

Modeling a Within-School Contact Network to Understand Influenza Transmission

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http://arxiv.org/PS_cache/arxiv/pdf/1109/1109.0262v2.pdf

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- Many influenza simulation models assume random mixing within mixing groups.
 - ▶ Within school
 - ▶ Within grade
- Schools are known to be a primary mechanism for influenza spread.

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We create a detailed contact network model based on friendship and contact data and perform simulations to answer these questions.

The National Longitudinal Study of Adolescent Health (Add Health)

- Representative sample of 80 high schools and 52 feeder schools in U.S. during 1994-95 school year
- We analyze data from one high school+feeder school combination.
- Students were given a school roster and identified up to 5 best male friends and 5 best female friends.
- We assume two students are friends if an un-reciprocated or reciprocated nomination occurred.
- We treat the friendship network data as complete (n=1074).

<http://www.cpc.unc.edu/projects/addhealth>
Carolina Population Center, University of North Carolina

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 - ▶ Students are more likely to contact their friends.
 - ▶ Students make longer social contacts with their friends.

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We supplement the Add Health data with a survey of contact behavior in schools to create a model capturing these two tendencies.

Social Contact Survey Data

A Survey on Epidemics in High Schools

- Survey administered in two Virginia high schools (2009)
 - ▶ 200 of 400 students surveyed
 - ▶ 120 of 1,000 students surveyed
- By a “contact,” we mean being in close proximity for more than roughly five minutes.
 - ▶ Average number of contacts during each break between classes
 - ▶ Average number of contacts during lunch break
 - ▶ Percentage of contacts during school hours to friends

Huadong Xia, Jiangzhuo Chen, Madhav V. Marathe and Henning S. Mortveit, (2010). *Synthesis & Embedding of Subnetworks for Individual-based Epidemic Models*. NDSSL Technical Report 10-139.

Modeling the contact network

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- Assume 7 classes (40 mins), 1 lunch break (50 mins), and 5 non-lunch breaks of 10 minutes each.
- The maximum number of contacts between any pair is 38.

Modeling the contact network

- 1 Model the friendship network with an exponential family random graph model (ERGM).

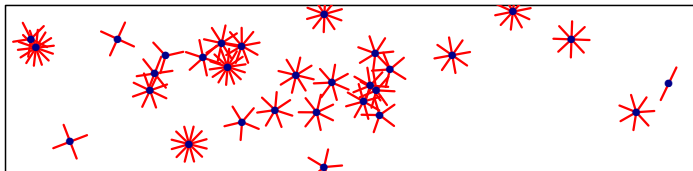
Modeling the contact network

- 1 Model the friendship network with an exponential family random graph model (ERGM).
- 2 Model the contact network conditional on the friendship network.
 - ▶ Break/lunch contact network
 - ▶ Class contact network

Modeling break and lunch contacts

Definition: degree = number of contacts a student makes

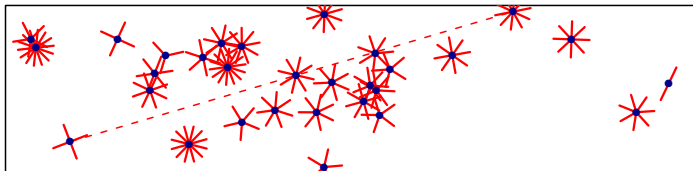
- Let D_{bl} denote the vector of break/lunch contact degrees.
- Let Y_{bl} denote the sociomatrix of break/lunch contacts.
- $P(Y_{bl} = y_{bl}) = \sum_{d_{bl}} P(Y_{bl} = y_{bl} | D_{bl} = d_{bl}) P(D_{bl} = d_{bl})$



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Modeling break and lunch contacts

- Model the break/lunch contact degree distribution by fitting negative binomial distributions to contact survey.
- Distribute 68% of contacts between friends

We use a similar approach to model the class contact network, but 50% of contacts are to friends.

Model Selection

- Dynamic contact network

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Influenza Simulations

- Incubation period has 2, 3, or 4 days with probability 0.3, 0.5, and 0.2.
- Infectiousness is proportional to viral load (sampled from challenge study data).
- 67% of infected students become symptomatic.
- 75% of symptomatic cases withdraw to home:
 - ▶ 20% on first day
 - ▶ 40% on second
 - ▶ 15% on third

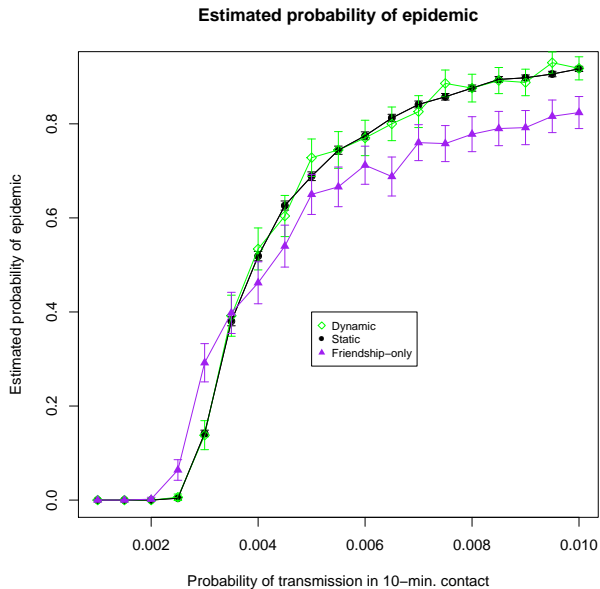
Chao, DE, Halloran, ME, Obenchain, VJ, and Longini, IM, (2010). "FluTE: a publicly available stochastic epidemic simulation model." *PLoS Computational Biology* vol.6, no.1

Influenza Simulations

- p_{ti} = per-10-minute transmission probability of person i on day t
- Y_{ij} = number of contacts between i and j on day t

$$P(i \text{ infects } j \text{ on day } t) = 1 - (1 - p_{ti})^{Y_{ij}}$$

Comparison of three network models



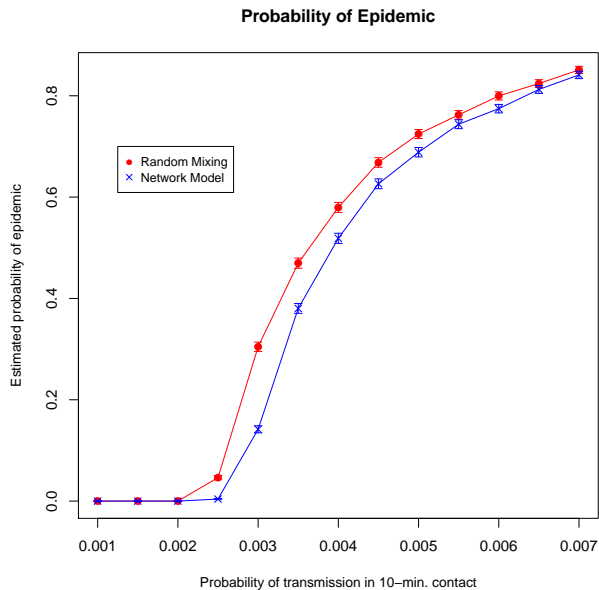
Model Selection

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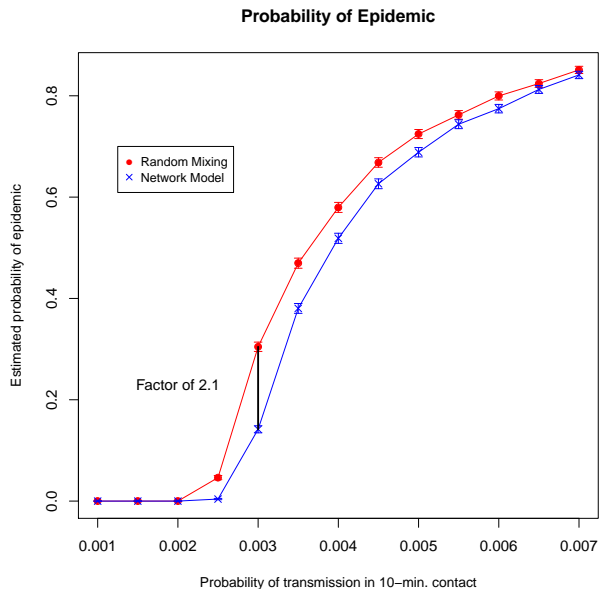
Influenza Simulations: Random Mixing

- Compare disease simulations over the contact network to those over a random mixing scenario.
- Calibrate so that the expected number of schoolmates contacted, as well as the total number of contacts, are the same in both models.

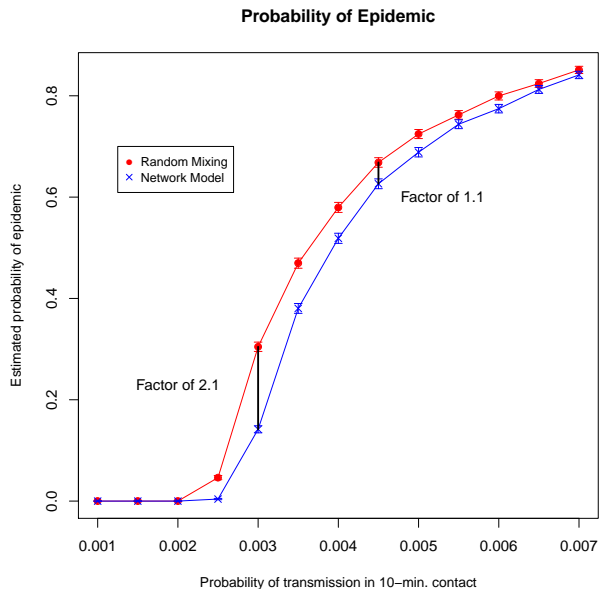
Influenza Simulation Results



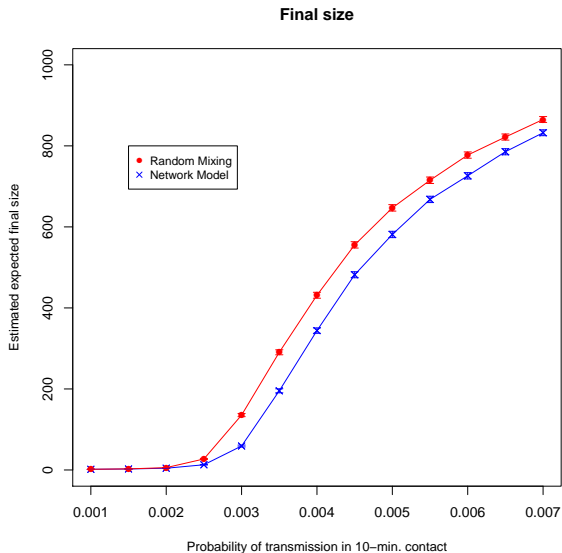
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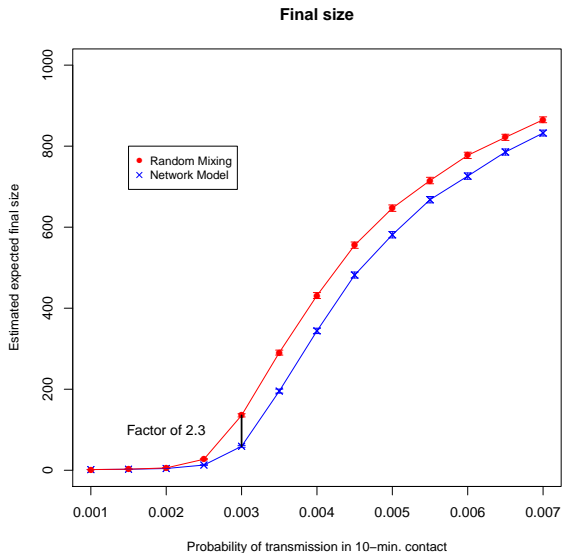
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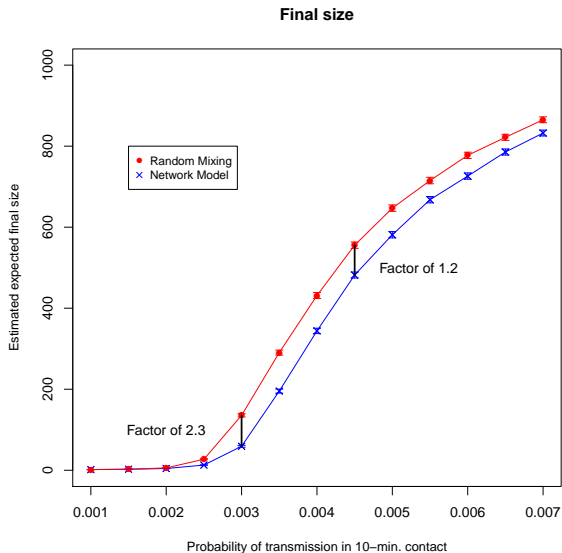
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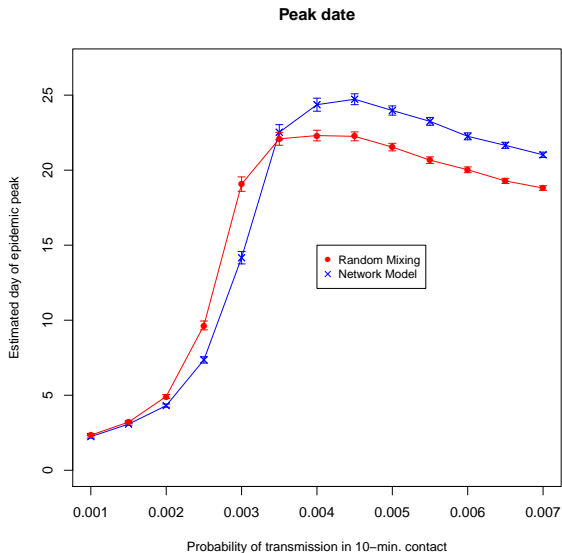
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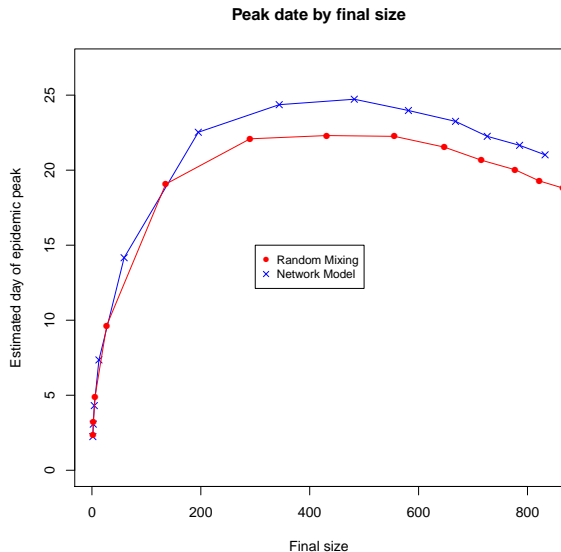
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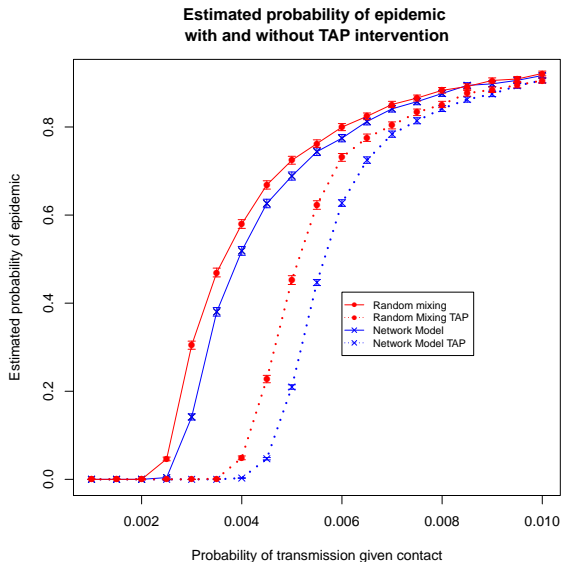
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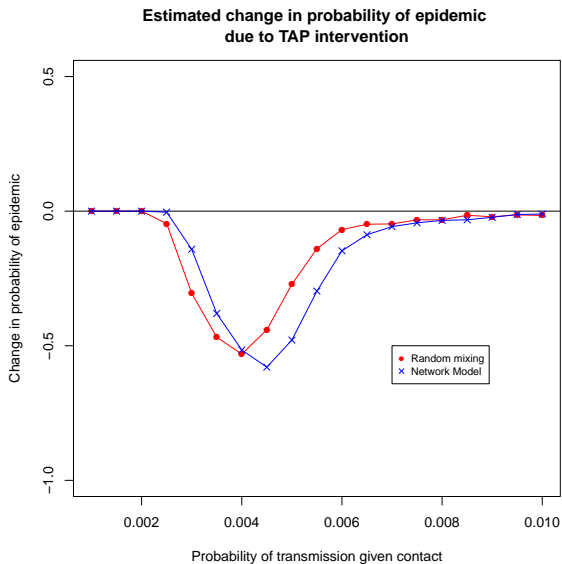
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 - ▶ Assume 67% of infected students are symptomatic.
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 - ▶ Assume $AVE_S = 0.63$, $AVE_I = 0.15$, $AVE_P = 0.56$

Halloran ME, Hayden FG, Yang Y, Longini, IM, Monto, AS (2007) *Antiviral Effects on Influenza Viral Transmission and Pathogenicity: Observations from Household-based Trials*. American Journal of Epidemiology 165(2): 212-221

TAP Intervention Results

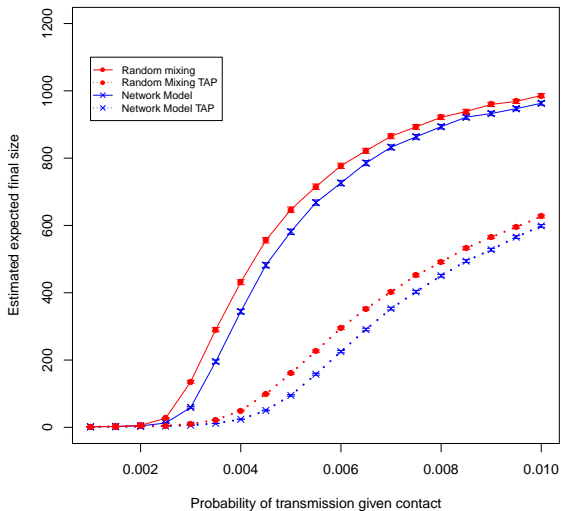


TAP Intervention Results

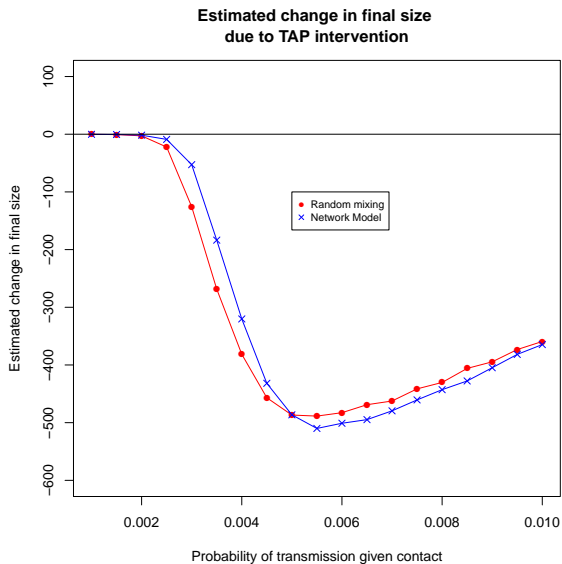


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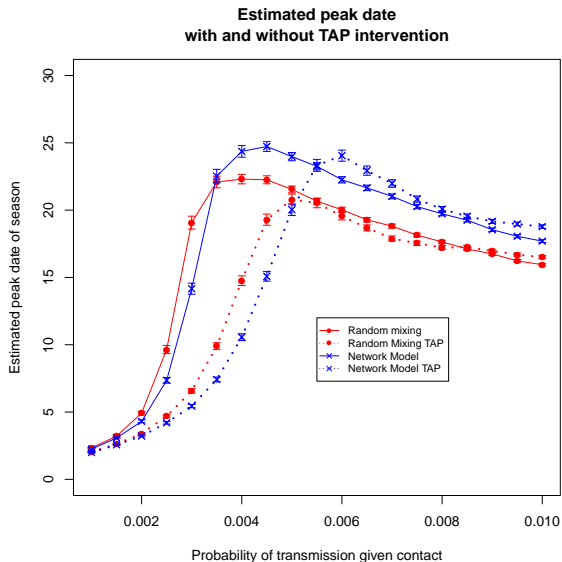
Estimated final size, with and without TAP



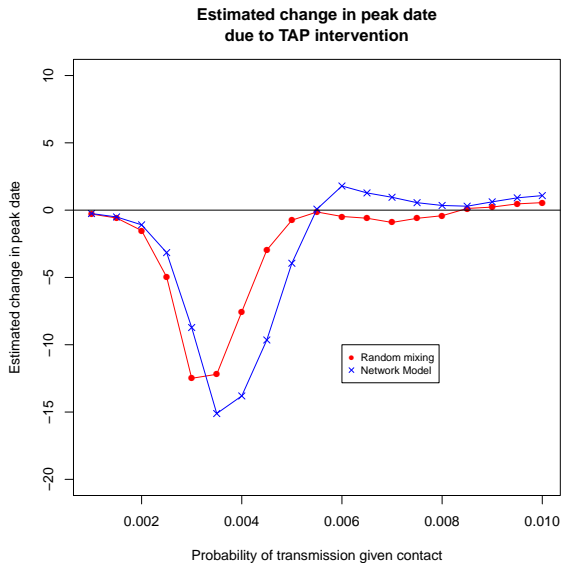
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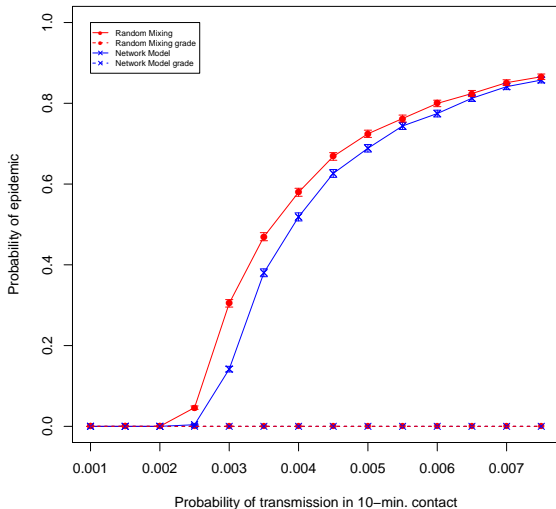


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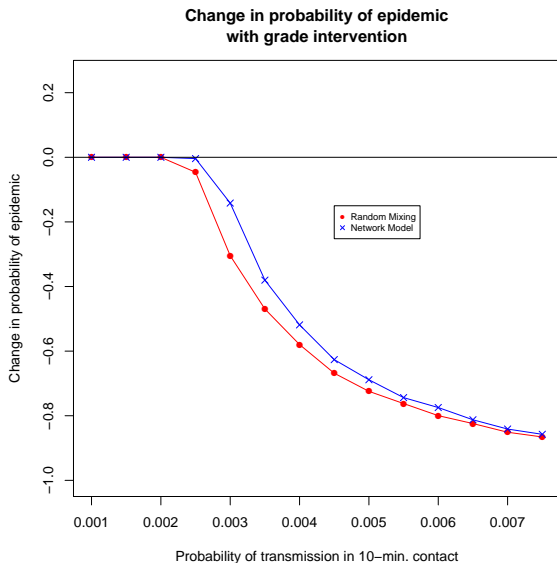


Grade Closure Intervention Results

Estimated probability of epidemic with and without grade intervention



Grade Closure Intervention Results



Limitations

- Measurement error in reports of “average number of contacts.”
- Within-classroom contact frequencies not informed by data.
- We assumed perfect observation of symptoms and perfect reporting of contact behavior.
- We treated the Add Health friendship network data as a complete network.
- Model is for within-school contacts only. Friends may contact each other outside school.

Conclusions

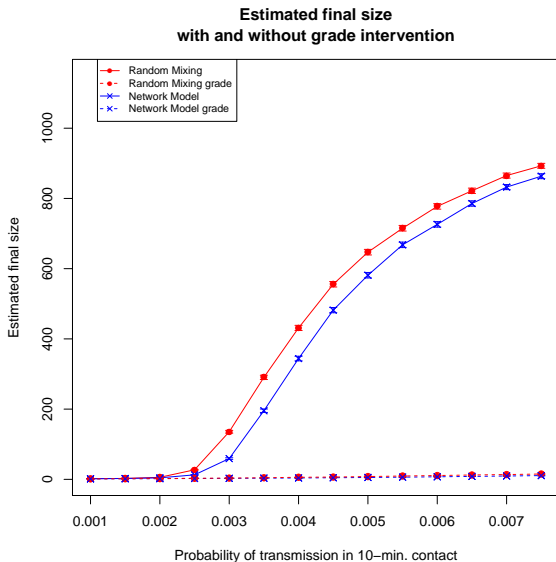
- We developed a data-driven model of contact behavior in a school.
- Model allows us to estimate epidemic parameters and estimate the effectiveness of interventions.
- Epidemic outcomes, with and without interventions, differ substantively from a random mixing scenario.
- The dynamic contact network model and static contact network model produced identical epidemic predictions.

We recommend further exploration of contact network structure with the aim of improving existing simulation models.

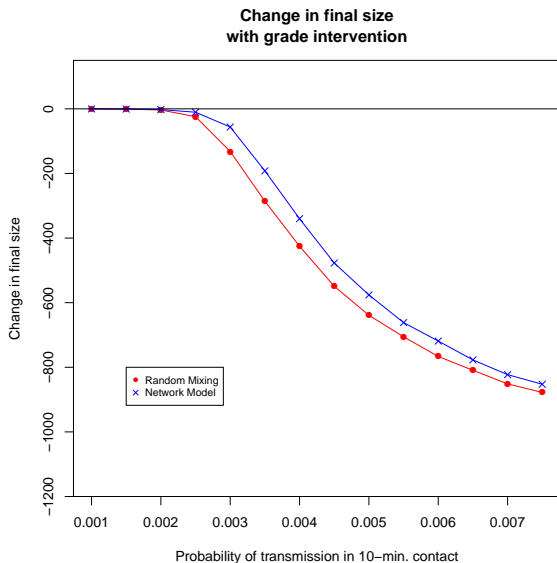
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- UW Social Network Modeling Group (Martina Morris and Steven Goodreau, PIs)
- Data: Stephen Eubank, Martina Morris
- Funding: National Institute of General Medical Sciences MIDAS grant U01-GM070749

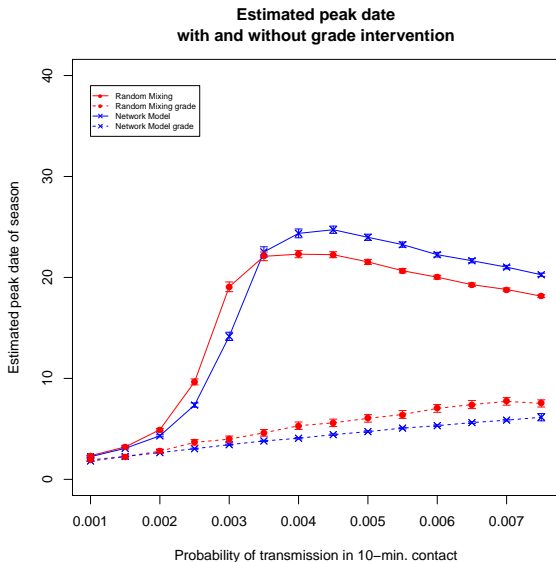
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