

R_0 for structured population epidemic models

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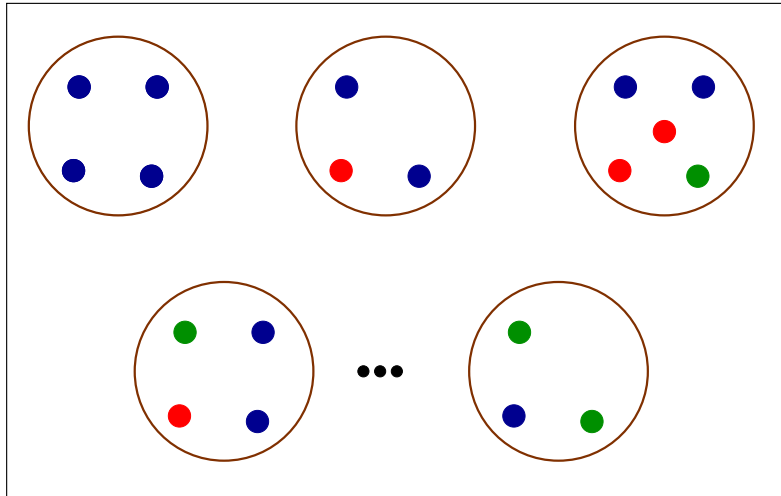
Outline of talk

- Households model and R_* .
- R_0 for households model.
- Relationship between R_0 and R_r (“estimate” of R_0 from real-time exponential growth rate r ignoring household structure).
- Concluding comments.

Pellis, L., Ball, F. and Trapman, P. (2012) Reproduction numbers for epidemic models with households and other social structures I: Definition and calculation of R_0 . *Math. Biosci.* **235**, 85–97.

Ball, F., Pellis, L. and Trapman, P. (2016) Reproduction numbers for epidemic models with households and other social structures II: comparisons and implications for vaccination. *Math. Biosci.* **274**, 108–139.

Households SIR epidemic model



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

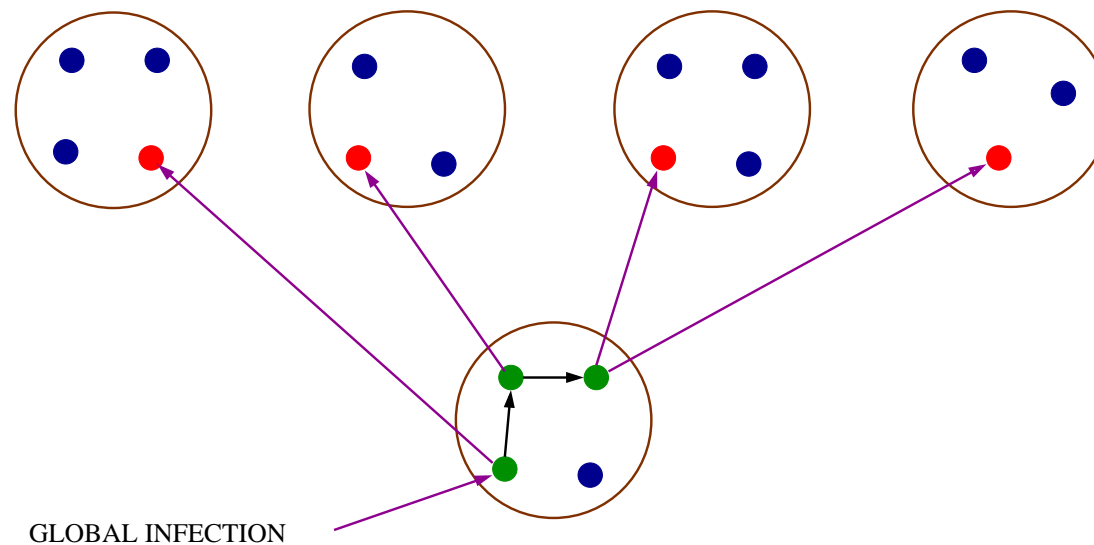
total no. of households $m = \sum_{n=1}^{n_{\max}} m_n$

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

- SIR (susceptible \rightarrow infective \rightarrow recovered)
- Infectious period $\sim I$, having an arbitrary but specified distribution
- Infection rates (individual \rightarrow individual)
 - local (within-household) λ_L
 - 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

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

where

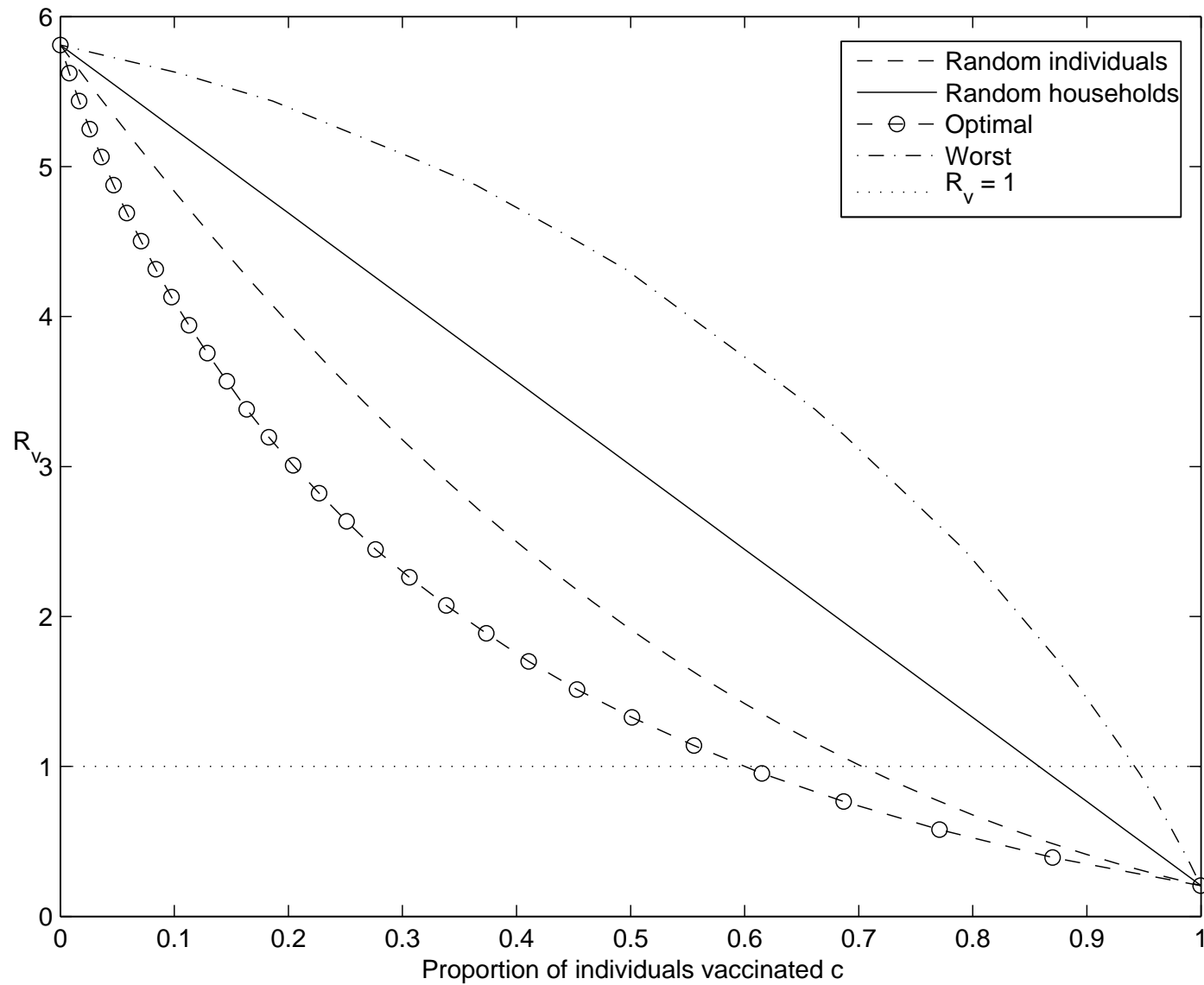
$$\tilde{\alpha}_n = \frac{nm_n}{N} = \text{P}(\text{randomly chosen person lives in a household of size } n)$$

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

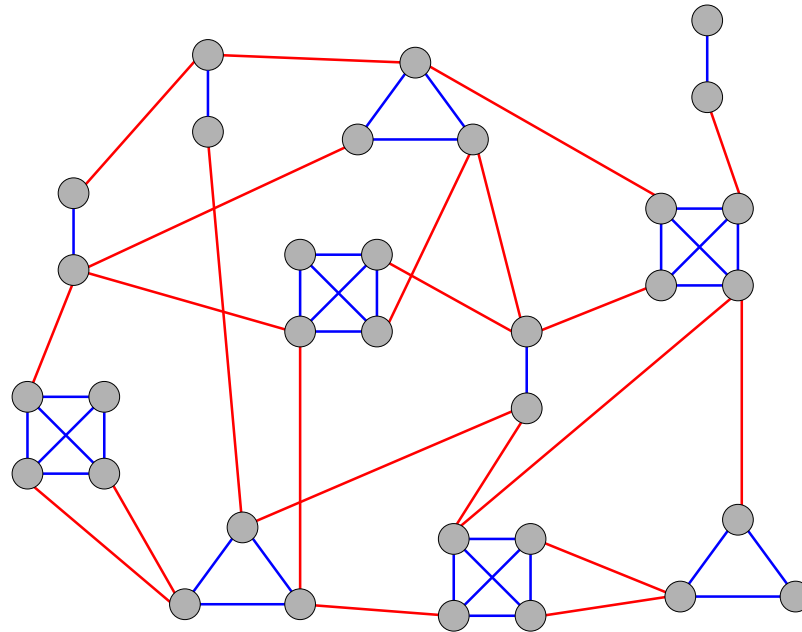
- $\text{P}(\text{global epidemic}) > 0 \iff R_* > 1$

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

Comparison of vaccination strategies



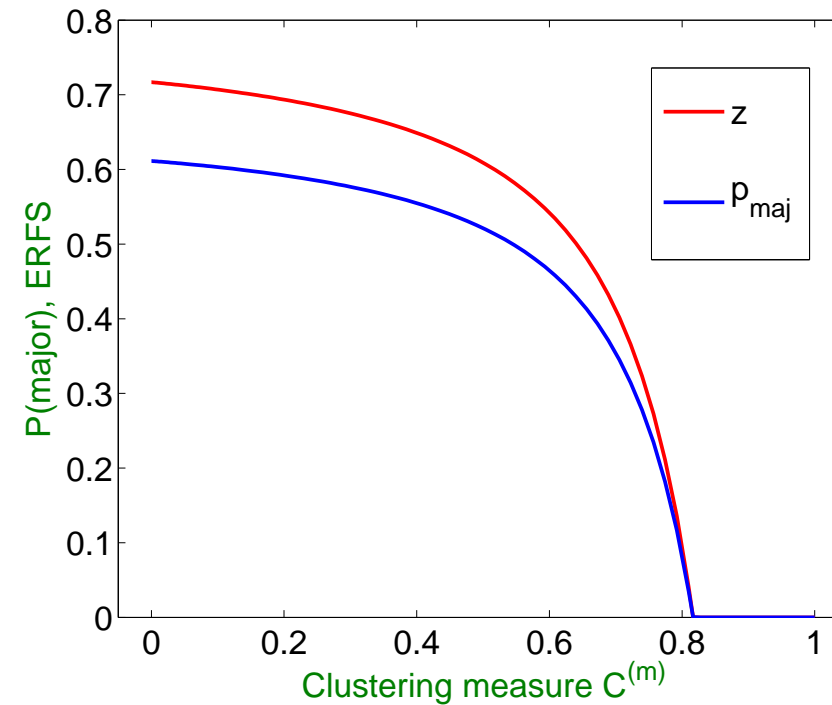
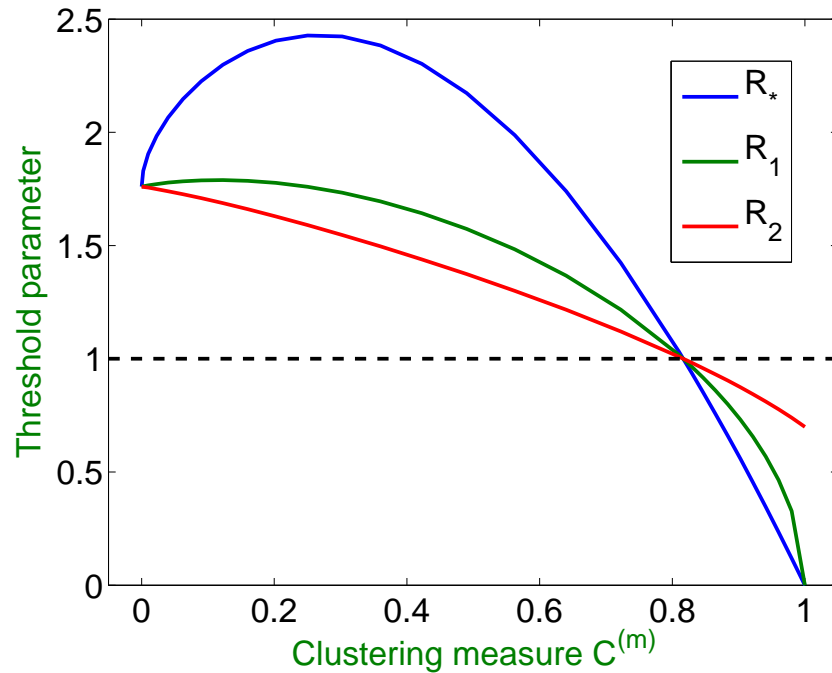
Network–households model



- Individuals infect along **household** edges at rate λ_L and **global** edges at rate λ_G .
- **Households** introduce **clustering** into network.

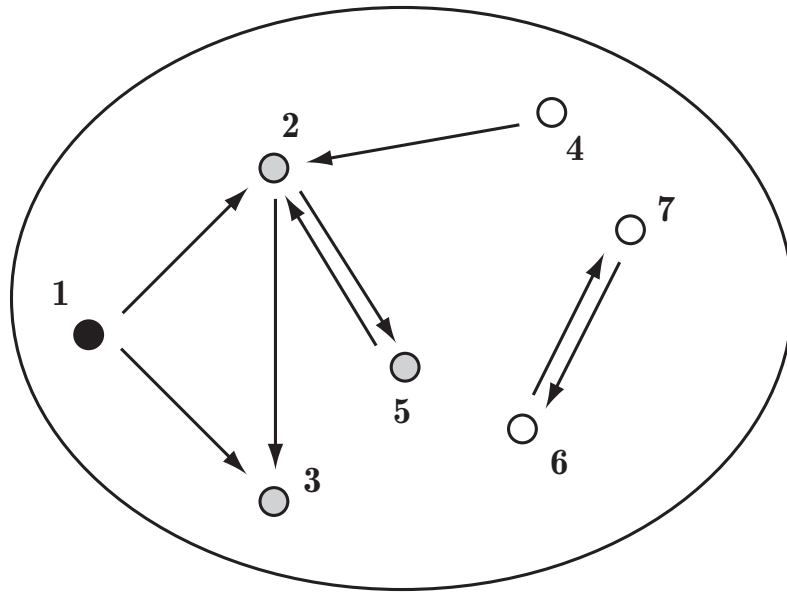
(Ball, Sirl and Trapman (2010))

Effect of clustering when $\lambda_L = \lambda_G$



Plots of threshold parameters and the probability p_{maj} and expected relative final size z of a major outbreak for networks with $H \sim \text{Poi}^+(\mu)$ and $D \sim \text{Poi}(10 - \mu)$, so Q is always $\text{Poi}(10)$ and $C^{(m)} \approx (\mu/10)^2$. Other parameters are $I \sim \text{Gamma}(3, 1/3)$ and $\lambda_L = \lambda_G = 1/5$.

Epidemic graph – generations of infectives



Generations of infectives

Generation 0: individual 1

Generation 1: individuals 2, 3

Generation 2: individual 5

- Suppose there is **one** initial infective in a population of size N . Let $Y_k^{(N)}$ be the number of **generation- k** infectives.

Definition of R_0

- Following Trapman (2007), define R_0 by

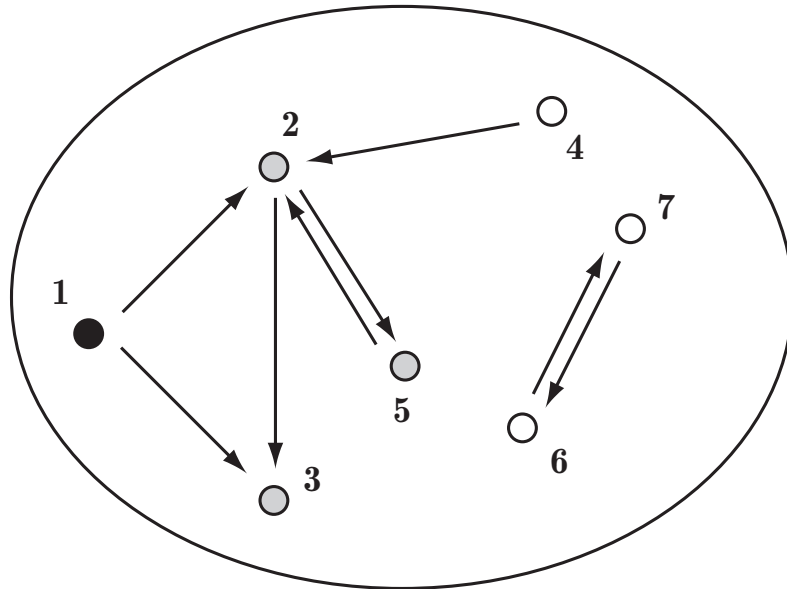
$$R_0 = \lim_{k \rightarrow \infty} \lim_{N \rightarrow \infty} \left(\mathbb{E} \left[Y_k^{(N)} \right] \right)^{\frac{1}{k}}. \quad (1)$$

- Yields usual R_0 if the process of **infectives** (viewed on a **generation** basis) in the epidemic model converges to a (**single** or **multitype**) Galton-Watson **branching process** as the population size $N \rightarrow \infty$. In which case, for large N ,

$$P(\text{major outbreak}) \approx P(\text{BP survives}) > 0 \iff R_0 > 1.$$

- We use (1) as our definition of R_0 for **structured population** epidemic models.

Household generations



Generations of infectives

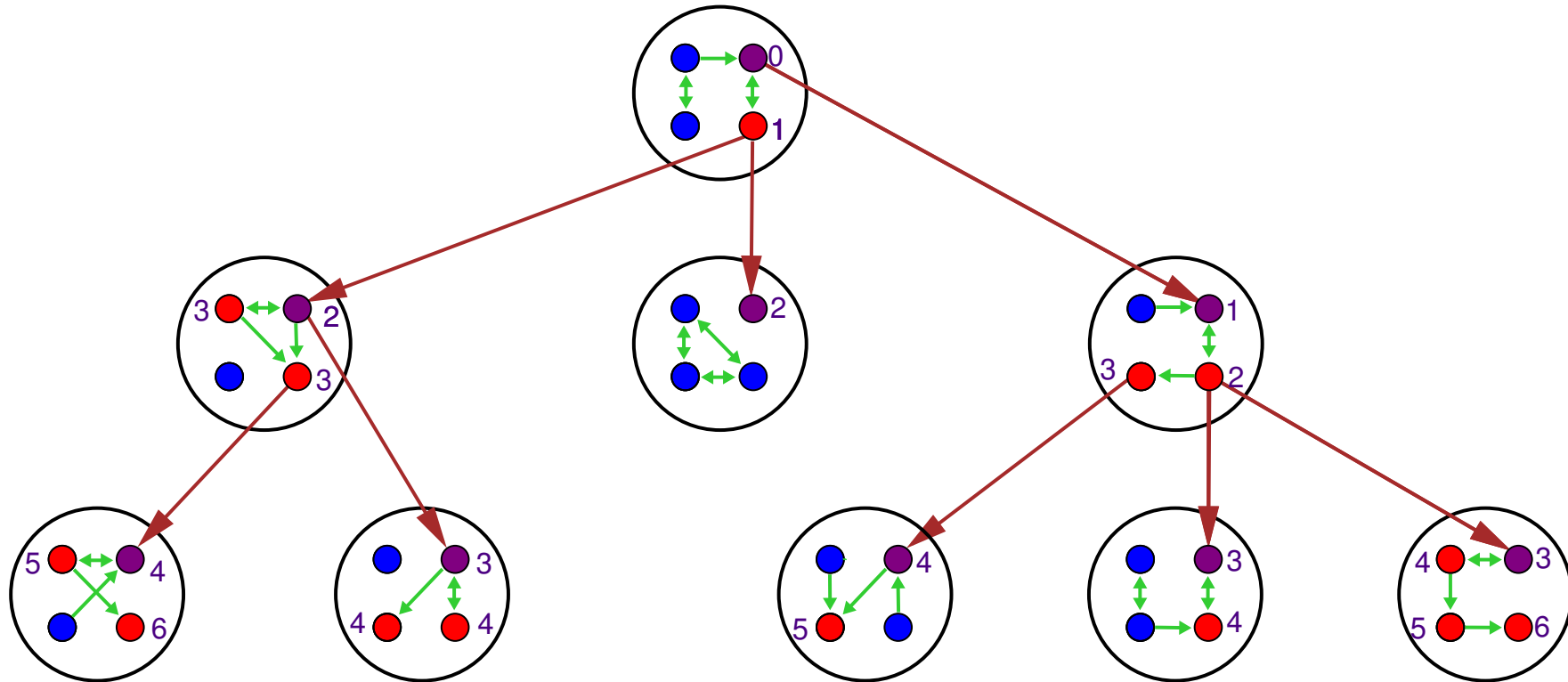
Generation 0: individual 1

Generation 1: individuals 2, 3

Generation 2: individual 5

- Let $\mu_i^{(n)}$ be the mean number of cases in generation i of a **single (size- n) household epidemic** ($\mu_0 = 1$).
- Let $\mu_i = \sum_{n=i+1}^{n_{\max}-1} \tilde{\alpha}_n \mu_i^{(n)}$ be the mean number of cases in generation i of a **typical single-household epidemic**.
- These are **rank** generations, which typically do **not** correspond to **real time** generations. The latter typically yield a different R_0 (cf. Neal (2019)).

Derivation of R_0



- Consider branching process of **infected households**, in which for each infected household the time of its birth is given by the **global generation** of the corresponding household **primary** case.

Derivation of R_0

- R_0 is given by the asymptotic (Malthusian) geometric growth rate of the mean population size of this branching process.
- Let $\mu_G = \lambda_G \mathbf{E}[I]$ be the mean number of global infections made by a typical infective. Then R_0 is the unique positive root of the discrete-time Lotka-Euler equation

$$\sum_{i=1}^{n_{\max}} \frac{\nu_i}{\lambda^i} = 1,$$

where

$$\nu_i = \begin{cases} \mu_G \mu_{i-1} & \text{if } i = 1, 2, \dots, n_{\max}, \\ 0 & \text{otherwise,} \end{cases}$$

is the mean number of offspring that a typical individual (i.e. infectious household) has at age i .

Reproduction number R_r

- Suppose that infectives have iid infectivity profiles $\{\Lambda(a) : a \geq 0\}$ satisfying $\mathbb{E}[\int_0^\infty \Lambda(a) da] = 1$.
- Infective with infectious age a makes global contacts at rate $\mu_G \Lambda(a)$ and contacts any given susceptible in its household independently at rate $\lambda_L \Lambda(a)$.
- “Infectious contact interval” W has pdf $w(t) = \mathbb{E}[\Lambda(t)]$ ($t > 0$) and Laplace transform $M_W(\theta) = \mathbb{E}[e^{-\theta W}] = \int_0^\infty e^{-\theta a} \mathbb{E}[\Lambda(a)] da$.
- Exponential-growth associated reproduction number R_r is defined (Goldstein et al. (2009)) by

$$R_r = 1/M_W(r),$$

i.e. by estimate of R_0 from real-time growth rate r ignoring household structure of population (e.g. Wallinga and Lipsitch (2007)).

Comparison of R_r and R_0

- Real-time growth rate r satisfies

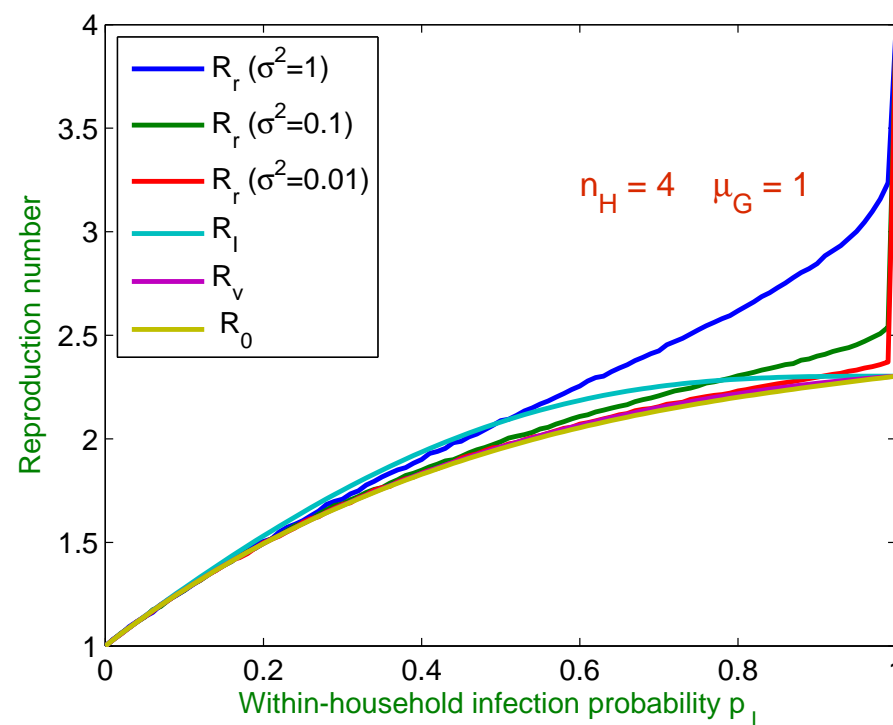
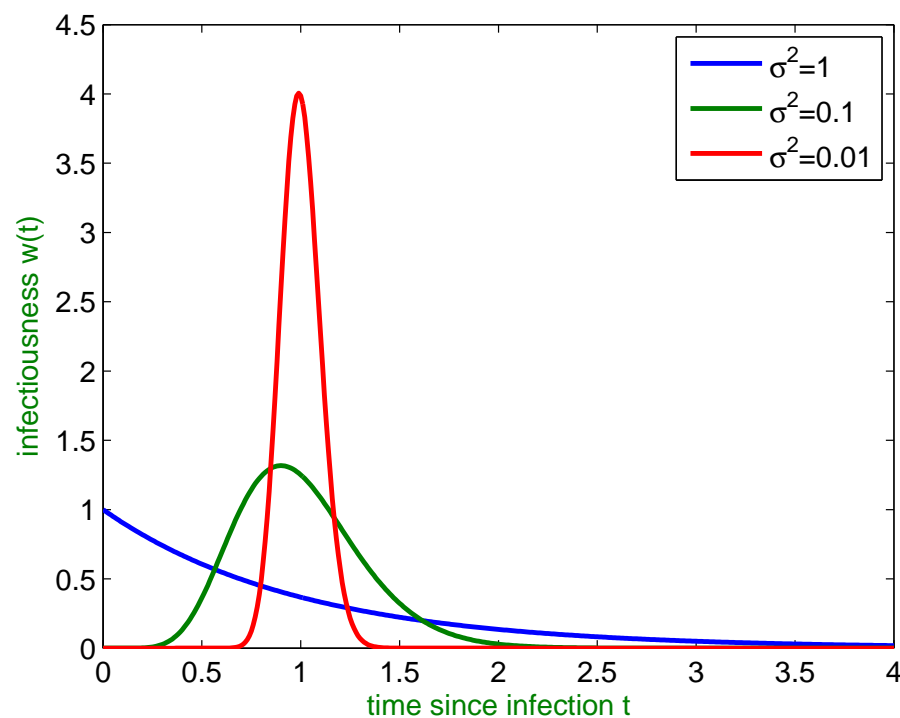
$$\int_0^{\infty} e^{-rt} \beta_H(t) dt = 1,$$

where $\beta_H(t)$ is the expected rate global contacts emanate from a typical single-household epidemic t time units after its infection.

- Proving comparisons between R_0 and R_r is generally difficult as $\beta_H(t)$ is complicated.
- $\text{var}(W) = 0 \implies R_r = R_0$.
- If the infectivity profile $\{\Lambda(a) : a \geq 0\}$ takes the form (i) $\Lambda(a) = Jw(a)$ for some random variable $J \geq 0$ with $\mathbb{E}[J] = 1$ or (ii) $\Lambda(a) = f(a)1_{\{I>a\}}$ for some deterministic function f , then

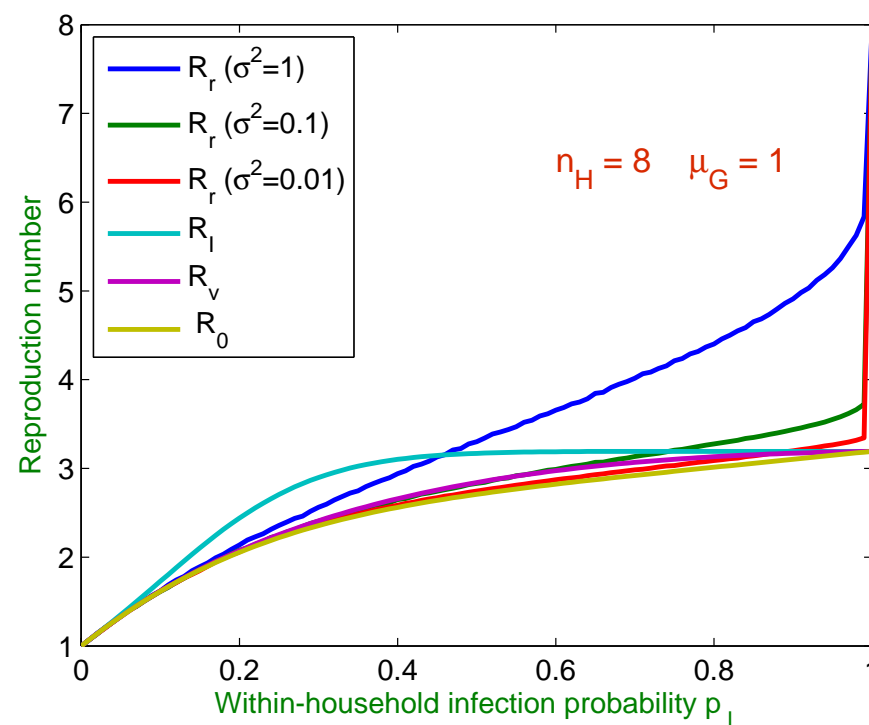
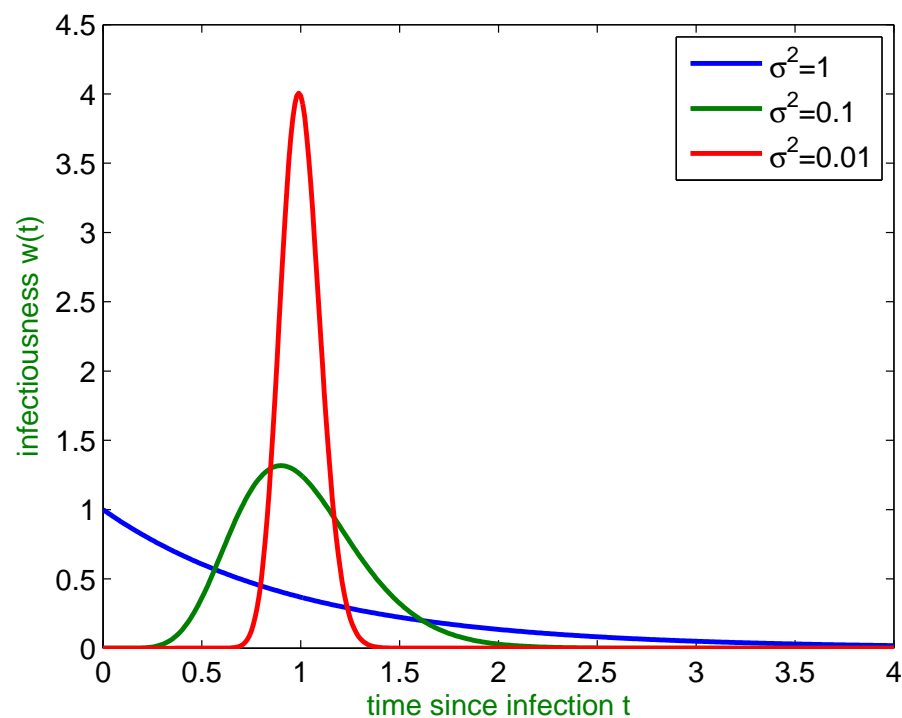
$R_r \geq R_0$ in a growing epidemic and $R_r \leq R_0$ in a declining epidemic.

Households model reproduction numbers



Reproduction numbers for **households** model with $\mu_G = 1$, household size = **4** and **non-random infectivity profile** $\Lambda(t) \equiv w(t)$ that follows a **gamma** distribution with mean **1**.

Households model reproduction numbers



Reproduction numbers for **households** model with $\mu_G = 1$, household size = **8** and **non-random infectivity profile** $\Lambda(t) \equiv w(t)$ that follows a **gamma** distribution with mean **1**.

Concluding comments

- Extends to other models with social structure such as the **households-workplaces** model.
- Needs an underlying **branching process** at some level for the **threshold** $R_0 = 1$ to have a meaningful interpretation.
- $R_r \geq R_0$ in a **growing** epidemic and $R_r \leq R_0$ in a **declining** epidemic.
- **Critical vaccination coverage** $v_c = 1 - R_0^{-1}$ if **ALL** households have **size** ≤ 3 , otherwise $v_c > 1 - R_0^{-1}$.