Epidemics on networks

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Outline of lecture

- Vaccination for SIR epidemics on configuration model networks
  - uniform vaccination,
  - acquaintance vaccination.
- Network-households model
  - threshold behaviour,
  - final outcome.
- Vaccination in network-households model
  - household-based vaccination schemes,
  - acquaintance vaccination.

Reminder on notation

- Configuration model network on population $\mathcal{N} = \{1, 2, \cdots, n\}$.
  - D= degree of typical individual; $p_k = \mathrm{P}(D = k) \quad (k = 0, 1, \cdots)$,

$$\mu_D = \mathrm{E}[D] \qquad \text{and} \qquad f_D(s) = \mathrm{E}[s^D].$$

  - $\tilde{D}$ = degree of typical neighbour of an individual,

$$\tilde{p}_k = \mathrm{P}(\tilde{D} = k) = \mu_D^{-1} k p_k \qquad (k = 1, 2, \cdots).$$

- SIR (susceptible $\to$ infective $\to$ recovered) epidemic.
  - infectious period $\sim I$; $\phi_I(\theta) = \mathrm{E}[\mathrm{e}^{-\theta I}]$.
  - individual-to-individual contact rate λ;

$$p_I = \mathrm{P}(\text{infective infects a given neighbour}) = 1 - \phi_I(\lambda).$$

- Basic reproduction number $R_0 = \mu_{\tilde{D}-1} p_I = \left(\mu_D + \mu_D^{-1}\sigma_D^2 - 1\right) p_I$.

Uniform vaccination

- Suppose that a proportion c, chosen uniformly at random, of the population is vaccinated with a perfect vaccine. Then R_0 is reduced to $R_v = (1-c)R_0$, so, if $R_0 > 1$,

  $R_v \leq 1 \iff c \geq 1 - R_0^{-1}$ – critical vaccination coverage c_{crit}

- Recall that $R_0 = \left(\mu_D + \frac{\sigma_D^2}{\mu_D} - 1\right) p_I$, so if $\sigma_D^2 = \infty$ then $c_{\text{crit}} = 1$!

Acquaintance vaccination

- Method of targetting high-degree individuals for vaccination.
- Each individual in the population is independently sampled a Poisson number of times with mean κ.
- Each time an individual is sampled it chooses a neighbour uniformly at random (with replacement), who is then nominated for vaccination.
- All individuals who are nominated at least once are vaccinated.
- The probability that an individual is not named by a given neighbour is

$$\alpha = \sum_{d=1}^{\infty} \tilde{p}_d \mathrm{e}^{-\kappa/d} \qquad [\tilde{p}_d = \mathrm{P}(\tilde{D} = d)],$$

so the vaccination coverage is

$$c(\kappa) = 1 - \sum_{d=0}^{\infty} p_d \alpha^d = 1 - f_D(\alpha) \qquad [p_d = \mathrm{P}(D = d)].$$

(Cohen, Havlin and ben-Avraham (2003), Britton, Janson and Martin-Löf (2007))

Perfect vaccine threshold parameter R_v

- Approximating forward branching process (BP) involves only unvaccinated (i.e. unnamed) individuals.
- Consider typical individual i^* in non-initial generation of this BP; denote its degree by $\tilde{D}_U$. Unconditionally, i^*'s degree is distributed as $\tilde{D}$, but we know that (i) i^* is unvaccinated (U) and (ii) i^* did not name its infector for vaccination (N^c). Hence, for $d = 1, 2, \ldots$,

$$\mathrm{P}(\tilde{D}_U = d) = \mathrm{P}(\tilde{D} = d | U, N^c) = \frac{\mathrm{P}(\tilde{D} = d, U, N^c)}{\mathrm{P}(U, N^c)} = \frac{\tilde{p}_d \alpha^{d-1} \mathrm{e}^{-\kappa/d}}{\sum_{k=1}^{\infty} \tilde{p}_k \alpha^{k-1} \mathrm{e}^{-\kappa/k}}$$

and

$$\mathrm{P}(U|N^c) = \frac{\sum_{k=1}^{\infty} \tilde{p}_k \alpha^{k-1} \mathrm{e}^{-\kappa/k}}{\sum_{k=1}^{\infty} \tilde{p}_k \mathrm{e}^{-\kappa/k}} = \sum_{k=1}^{\infty} \tilde{p}_k \alpha^{k-2} \mathrm{e}^{-\kappa/k}.$$

- $R_v = \sum_{d=1}^{\infty} \mathrm{P}(\tilde{D}_U = d)(d-1)\mathrm{e}^{-\kappa/d}\mathrm{P}(U|N^c)p_I = p_I \sum_{d=1}^{\infty} \tilde{p}_d \alpha^{d-2} \mathrm{e}^{-2\kappa/d}(d-1)$.
- Critical vaccination coverage is < 1 even if $\sigma_D^2 = \infty$.

Vaccine response model

- Response of vaccinated individual described by a random vector (A, B)

  A = relative susceptibility compared to an unvaccinated individual

  [all infection rates to that individual are multiplied by A]

  B = relative infectivity should vaccinee become infected

  [all infection rates from that individual are multiplied by B]

- All-or-nothing $\mathrm{P}(A = 0, B = 0) = 1 - \mathrm{P}(A = 1, B = 1) = \varepsilon$

  Non-random $\mathrm{P}(A = a, B = b) = 1$

  Leaky $a = 1 - \varepsilon, b = 1$

- Vaccine efficacy: $VE_{\mathrm{SI}} = 1 - \mathrm{E}[AB]$ $(= \varepsilon)$

(Becker and Starczak (1998))

Marginal transmission probabilities

- Let p_{UV} be the probability that a given unvaccinated infective infects a given vaccinated susceptible neighbour and define p_{UU}, p_{VU} and p_{VV} similarly.
- All-or-nothing vaccine

$$P^{AoN} = \begin{bmatrix} p_{UU}^{AoN} & p_{UV}^{AoN} \\ p_{VU}^{AoN} & p_{VV}^{AoN} \end{bmatrix} = p_I \begin{bmatrix} 1 & 1-\varepsilon \\ 1 & 1-\varepsilon \end{bmatrix}$$

- Non-random vaccine

$$P^{NR} = \begin{bmatrix} p_{UU}^{NR} & p_{UV}^{NR} \\ p_{VU}^{NR} & p_{VV}^{NR} \end{bmatrix} = \begin{bmatrix} 1-\phi_I(\lambda) & 1-\phi_I(a\lambda) \\ 1-\phi_I(b\lambda) & 1-\phi_I(ab\lambda) \end{bmatrix}$$

Acquaintance vaccination

- Suppose that the vaccine is imperfect, so some vaccinated individuals become infected. Forward and backward BPs may include vaccinated individuals, which can lead to sibling dependence.
- In forward BP, individuals need to be typed by their vaccination status (N, V or U) and by their degree d, leading to the type space $\mathcal{T} = \{N_d, V_d, U_d : d = 1, 2, \ldots\}$, where
  - N means an individual was named by its infector and hence is vaccinated
  - V means it was not named by its infector but is still vaccinated (i.e. it was named by another neighbour)
  - U means it is unvaccinated (i.e. not named by any neighbour)
- A similar typing is required in the backward BP.

Forward process mean matrix

- Mean matrix $M = (m_{t,t'},\, t, t' \in \mathcal{T})$, where $\mathcal{T} = \{N_d, V_d, U_d : d = 1, 2, \ldots\}$.
- Type N_d individual
  - The degrees of its $d-1$ forward neighbours are independent copies of $\tilde{D}$.
  - Each such neighbour is named with probability $1 - \mathrm{e}^{-\kappa/d}$. If the neighbour is of degree d' and not named then it is unvaccinated with probability $\alpha^{d'-1}$, otherwise it is vaccinated.
  - For $d, d' = 1, 2, \ldots$,

$$
\begin{aligned}
m_{N_d,N_{d'}} &= (d-1)(1-\mathrm{e}^{-\kappa/d})\tilde{p}_{d'}p_{VV}, \\
m_{N_d,V_{d'}} &= (d-1)\mathrm{e}^{-\kappa/d}\tilde{p}_{d'}(1-\alpha^{d'-1})p_{VV}, \\
m_{N_d,U_{d'}} &= (d-1)\mathrm{e}^{-\kappa/d}\tilde{p}_{d'}\alpha^{d'-1}p_{VU}.
\end{aligned}
$$

Forward process mean matrix

- Type U_d individual, i^*.
  - Each of i^*'s $d-1$ forward neighbours failed to name i^*, so the degrees of these $d-1$ neighbours are independent copies of the random variable $\tilde{D}^U$ having distribution $\mathrm{P}(\tilde{D}^U = d') = \alpha^{-1}\tilde{p}_{d'}\mathrm{e}^{-\kappa/d'}$ $(d' = 1, 2, \ldots)$.
  - Each such neighbour is named with probability $1 - \mathrm{e}^{-\kappa/d}$. If the neighbour is of degree d' and not named then it is unvaccinated with probability $\alpha^{d'-1}$, otherwise it is vaccinated.
  - For $d, d' = 1, 2, \ldots$,

$$
\begin{aligned}
m_{U_d,N_{d'}} &= (d-1)(1-\mathrm{e}^{-\kappa/d})\tilde{p}_{d'}\mathrm{e}^{-\kappa/d'}\alpha^{-1}p_{UV}, \\
m_{U_d,V_{d'}} &= (d-1)\mathrm{e}^{-\kappa/d}\tilde{p}_{d'}\mathrm{e}^{-\kappa/d'}\alpha^{-1}(1-\alpha^{d'-1})p_{UV}, \\
m_{U_d,U_{d'}} &= (d-1)\mathrm{e}^{-\kappa/d}\tilde{p}_{d'}\mathrm{e}^{-\kappa/d'}\alpha^{-1}\alpha^{d'-1}p_{UU}.
\end{aligned}
$$

Forward process mean matrix

- Type V_d individual, i^*. Note d must be ≥ 2.
  - Let $D_1^V, D_2^V, \ldots, D_{d-1}^V$ denote the degrees of i^*'s $d-1$ forward neighbours. At least one of these neighbours named i^*, so

$$\mathrm{P}(D_1^V = d_1', \ldots, D_{d-1}^V = d_{d-1}') = \frac{\tilde{p}_{d_1'}\tilde{p}_{d_2'}\cdots\tilde{p}_{d_{d-1}'}\,(1 - \mathrm{e}^{-\kappa/d_1'}\mathrm{e}^{-\kappa/d_2'}\cdots\mathrm{e}^{-\kappa/d_{d-1}'})}{1-\alpha^{d-1}}.$$

  - Thus, $D_1^V, D_2^V, \ldots, D_{d-1}^V$ are dependent, though exchangeable, with

$$\mathrm{P}(D_1^V = d_1') = \frac{\tilde{p}_{d_1'}}{1-\alpha^{d-1}}\,(1 - \mathrm{e}^{-\kappa/d_1'}\alpha^{d-2}) \qquad (d_1' = 1, 2, \ldots).$$

  - For $d = 2, 3, \ldots$ and $d' = 1, 2, \ldots$,

$$\begin{aligned}
m_{V_d,N_{d'}} &= (d-1)(1-\mathrm{e}^{-\kappa/d})\tilde{p}_{d'}(1-\mathrm{e}^{-\kappa/d'}\alpha^{d-2})(1-\alpha^{d-1})^{-1}p_{VV},\\
m_{V_d,V_{d'}} &= (d-1)\mathrm{e}^{-\kappa/d}\tilde{p}_{d'}(1-\mathrm{e}^{-\kappa/d'}\alpha^{d-2})(1-\alpha^{d-1})^{-1}(1-\alpha^{d'-1})p_{VV},\\
m_{V_d,U_{d'}} &= (d-1)\mathrm{e}^{-\kappa/d}\tilde{p}_{d'}(1-\mathrm{e}^{-\kappa/d'}\alpha^{d-2})(1-\alpha^{d-1})^{-1}\alpha^{d'-1}p_{VU}.
\end{aligned}$$

Threshold behaviour

- If D has finite support then standard multitype branching process theory applies, so assume that D has countable support and for simplicity that $p_d > 0$ $(d = 1, 2, \ldots)$.
- Except for the initial generation, individuals with degree 1 have no offspring in the forward branching process.
- Let $\tilde{\mathcal{B}}_F$ be the BP process with type space $\tilde{\mathcal{T}} = \{N_d, V_d, U_d : d = 2, 3, \ldots\}$ and offspring distributions defined implicitly above.
- For $d^* = 2, 3, \ldots$, let $\tilde{\mathcal{B}}_F^{(d^*)}$ be the BP derived from $\tilde{\mathcal{B}}_F$ by ignoring all individuals with degree $> d^*$ (and their progeny).
- For $t \in \tilde{\mathcal{T}}$, let $\tilde{\pi}_t$ be the probability that $\tilde{\mathcal{B}}_F$ goes extinct given that initially there is one individual whose type is t. Define $\tilde{\pi}_t^{(d^*)}$ similarly for $\tilde{\mathcal{B}}_F^{(d^*)}$.

Threshold parameter R_A

- Let $\tilde{M}$ and $\tilde{M}^{(d^*)}$ be the mean offspring matrices for $\tilde{\mathcal{B}}_F$ and $\tilde{\mathcal{B}}_F^{(d^*)}$.
- Every element of $\tilde{M}$ is strictly positive, so

$$\tilde{\pi}_t < 1 \iff \tilde{\pi}_{t'} < 1 \quad (t, t' \in \tilde{\mathcal{T}}).$$

- Let $R_A^{(d^*)}$ be the dominant eigenvalue of $\tilde{M}^{(d^*)}$. Then $\left(R_A^{(d^*)}\right)$ is strictly increasing, so let $R_A = \lim_{d^* \to \infty} R_A^{(d^*)}$.
- Let t_0 be the type U_2. There exists $p_0 > 0$ such that, for any $t \in \tilde{\mathcal{T}}$, the probability a type-t individual has at least one type-t_0 child is at least p_0. Exploiting natural single-type (t_0) Galton–Watson processes embedded in $\tilde{\mathcal{B}}_F$ and $\tilde{\mathcal{B}}_F^{(d^*)}$ $(d^* \geq 2)$ then yields, for $t \in \tilde{\mathcal{T}}$, that

$$\tilde{\pi}_t = \lim_{d \to \infty} \tilde{\pi}_t^{(d^*)} \qquad \text{and} \qquad \tilde{\pi}_t < 1 \iff R_A > 1.$$

New acquaintance vaccination model

- The original model for acquaintance vaccination is generally numerically infeasible for imperfect vaccines as the type space required for analysis is too large.
- Problem caused by degrees of neighbours of vaccinated individuals being dependent which gives rise to sibling dependence in approximating branching processes.
- Ball and Sirl (2013) proposed a new model for acquaintance vaccination which circumvents these difficulties.

New acquaintance vaccination model

- Each individual in the population is sampled independently with probability p_S.
- Each sampled individual nominates each of its neighbours independently with probability p_N.
- All individuals who are nominated at least once are vaccinated.
- The probability that an individual is not named by a given neighbour is $\alpha = 1 - p_N p_S$, so the vaccination coverage is

$$c(p_S, p_N) = 1 - \sum_{d=0}^{\infty} p_d \alpha^d = 1 - f_D(\alpha).$$

- The probability that a given individual, i^* say, nominates a given neighbour is now independent of i^*'s degree, so the sibling dependence problems are alleviated.

Perfect vaccine threshold parameter R_v

- Approximating forward branching process (BP) involves only unvaccinated (i.e. unnamed) individuals.
- Consider typical individual i^* in non-initial generation of this BP; denote its degree by $\tilde{D}_U$.

$$\mathrm{P}(\tilde{D}_U = d) = \mathrm{P}(\tilde{D} = d|U) = \frac{\mathrm{P}(\tilde{D} = d, U)}{\mathrm{P}(U)} = \frac{\tilde{p}_d \alpha^{d-1}}{\sum_{k=1}^{\infty} \tilde{p}_k \alpha^{k-1}} = \frac{\tilde{p}_d \alpha^{d-1}}{f_{\tilde{D}-1}(\alpha)}.$$

and, since i^* did not name its infector for vaccination (N^c),

$$\tilde{p}_{SU} = \mathrm{P}(i^* \text{ sampled}|N^c) = \frac{p_S(1-p_N)}{1-p_S p_N} = \frac{p_S(1-p_N)}{\alpha}.$$

- $R_v = \mu_{\tilde{D}_U - 1}[1 - \tilde{p}_{SU} + \tilde{p}_{SU}(1-p_N)] f_{\tilde{D}-1}(\alpha) p_I$.
- Critical vaccination coverage is < 1 even if $\sigma_D^2 = \infty$.

Perfect vaccine

- Vaccination coverage is $c = 1 - f_D(\alpha)$, where $\alpha = 1 - p_S p_N$.
- Post-vaccination basic reproduction number

$$R_v = p_I \left[\alpha - (1-\alpha)(1-p_N)\right] f^{(1)}_{\tilde{D}-1}(\alpha).$$

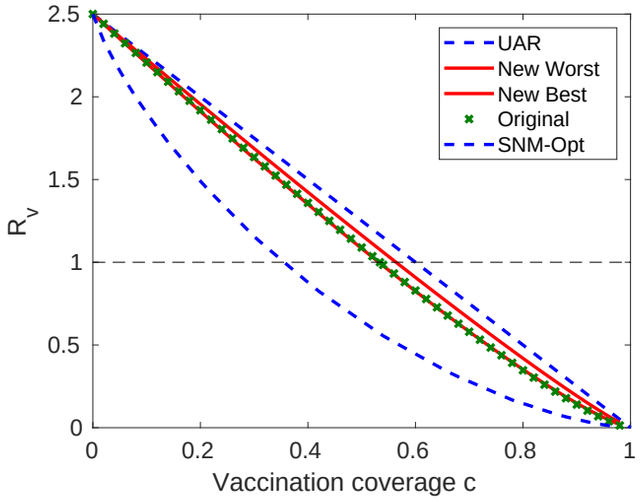
- For fixed vaccination coverage (and hence fixed α), R_v is greatest when $p_N = 1$ (so $p_S = 1 - \alpha$) [WORST model] and R_v is least when $p_S = 1$ (so $p_N = 1 - \alpha$) [BEST model].

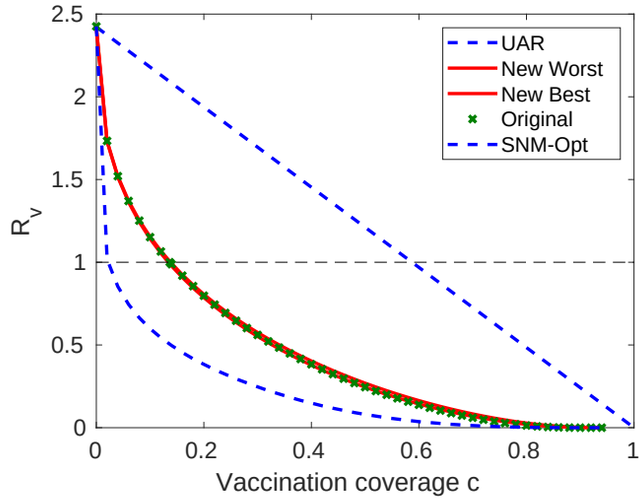
Imperfect vaccine

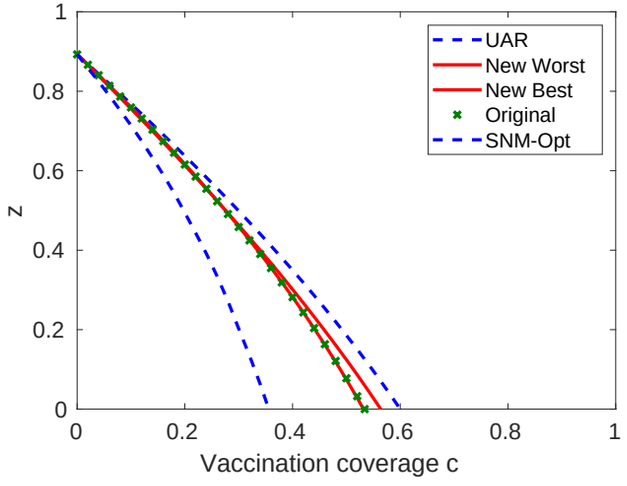
- In the forward and backward BPs individuals are typed by
  - whether they are named (N), vaccinated (V) or unvaccinated (U), as before, and
  - whether or not they are sampled and thus might name their neighbours for vaccination (S and S^c),

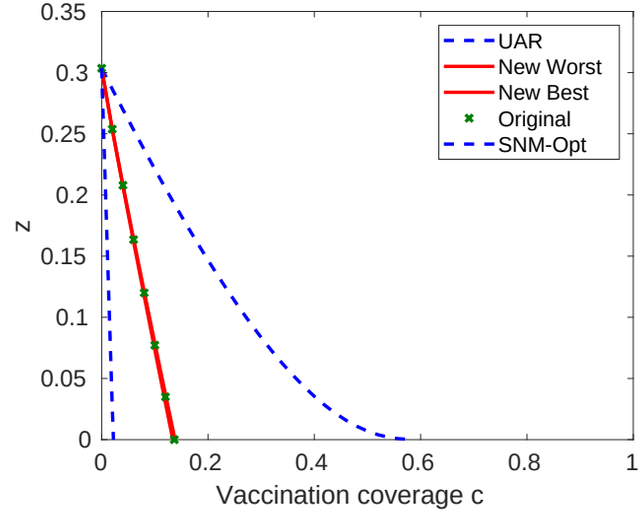
  so there are 6 types of individuals: (N, S), (V, S), (U, S), (N, S^c), (V, S^c) and (U, S^c).
- Post-vaccination threshold parameter R_v, probability of a major epidemic ($p_{\mathrm{maj}}^{(U)}$ and $p_{\mathrm{maj}}^{(V)}$) and large-population proportions of vaccinated and unvaccinated individuals ultimately infected by a major epidemic ($z^{(U)}$ and $z^{(V)}$) are derived using multitype BPs in the obvious fashion.

Perfect vaccine R_v and z





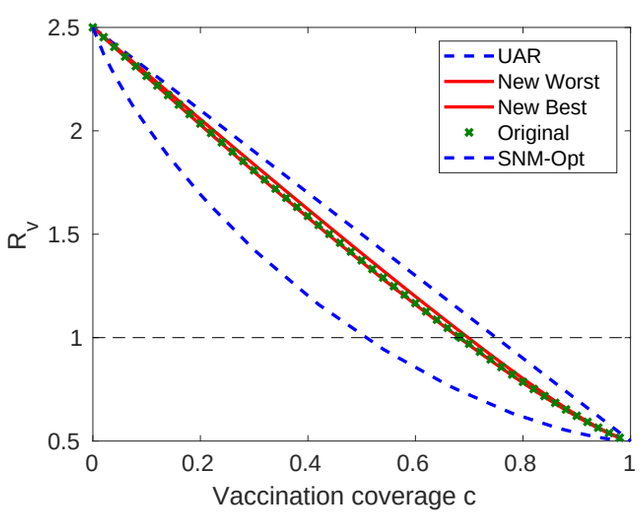


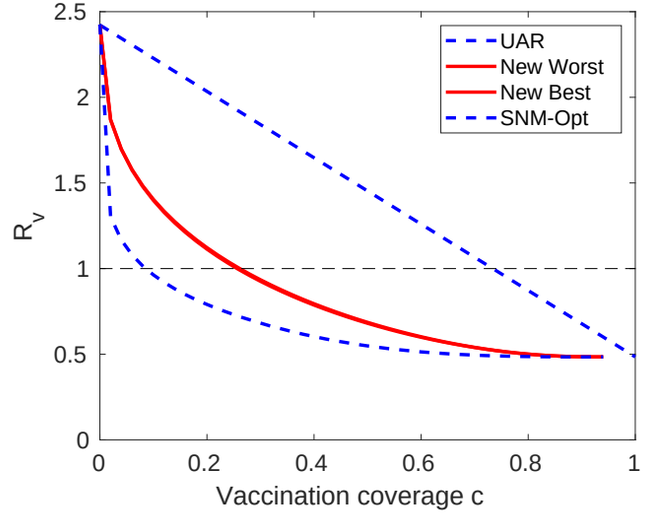


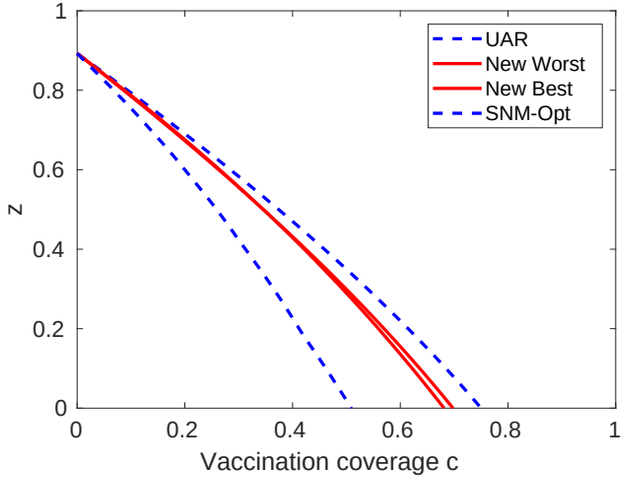
LEFT: $D \sim \text{Poisson}(10), I \sim \text{Exp}(3), \lambda = 1$

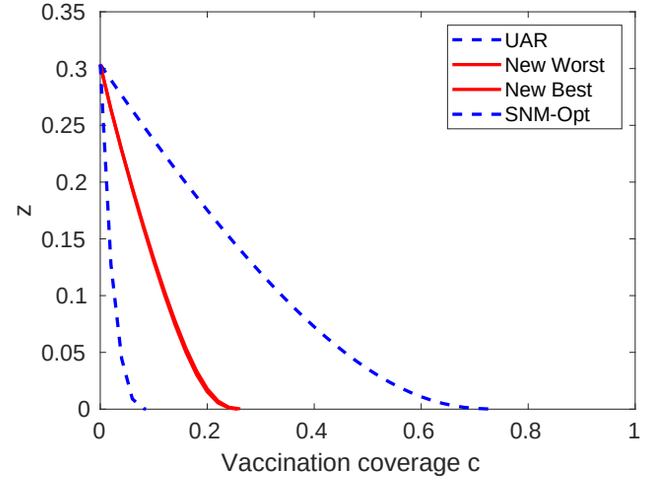
RIGHT: $\mathrm{P}(D = k) \propto (\max(12, k))^{-3.4}$ $(k = 1, 2, \cdots), I \sim \text{Exp}(10), \lambda = 1$.

All-or-nothing vaccine, $\varepsilon = 0.8$









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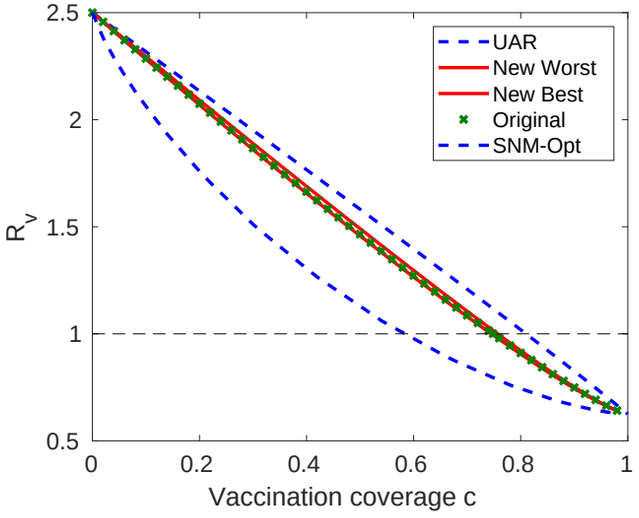
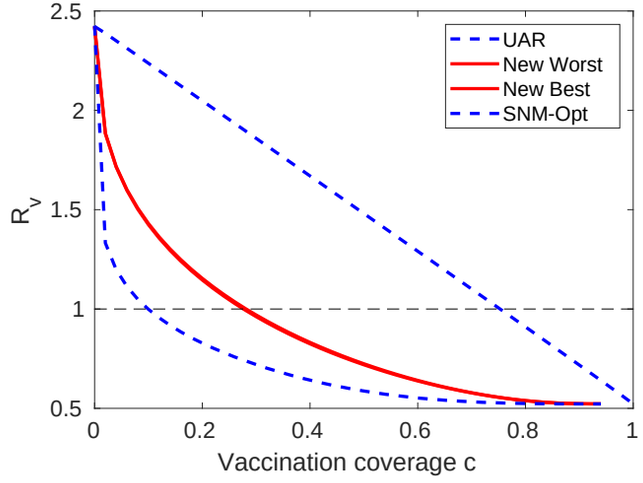
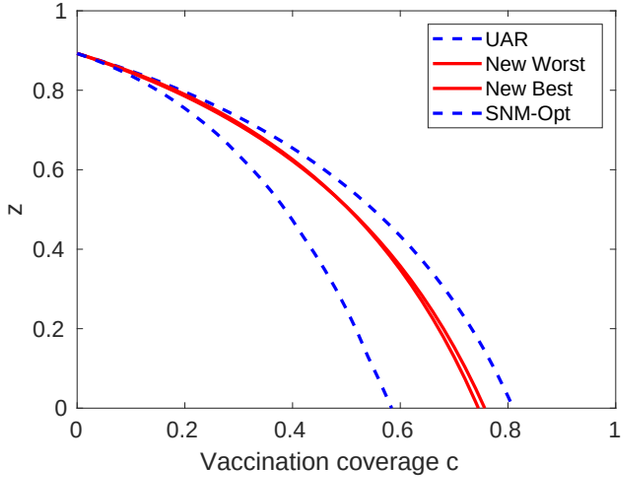
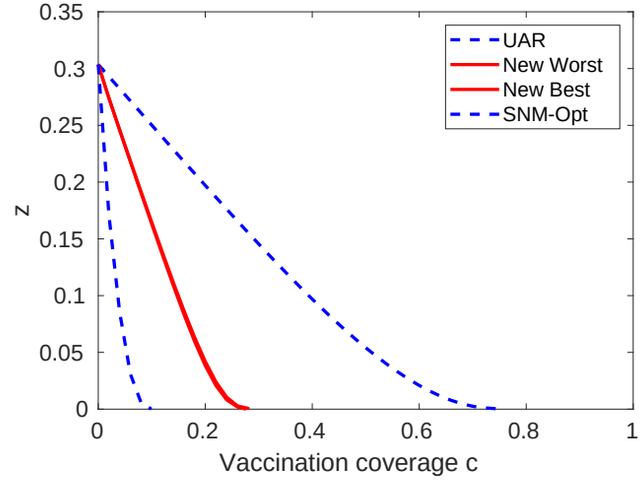
RIGHT: $\text{P}(D = k) \propto (\max(12, k))^{-3.4}$ $(k = 1, 2, \cdots), I \sim \text{Exp}(10), \lambda = 1$.

Non-random vaccine, $a = b = \sqrt{0.2}$









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Network–households model

- Population structure

  Population of N individuals partitioned into m households, of which m_n are of size n $(n = 1, 2, \ldots)$.

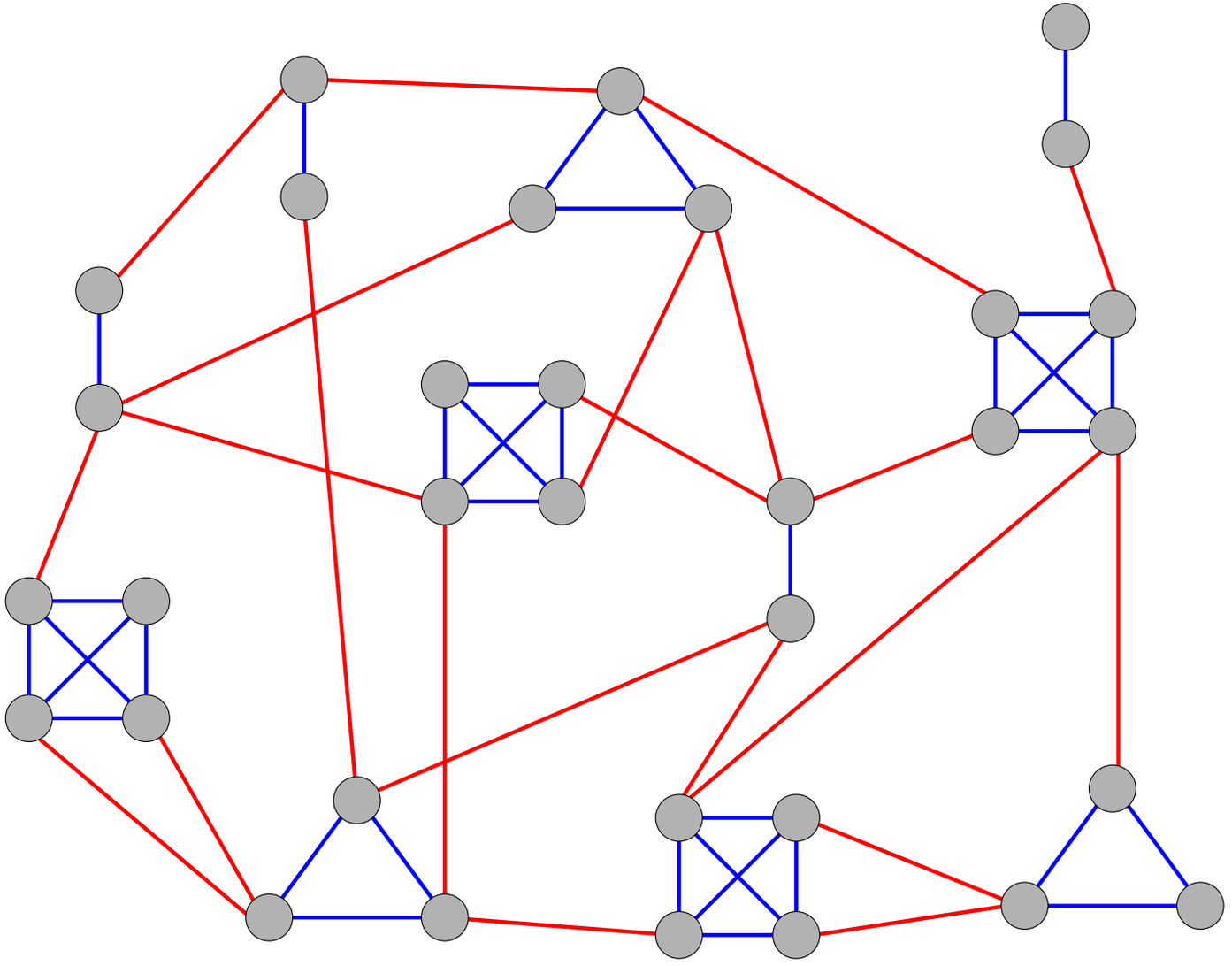
  - Configuration model with degree random variable D for network of possible global contacts.

- SIR epidemic model

  - Infectious periods $\overset{\text{iid}}{\sim} I$.
  - Whilst infectious, individuals contact each of their local (global) neighbours independently at rate λ_{L} (λ_{G}).
  - Single initial infective chosen uniformly at random from entire population.

(Ball, Sirl and Trapman (2009,2010); cf. Stegehuis, van der Hofstad and van Leeuwaarden (2016))

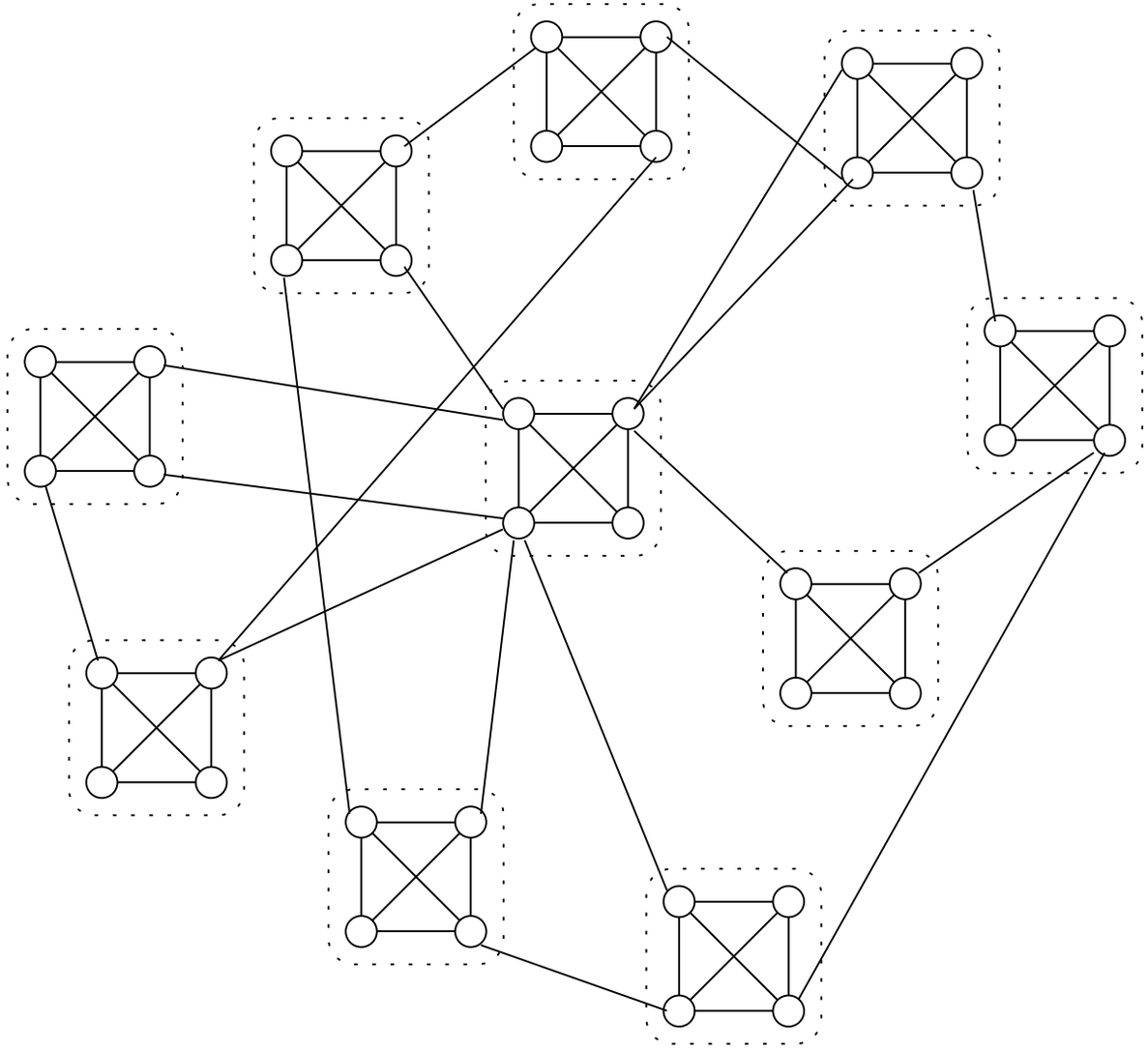
Example of (very small) population



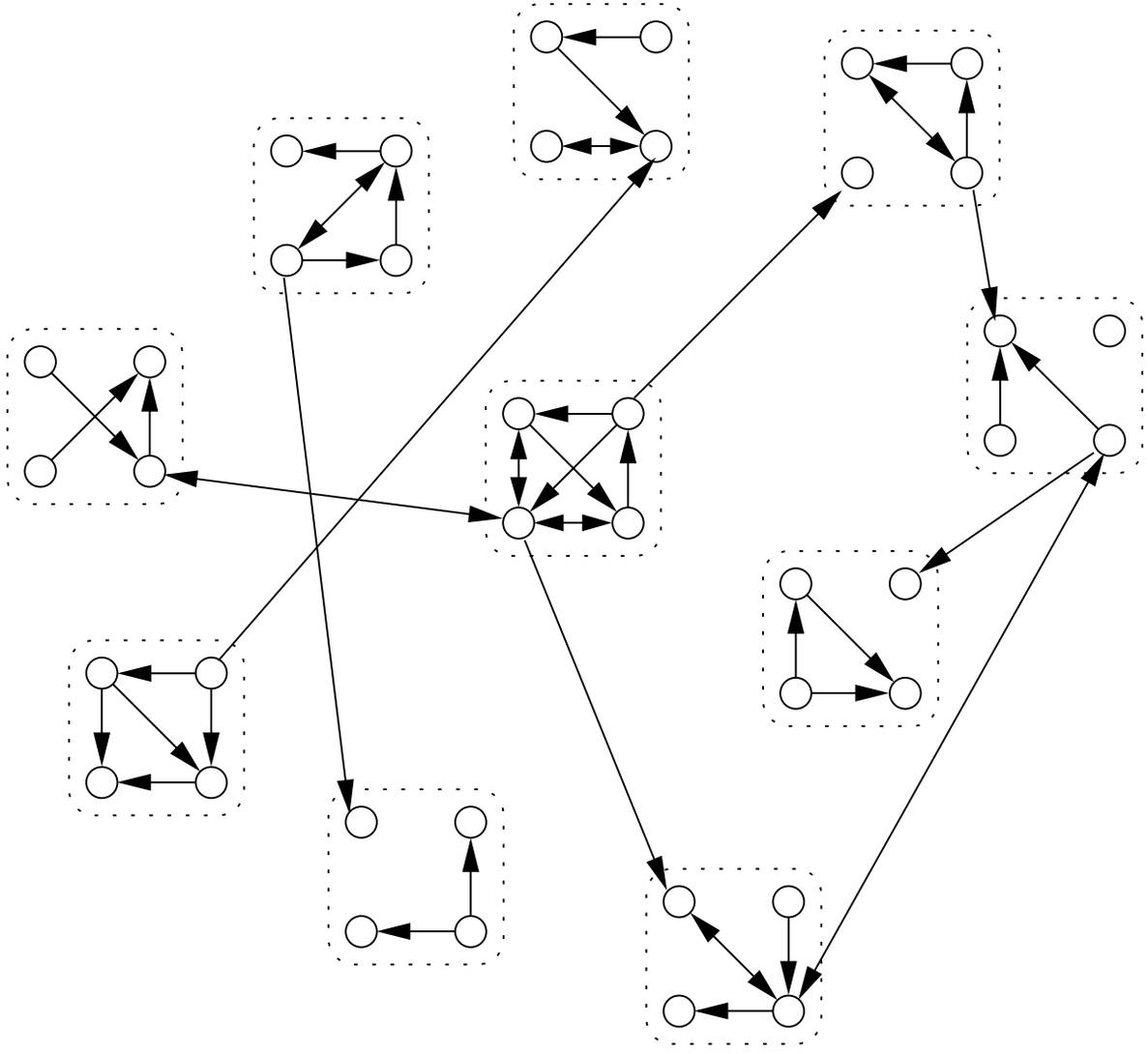
Why households?

- Household structure is a key component of human populations which can have significant impact on disease dynamics.
- There are outbreak control measures associated with households and similar structures (e.g. schools and workplaces)
- Epidemic data are often collected at the household level
- Households models are mathematically reasonably tractable and consequently are generally easier to interpret than complex simulation models
- A tool for incorporating clustering into a network ($\lambda_{\mathrm{L}} = \lambda_{\mathrm{G}}$);
  cf. Trapman (2007) and Coupechoux and Lelarge (2014).

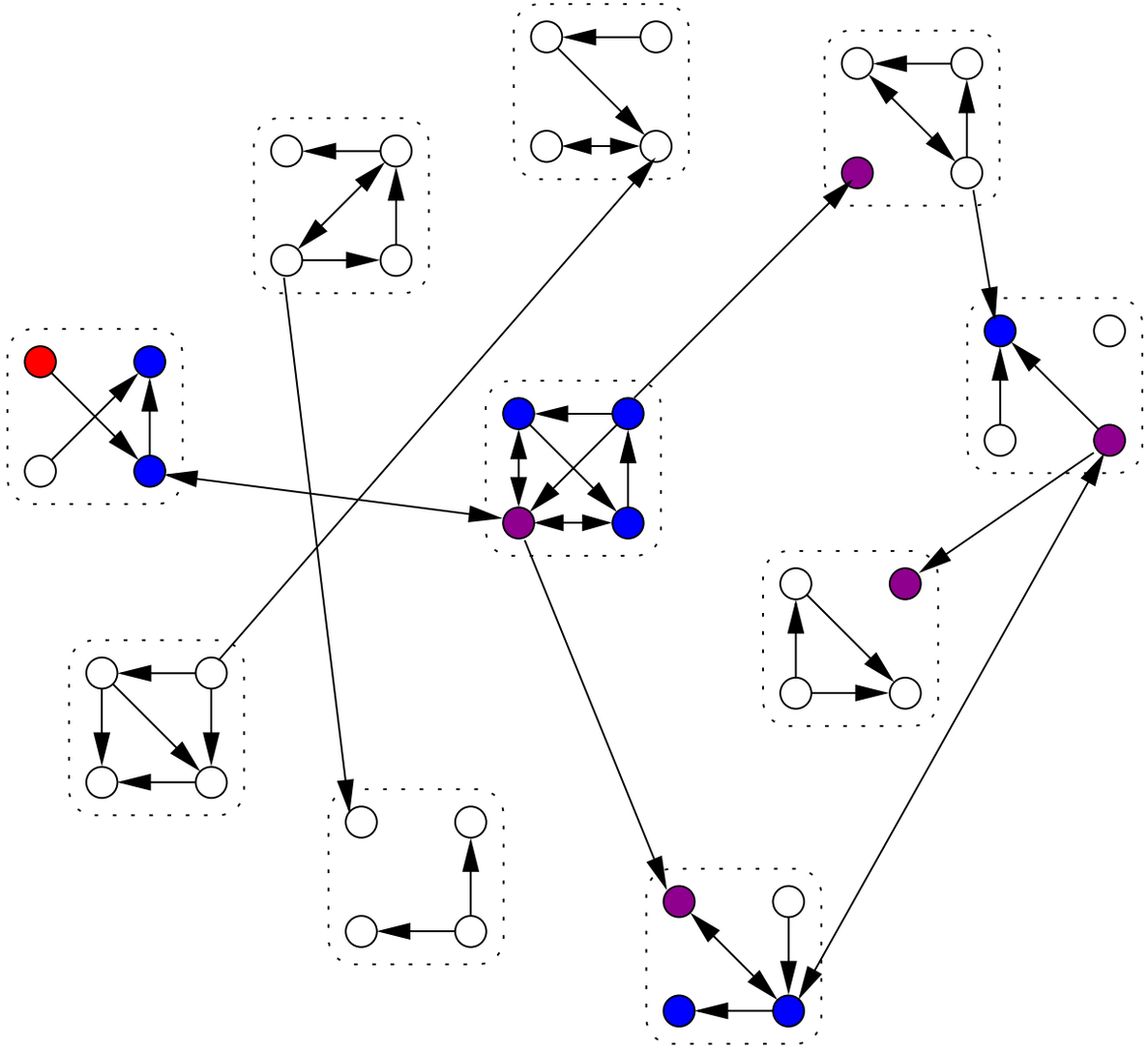
Example network



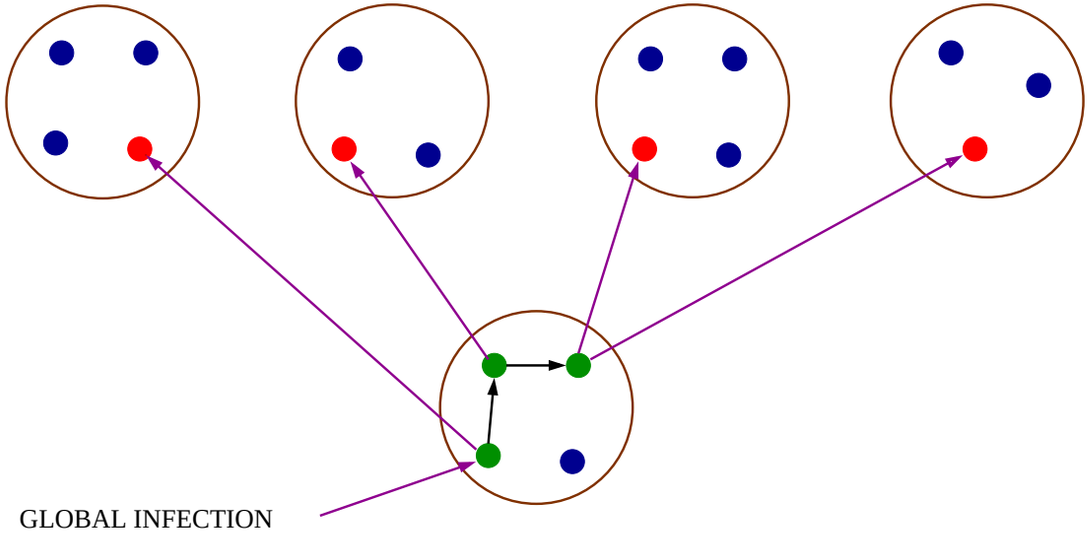
Digraph of potential infections



Realisation of epidemic



Threshold parameter R_*



- R_* = mean number of global neighbours infected by a typical single-household epidemic

$$R_* = \sum_{n=1}^{\infty} \tilde{\rho}_n \mathrm{E}[\tilde{C}^{(n)}],$$

where

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

$\tilde{C}^{(n)}$ = number of global neighbours infected by a typical [size-n] single-household epidemic with one initial infective.

- $\mathrm{P}(\text{major outbreak}) > 0 \iff R_* > 1$.

Calculation of $\mathrm{E}[\tilde{C}^{(n)}]$

- $\mathrm{E}[\tilde{C}^{(n)}] = \mathrm{E}[C_0] + \mathrm{E}[T^{(n)}]\mathrm{E}[C_1]$,
  - $T^{(n)} =$ final size of single-household epidemic (excluding initial case),
  - C_0 and C_1 are the numbers of global neighbours infected by the primary and typical secondary infective in the household.
- $C_i \sim \mathrm{Bin}(K_i, 1 - \exp(-\lambda_{\mathrm{G}} I_i)) \implies \mathrm{E}[C_i] = \mathrm{E}[K_i] p_{\mathrm{G}}$,
  - K_0 and K_1 are the numbers of global neighbours of primary and typical secondary case,
  - $p_{\mathrm{G}} = 1 - \mathrm{E}[\exp(-\lambda_{\mathrm{G}} I)]$ is the probability an infective infects a given global neighbour.
- For initial generation, $K_0, K_1 \sim D$. For all subsequent generations, $K_0 \sim \tilde{D} - 1$ and $K_1 \sim D$.

Threshold parameter R_*

$$
\begin{aligned}
R_* &= \sum_{n=1}^{\infty} \tilde{\rho}_n \mathrm{E}[\tilde{C}^{(n)}] \\
&= \sum_{n=1}^{\infty} \tilde{\rho}_n \left(\mathrm{E}[C_0] + \mathrm{E}[C_1]\mathrm{E}[T^{(n)}] \right) \\
&= \sum_{n=1}^{\infty} \tilde{\rho}_n \left(\mu_{\tilde{D}-1} + \mu_D \mu_{T^{(n)}} \right) p_{\mathrm{G}} \\
&= \left(\mu_D(\mu_T + 1) + \frac{\sigma_D^2}{\mu_D} - 1 \right) p_{\mathrm{G}},
\end{aligned}
$$

where $\mu_T = \sum_{n=1}^{\infty} \tilde{\rho}_n \mu_{T^{(n)}}$ is the size-biased mean within-household final size.

Early stages of epidemic

- Approximate process of infected households by a (forward) branching process $\mathcal{B}_F = \mathrm{BP}(1, C, \tilde{C})$ having one initial ancestor, and offspring distribution C for the initial generation and $\tilde{C}$ in subsequent generations. (Exact as $m \to \infty$).
- $R_* = \mathrm{E}[\tilde{C}]$.
- The probability of a major outbreak, p_{maj}, is approximated by the probability $\mathcal{B}_F$ avoids extinction.
- $p_{\mathrm{maj}} = 1 - f_C(\sigma)$, where σ is the smallest solution of $f_{\tilde{C}}(s) = s$ in $[0, 1]$ and e.g. $f_{\tilde{C}}(s) = \mathrm{E}[s^{\tilde{C}}]$.
- $$f_C(s) = \sum_{n=1}^{\infty} \tilde{\rho}_n f_{C^{(n)}}(s) \qquad \text{and} \qquad f_{\tilde{C}}(s) = \sum_{n=1}^{\infty} \tilde{\rho}_n f_{\tilde{C}^{(n)}}(s).$$
- Calculation of $f_C(s)$ and $f_{\tilde{C}}(s)$ complicated unless I is constant.

Standard SIR epidemic model

- Homogeneously mixing population with initially n susceptibles and a infectives.
- Infectious periods $\overset{\text{iid}}{\sim} I$.
- Individual to individual infection rate λ.
- i.e. SIR epidemic on complete graph with $n + a$ vertices.
- Denote model by $E_{n,a}(\lambda, I)$.
- Let S denote the final number of susceptibles.

Final state random variables

- Let $\boldsymbol{R} = (R_1, R_2, \cdots, R_p)$ be a random vector associated with a typical infective.
  - E.g. $p = 2$,

    R_1 = infectious period

    R_2 = number of global neighbours infected in network-households model
- Let $T_{\boldsymbol{R}}$ be the sum of the R-vectors over all infectives in $E_{n,a}(\lambda, I)$.
- $C^{(n)}$ is given by the R_2 component of $T_{\boldsymbol{R}}$ for $E_{n-1,1}(\lambda, I)$.

Gontcharoff polynomials

- **Definition** Given a sequence of real numbers $\mathcal{U} = u_0, u_1, \cdots$, define a family of polynomials $G_k(x\,|\,\mathcal{U})$ $(k = 0, 1, \cdots)$ by

$$\sum_{i=0}^{k} \frac{u_i^{k-i}}{(k-i)!} G_i(x\,|\,\mathcal{U}) = \frac{x^k}{k!} \qquad (k = 0, 1, \cdots).$$

- **Note**
  - $G_k(x\,|\,\mathcal{U})$ is a polynomial of degree k in x.
  - For fixed x, it is “easy" to compute $G_0(x\,|\,\mathcal{U}), G_1(x\,|\,\mathcal{U}), \cdots$ recursively.
- **Differentiation**

$$G_k^{(i)}(x\,|\,\mathcal{U}) = G_{k-i}(x\,|\,E^i\mathcal{U}) \qquad (0 \le i \le k),$$

where $E^i\mathcal{U}$ is the sequence $u_i, u_{i+1}, \cdots$.

(Gontcharoff (1937), Lefèvre and Picard (1990))

Final state random variables

- Consider a typical infective, i_*, with infectious period I and associated random vector $\boldsymbol{R}$. For $k = 1, 2, \cdots$, let A_k be the event that i_* fails to infect anyone in a given set of k susceptibles.
- For $\boldsymbol{\theta} \in \mathbb{R}^p$, let $q_0(\boldsymbol{\theta}) = \mathrm{E}\left[\mathrm{e}^{-\boldsymbol{\theta}\boldsymbol{R}^\top}\right]$ and, for $k = 1, 2, \cdots$, let

$$q_k(\boldsymbol{\theta}) = \mathrm{E}\left[\mathrm{e}^{-\boldsymbol{\theta}\boldsymbol{R}^\top} 1_{A_k}\right] = \mathrm{E}\left[\mathrm{e}^{-(\boldsymbol{\theta}\boldsymbol{R}^\top + \lambda k I)}\right].$$

Theorem 1 For $n, a = 0, 1, \cdots$,

$$\mathrm{E}\left[x^S \mathrm{e}^{-\boldsymbol{\theta}\boldsymbol{T}_{\boldsymbol{R}}^\top}\right] = \sum_{i=0}^{n} \frac{n!}{(n-i)!} q_i(\boldsymbol{\theta})^{n+a-i} G_i(x \,|\, \mathcal{U}(\boldsymbol{\theta})),$$

where $\mathcal{U}(\boldsymbol{\theta})$ is given by $u_k(\boldsymbol{\theta}) = q_k(\boldsymbol{\theta})$ $(k = 0, 1, \cdots)$.

(Ball and O'Neill (1999))

Application to network-households model

- Let $T^{(n)}$ be the size of single-household epidemic (excluding initial infective). Then

$$C^{(n)} = \sum_{i=0}^{T^{(n)}} C_i \qquad \text{and} \qquad \tilde{C}^{(n)} = \tilde{C}_0 + \sum_{i=1}^{T^{(n)}} C_i,$$

  where $C_i \sim \mathrm{Bin}(D, 1 - \mathrm{e}^{-\lambda_{\mathrm{G}} I})$ and $\tilde{C}_0 \sim \mathrm{Bin}(\tilde{D} - 1, 1 - \mathrm{e}^{-\lambda_{\mathrm{G}} I})$.

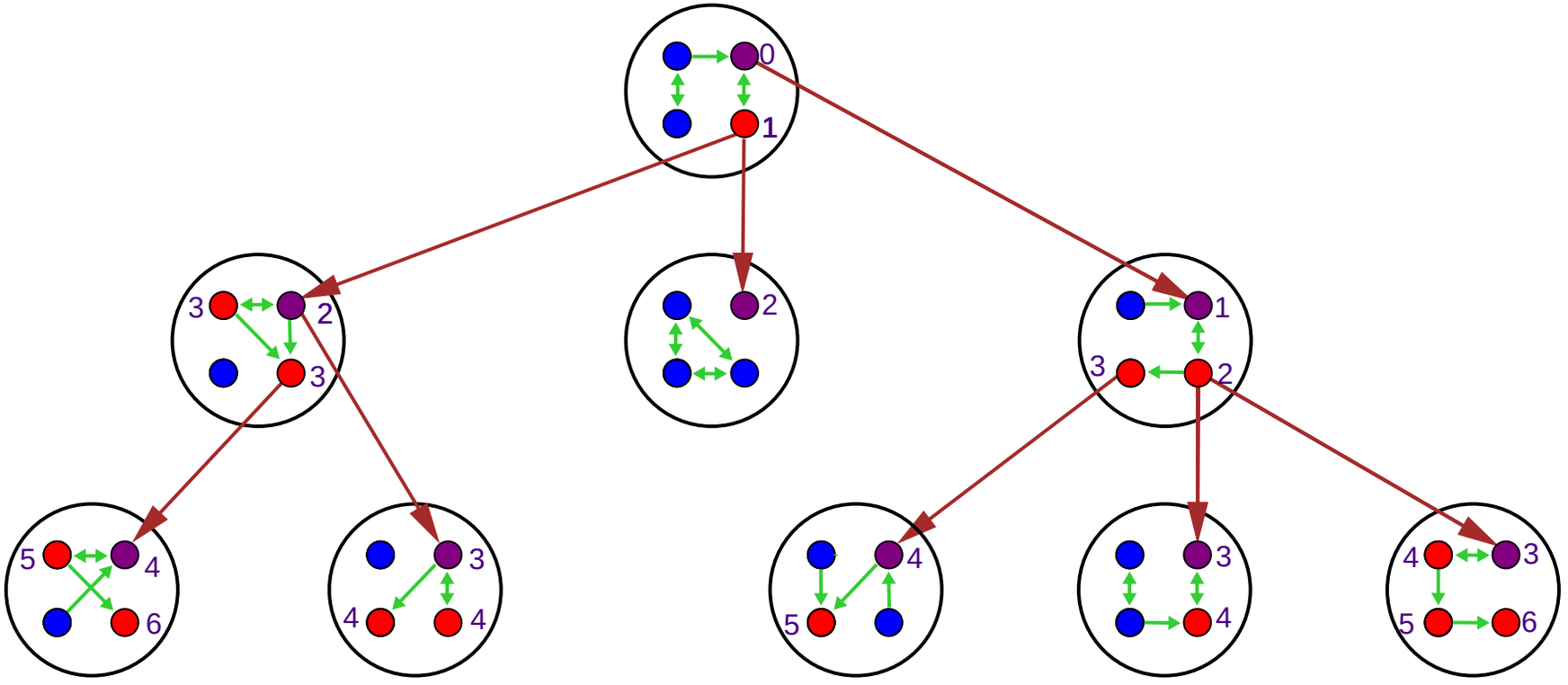
- Need version of Theorem 1 in which for the initial infectives, $q_k(\boldsymbol{\theta}) = \hat{q}_k(\boldsymbol{\theta})$ $(k = 0, 1, \cdots)$.

Theorem 2 (Ball (2018)) For $n, a = 0, 1, \cdots$,

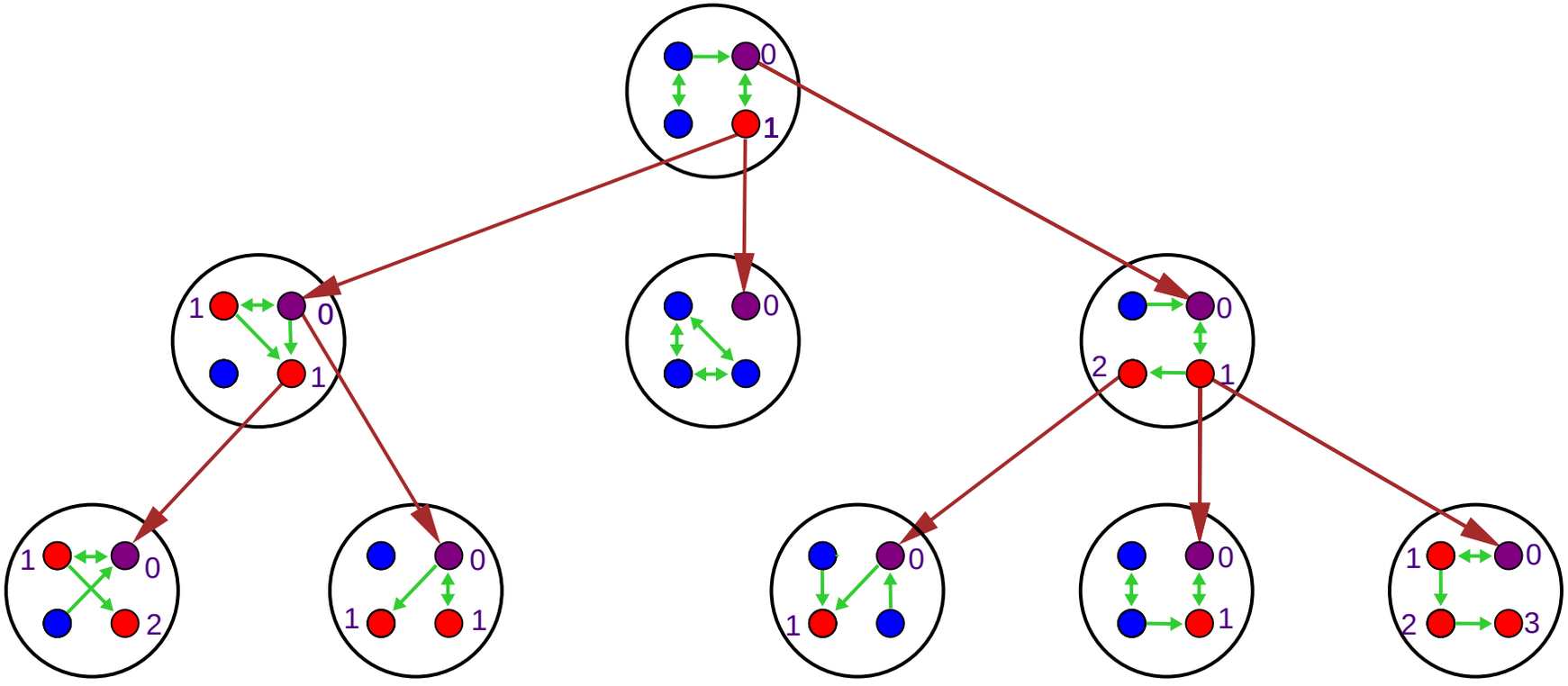
$$\mathrm{E}\left[x^S \mathrm{e}^{-\boldsymbol{\theta} \boldsymbol{T}_{\boldsymbol{R}}^{\top}}\right] = \sum_{i=0}^{n} \frac{n!}{(n-i)!} q_i(\boldsymbol{\theta})^{n-i} \hat{q}_i(\boldsymbol{\theta})^a G_i(x \,|\, \mathcal{U}(\boldsymbol{\theta})),$$

where $\mathcal{U}(\boldsymbol{\theta})$ is given by $u_k(\boldsymbol{\theta}) = q_k(\boldsymbol{\theta})$ $(k = 0, 1, \cdots)$.

Forward BP $\mathcal{B}_F$ – global generations

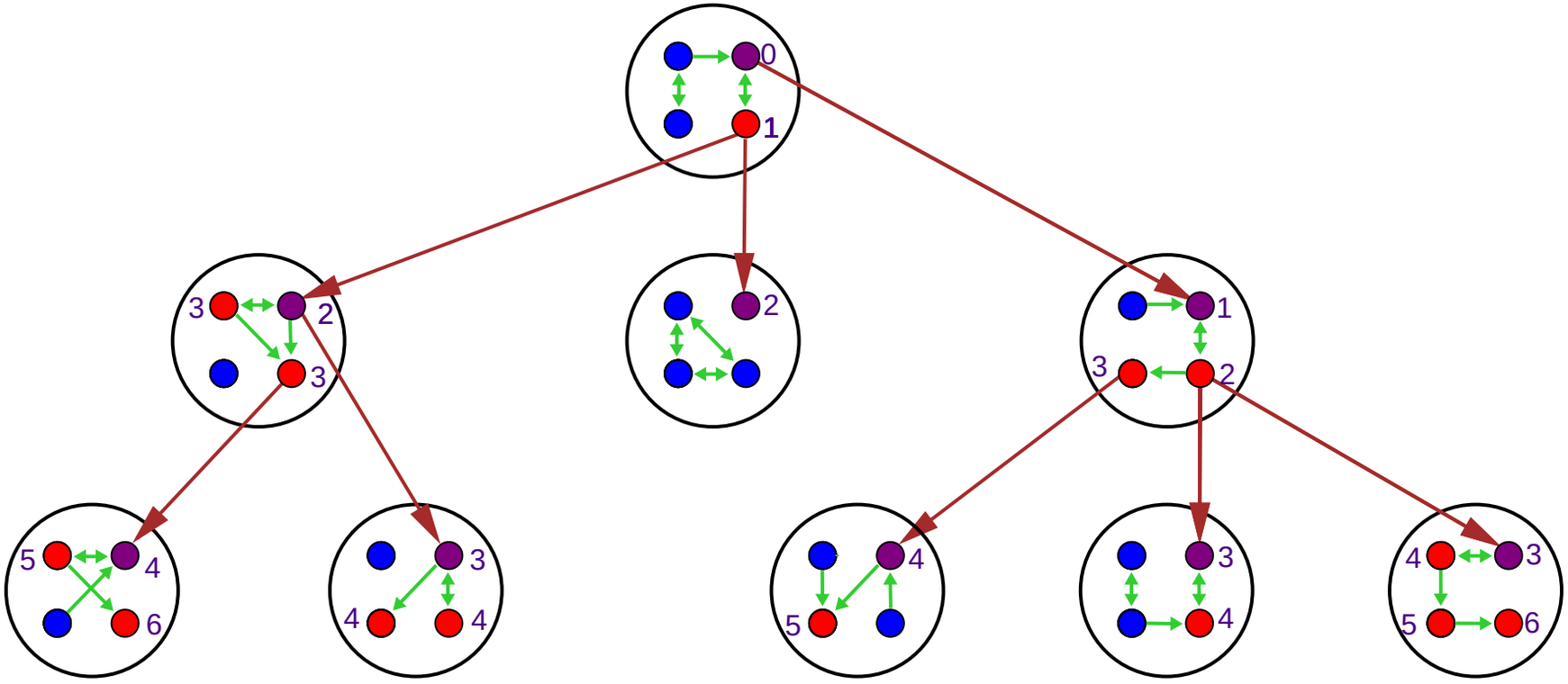


Household generations



Forward branching process $\mathcal{B}_F$.

Basic reproduction number R_0



- Consider BP $\tilde{\mathcal{B}}_F$, in which for each infected household the time of its birth is given by the global generation of the corresponding household primary case.

Basic reproduction number R_0

- R_0 is defined to be the asymptotic (Malthusian) geometric growth rate of $\tilde{\mathcal{B}}_F$.
- R_0 is given by the unique positive root of the discrete-time Lotka-Euler equation

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

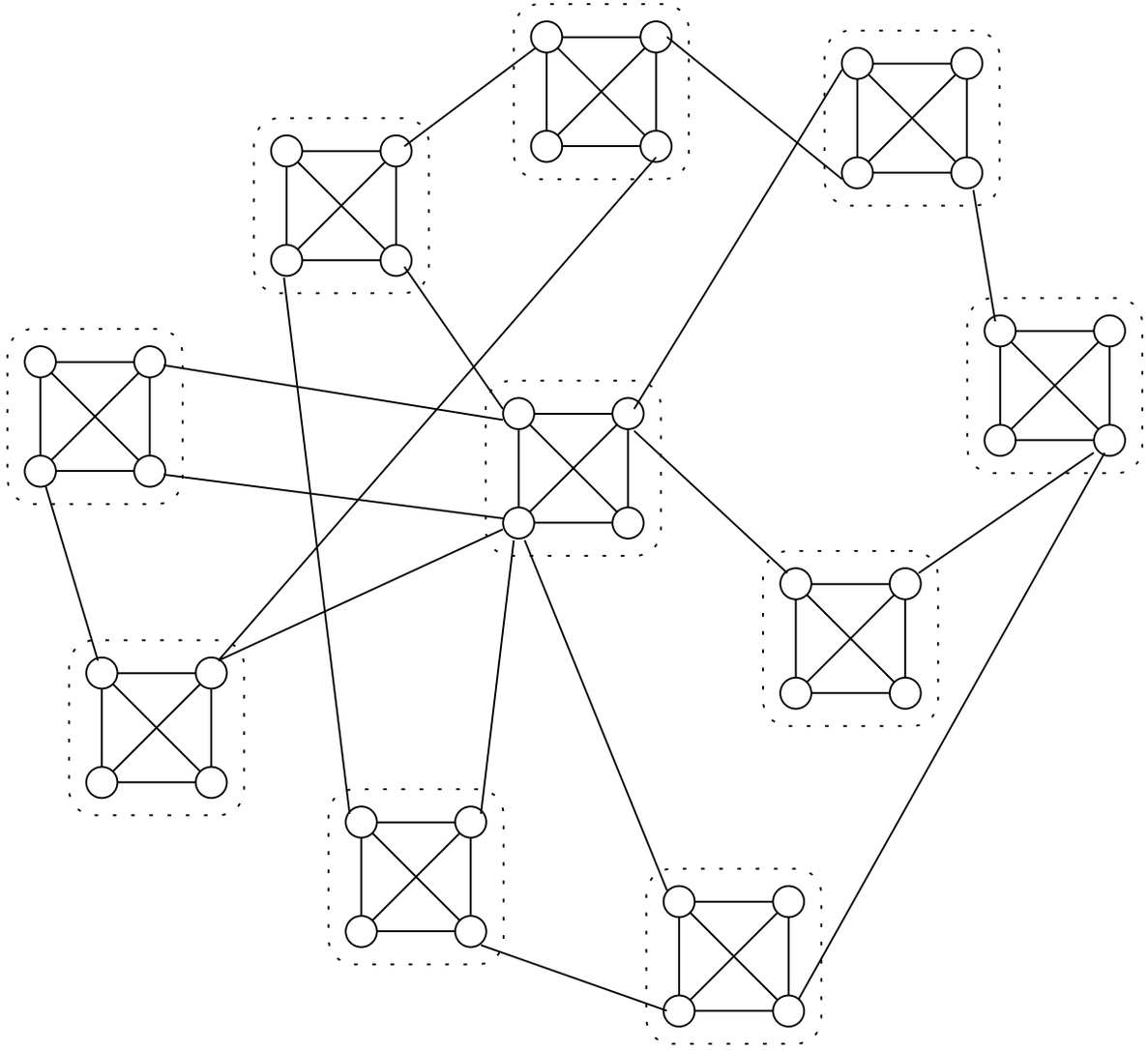
where

$$\nu_i = \begin{cases} \mu_{\tilde{D}-1} p_G & \text{if } i = 1, \\ \left(\sum_{n=i}^{\infty} \tilde{\rho}_n \mu_{n,i-1}\right) \mu_D p_G & \text{if } i = 2, 3, \cdots, \end{cases}$$

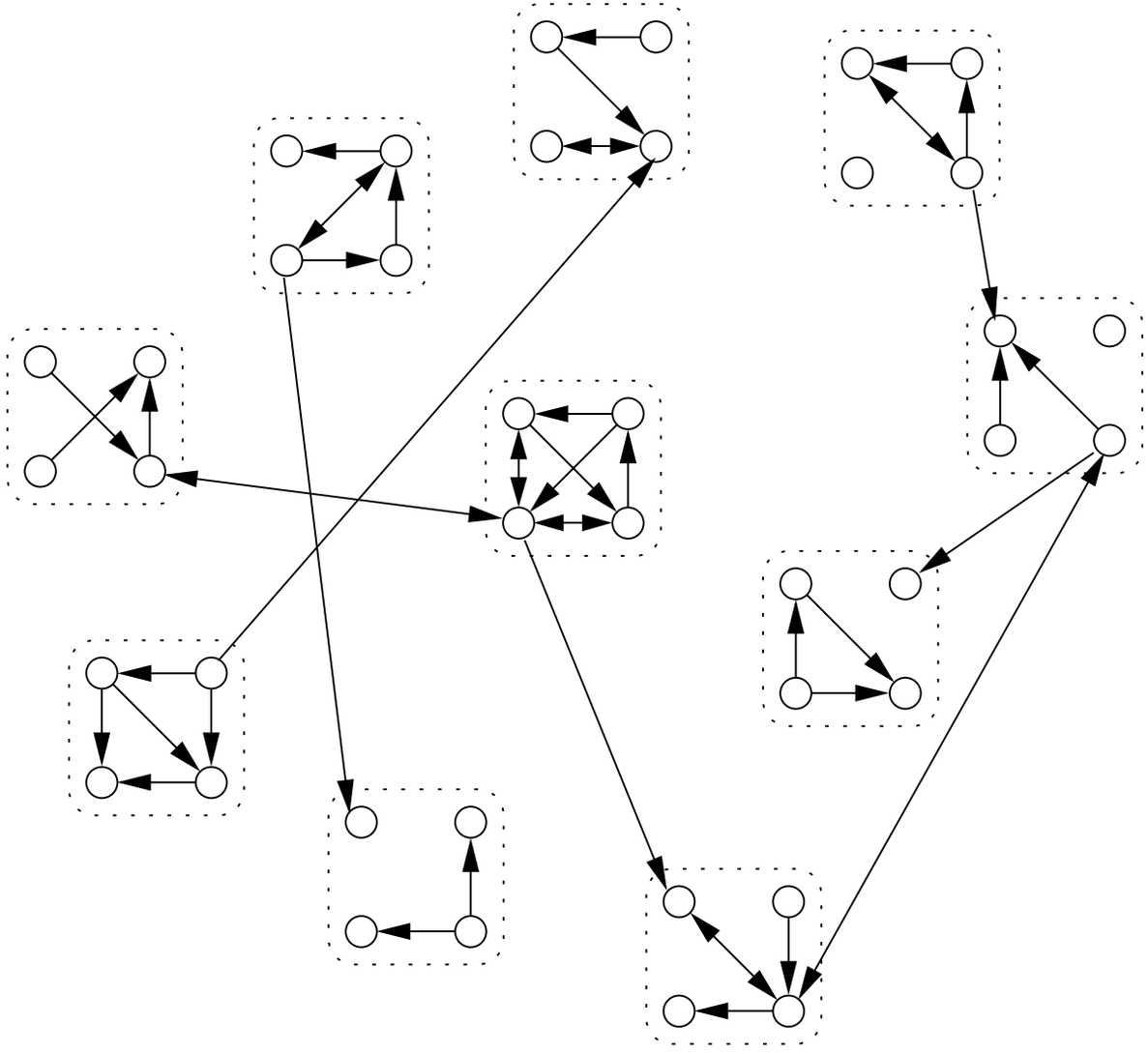
is the mean number of offspring that a typical individual (i.e. infectious household) in $\tilde{\mathcal{B}}_F$ has at age i and $\mu_{n,i}$ is the mean size of the ith generation in a typical size-n single-household epidemic.

(Pellis, Ball and Trapman (2012), Ball, Pellis and Trapman (2016))

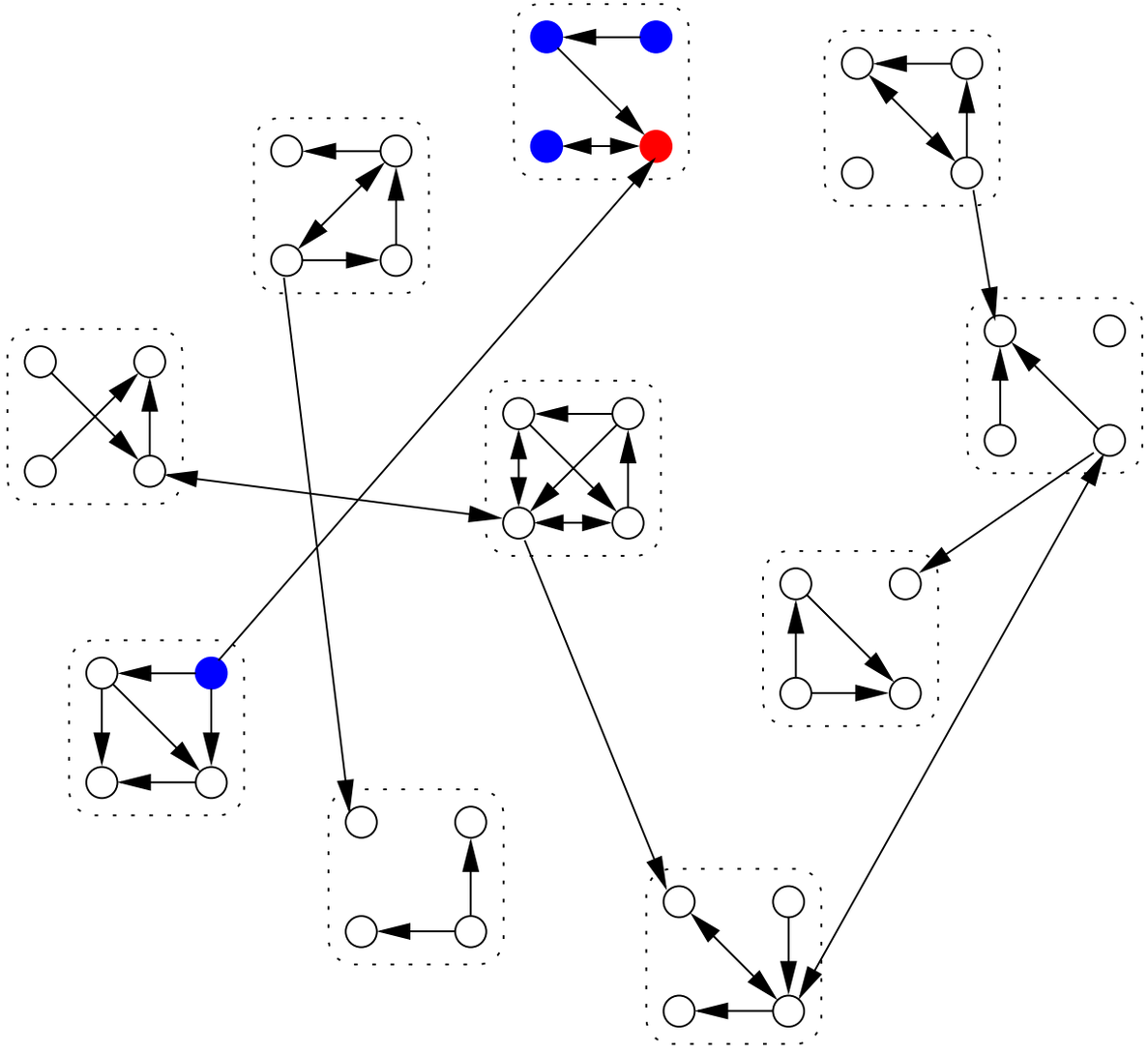
Example network



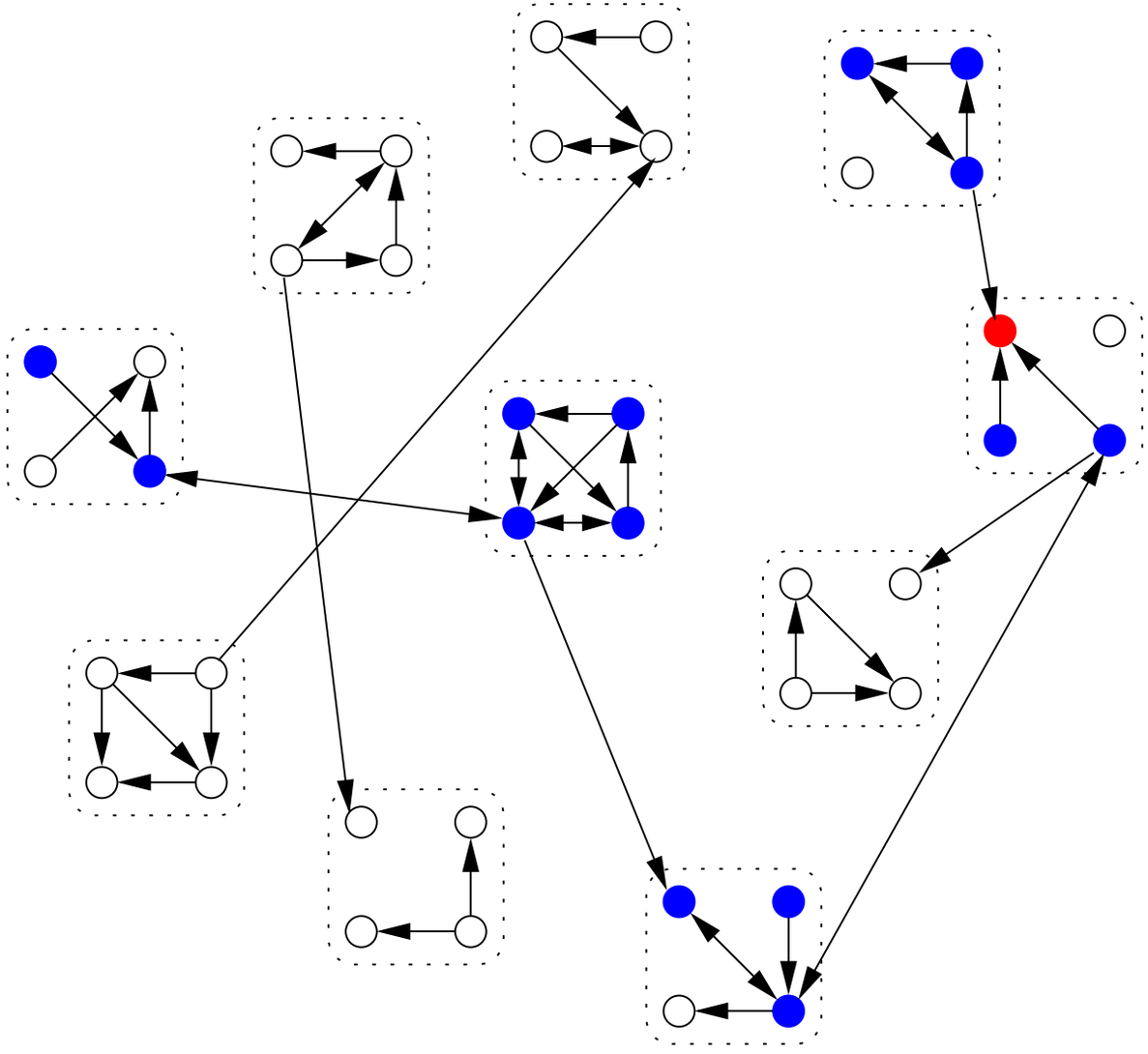
Digraph of potential infections



Susceptibility set, Example 1



Susceptibility set, Example 2



Final size of major outbreak

- Expected proportion of population ultimately infected by a major outbreak, z say, is given by the probability that a typical susceptible, i_* say, is ultimately infected.
- Approximate i_*'s susceptibility set, $\mathcal{S}_{i_*}$, by a households based (backward) branching process $\mathcal{B}_B = \mathrm{BP}(1, B, \tilde{B})$.
- $\mathrm{P}(i_*$ ultimately infected$) = \mathrm{P}(\mathcal{B}_B$ avoids extinction$)$
- $z = 1 - f_B(\xi)$, where ξ is the smallest solution of $f_{\tilde{B}}(s) = s$ in $[0, 1]$.
- Distribution of within-household final size (WHFS) in the event of a major outbreak is available. If $(z, \lambda_{\mathrm{L}})$ and the distribution of I are fixed, then the distribution of WHFS is invariant to the degree distribution D.

Backward branching process $\mathcal{B}_B$

- Conditioning on household size n of initial member of a local susceptibility set,

$$f_B(s) = \sum_{n=1}^{\infty} \tilde{\rho}_n f_{B^{(n)}}(s) \qquad \text{and} \qquad f_{\tilde{B}}(s) = \sum_{n=1}^{\infty} \tilde{\rho}_n f_{\tilde{B}^{(n)}}(s).$$

- Let $M^{(n)}$ be the size of a local susceptibility set in a household of size n. Then

$$B^{(n)} = \sum_{i=0}^{M^{(n)}} B_i \qquad \text{and} \qquad \tilde{B}^{(n)} = \tilde{B}_0 + \sum_{i=1}^{M^{(n)}} B_i,$$

where $M^{(n)}, \tilde{B}_0, B_0, B_1, \cdots$ are independent with $\tilde{B}_0 \sim \mathrm{Bin}(\tilde{D}-1, p_{\mathrm{G}})$ and $B_i \sim \mathrm{Bin}(D, p_{\mathrm{G}})$.

Backward branching process $\mathcal{B}_B$

- Recall

$$B^{(n)} = \sum_{i=0}^{M^{(n)}} B_i \qquad \text{and} \qquad \tilde{B}^{(n)} = \tilde{B}_0 + \sum_{i=1}^{M^{(n)}} B_i,$$

where $\tilde{B}_0, B_0, B_1, \cdots$ are independent with $\tilde{B}_0 \sim \mathrm{Bin}(\tilde{D}-1, p_{\mathrm{G}})$ and $B_i \sim \mathrm{Bin}(D, p_{\mathrm{G}})$.

- Thus,

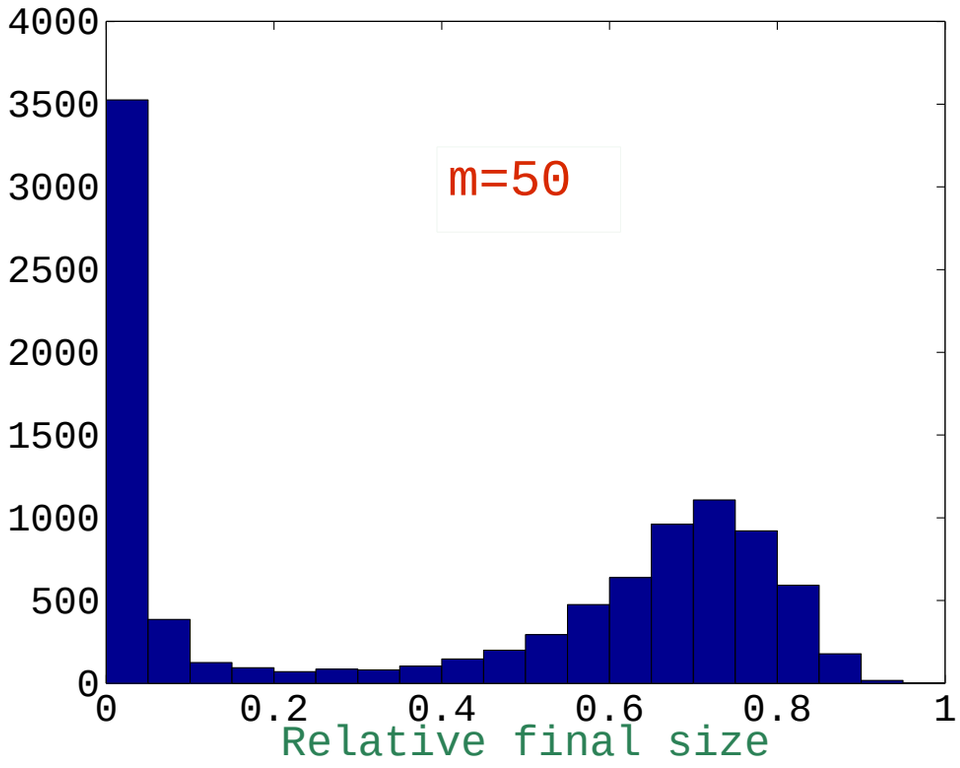
$$f_{B^{(n)}}(s) = f_D(1-p_{\mathrm{G}}+p_{\mathrm{G}}s) f_{M^{(n)}}(f_D((1-p_{\mathrm{G}}+p_{\mathrm{G}}s)),$$
$$f_{\tilde{B}^{(n)}}(s) = f_{\tilde{D}-1}(1-p_{\mathrm{G}}+p_{\mathrm{G}}s) f_{M^{(n)}}(f_D((1-p_{\mathrm{G}}+p_{\mathrm{G}}s)).$$

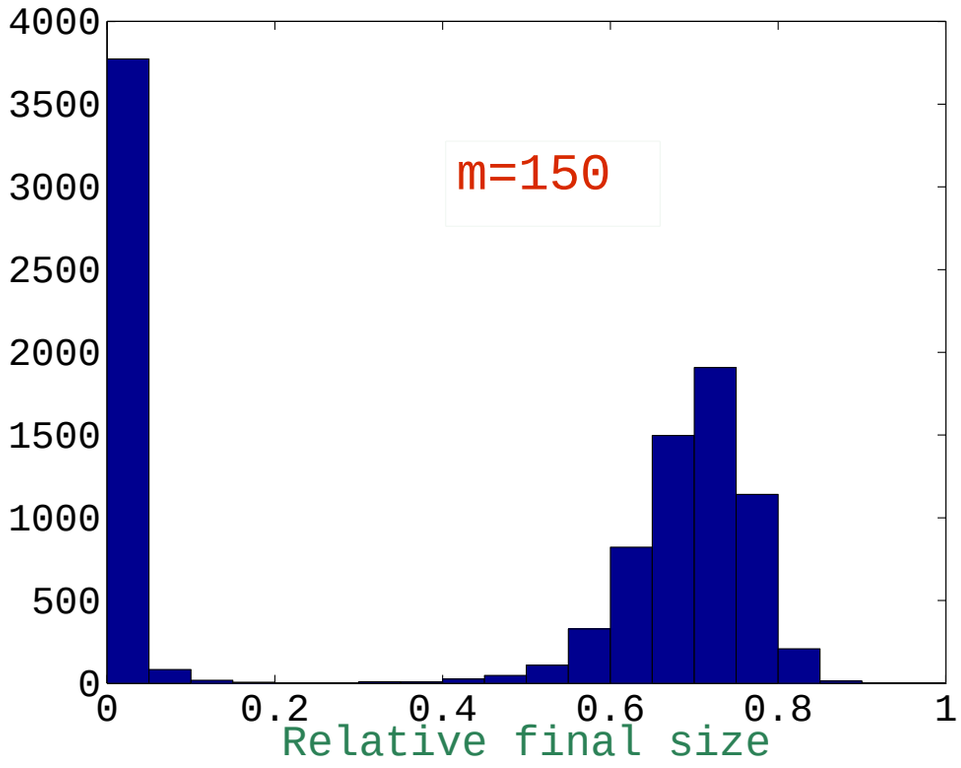
- Let $q_k = \phi_I(k\lambda_{\mathrm{L}}\ (k=0,1,\cdots)$. Then

$$\mathrm{P}(M^{(n)}=k) = \frac{(n-1)!}{(n-1-k)!} q_{k+1}^{n-1-k} G_{k+1}(1\,|\,\mathcal{U}) \qquad (k=0,1,\cdots,n-1),$$

where $\mathcal{U}$ is given by $u_k = q_{k+1}(\boldsymbol{\theta})\ (k=0,1,\cdots)$.

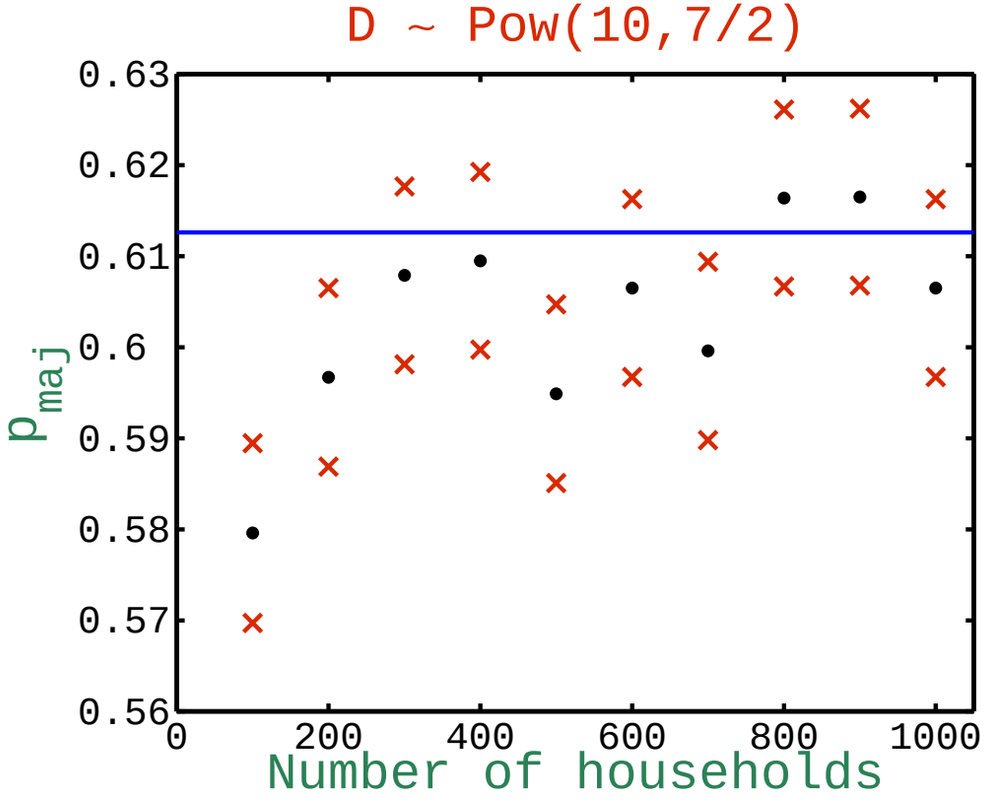
Simulations of final size

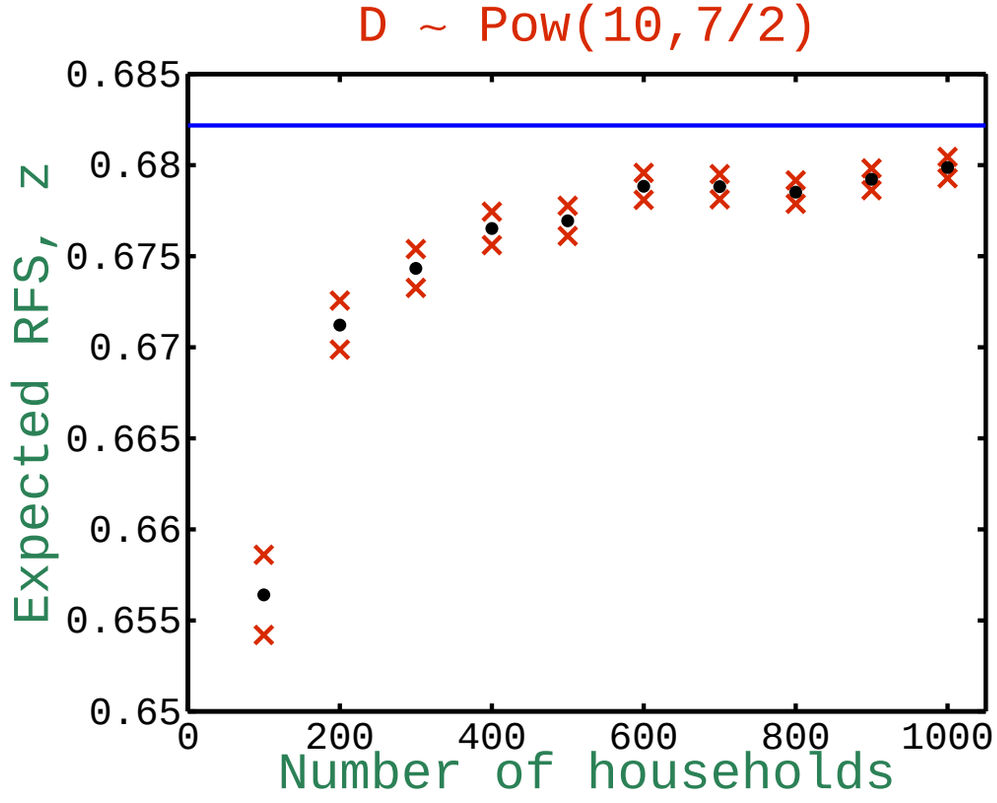




Histograms of relative final sizes from 10,000 simulations of the model with $H \sim (0.2, 0.25, 0.25, 0.25, 0.04, 0.01)$, $\lambda_{\mathrm{L}} = 1$, $\lambda_{\mathrm{G}} = 1/10$, $D \sim \mathrm{Poi}(8)$ and $I \sim \mathrm{Gamma}(3, 1/3)$ on networks of 50 and 150 households.

Simulation results for p_{maj} and z

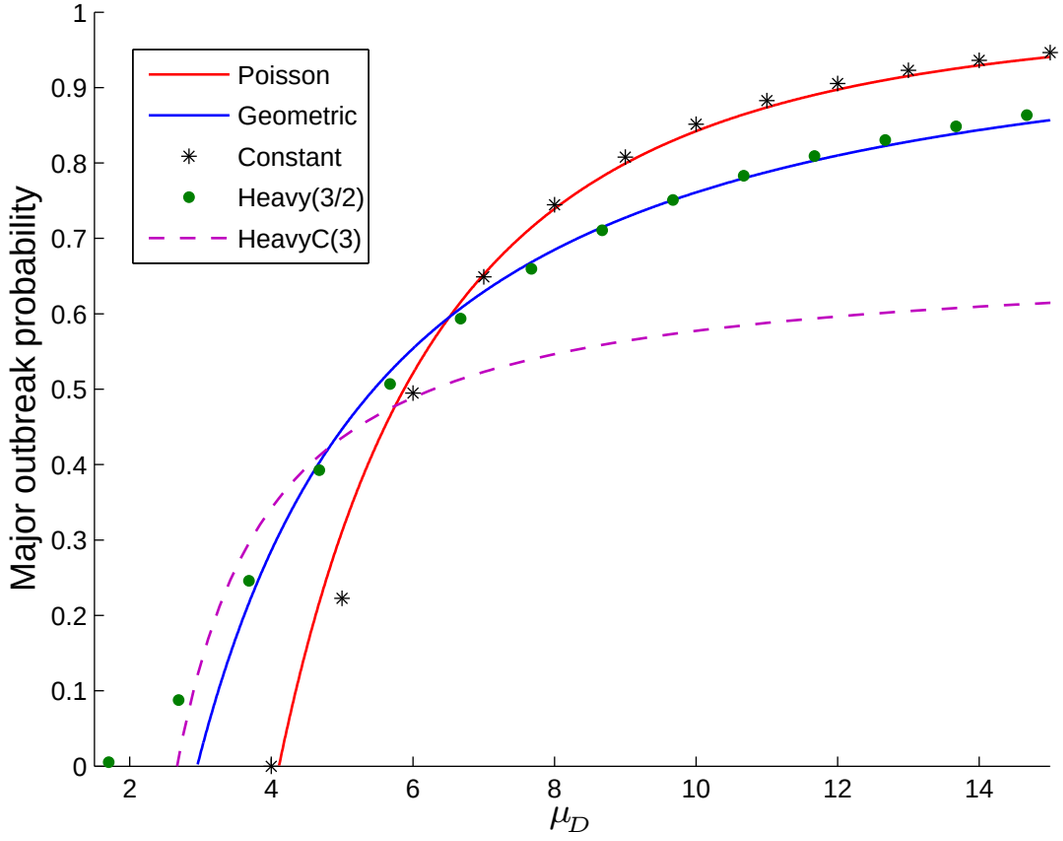




Comparison of simulation-based estimates of probability p_{maj} and expected relative final size z of a major outbreak for finite populations with asymptotic results (horizontal lines), based on 10,000 simulations for each m.

[$D \sim \mathrm{Pow}(k_*, a)$ means $\mathrm{P}(D = k) \propto (\max(k_*, k))^{-a}$ $(k = 1, 2, \ldots)$.]

Effect of degree distribution, D



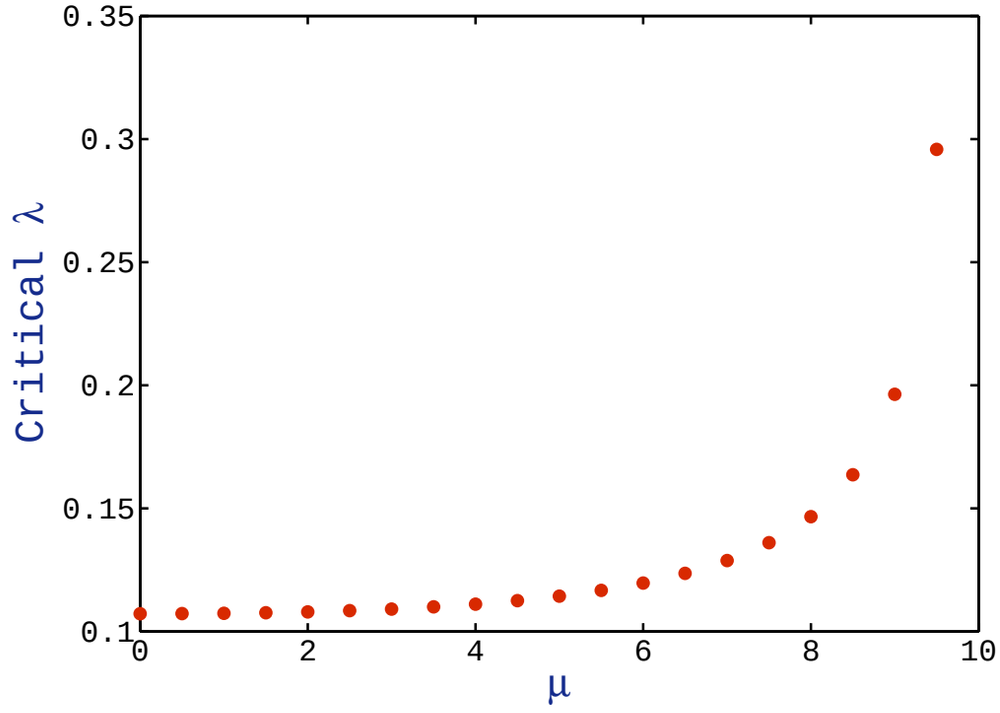
Dependence of probability of a major outbreak p_{maj} on degree distribution D. Other parameters are $H \equiv 3$, $I \equiv 1$, $\lambda_L = 1$, $\lambda_G = 1/10$.

[$\mathrm{Heavy}(3/2)$ is $\mathrm{Pow}(k_*, 3/2)$ with varying k_*. The mass function of $\mathrm{HeavyC}(3)$ is $\mathrm{P}(D = k) \propto k^{-3} \exp(-k/\kappa)$ $(k = 1, 2, \dots)$ with varying κ.]

Comparison to standard network model

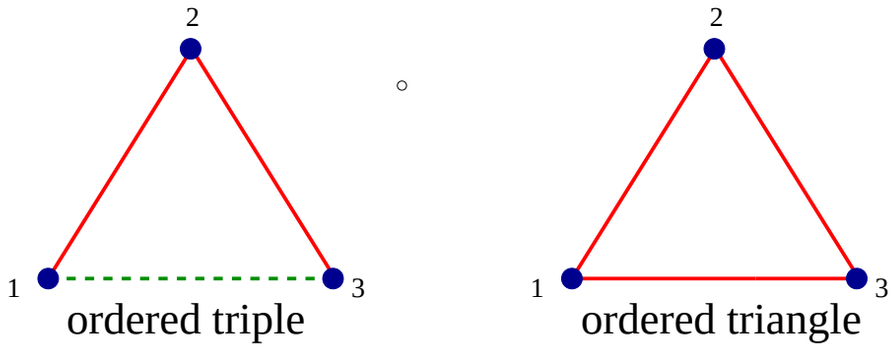
- Standard network model (see e.g. Newman(2002)) is obtained when all households have size 1.
- In network household model (NHM) let H denote the household size distribution and $\tilde{H}$ denote the size-biased household size distribution.
  [$\mathrm{P}(\tilde{H}=n)=\mu_H^{-1}n\mathrm{P}(H=n)\ (n=1,2,\dots)$.]
- Total degree (local $+$ global) of individual in NHM $\sim Q \stackrel{\mathcal{D}}{=} \tilde{H}-1+D$.
- Assume $\lambda_{\mathrm{L}}=\lambda_{\mathrm{G}}=\lambda$ and compare critical value of λ with that of standard network model (SNM) with degree distribution Q.

Comparison to standard network model



Plot of critical infection rate $\lambda_{\mathrm{L}} = \lambda_{\mathrm{G}} = \lambda$ for models with $H \sim \mathrm{Poi}^{+}(\mu)$ and $D \sim \mathrm{Poi}(10 - \mu)$ (so Q is always $\mathrm{Poi}(10)$ and $\mu = 0$ gives SNM) when $I \sim \mathrm{Gamma}(3, 1/3)$.

Clustering



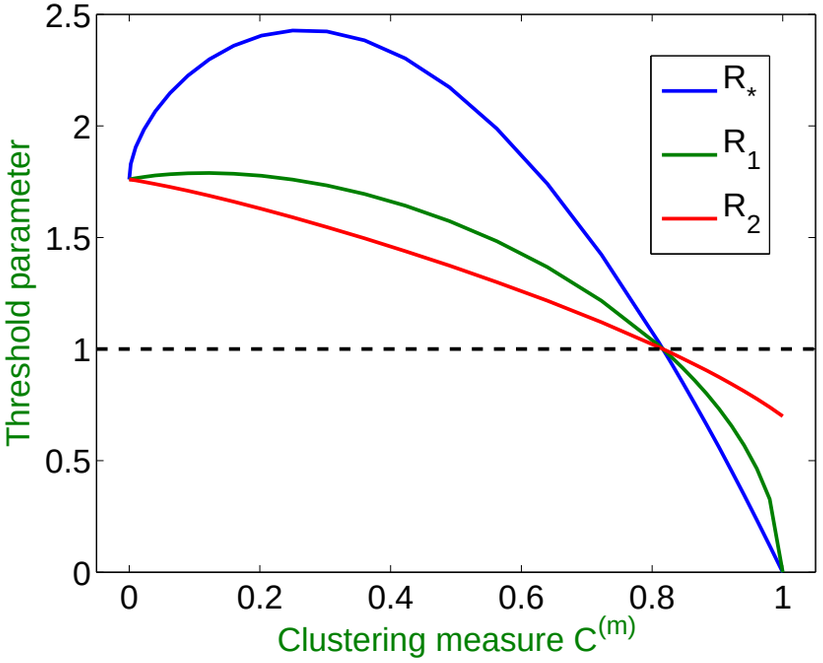
- Clustering measure

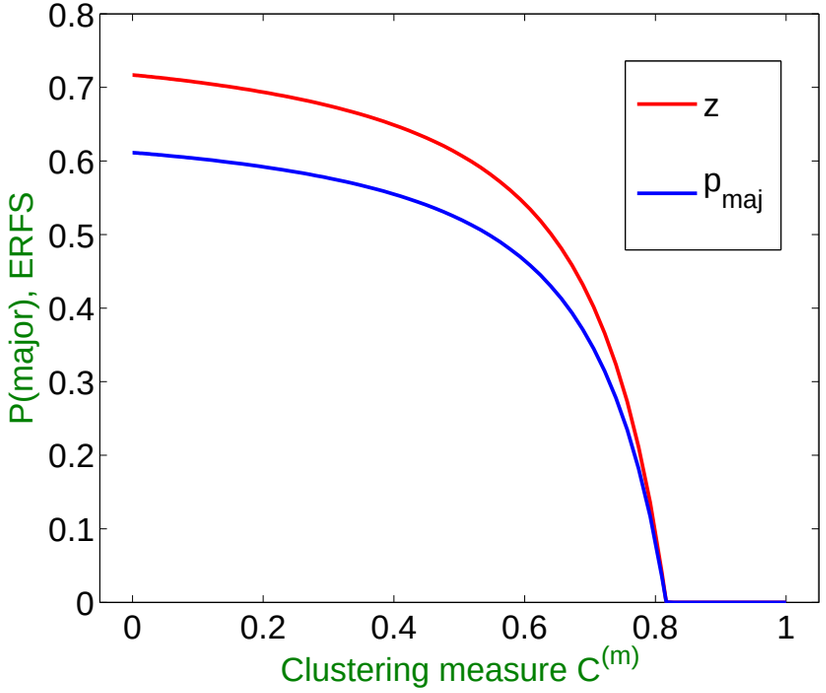
$$\mathcal{C}^{(m)} = \frac{\text{total number of ordered triangles in network}}{\text{total number of ordered triples in network}}.$$

- As $m \to \infty$, number of triangles not entirely in the same household per individual $\xrightarrow{a.s.} 0$, so

$$\mathcal{C}^{(m)} \xrightarrow{a.s.} \mathcal{C} = 1 - \frac{\mathrm{E}[H\{2D(H-1) + D(D-1)\}]}{\mathrm{E}[H(D+H-1)(D+H-2)]}.$$

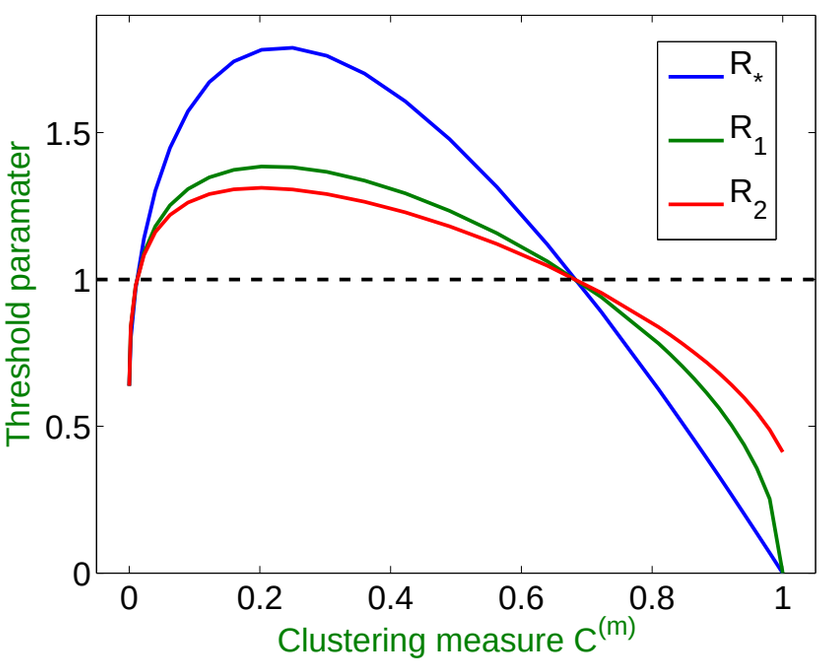
Effect of clustering when $\lambda_{\mathrm{L}} = \lambda_{\mathrm{G}}$

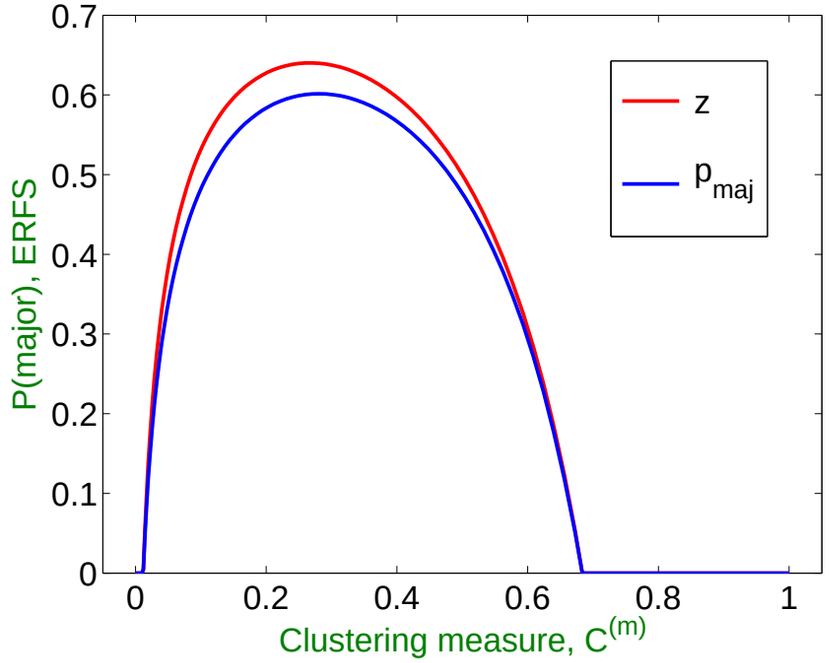




Plots of threshold parameters and the probability p_{maj} and expected relative final size z of a major outbreak for networks with $H \sim \mathrm{Poi}^{+}(\mu)$ and $D \sim \mathrm{Poi}(10-\mu)$, so Q is always $\mathrm{Poi}(10)$ and $\mathcal{C}^{(m)} \approx (\mu/10)^2$. Other parameters are $I \sim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

Effect of clustering when $\lambda_{\mathrm{L}} > \lambda_{\mathrm{G}}$





Plots of threshold parameters and the probability p_{maj} and expected relative final size z of a major epidemic for networks with $H \sim \mathrm{Poi}^{+}(\mu)$ and $D \sim \mathrm{Poi}(10-\mu)$, so Q is always $\mathrm{Poi}(10)$ and $\mathcal{C}^{(m)} \approx (\mu/10)^2$. Other parameters are $I \sim \mathrm{Gamma}(3, 1/3)$, $\lambda_{\mathrm{L}} = 1$ and $\lambda_{\mathrm{G}} = 1/15$.

Households-based vaccination

- Consider all-or-nothing vaccine – vaccinees are rendered fully immune with probability ε, otherwise the vaccine has no effect.
- Potential infectious global contact. Consider an infective i and a given global neighbour j of i.
  - j is a potential infectious global contact of i iff i contacts j.
  - j becomes an actual infectious global contact of i if either j is susceptible or j is vaccinated and the vaccine fails.
- Approximate process of potentially infected households by a (forward) branching process $\mathcal{B}'_F$.

All-or-nothing vaccination

- For $n = 1, 2, \ldots$ and $v = 0, 1, \ldots, n$, let

  x_{nv} = proportion of size-n households that have v members vaccinated

  μ_{nv} = mean number of potential global contacts that emanate from a typical single-household epidemic in a household in state (n, v), initiated by a potential global contact with an individual chosen uniformly at randomly from that household.

- Post-vaccination

$$R_v = \sum_{n=1}^{\infty} \tilde{\rho}_n \sum_{v=0}^{n} x_{nv} \mu_{nv}$$

- Vaccination coverage

$$c = \sum_{n=1}^{\infty} \tilde{\rho}_n \sum_{v=0}^{n} \frac{v}{n} x_{nv}$$

- Determination of optimal vaccination scheme (e.g. to reduce R_v to 1 with minimum vaccination coverage) is a linear programming problem, whose solution can be constructed explicitly.

(Becker and Starczak (1997), Ball and Lyne (2002, 2006), Ball and Sirl (2018))

Calculation of μ_{nv}

x_{nv} = proportion of size-n households that have v members vaccinated

μ_{nv} = mean number of potential global contacts that emanate from a typical single-household epidemic in a household in state (n, v), initiated by a potential global contact with an individual chosen uniformly at randomly from that household.

$$\mu_{nv} = \sum_{k=0}^{v} \underbrace{\binom{v}{k} \varepsilon^k (1-\varepsilon)^{v-k}}_{(1)} \underbrace{\frac{n-k}{n}}_{(2)} \underbrace{\mathrm{E}[\tilde{C}^{(n-k)}]}_{(3)}$$

(1) $\mathrm{P}(k$ vaccinations are successful$)$

(2) $\mathrm{P}($potential contact leads to infection$)$

(3) Mean number of potential global contacts emanating from single-household epidemic

Optimal vaccination schemes

- Let

  $h_{nv} = m_n x_{nv}$ = number of households of size n with v members vaccinated.

- Recalling $\tilde{\rho_n} = nm_n/N$,

  $$R_v = \sum_{n=1}^{\infty} \tilde{\rho}_n \sum_{v=0}^{n} x_{nv}\mu_{nv}$$

  $$= \sum_{n=1}^{\infty} \sum_{v=0}^{n} h_{nv} M_{n,v}, \quad \text{SUM OVER HOUSEHOLDS}$$

  where $M_{n,v} = n\mu_{nv}/N$.

- Consider vaccine gain

  $G_{n,v} = M_{n,v} - M_{n,v+1}$ — reduction in R_v obtained by vaccinating one further member of a household in state (n, v)

Vaccine gain matrix

n	$v=$ 0	1	2	3
1	0.5625^{10}			
2	1.5000^{6}	0.7969^{9}		
3	2.6506^{3}	1.7876^{5}	1.0446^{8}	
4	3.8165^{1}	2.9420^{2}	2.0762^{4}	1.3025^{7}

Vaccine gain matrix $G_{n,v}$ for a population consisting of 100 households of each size 1, 2, 3 and 4, when $T_I \sim \mathrm{Exp}(1)$, $\lambda_L = 5$ and $\lambda_G = 0.75$, for an all-or-nothing vaccine with $\varepsilon = 0.75$.

Non-random vaccine response

- Need to use 2-type forward and backward branching processes.
- Individuals in the forward BP $\mathcal{B}'_F$ correspond to infected households in the epidemic process and are typed by the vaccine status, V or U, of the initial infective in the corresponding single-household epidemic.
- R_v is the maximum eigenvalue of the offspring mean matrix $\tilde{M}$ of $\mathcal{B}'_F$.
- Marginal global transmission probabilities

$$P_G^{NR} = \begin{bmatrix} p_G^{NR}(U,U) & p_G^{NR}(U,V) \\ p_G^{NR}(V,U) & p_G^{NR}(V,V) \end{bmatrix} = \begin{bmatrix} 1-\phi_I(\lambda_G) & 1-\phi_I(a\lambda_G) \\ 1-\phi_I(b\lambda_G) & 1-\phi_I(ab\lambda_G) \end{bmatrix}.$$

- $\text{rank}(P_G^{NR}) = 1 \implies \text{rank}(\tilde{M}) = 1 \implies R_v = \text{trace}(\tilde{M})$

  and determination of optimal vaccination scheme is a linear programming problem as before.
- $\text{rank}(P_G^{NR}) = 1$ if $a = 1$ or $b = 1$ (leaky vaccine).

Vaccine gain matrices

All-or-nothing, $\varepsilon = 0.75$

n	$v =$	0	1	2	3
1		0.5625^{10}			
2		1.5000^{6}	0.7969^{9}		
3		2.6506^{3}	1.7876^{5}	1.0446^{8}	
4		3.8165^{1}	2.9420^{2}	2.0762^{4}	1.3025^{7}

Non-random, $a = b = 0.5$

n	$v =$	0	1	2	3
1		0.5625^{10}			
2		1.2768^{7}	0.8899^{9}		
3		2.0582^{4}	1.6686^{6}	1.2706^{8}	
4		2.8224^{1}	2.4464^{2}	2.0640^{3}	1.6714^{5}

Leaky, $a = 0.25$

n	$v =$	0	1	2	3
1		0.5625^{10}			
2		1.2396^{8}	0.9271^{9}		
3		1.8857^{5}	1.7141^{6}	1.3976^{7}	
4		2.4365^{1}	2.3821^{2}	2.2418^{3}	1.9437^{4}

Acquaintance vaccination

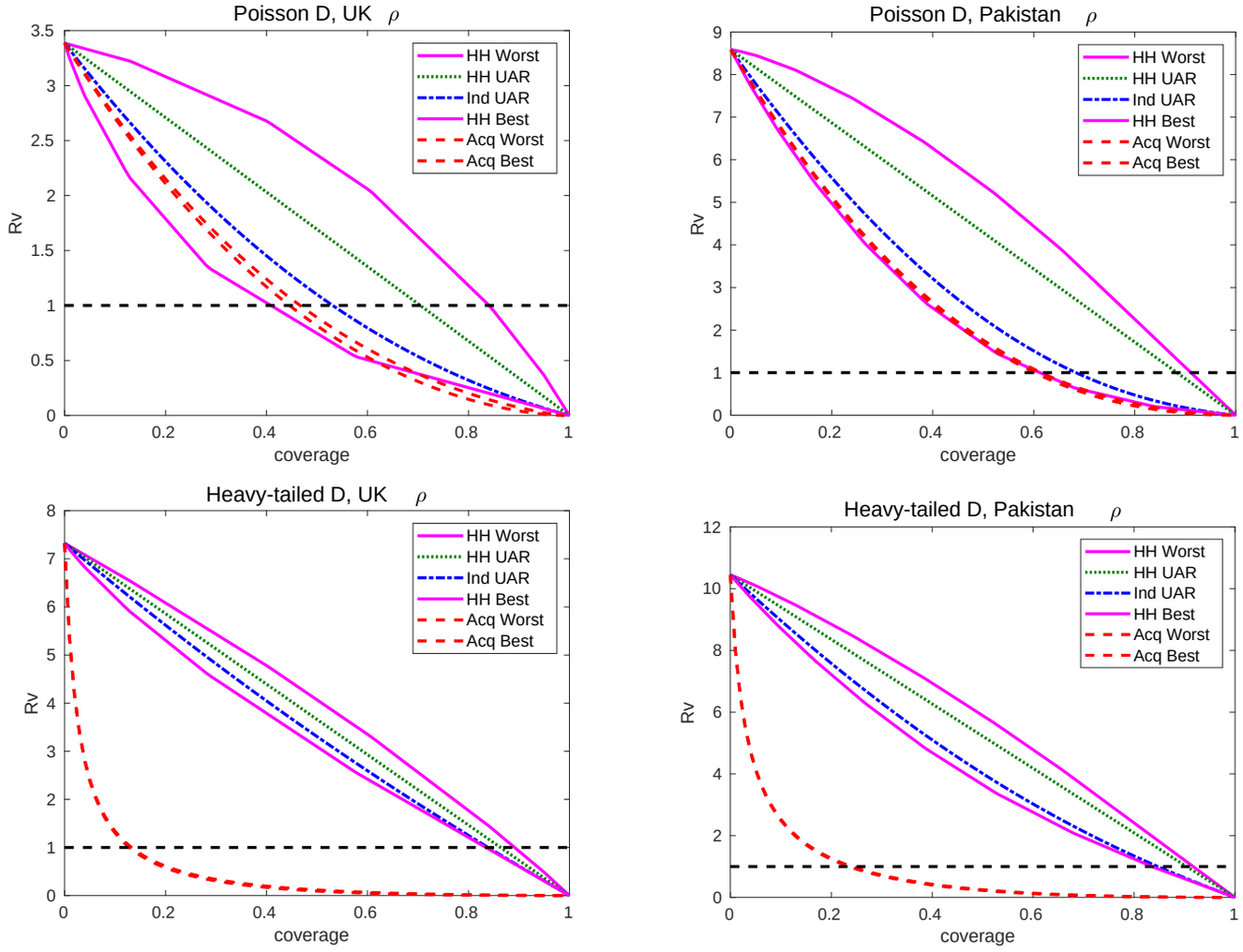
- Analysis of new model for acquaintance vaccination may be extended to the network-households model, using multitype branching processes to approximate the early stages of the epidemic and the susceptibility set of an individual.
- Individuals in the forward branching process correspond to infected households in the epidemic process, with the type of an individual ((N,S), (V,S), (U,S), (N,S^c), (V,S^c) or (U,S^c)) being given by the type of the initial infective in the corresponding single-household epidemic.
- Individuals in the backward branching process correspond to local (within-household) susceptibility sets, with the type of an individual being given by the type of the initial member of the corresponding local susceptibility set.
- R_v, $(p_{\mathrm{maj}}^{(U)}, p_{\mathrm{maj}}^{(V)})$ and $(z^{(U)}, z^{(V)})$ follow.

Numerical illustrations

- Household size distributions
  $\rho_n = \mathrm{P}(H = n)$ $(n = 1, 2, \ldots, n_{\max})$.
  - UK $\rho_{\mathrm{UK}} = (0.31, 0.32, 0.16, 0.14, 0.05, 0.02)$
    mean 2.4, $n_{\max} = 6$.
  - Pakistan $\rho_{\mathrm{Pak}} =$
    $(0.009, 0.045, 0.077, 0.118, 0.141, 0.146, 0.123, 0.237)$
    mean 6.8, $n_{\max} = 9$.

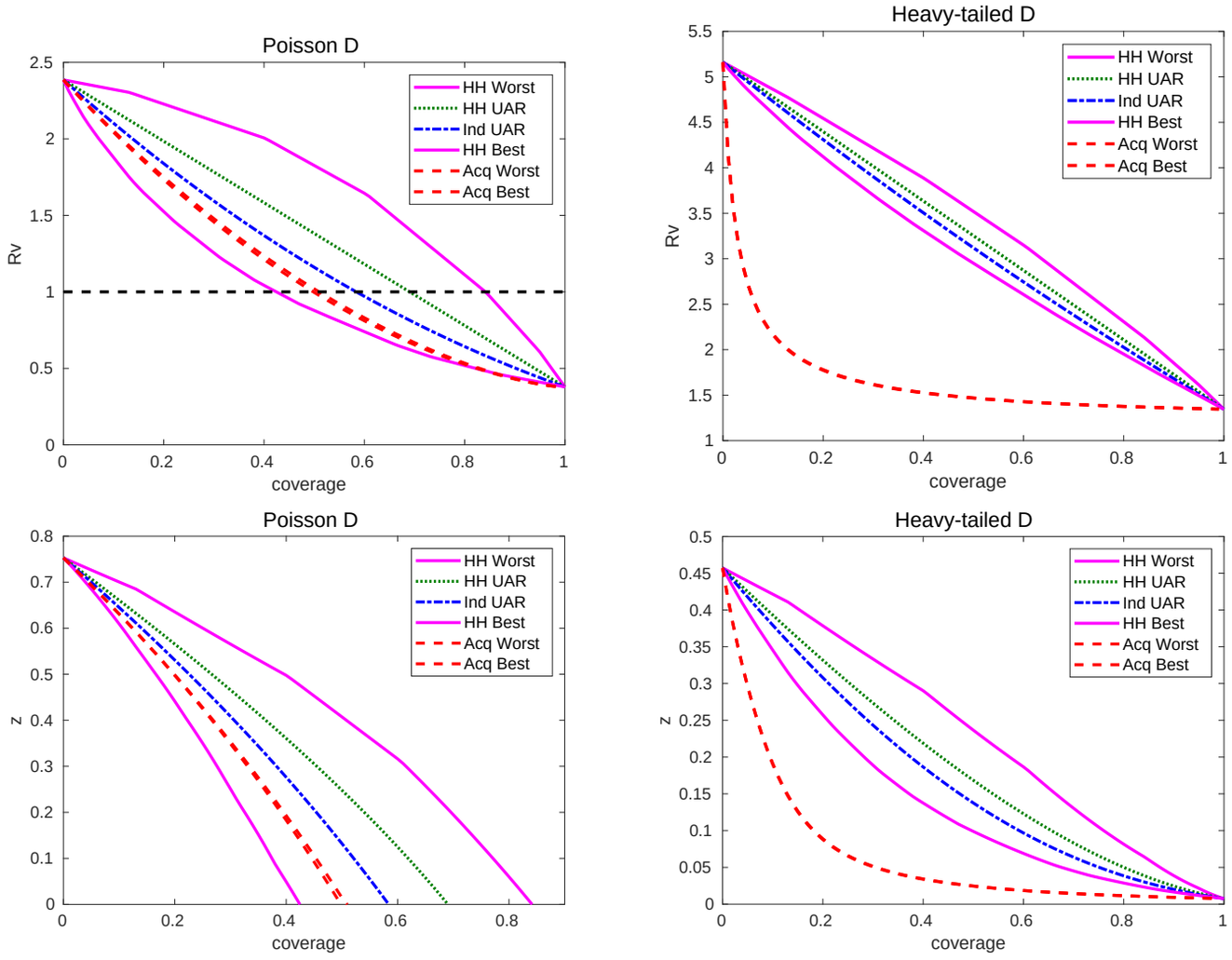
- Degree distributions
  - $D \sim \mathrm{Poisson}(5)$.
  - $D \sim \mathrm{Power}(2, 120)$: $p_k \propto k^{-2}\mathrm{e}^{-k/120}$ $(k = 1, 2, \cdots)$.
    $\mathrm{E}[D] \approx 3.001, \sigma_D^2 \approx 66$.

Perfect vaccine R_v



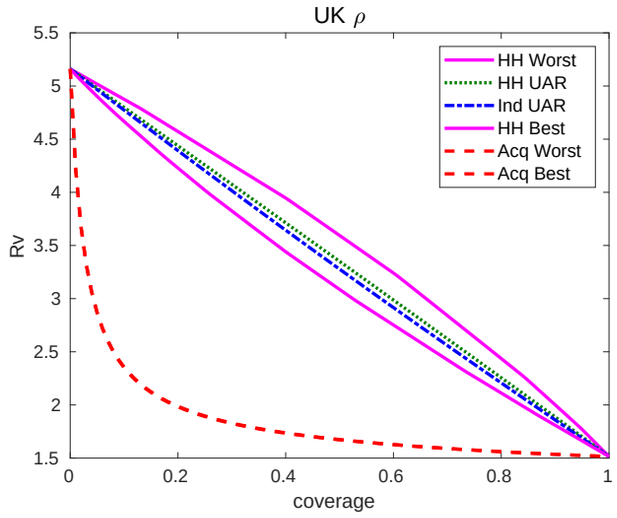
Plots of R_v for epidemics with $\lambda_L = 1, \lambda_G = 0.3$ and $I \sim \text{Gamma}(5, 1/5)$.

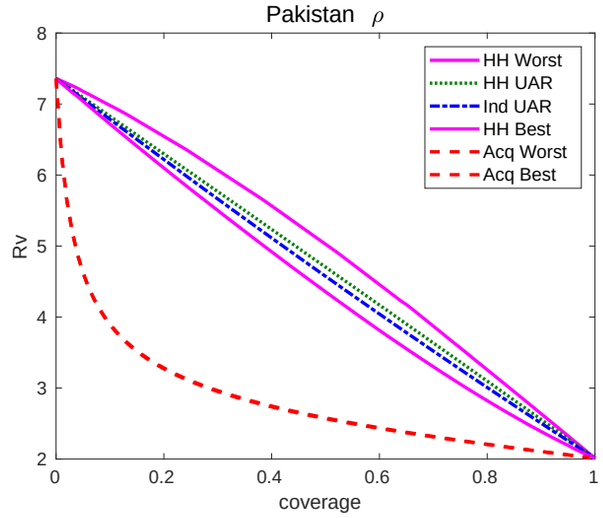
All-or-nothing vaccine R_v

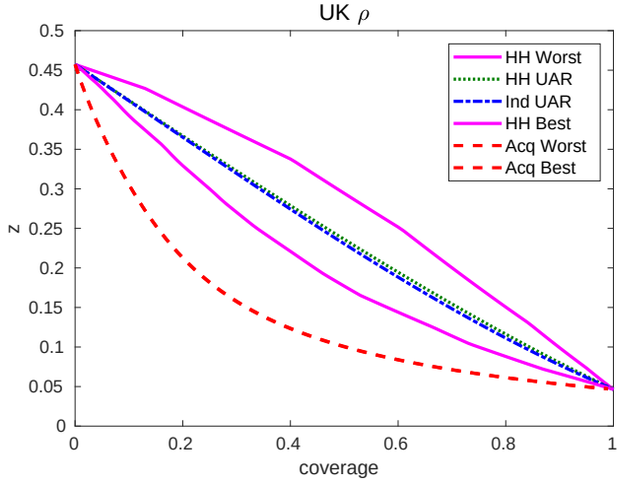


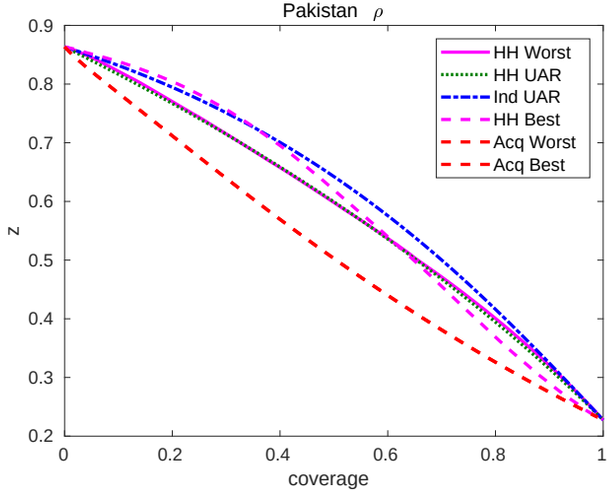
Plots of R_v and z for epidemics with UK household size distribution, $\lambda_L = 1, \lambda_G = 0.2$ and $I \sim \text{Gamma}(5, 1/5)$. Vaccination success probability $\varepsilon = 0.7$.

Non-random R_v









Plots of R_v and z for epidemics with $D \sim \text{Power}(2, 120), \lambda_L = 1, \lambda_G = 0.2$ and $I \sim \text{Gamma}(5, 1/5)$. Vaccine relative susceptibility and infectivity $a = 0.5$ and $b = 0.6$.

Concluding comments

- Described a number of methods for analysing SIR epidemics on configuration model and related networks.
- CLTs for final outcome of epidemic and size of largest connected component in bond and site percolation extend in principle to network-households model.
- Household structure, degree distribution and clustering each have a significant impact on disease dynamics and performance of vaccination schemes.
- Acquaintance vaccination can outperform appreciably households-based vaccination.

Concluding comments

- Extensions
  - multitype epidemics (e.g. adults and children).
  - Include tunable degree correlation.
  - Include casual contacts.
- Challenges include
  - Models with dynamic networks.
  - Models with adaptive dynamics.

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