Parametersing Markovian epidemic models using household level data

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Household models

- Strong mixing within households.
- Weaker mixing between households.
Why do we like household models?

- Capture some realistic heterogeneity, but still simple to solve.
- Households are small, so must model dynamics stochastically.
- State space is small.
- Lots of data available.
Household data collection

Monitoring and tracking all a person's contacts is difficult.

Monitoring a household is much easier.

▶ FF100

If available, antivirals are given to whole households.

Challenge

Use all this data from within households to parametrise our models.
Within-household dynamics

generation time: the interval of time between successive infection events.
Within-household dynamics

serial interval: the time between the onset of symptoms in an index case and that of a secondary.
Observed events

- Chain of symptomatic events.
- Estimating recovery is more difficult.
Serial interval data

Most people just fit a parametric distribution to this and consider that a job well done.

To learn something interesting from this data we need to fit a transmission model.
### Stochastic $SE(j)I(k)R$ model

<table>
<thead>
<tr>
<th>Event</th>
<th>Transition</th>
<th>Rate</th>
</tr>
</thead>
<tbody>
<tr>
<td>Infection</td>
<td>$(S, E_1) \rightarrow (S - 1, E_1 + 1)$</td>
<td>$\beta \frac{S \sum_{1}^{k} I_m}{(N-1)}$</td>
</tr>
<tr>
<td>exposed progression, $(n = 1, \ldots, j - 1)$</td>
<td>$(E_n, E_{n+1}) \rightarrow (E_n - 1, E_{n+1} + 1)$</td>
<td>$j \sigma E_n$</td>
</tr>
<tr>
<td>Start shedding</td>
<td>$(E_j, I_1) \rightarrow (E_j - 1, I_1 + 1)$</td>
<td>$j \sigma E_j$</td>
</tr>
<tr>
<td>Infection progression, $(m = 1, \ldots, k - 1)$</td>
<td>$(I_m, I_{m+1}) \rightarrow (I_m - 1, I_{m+1} + 1)$</td>
<td>$k \gamma I_m$</td>
</tr>
<tr>
<td>Recovery</td>
<td>$I_k \rightarrow I_k - 1$</td>
<td>$k \gamma I_k$</td>
</tr>
</tbody>
</table>

**Individual level:**

- **Within-household transmission:**
  
  \[ \beta \frac{S(I_1 + I_2)}{N - 1} \]
Calculating the serial interval

Dynamics of model,

\[ \frac{dp(t)}{dt} = p(t)Q \]  \hspace{1cm} (1)

where \( Q \) is the stochastic transition matrix.

- Initial condition: \( (I_1 = 1, S = N - 1) \).
- Make the states which correspond to an serial interval event absorbing.
- Integrate forward the dynamics.

\[ p(t) = p(0) \exp(Qt) \]  \hspace{1cm} (2)
Calculating the serial interval

The cdf of the serial interval is then,

\[ F(t) = \frac{1}{c} \sum_{s \in B} p_s(t), \quad (3) \]

where \( c \) is the probability of infecting at least 1 person before recovering.

How we evaluate the dynamics is important. There are two methods we use:

- Expokit for calculating matrix exponentials.
- Lexicographic ordering, and forward substitution.
Basic results

The serial interval distribution depends on the household size.
Antiviral efficacy model

The impact of antivirals was limited in the 2009 influenza A(H1N1) pandemic.

We wanted to assess the impact of antivirals: were they not effective or was the delay too large?

There has already been a lot of modelling for this problem. What sets this apart?

Already have posteriors for $\beta$ and serial interval data. Use Bayesian MCMC to estimate $\gamma$ and $\sigma$. 
Pandemic Influenza model - parameters

(a) $\beta_2$

(b) $\beta_3$

(c) $\beta_4$

(d) $\beta_5$

(e) $\beta_6$

(f) $\beta_7$

(g) $\beta_8$

(h) Serial interval distribution

(i) Cases distribution

(j) Infectious period parameter, $\gamma$ (days$^{-1}$)

(k) Latent period parameter, $\sigma$ (days$^{-1}$)

(l) Parameter $\tau$

(m) Parameter $\rho$
Model with explicit household size

Generate some test data, now stratified by household size.

Parameters: $\beta = 2$, $\gamma = 1/2$, $\sigma = 1/4$, $j = k = 2$. 
Posterior distributions

A

B

C

serial interval (days)

probability density
Complications

- Symptoms and infectiousness don’t coincide.
- Asymptomatic individuals.
- External infections.
- Potentially wasteful.
In collaboration with:
Joshua Ross, Thomas House and Matt Keeling.

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**Epidemiological consequences of household-based antiviral prophylaxis for pandemic influenza**

**Estimating a Markovian epidemic model using household serial interval data from the early phase of an epidemic**
Andrew J. Black and Joshua V. Ross (2013)