$R_0$ for structured population epidemic models

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Outline of talk

- Households model and $R_0$.
- $R_0$ 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.


Households SIR epidemic model

$m_n$ households of size $n$

($n = 1, 2, \cdots, n_{\text{max}}$)

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

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

- **SIR** (susceptible $\rightarrow$ infective $\rightarrow$ recovered)
- Infectious period $\sim I$, having an arbitrary but specified distribution
- Infection rates (individual $\rightarrow$ individual)
  - (i) local (within-household) $\lambda_L$
  - (ii) global (between-household) $\lambda_G/N$
- 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

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

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

![Graph showing comparison of vaccination strategies]

- Random individuals
- Random households
- Optimal
- Worst
- \( R_v = 1 \)

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Network–households model

- Individuals infect along household edges at rate $\lambda_L$ and global edges at rate $\lambda_G$.
- 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 $\lambda_L = \lambda_G = 1/5$. 
Suppose there is one initial infective in a population of size $N$. Let $Y_k^{(N)}$ be the number of generation-$k$ infectives.
Following Trapman (2007), define $R_0$ by

$$R_0 = \lim_{k \to \infty} \lim_{N \to \infty} \left( E \left[ Y^{(N)}_k \right] \right)^{\frac{1}{k}}.$$  

(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 $N \to \infty$. 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

Let $\mu_i^{(n)}$ be the mean number of cases in generation $i$ of a single (size-$n$) household epidemic ($\mu_0 = 1$).

Let $\mu_i = \sum_{n=i+1}^{n_{\text{max}}-1} \tilde{\alpha}_n \mu_i^{(n)}$ 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)).
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 $\mu_G = \lambda_G E[I]$ be the mean number of global infections made by a typical infective. Then $R_0$ is the unique positive root of the discrete-time Lokta-Euler equation

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

where

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

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

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Suppose that infectives have iid infectivity profiles \( \{ \Lambda(a) : a \geq 0 \} \) satisfying \( E[\int_0^\infty \Lambda(a) da] = 1 \).

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 \( w(t) = E[\Lambda(t)] \ (t > 0) \) and Laplace transform \( M_W(\theta) = E[e^{-\theta W}] = \int_0^\infty e^{-\theta a} E[\Lambda(a)] da \).

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) $\Lambda(a) = J w(a)$ 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.
Reproduction numbers for households model with $\mu_G = 1$, household size $n_H = 8$ 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 $\leq 3$, otherwise $v_c > 1 - R_0^{-1}$. 