Social and Information Networks

Tutorial #9: Disease Modelling

University of Toronto CSC303
Winter/Spring 2021
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Week 10: Mar 25-29 (2021)

Today's agenda

In lecture we've covered Chapter 3 of the textbook looking at Strong and weak ties.

Today:

- Questions from Lecture
- Real world modeling of COVID-19
- Quercus Quiz

Questions?

Modelling COVID-19

- Today we'll be looking at *real* research modeling the spread of COVID under various strategies, published March of last year in the Lancet `https://doi.org/10.1016/S2468-2667(20)30073-6`

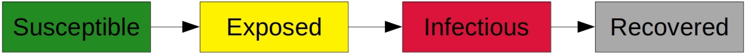
The effect of control strategies to reduce social mixing on outcomes of the COVID-19 epidemic in Wuhan, China: a modelling study

Kiesha Prem, Yang Liu*, Timothy W Russell, Adam J Kucharski, Rosalind M Eggo, Nicholas Davies, Centre for the Mathematical Modelling of Infectious Diseases COVID-19 Working Group†, Mark Jit, Petra Klepac*

- Prem et al.'s work uses a modification of the SIR model discussed in class

SEIR

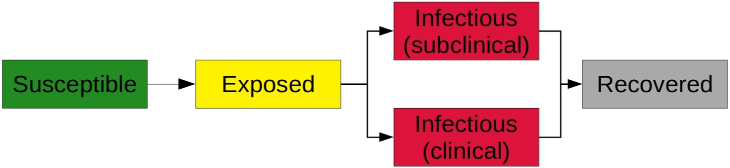
- The SEIR model has four states:
  - Susceptible
  - Exposed
  - Infectious
  - Recovered



- During the *Exposed* state, a node has been infected, but is not yet infectious

SEIR with asymptomatic (subclinical) infection

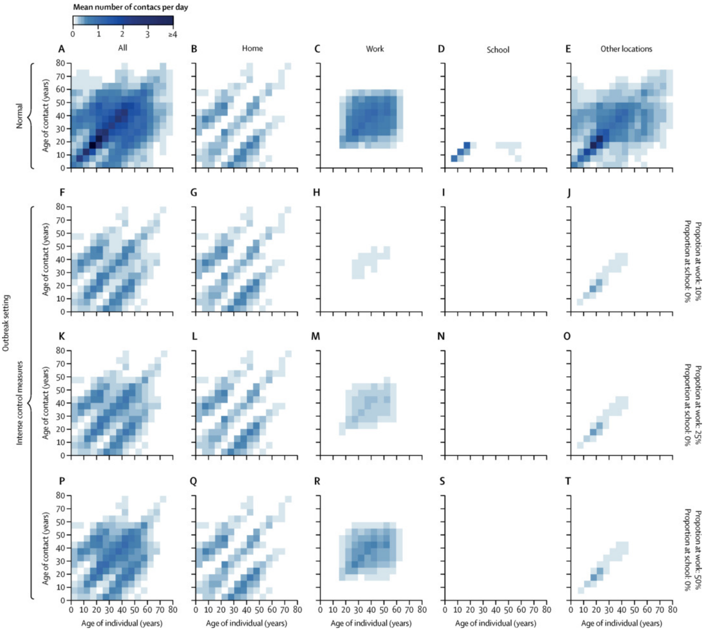
- To further model asymptomatic (subclinical) vs symptomatic (clinical) cases, the authors divided the infectious state into I^{sc} and I^{c}



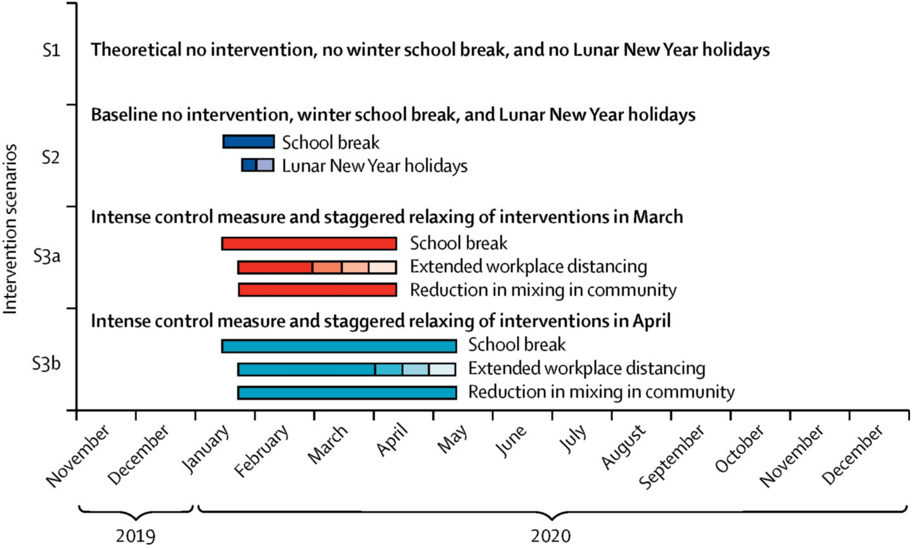
- During the *Exposed* state, a node has been infected, but is not yet infectious

Spread between age groups

- In class we modeled individuals, instead Prem et al. modelled age groups
  - In part this was to account for different probabilities of being asymptomatic based on age
- Instead of contact networks at the level of individuals like we saw in class, Prem et al. instead produced a weighted graph of exposure between different age groups under various physical distancing scenarios
- These weights were produced by combining the weights estimated for 4 key environments: Home, Work, School, and "Other"
- As these scenarios used different restrictions over time, the weights changed over time
- The weight between age groups i and j adjacency matrix at time t was dubbed $C_{(i,j),t}$. This is the average number of people of age j that a person of age i is exposed to, on day t



[From Prem et al.]



[From Prem et al.]

Spread between age groups

- As Prem et al. did not model individuals, they instead tracked the variables $S_{i,t}, E_{i,t}, I^{c}_{i,t}, I^{sc}_{i,t}$ and $R_{i,t}$
- Here i is the age group (in buckets of 5 year ranges, and 75+), and t is the day
- Each variable is the average number of people in this state

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$$S_{i,t+1} = S_{i,t} - \left[\beta S_{i,t} \sum_{j=1}^{n} C_{(i,j),t} I^{c}_{j,t} + \alpha\beta S_{i,t} \sum_{j=1}^{n} C_{(i,j),t} I^{sc}_{j,t}\right]$$

- β is the transmission rate, scaled based on R_0
- α is a discounting factor to adjust for asymptomatic individuals being less infectious

Spread between age groups

$$E_{i,t+1} = (1-\kappa)E_{i,t} + \left[\beta S_{i,t} \sum_{j=1}^{n} C_{(i,j),t} I^{c}_{j,t} + \alpha\beta S_{i,t} \sum_{j=1}^{n} C_{(i,j),t} I^{sc}_{j,t}\right]$$

- κ is the probability of an exposed individual becoming infectious within a day
  - Based on the exponential distribution, $\kappa = 1 - \exp(1/d_L)$ where d_L is the average incubation period in days

Spread between age groups

$$I^{c}_{i,t+1} = \rho_i \kappa E_{i,t} + (1-\gamma) I^{c}_{i,t}$$

$$I^{sc}_{i,t+1} = (1-\rho_i) \kappa E_{i,t} + (1-\gamma) I^{sc}_{i,t}$$

- ρ_i is the probability that an infectious individual in age group i is asymptomatic
- γ is the probability that an individual recovers in a day or less
  - Again by the exponential distribution, $\gamma = 1 - \exp(-1/d_I)$ where d_I is the average duration of infection in days

Spread between age groups

$$R_{i,t+1} = R_{i,t} + \gamma I^{c}_{i,t+1} + \gamma I^{sc}_{i,t+1}$$

- γ is the probability that an individual recovers in a day or less

Source of Parameters

- The $C_{(i,j),t}$ values were synthetic
- Other parameters were estimated based on published research

	Values	References
Basic reproduction number, R_0	2·2 (1·6–3·0)*	Kucharski et al[14]
Average incubation period, d_L	6·4 days	Backer et al[16]
Average duration of infection, d_I	3 days or 7 days	Woelfel et al[22]
Initial number of infected, I_0	200 or 2000	Abbott et al[15]
Pr(infected case is clinical), ρ_i	0 or 0·4, for $i \leq 4$	Bi et al[20]
Pr(infected case is clinical), ρ_i	0 or 0·8, for $i > 4$	Davies[21]
Pr(infection acquired from subclinical), α	0·25	Liu et al[19]

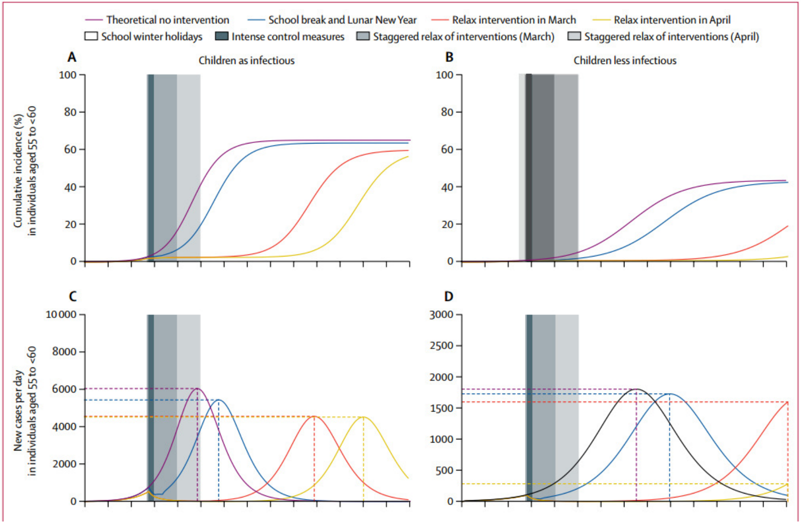
*Data are median (IQR). Pr represents the probability of an event. The parameters d_L and d_I represent the mean incubation period and duration of infectiousness, respectively.

Table: **Parameters of the susceptible-exposed-infected-removed model**

[From Prem et al.]

- Model parameters were validated by comparison with the number of confirmed cases in Wuhan from 16th January to 12th February
- Prem et al. considered two scenarios, one where children where more likely to be asymptomatic, and one where children were equally likely to be asymptomatic

Results



[Modified From Prem et al.]

Conclusions

- The authors concluded that measures that reduced social mixing were effective at reducing the magnitude of an outbreak, and at delaying the peak
- They found the effect of the measures varied by age group, with the largest impact on children and older individuals, and the least impact on working-age individuals
- They found that whether children were more likely to be asymptomatic had a large impact
- The incubation period was found to be critical to when measures can be relaxed
  - under an incubation period of 3 days measures could be relaxed in March, to produce the same effect under an incubation period of 7 days measures had to be lifted a month later in April

Quercus Quiz