Household, network and other models of heterogeneity

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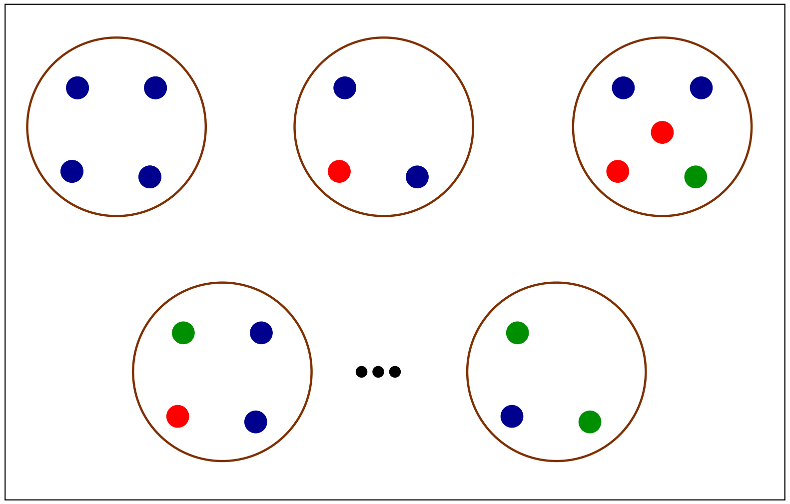
Households SIR epidemic model



m_n households of size n
$(n = 1, 2, \cdots, n_{\max})$

total no. of households $m = \sum_{n=1}^{n_{\max}} m_n$

total no. of individuals $N = \sum_{n=1}^{n_{\max}} n m_n < \infty$

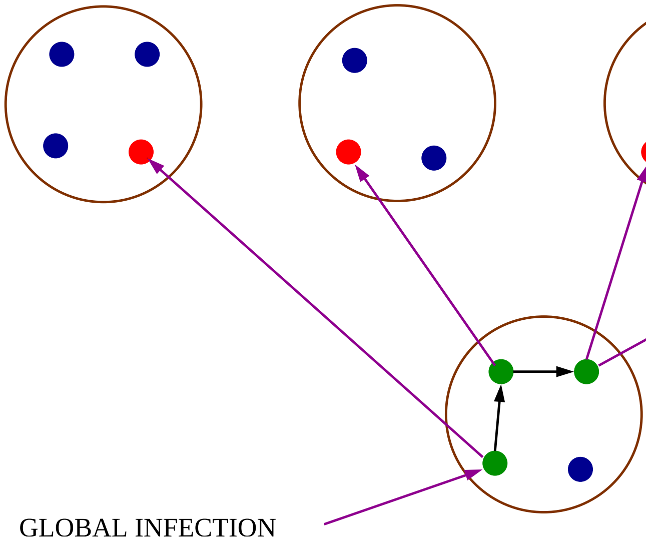
- Infectious period $\sim I$, having an arbitrary but specified distribution
- Infection rates (individual $\to$ individual)

  (i) local (within-household) λ_L

  (ii) global (between-household) λ_G / N
- Latent period/infectivity profiles

  (Bartoszyński (1972), Becker and Dietz (1995), Ball, Mollison and Scalia-Tomba (1997))

Threshold parameter R_*



- R_* = mean number of global contacts emanating from a typical single-household epidemic

$$R_* = \sum_{n=1}^{n_{\max}} \tilde{\alpha}_n \mu_n(\lambda_L) \lambda_G \mathrm{E}[I],$$

where

$\tilde{\alpha}_n = \frac{n m_n}{N}$ = $\mathrm{P}($randomly chosen person lives in a household of size $n)$

$\mu_n(\lambda_L)$ = mean size of single (size-n) household epidemic with 1 initial infective

- $\mathrm{P}($global epidemic$) > 0 \iff R_* > 1$

(Ball, Mollison and Scalia-Tomba (1997), Becker and Dietz (1995))

Variola Minor, Sao Paulo, 1956

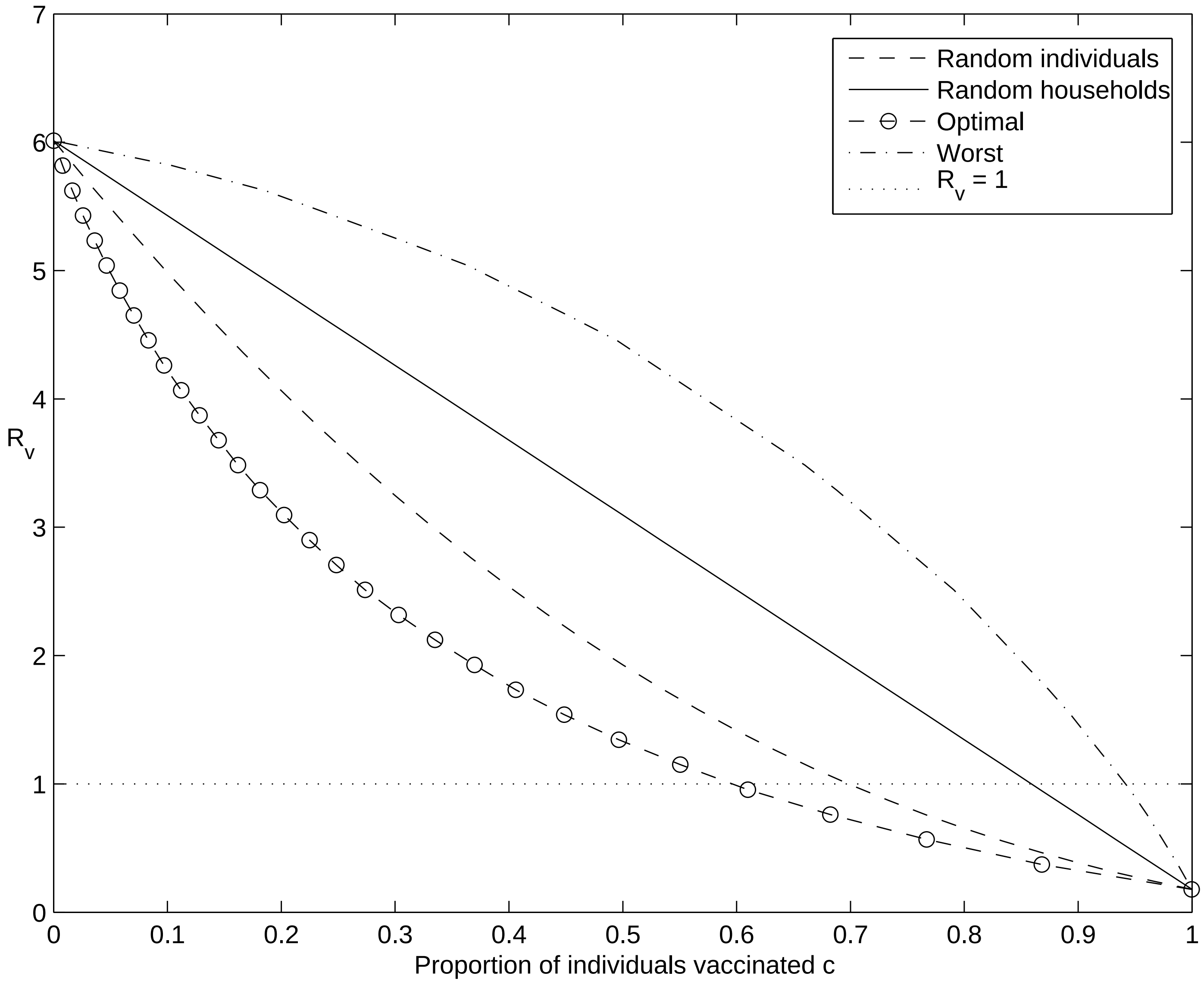
- Data comprise final numbers infected in each of 338 households. Household size varied from 1 to 12 (mean $= 4.56$)
- Each individual labelled vaccinated or unvaccinated

  773 unvaccinated — 425 infected (58%)
  809 vaccinated — 85 infected (11%)

- Fit households SIR model with non-random vaccine response, assuming infectious period $T_I \equiv 1$, using pseudolikelihood method of Ball and Lyne (2010) to obtain the estimates

$$\hat{\lambda}_L = 0.3821, \hat{\lambda}_G = 1.4159, \hat{a} = 0.1182, \hat{b} = 0.8712$$

Comparison of vaccination strategies



Configuration model networks

- Population $\mathcal{N} = \{1, 2, \cdots, n\}$.
- D= degree of typical individual

$$p_k = \mathrm{P}(D = k) \quad (k = 0, 1, \cdots) \quad \text{specified} \qquad \mu_D = \mathrm{E}[D].$$

- $D_1, D_2, \cdots, D_n$ iid copies of D.
- Attach D_i stubs (half-edges) to individual i $(i = 1, 2, \cdots, n)$.
- Pair up the stubs uniformly at random to form the Newman–Strogratz–Watts (NSW) network.
- Degree $\tilde{D}$ of a typical neighbour of an individual has the size-biased distribution

$$\mathrm{P}(\tilde{D} = k) = \frac{kp_k}{\mu_D} \quad (k = 1, 2, \cdots).$$

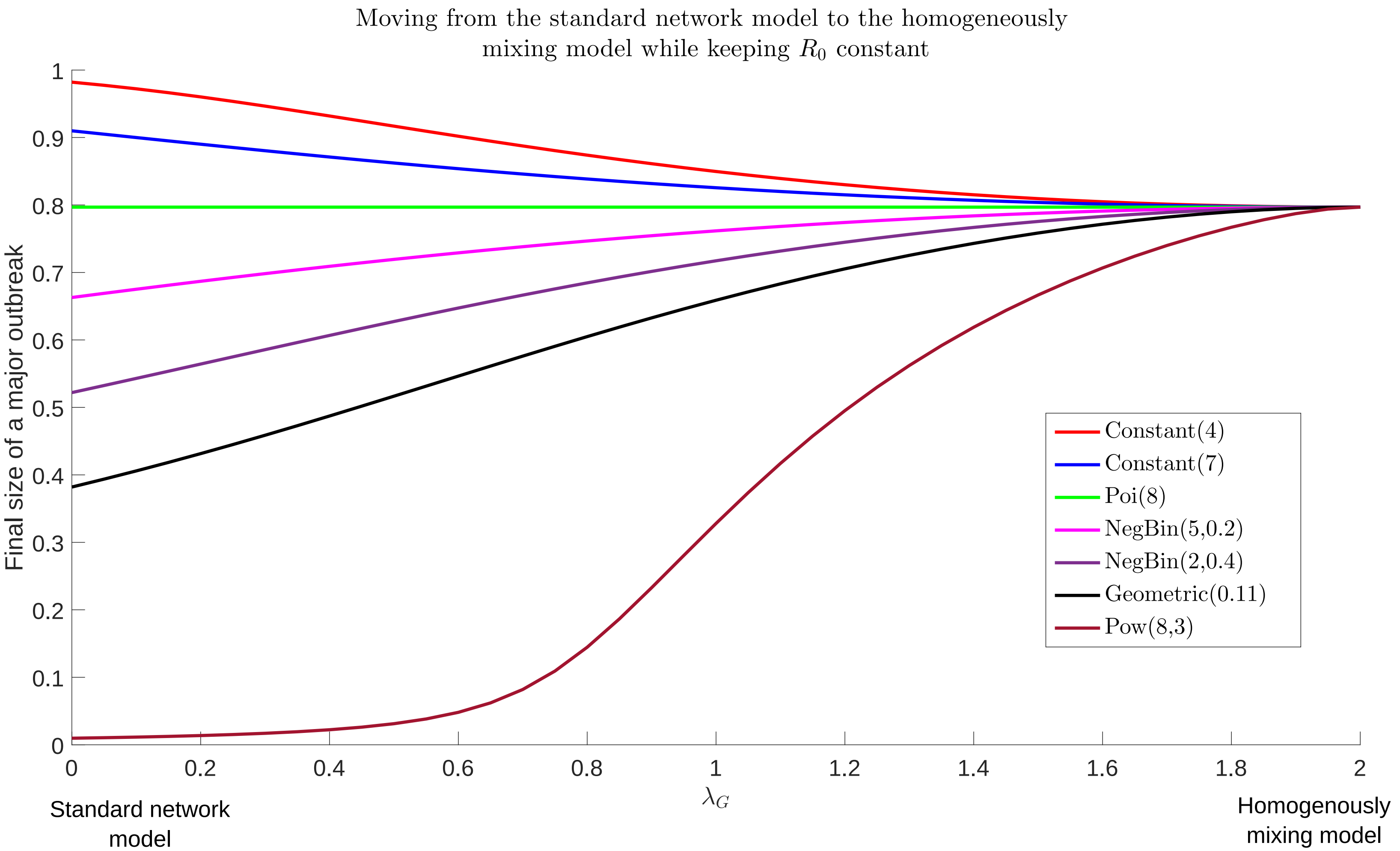
SIR Epidemic model

- Infectious periods iid according to a random variable I having an arbitrary but specified distribution.
- Whilst infectious, individuals contact each of their neighbours independently at rate β.
- $$R_0 = \mathrm{E}[\tilde{D} - 1] p_I = (\mu_D + \mu_D^{-1} \sigma_D^2 - 1) p_I,$$

  where $p_I = 1 - \mathrm{E}[\mathrm{e}^{-\beta I}]$ is the probability an infective infects a given neighbour.

(Diekmann et al. (1998), Andersson (1999), Newman (2002))

Network model with casual contacts



Final size of major outbreak with fixed $R_0 = 2$ (Davis (2017))

Some challenges

- Endemic models with household (or network) structure – incorporate waning immunity
- Extension to more complex social structures, while maintaining mathematical tractability
  - Households on a network
  - Overlapping-groups models (e.g. households-workplaces models)
  - More realistic network models
- Inferential methods for emerging diseases
- Computationally efficient calculation of thresholds and early exponential growth rates