

# Parametersing Markovian epidemic models using household level data

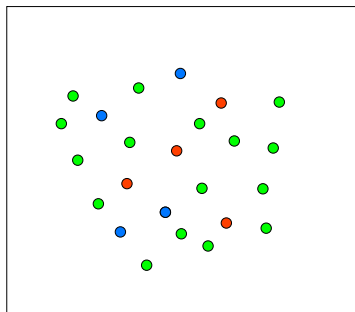
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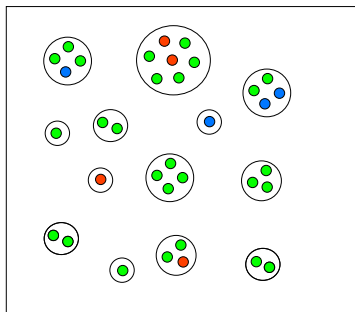
School of Mathematical Sciences  
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# Household models



homogeneous population  
of individuals



heterogeneous population  
of households

- ▶ 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 persons contacts is difficult.

Monitoring a household is much easier.

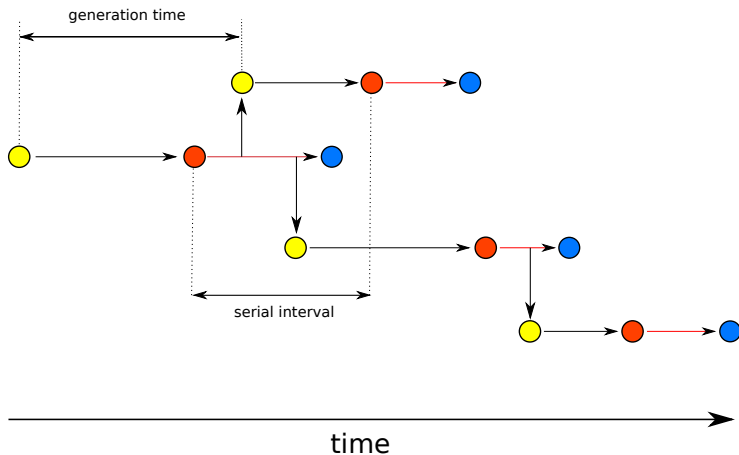
- ▶ FF100

If available, antivirals are given to whole households.

## Challenge

Use all this data from within households to parametrise our models.

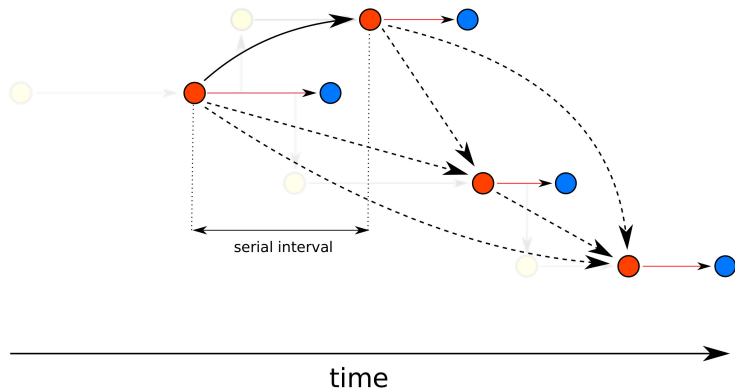
# Within-household dynamics



generation time: the interval of time between successive infection events.

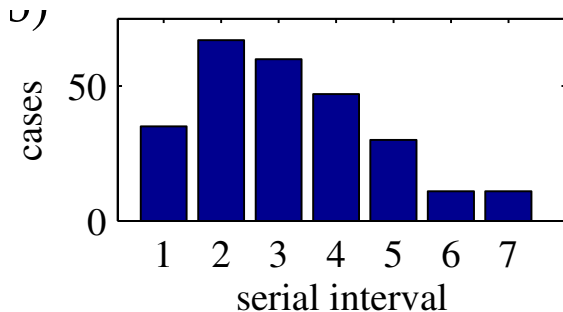


# Observed events



- ▶ Chain of symptomatic events.
- ▶ Estimating recovery is more difficult.

## Serial interval data



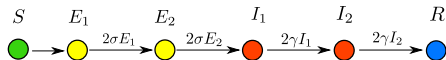
- ▶ Most people just fit a parametric distribution to this and consider that a job well done.
- ▶ To learn something interesting from this data we need to fit a transmission model.



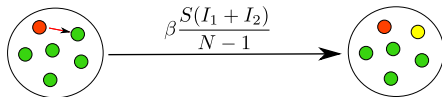
# Stochastic $SE(j)I(k)R$ model

Event	Transition	Rate
Infection	$(S, E_1) \rightarrow (S - 1, E_1 + 1)$	$\beta \frac{S \sum_1^k I_m}{(N-1)}$
exposed progression, $(n = 1, \dots, j - 1)$	$(E_n, E_{n+1}) \rightarrow (E_n - 1, E_{n+1} + 1)$	$j\sigma E_n$
Start shedding	$(E_j, I_1) \rightarrow (E_j - 1, I_1 + 1)$	$j\sigma E_j$
Infection progression, $(m = 1, \dots, k - 1)$	$(I_m, I_{m+1}) \rightarrow (I_m - 1, I_{m+1} + 1)$	$k\gamma I_m$
Recovery	$I_k \rightarrow I_k - 1$	$k\gamma I_k$

Individual level:



Within-household transmission:



# Calculating the serial interval

Dynamics of model,

$$\frac{dp(t)}{dt} = p(t)Q \quad (1)$$

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.

$$p(t) = p(0) \exp(Qt). \quad (2)$$

## Calculating the serial interval

The cdf of the serial interval is then,

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

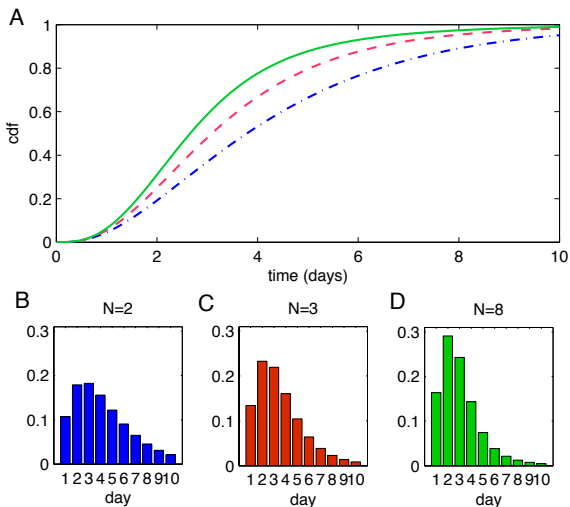
where  $c$  is the probability of infecting at least 1 person before recovering.

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

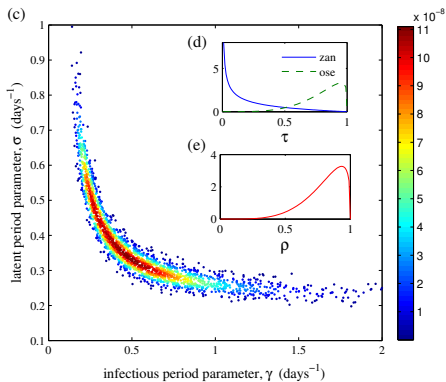
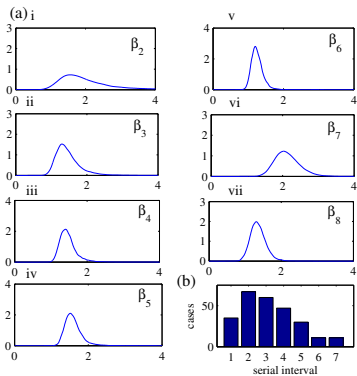
The impact of antivirals was limited in the 2009 influenza A(H1N1) pandemic.

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?

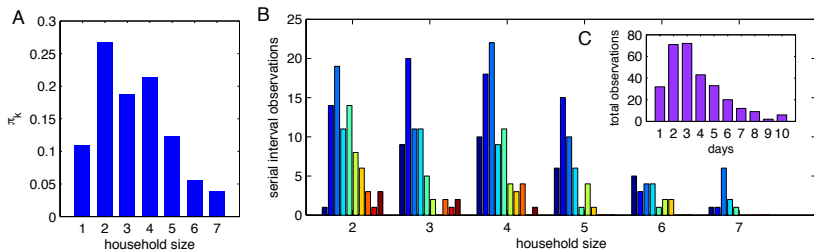
Already have posteriors for  $\beta$  and serial interval data. Use Bayesian MCMC to estimate  $\gamma$  and  $\sigma$

# Pandemic Influenza model - parameters



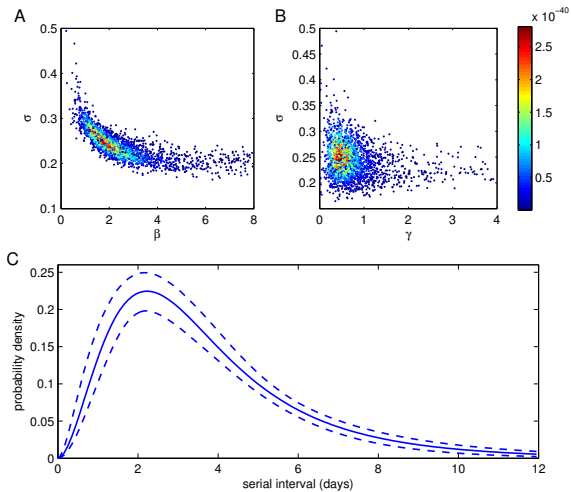
# Model with explicit household size

Generate some test data, now stratified by household size.



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

# Posterior distributions





# Complications

- ▶ Symptoms and infectiousness don't coincide.
- ▶ Asymptomatic individuals.
- ▶ External infections.
- ▶ Potentially wasteful.

# Acknowledgements and Papers

In collaboration with:

Joshua Ross, Thomas House and Matt Keeling.

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

Black, A.J., House, T., Keeling, M.J. and Ross, J.V. (2012)  
J. R. Soc. Interface 10, 20121019.

## **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)