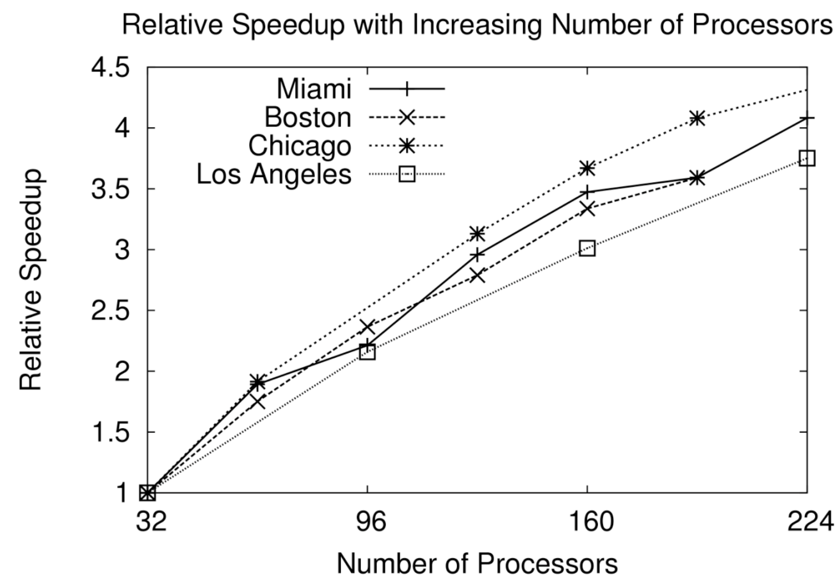


- C++/MPI implementation, tested on commodity clusters and SGI Altix systems.
- Los Angeles population: 16 million people.
  - 180 days of epidemic duration.
  - With and without interventions.
  - 25 replicates for each configuration.
  - Each replicate takes < 15 minutes.

[C. Barrett, K. Bisset, J. Chen, X. Feng, A. Vullikanti, M. Marathe, ICS, 2009]

EpiFast: scaling





Population	Population Size	CPU Number	Running Time (seconds) per simulation day
Miami	2.09	32	0.47
Boston	4.15	64	0.54
Chicago	9.05	128	0.54

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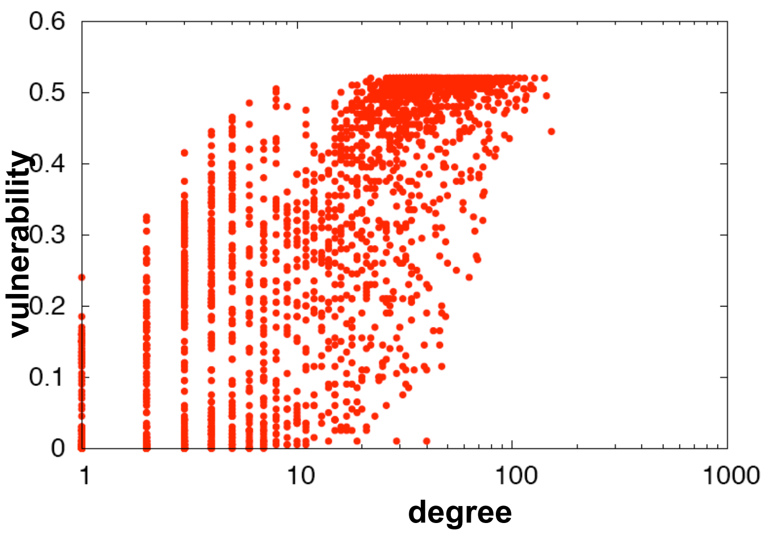
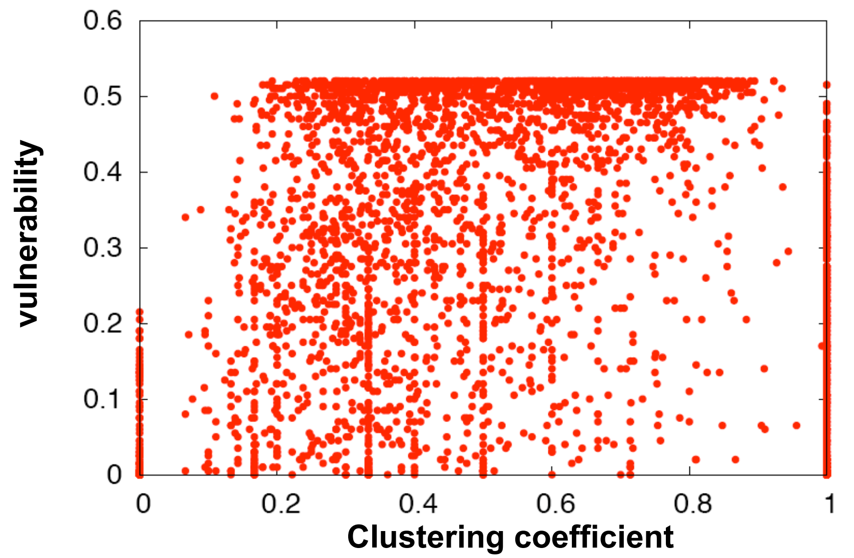
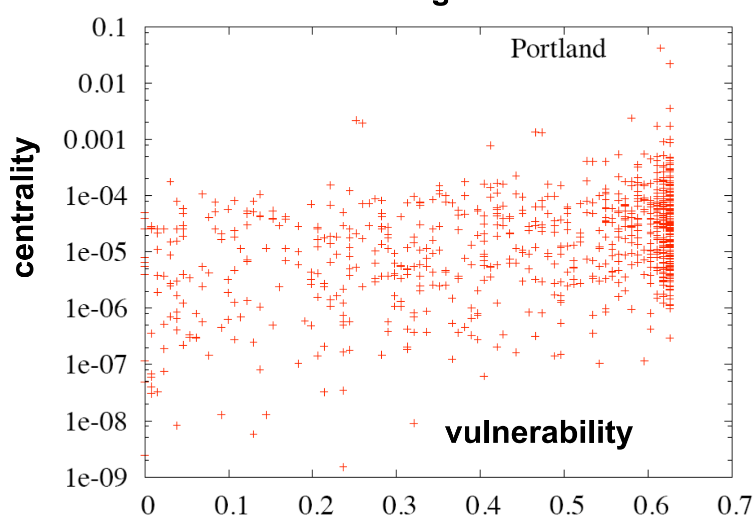
Correlation with static graph measures

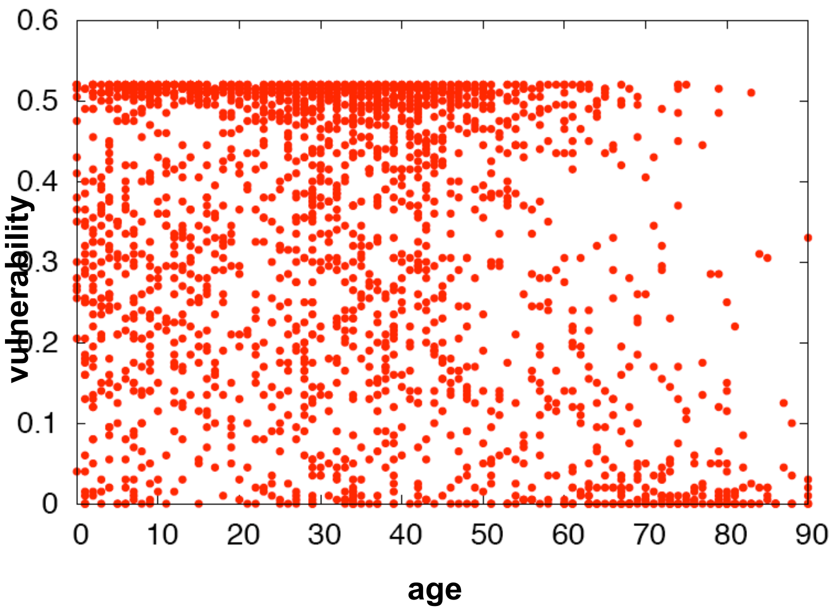


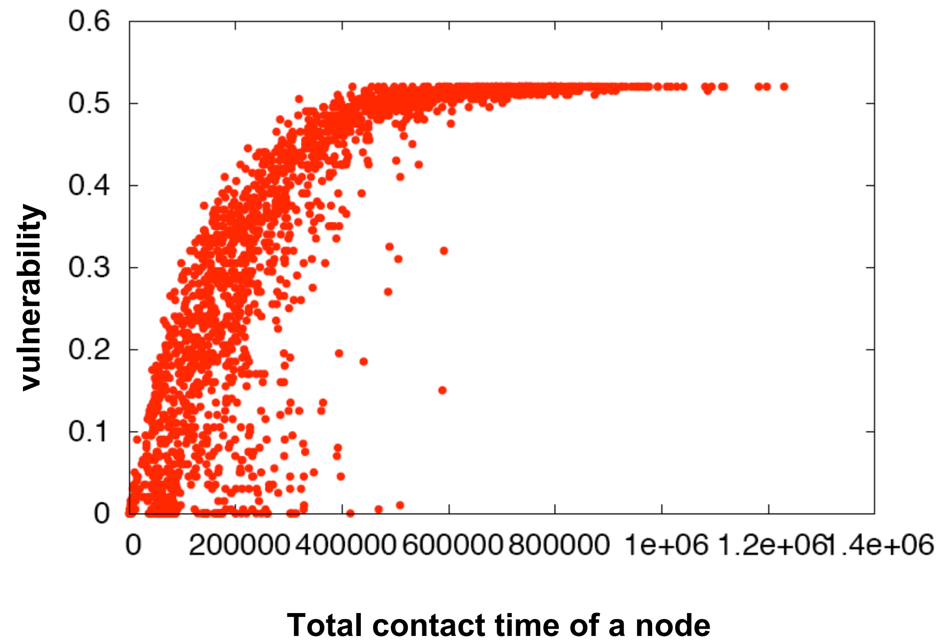




Very little information from static graph measures

Correlations with labels





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

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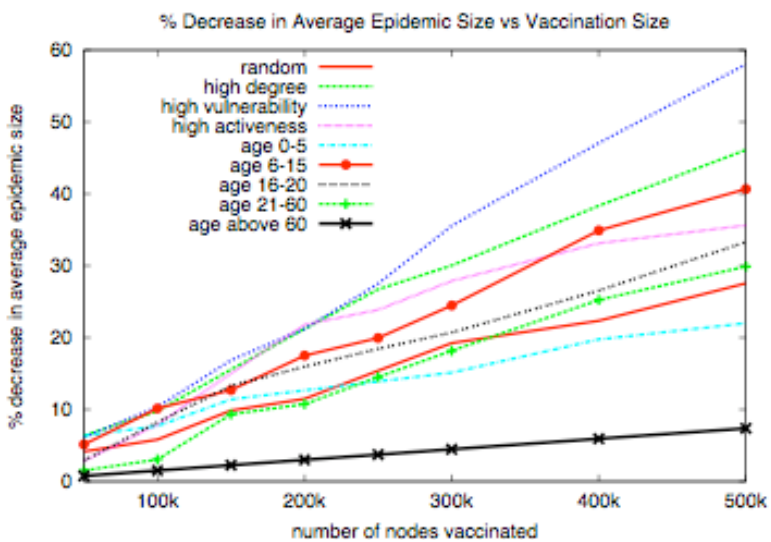
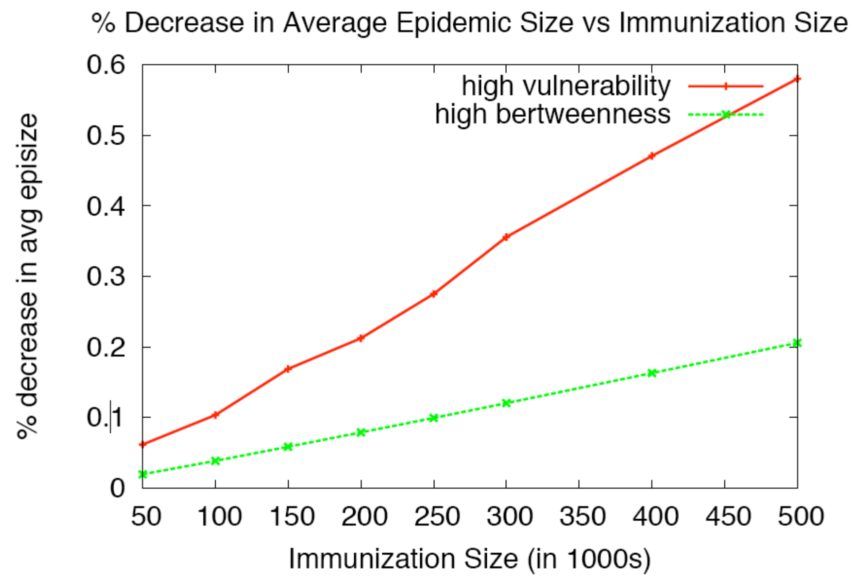
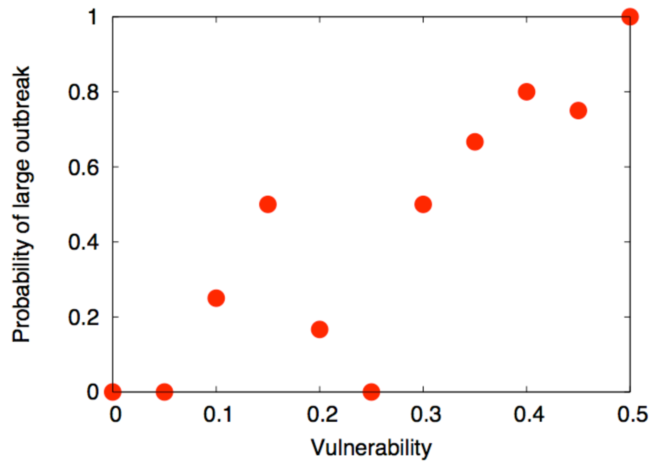
Application: Vaccination based on vulnerability rank order

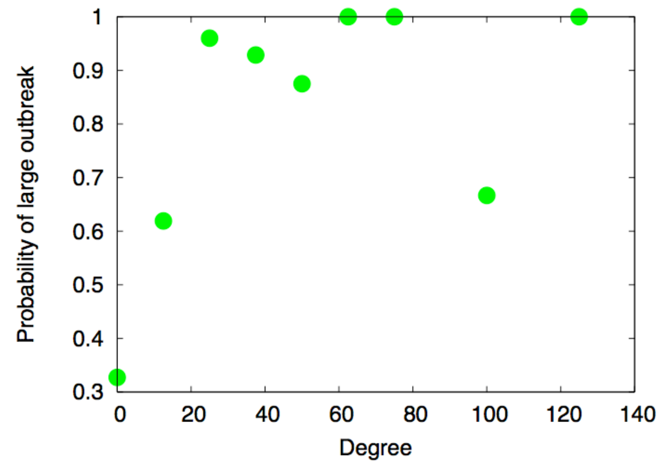


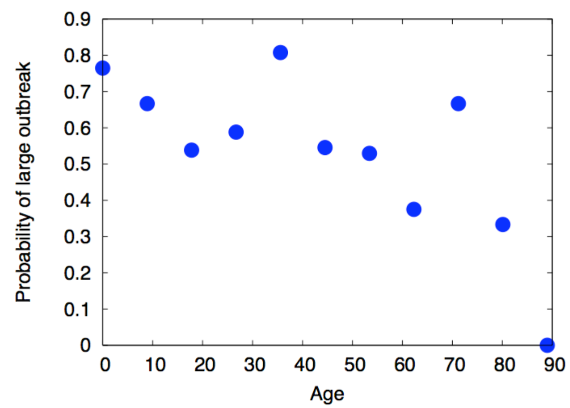


- Contact graph on Chicago, ~ 8 million people
- Highly vulnerable nodes are also most critical for this network

Application: which outbreaks take off?







Epidemic starting at higher vulnerability node is more likely to result in an outbreak

Conclusions

- Vulnerability measure
  - Useful for understanding disease propagation
  - Not first order properties
  - Not well correlated with other “standard” graph measures
  - Computationally intensive: efficient sequential and parallel algorithms
  - Need for good graph modeling