

# Epidemics with two levels of mixing

Frank Ball

Frank.Ball@nottingham.ac.uk

University of Nottingham

Modelling Complex Systems, University of Manchester

21st June 2010

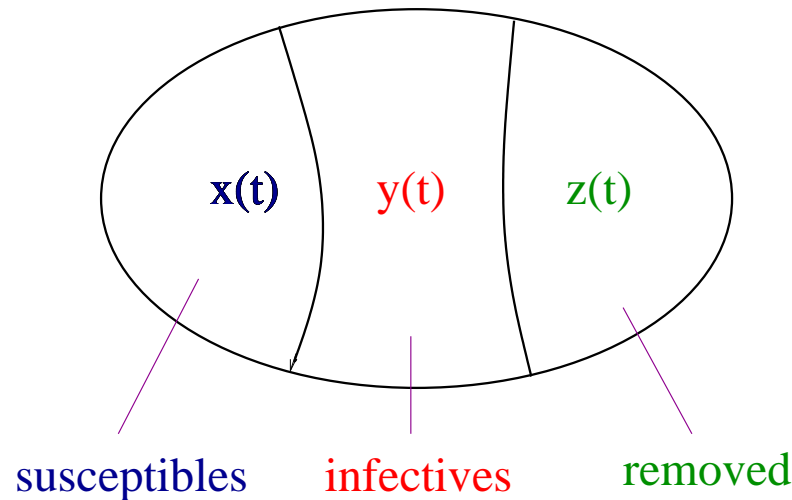
Joint work with Peter Neal (University of Manchester) and Owen Lyne (University of Kent)

Research supported by EPSRC and The Leverhulme Trust

# Outline of talk

- Background on **homogeneously mixing SIR** (susceptible → infective → removed) epidemic models
- General **two-level-mixing SIR** epidemic model
  - Special cases
    - households model
    - overlapping groups model
    - great circle model
    - network model with **casual** contacts
  - Threshold behaviour and final outcome of **global** epidemic
    - general results
    - applications to special cases
    - numerical illustrations
- **Vaccination** in **Households SIR** model
- Concluding comments

# General deterministic epidemic



$$(x(0), y(0), z(0)) = (N, a, 0)$$

$\beta$  = infection rate

$\gamma$  = removal rate

● SIR (susceptible  $\rightarrow$  infective  $\rightarrow$  removed)

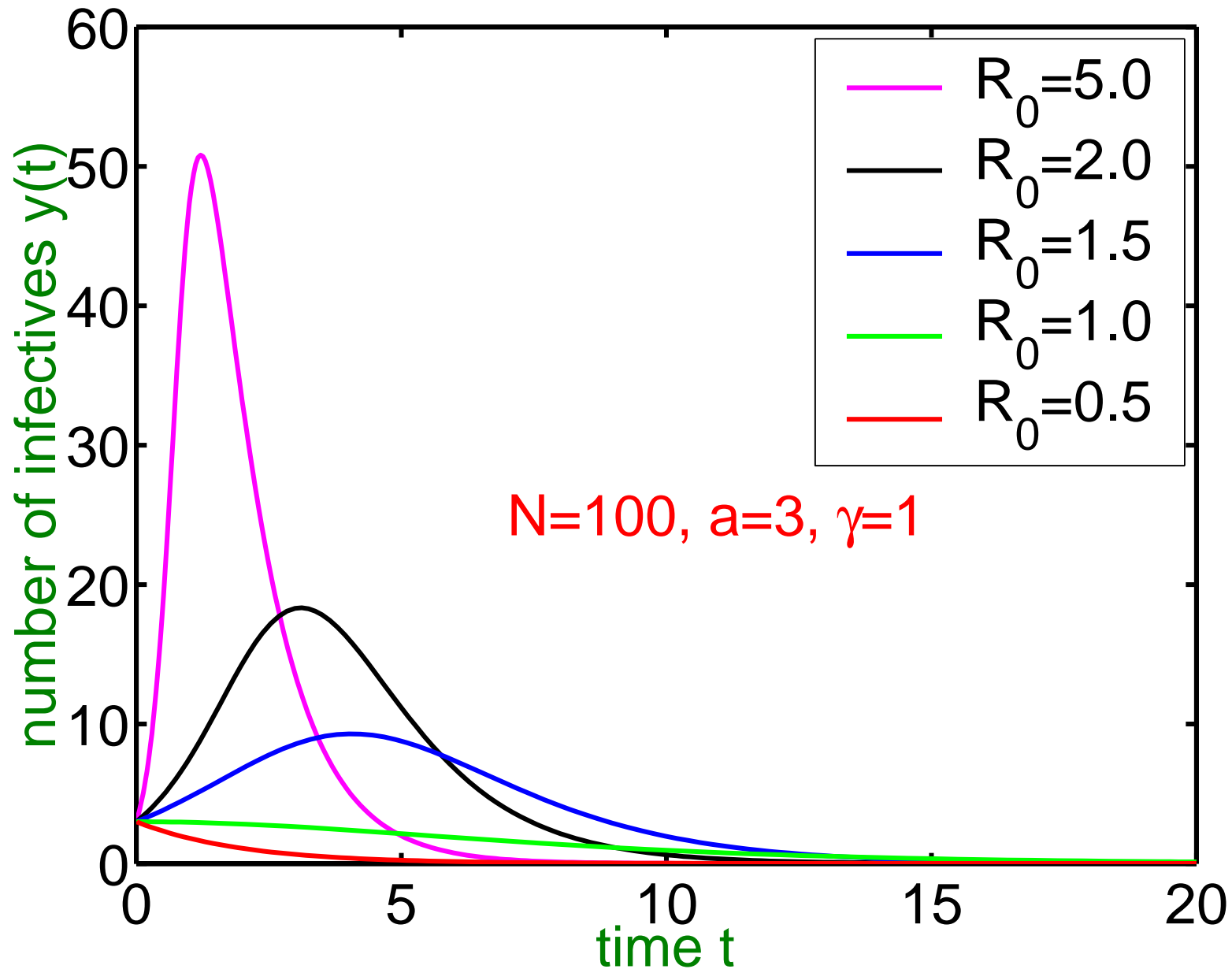
●  $\frac{dx}{dt} = -\beta xy, \frac{dy}{dt} = \beta xy - \gamma y, \frac{dz}{dt} = \gamma y$

●  $\frac{dy}{dt} > 0 \iff \beta xy - \gamma y > 0 \iff x > \gamma/\beta$

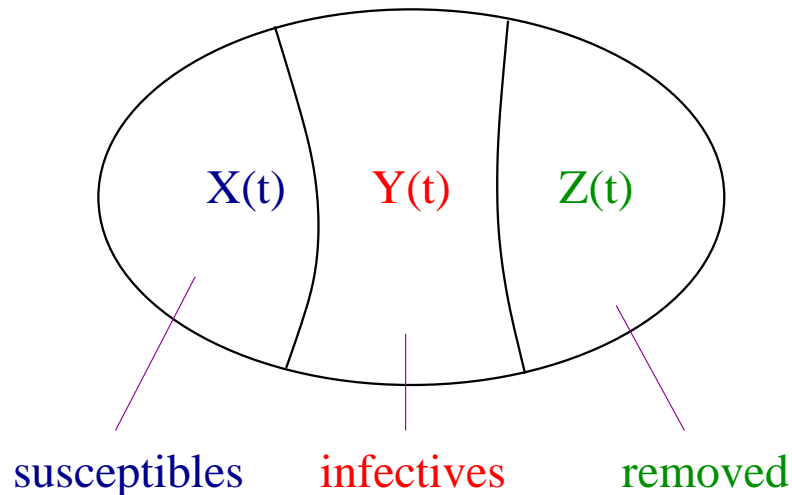
● Epidemic takes off  $\iff N > \gamma/\beta \iff R_0 = N\beta/\gamma > 1$

(Kermack and McKendrick (1927))

# General deterministic epidemic



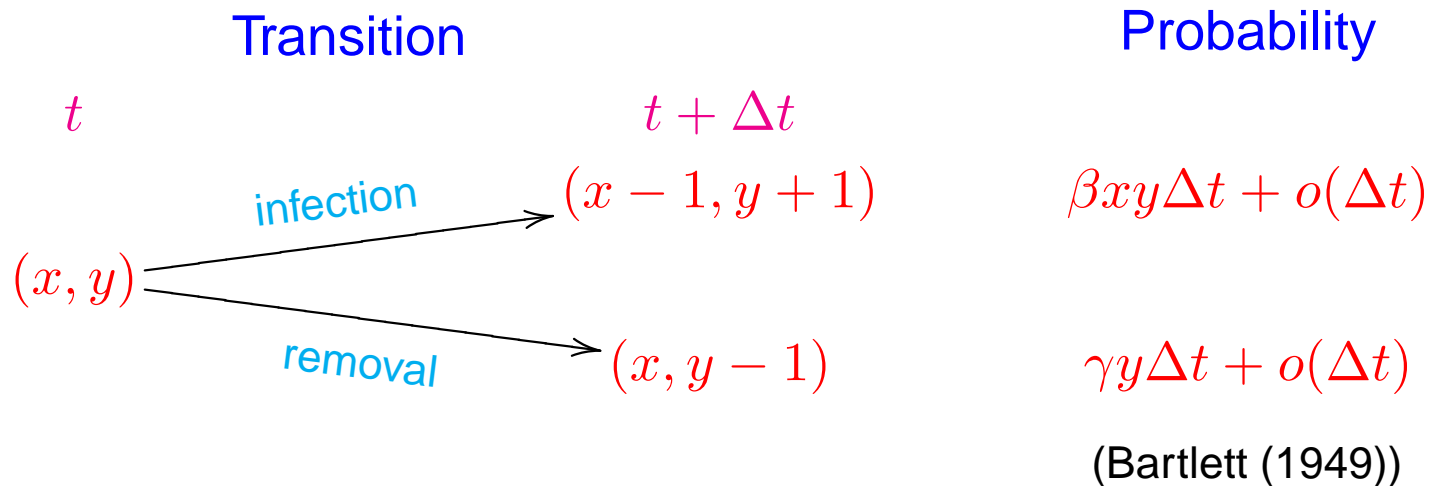
# General stochastic epidemic



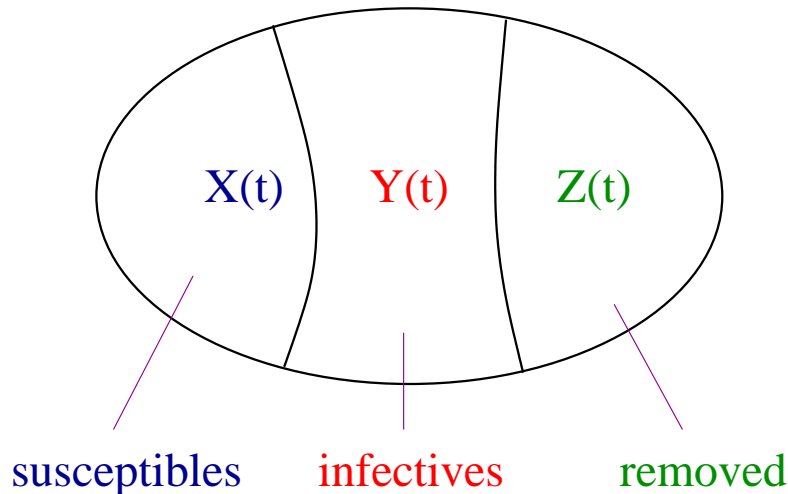
$$X(0) = N$$

$$Y(0) = a$$

$$Z(0) = 0$$



# General stochastic epidemic



$$X(0) = N$$

$$Y(0) = a$$

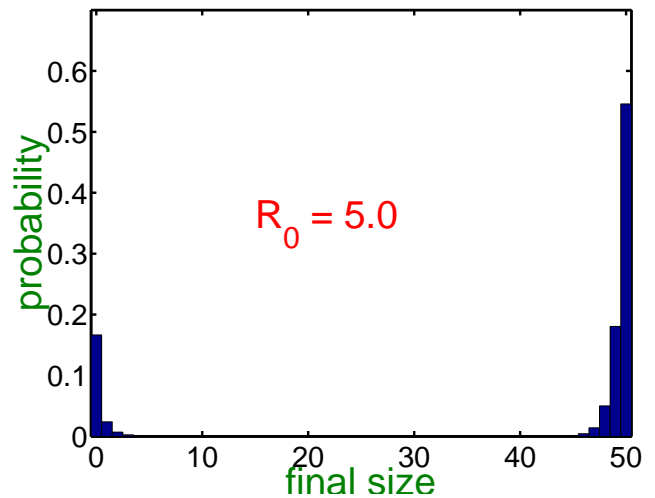
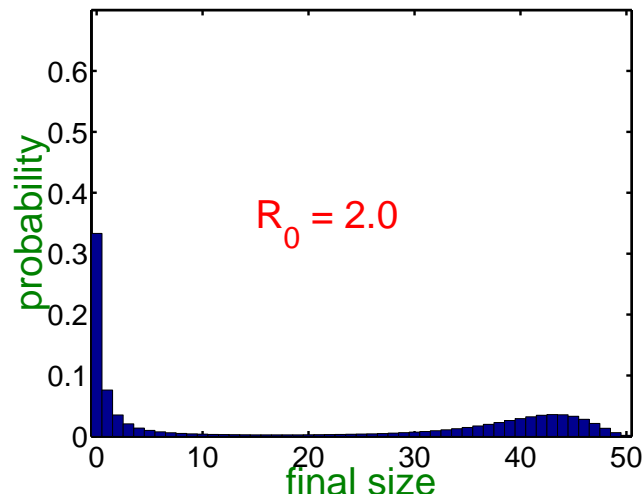
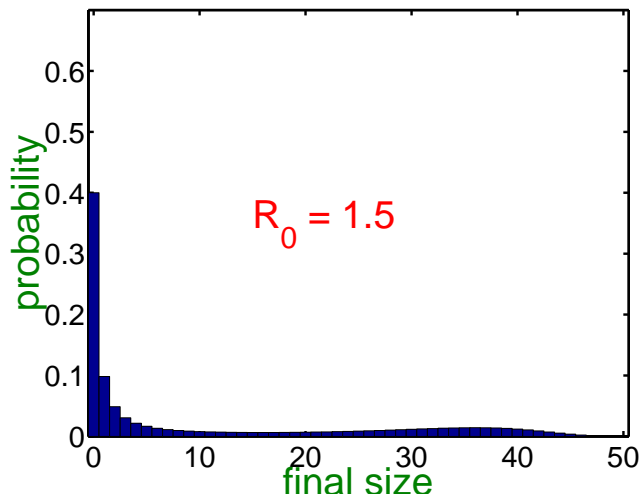
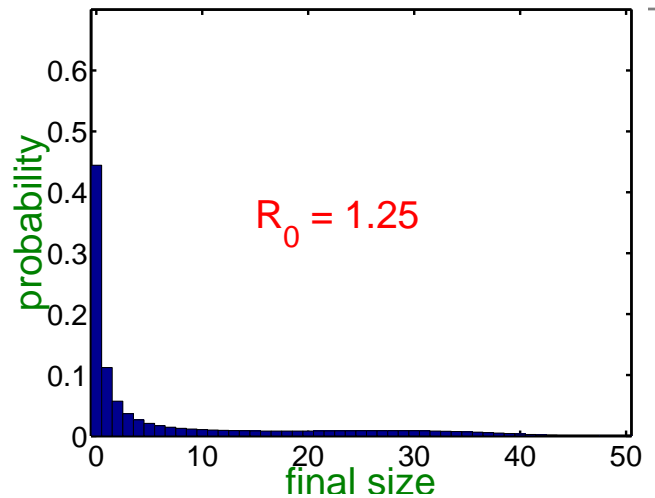
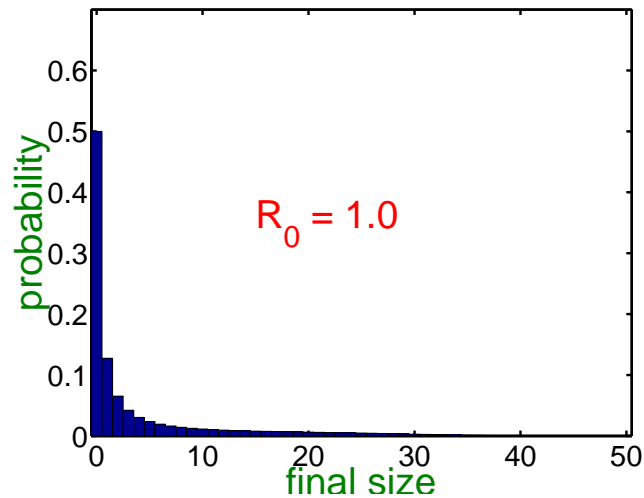
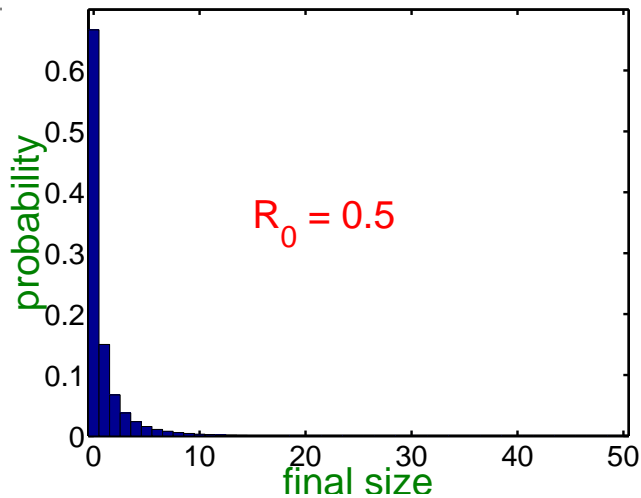
$$Z(0) = 0$$

- **Final size**  $T = N - X(\infty)$  — number of susceptibles ultimately infected
- Let  $P_j = P(T = j)$  ( $j = 0, 1, \dots, N$ ). Then

$$\sum_{j=0}^i \binom{N-j}{N-i} \left(1 + \left(1 - \frac{i}{N} R_0\right)\right)^{a+j} P_j = \binom{N}{i} \quad (i = 0, 1, \dots, N)$$

(Whittle (1955))

# Final size



Final size distribution for **general stochastic epidemic** with **1** initial infective and **50** initial susceptibles

# Threshold behaviour

- Consider epidemic with initially **few infectives** and **many susceptibles**
- If  $R_0 \leq 1$ , then
  - Only **minor outbreaks** occur
  - Size of outbreak distributed according to total progeny of approximating **branching process**,  $Z$  say, in which **all** contacts lead to an infection
- If  $R_0 > 1$ ,
  - $P(\text{major outbreak}) = 1 - P(Z \text{ goes extinct}) > 0$
  - Size of **minor outbreak** distributed according to total progeny of  $Z$ , conditional upon **extinction**
  - Size of **major outbreak** satisfies a **central limit theorem** with mean given by **deterministic** model

(von Bahr and Martin-Löf (1980))



# Basic reproduction number $R_0$

- $R_0 =$  "the expected number of **secondary** cases produced by a **typical** infected individual during its entire infectious period, in a population consisting of **susceptibles** only" (Heesterbeek and Dietz (1996))
- **Major outbreak** can occur  $\iff R_0 > 1$
- If proportion  $c$  of susceptibles is **vaccinated** with a **perfect** vaccine,  $R_0$  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**

(Smith (1964))

# Multitype general deterministic epidemic

- $m$  types of individual, labelled  $1, 2, \dots, m$ , reflecting e.g. age, vaccine status, geographical location.

$$\frac{dx_i}{dt} = -x_i \sum_{j=1}^m \beta_{ji} y_j,$$

$$\frac{dy_i}{dt} = x_i \sum_{j=1}^m \beta_{ji} y_j - \gamma_i y_i,$$

$$\frac{dz_i}{dt} = \gamma_i y_i \quad (i = 1, 2, \dots, m),$$

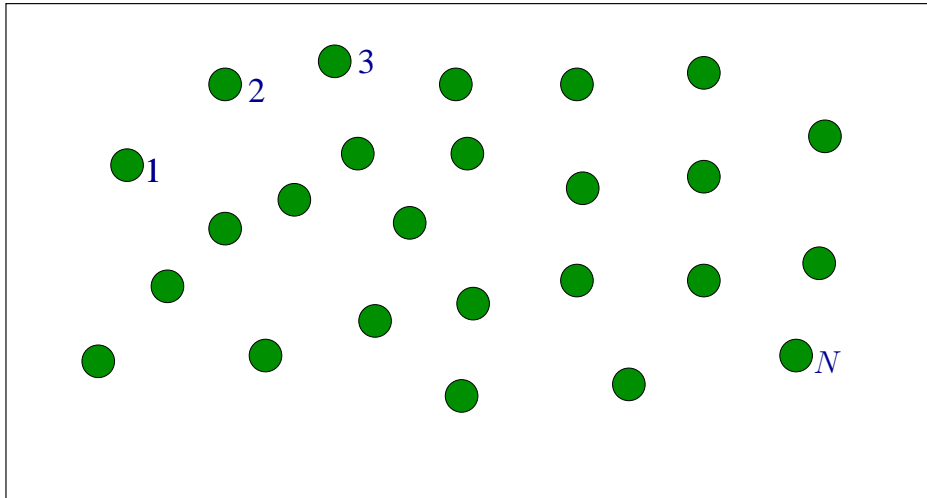
with  $(x_i(0), y_i(0), z_i(0)) = (N_i, a_i, 0)$

- Analogues of all previous results hold **BUT** threshold behaviour requires  $N_i \rightarrow \infty$  ( $i = 1, 2, \dots, m$ ), i.e. that the population is **LOCALLY LARGE**

# Non-locally-large models

- Spatial models
  - percolation
  - structure too rigid for human populations
- Network models
- Multi-level mixing models
  - metapopulation/households models
- Complex simulation models
  - more realistic but can be computationally expensive and difficult to interpret

# General two-level-mixing epidemic model



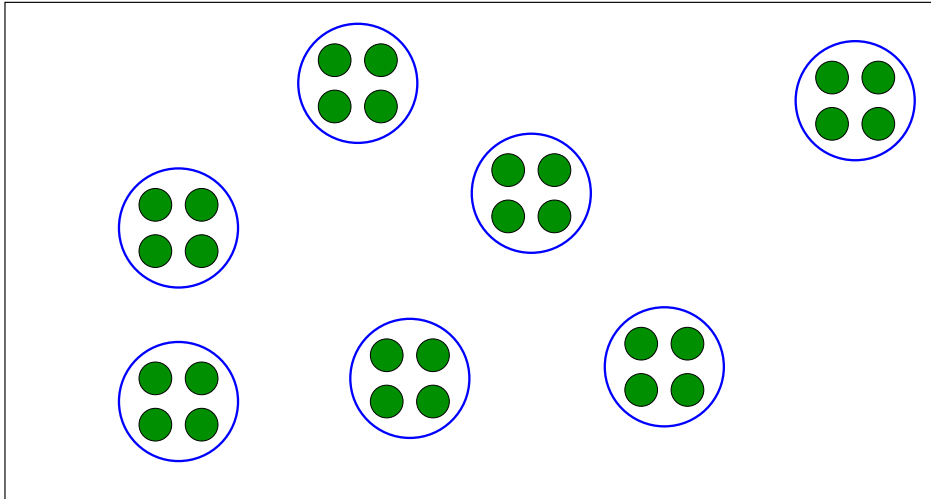
Population

$$\mathcal{N} = \{1, 2, \dots, N\}$$

- SIR (susceptible  $\rightarrow$  infective  $\rightarrow$  removed)
- Infectious periods  $I_1, I_2, \dots, I_N$  iid  $\sim I$  (arbitrary but specified)
- Infection rates (individual  $\rightarrow$  individual)
  - local  $\lambda_{ij}^L$
  - global  $\lambda_G/N$
- Latent period

(Ball and Neal (2002))

# Households model



$m$  households, each of size  $n$

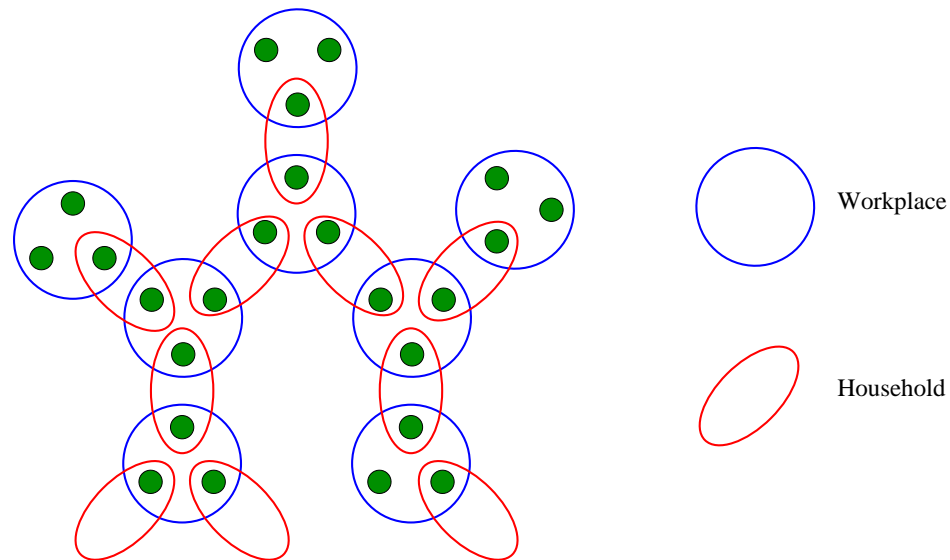
$$N = mn$$

●  $\lambda_{ij}^L = \begin{cases} \lambda_L & \text{if } i \text{ and } j \text{ belong to same household} \\ 0 & \text{otherwise} \end{cases}$

● Unequal-sized households.

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

# Overlapping groups model

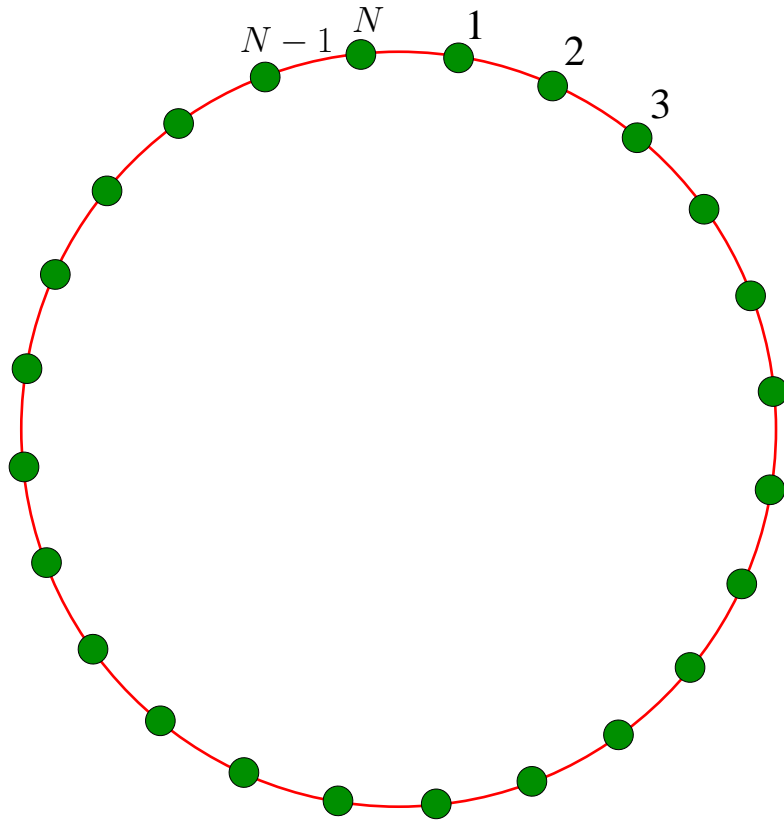


- $m_\alpha$  households, each of size  $n_\alpha$ ,  $m_\beta$  workplaces, each of size  $n_\beta$ , so  $N = m_\alpha n_\alpha = m_\beta n_\beta$

- $\lambda_{ij}^L = \begin{cases} \lambda_\alpha^L & \text{if } i \text{ and } j \text{ belong to same household} \\ \lambda_\beta^L & \text{if } i \text{ and } j \text{ belong to same workplace} \\ 0 & \text{otherwise} \end{cases}$

(Ball and Neal (2002), cf. Andersson (1997))

# Great circle model



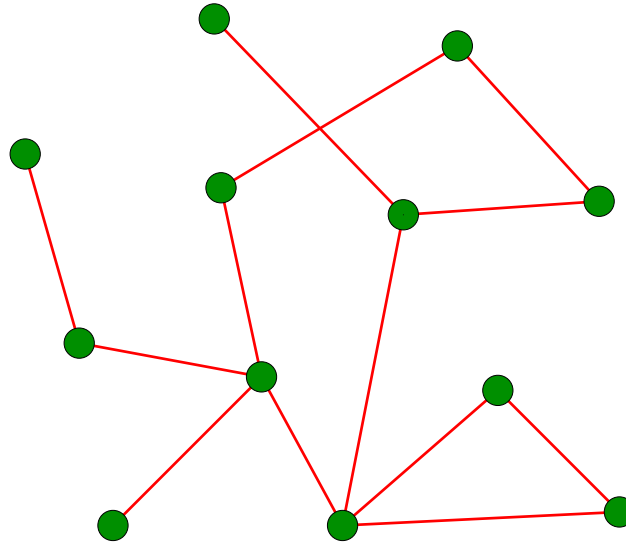
$$\lambda_{ij}^L = \begin{cases} \lambda_L & \text{if } i \text{ and } j \text{ are neighbours} \\ 0 & \text{otherwise} \end{cases}$$

'Small-world' networks

More general contact distribution

(Ball, Mollison and Scalia-Tomba (1997), Ball and Neal (2002, 2003))

# Networks with casual contacts



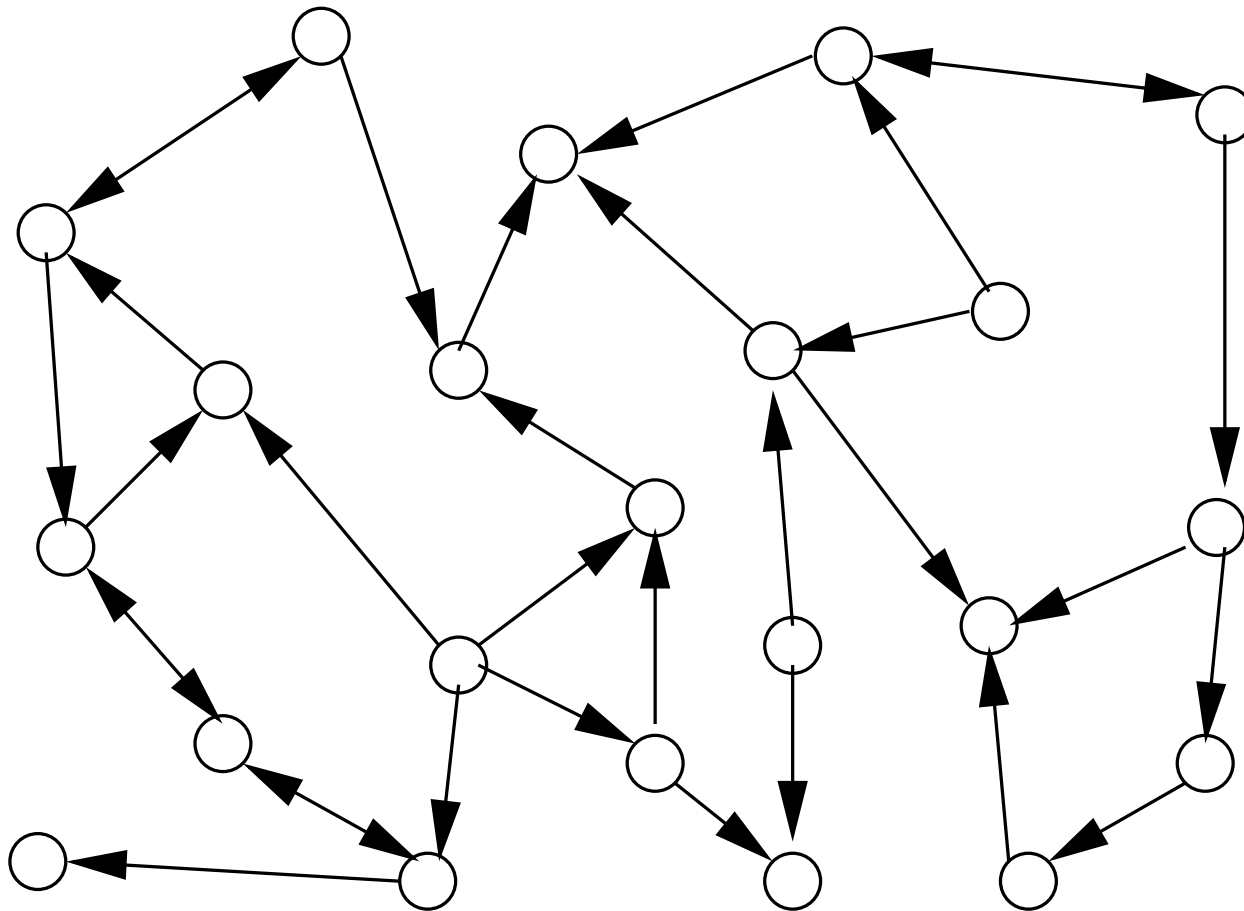
- ‘independent’ random graph of possible local contacts with specified degree distribution  $p_k = P(D = k)$  ( $k = 0, 1, \dots$ )

- $\lambda_{ij}^L = \begin{cases} \lambda_L & \text{if } i \text{ and } j \text{ are neighbours} \\ 0 & \text{otherwise} \end{cases}$

(Diekmann et al. (1998), Ball and Neal (2002), (2008), Kiss et al. (2006); Newman (2002))



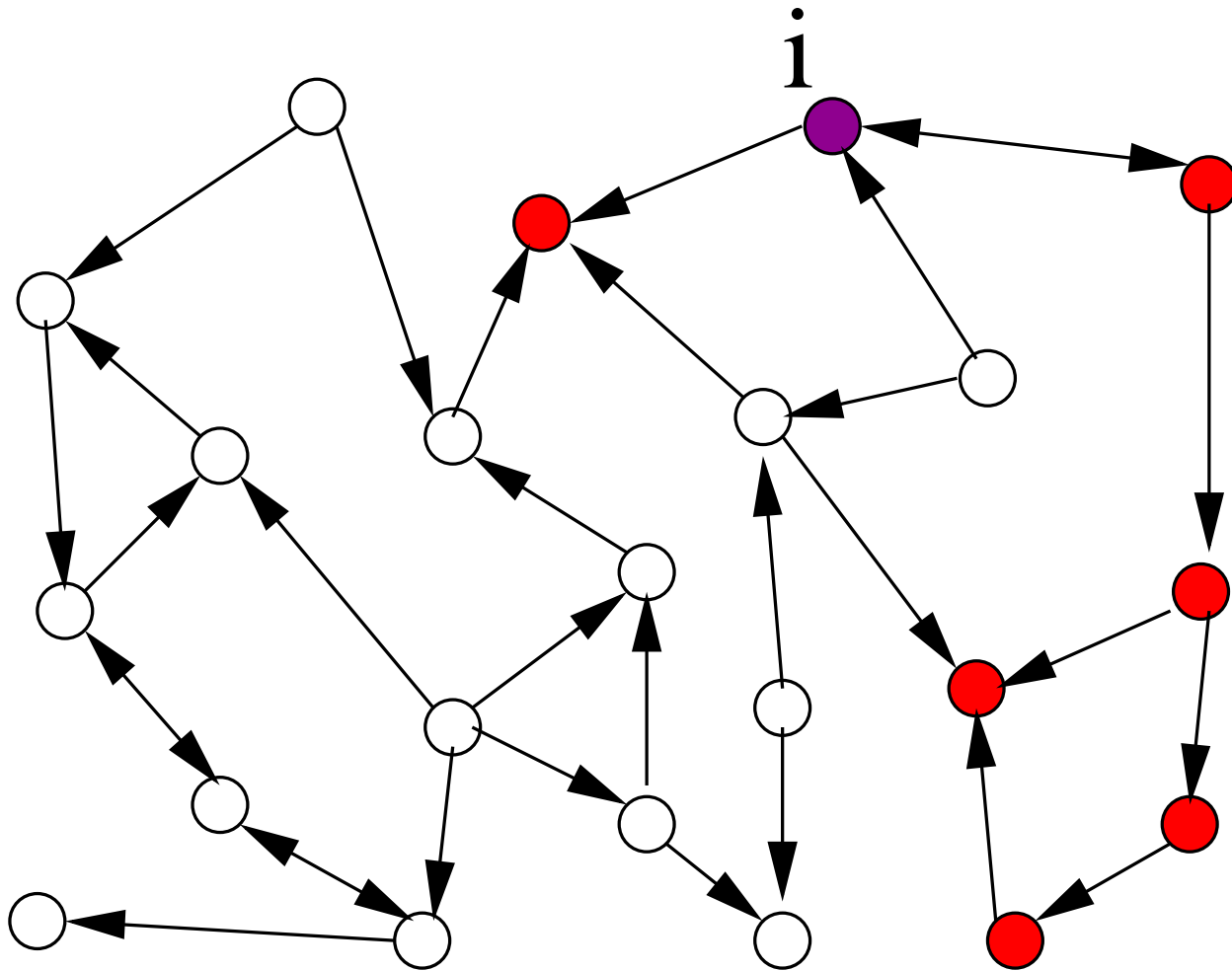
# Directed graph of potential local contacts



$i \rightarrow j$  if and only if  $i$ , if **infected**, contacts  $j$  **locally**.

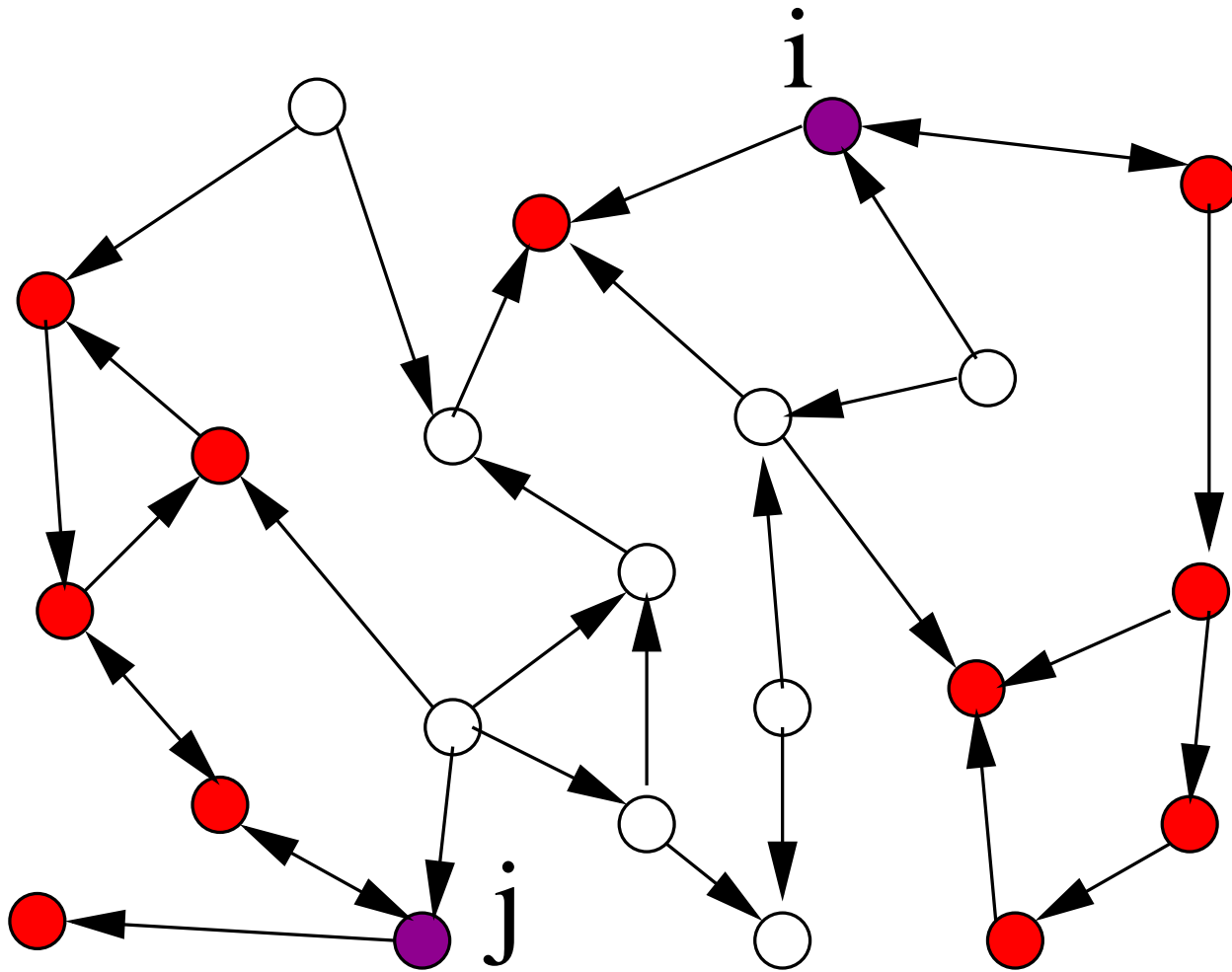
Given infectious periods  $I_1, I_2, \dots, I_N$ ,  $P(i \rightarrow j) = 1 - e^{-\lambda_L I_i}$   
independently for **distinct**  $(i, j)$ .

# Local infectious clump $\mathcal{C}_i^N$



$\mathcal{C}_i^N = \{j \in \mathcal{N} : i \rightsquigarrow j\}$ , where  $i \rightsquigarrow j$  if and only if there exists a **chain** of directed arcs **from  $i$  to  $j$** , and  $C_i^N = |\mathcal{C}_i^N|$ .

# Local infectious clumps

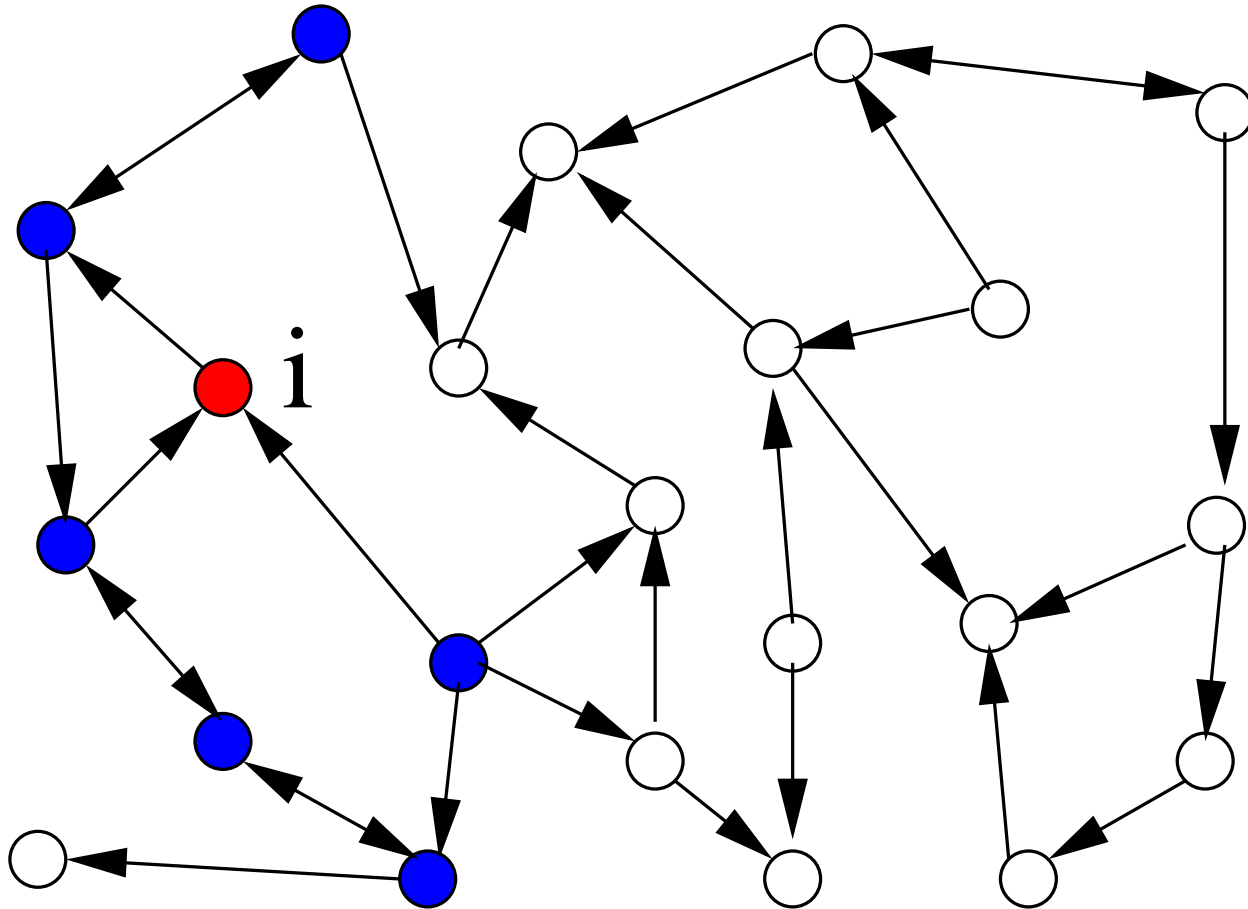


$\mathcal{C}_i^N = \{j \in \mathcal{N} : i \rightsquigarrow j\}$ , where  $i \rightsquigarrow j$  if and only if there exists a **chain** of directed arcs **from**  $i$  **to**  $j$ , and  $C_i^N = |\mathcal{C}_i^N|$ .

# Threshold parameter $R_*$

- As  $N \rightarrow \infty$ , process of **infected clumps** tends to a **branching process** having **offspring** random variable  $R \sim \text{Poisson}(\lambda_G A)$ , where  $A = \sum_{j \in \mathcal{C}} I_j$
- **Global** epidemic occurs if and only if this branching process does not go extinct
- $R_* = E[R] = \lambda_G E[A] = \lambda_G E \left[ \sum_{j \in \mathcal{N}} I_j 1_{\{j \in \mathcal{C}\}} \right] = \lambda_G \sum_{j=1}^N E[I_j] P(j \in \mathcal{C}) = \lambda_G \mu_I E[C]$
- $P(\text{global epidemic}) > 0 \iff R_* > 1$

# Local susceptibility set $\mathcal{S}_i^N$



$$\mathcal{S}_i^N = \{j \in \mathcal{N} : j \rightsquigarrow i\} \text{ and } S_i^N = |\mathcal{S}_i^N|.$$

# Final outcome of global epidemic

- Suppose  $N$  is large and there are few initial infectives. Let  $z$  be the expected proportion of the population who are infected by the epidemic. Then

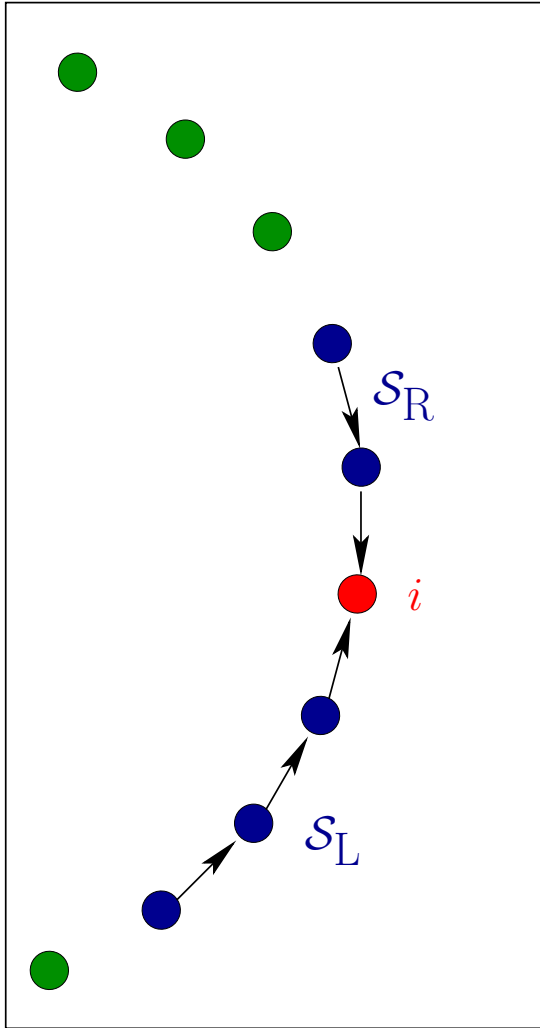
$$\pi = \text{P}(\text{typical susceptible avoids global infection}) = \exp\left(-\frac{\lambda_G}{N} N z \mu_I\right) = \exp(-\lambda_G z \mu_I)$$

and

$$\begin{aligned} 1 - z &= \text{P}(\text{typical susceptible avoids infection by epidemic}) \\ &= \text{P}(\text{typical local susceptibility set avoids global infection}) \\ &= \sum_{k=1}^{\infty} \text{P}(S = k) \pi^k = f_S(\pi) = f_S(e^{-\lambda_G z \mu_I}) \end{aligned} \tag{1}$$

- $R_* = \lambda_G \mu_I \text{E}[C] = \lambda_G \mu_I \text{E}[S]$
- $R_* \leq 1$   $z = 0$  is the only solution of (1) in  $[0, 1]$
- $R_* > 1$  unique second solution  $\hat{z} \in (0, 1)$ , giving mean 'size' of global epidemic
- Fully rigorous proof and central limit theorem for final size of global epidemic is available using Scalia-Tomba (1985) embedding technique

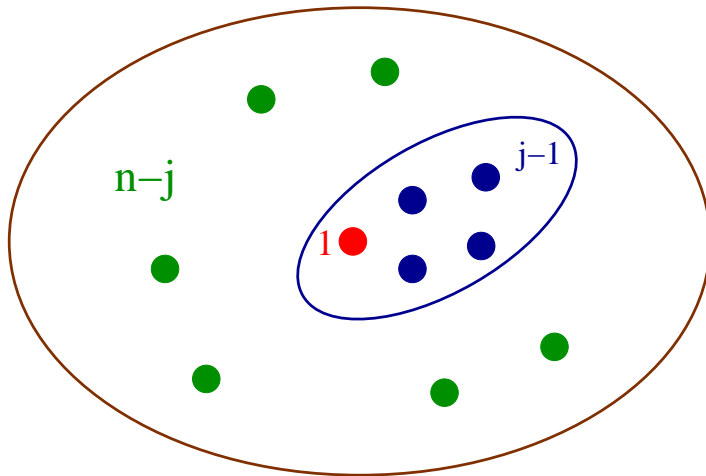
# Great circle model



- $S_i = \{i\} \cup S_L \cup S_R$
- $p_L = \text{P}(i \text{ infects } i+1 \text{ locally}) = 1 - \text{E}[e^{-\lambda_L I}]$
- $\text{P}(S_L = k) = \text{P}(S_R = k) = (1 - p_L)p_L^k$   
( $k = 0, 1, \dots$ )
- $S_L$  and  $S_R$  are independent, so  
 $\text{P}(S = k) = (1 - p_L)^2 p_L^{k-1}$  ( $k = 1, 2, \dots$ )
- $\text{E}[S] = 2p_L^{-1} - 1$

# Households model

Consider household of  $n$  individuals, labelled  $1, 2, \dots, n$ , and let  $S$  be the local susceptibility set of individual 1.



Let  $P_j^{(n)} = P(S = j) \quad (j = 1, 2, \dots, n)$

$q_k = E[e^{-k\lambda_L I}]$  be the probability that a given set of  $k$  susceptibles avoids local infection from a given infective

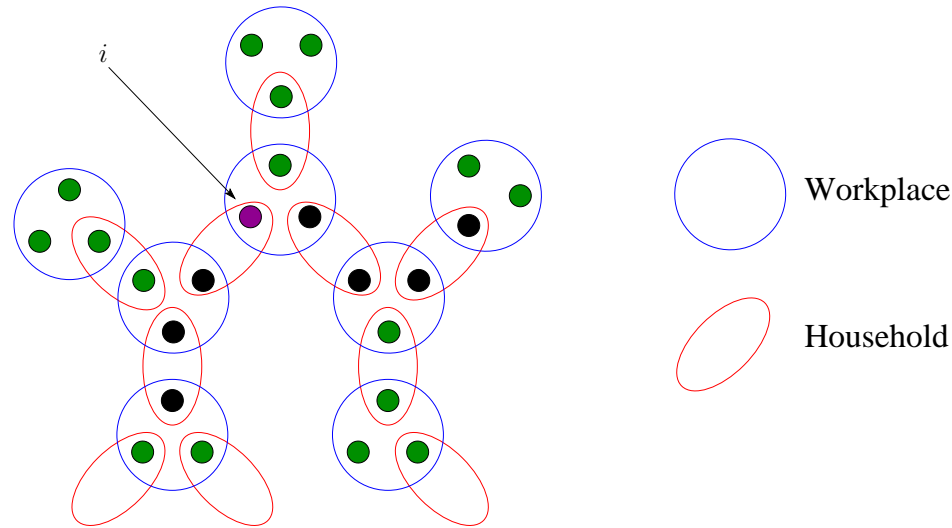
$$P_j^{(n)} = \binom{n-1}{j-1} P_j^{(j)} q_j^{n-j} \quad (j = 1, 2, \dots, n)$$

$$\begin{aligned} \sum_{j=1}^k P_j^{(k)} = 1 &\implies \sum_{j=1}^k \binom{k-1}{j-1} P_j^{(j)} q_j^{k-j} = 1 \\ &\implies \frac{\sum_{j=1}^k \binom{n-k}{n-j} P_j^{(n)}}{q_j^{n-k}} = \binom{n-1}{k-1} \quad (k = 1, 2, \dots, n) \end{aligned}$$

● Triangular system of linear equations for  $P(S = j) \quad (j = 1, 2, \dots, n)$



# Overlapping groups model



- Construct **local susceptibility set**  $\mathcal{S}$  of typical individual  $i$  via a **two-type branching process** in which individuals beget only the **opposite** type and the offspring of a type  $\alpha$  ( $\beta$ ) individual are the individuals in its **workplace** (**household**) susceptibility set.
- If  $\mu_\alpha$  ( $\mu_\beta$ ) is the mean size of a **household** (**workplace**) susceptibility set, then

$$E[\mathcal{S}] = \begin{cases} \frac{\mu_\alpha \mu_\beta}{\mu_\alpha + \mu_\beta - \mu_\alpha \mu_\beta} & \text{if } (\mu_\alpha - 1)(\mu_\beta - 1) < 1 \\ \infty & \text{otherwise} \end{cases}$$

# NETWORK — Configuration model

- Population  $\mathcal{N} = \{1, 2, \dots, N\}$

- $D$  = degree of typical individual

$$p_k = \mathbb{P}(D = k) \quad (k = 0, 1, \dots) \quad \text{specified} \quad \mu_D = \mathbb{E}[D]$$

- $D_1, D_2, \dots, D_N$  iid copies of  $D$ , conditioned on  $S_N = D_1 + D_2 + \dots + D_N$  being even

- Attach  $D_i$  half-edges to individual  $i$  ( $i = 1, 2, \dots, N$ )

- Pair up the  $S_N$  half-edges uniformly at random to form the network

IMPERFECTIONS — sparse if  $\sigma_D^2 = \text{var}(D) < \infty$

(Bollobás (2001))

# Networks with casual contacts

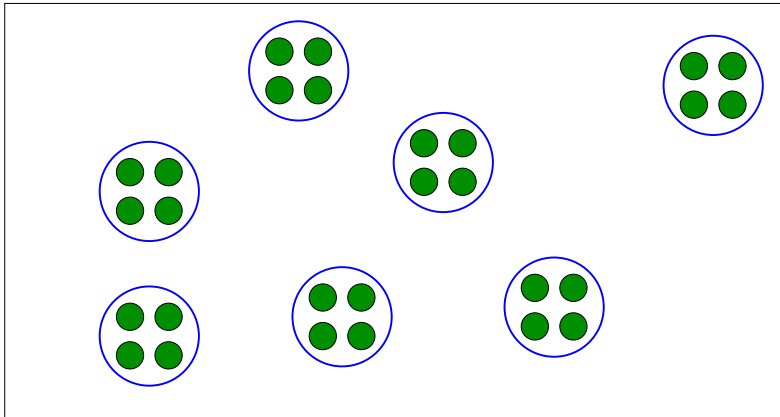
- Let  $\tilde{D}$  = degree of typical neighbour of typical individual in the network and  $\mu_{\tilde{D}} = \mathbb{E}[\tilde{D}]$ . Then

$$P(\tilde{D} = k) = kp_k / \mu_D \quad (k = 1, 2, \dots) \text{ and } \mu_{\tilde{D}} = \frac{\text{var}(D) + \mu_D^2}{\mu_D}.$$

- Size of typical local susceptibility set  $S^N \xrightarrow{a.s.} S$  as  $N \rightarrow \infty$ , where  $S$  is the total size of a branching process having offspring law  $\text{Bin}(D, p_L)$  for the initial individual and  $\text{Bin}(\tilde{D} - 1, p_L)$  for all subsequent individuals

- $$\mathbb{E}[S] = \begin{cases} 1 + \frac{\mu_D p_L}{1 - (\mu_{\tilde{D}} - 1)p_L} & \text{if } (\mu_{\tilde{D}} - 1)p_L < 1 \\ \infty & \text{otherwise} \end{cases}$$

# 'Deterministic' households model



$m$  households of size  $n$ , labelled  $1, 2, \dots, m$ .

Let  $x_i(t)$  and  $y_i(t)$  be the number of susceptibles and infectives in household  $i$  at time  $t$ .

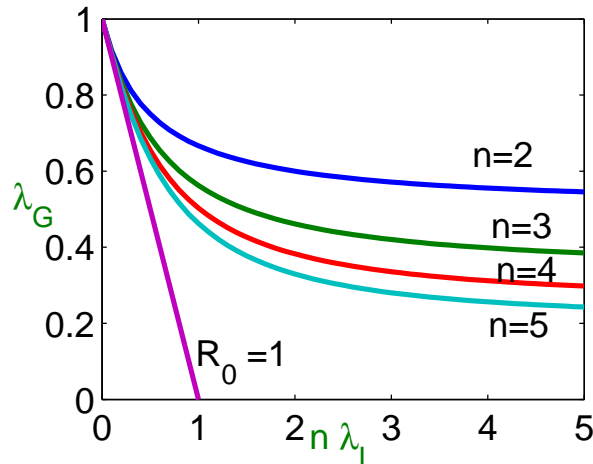
$$\frac{dx_i}{dt} = -(\lambda_L y_i + N^{-1} \lambda_G \sum_{j=1}^m y_j) x_i,$$

$$\frac{dy_i}{dt} = (\lambda_L y_i + N^{-1} \lambda_G \sum_{j=1}^m y_j) x_i - \gamma y_i \quad (i = 1, 2, \dots, m),$$

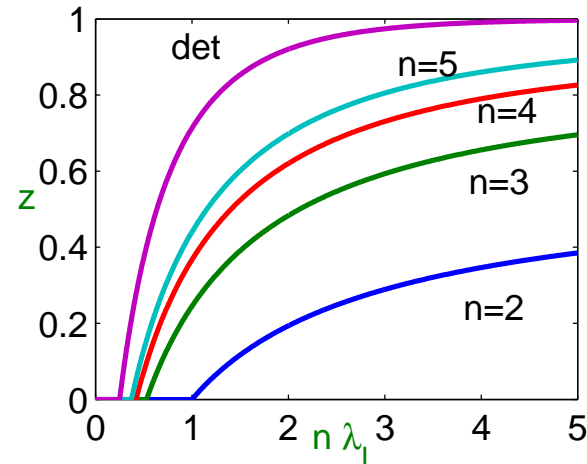
- Basic Reproduction number  $R_0 = (\lambda_G + n\lambda_L)/\gamma$
- Proportion of susceptibles ultimately infected,  $\hat{z}_{\text{det}}$  given by largest root in  $[0, 1]$  of  $1 - z = \exp(-R_0 z)$

# Households and great circle models

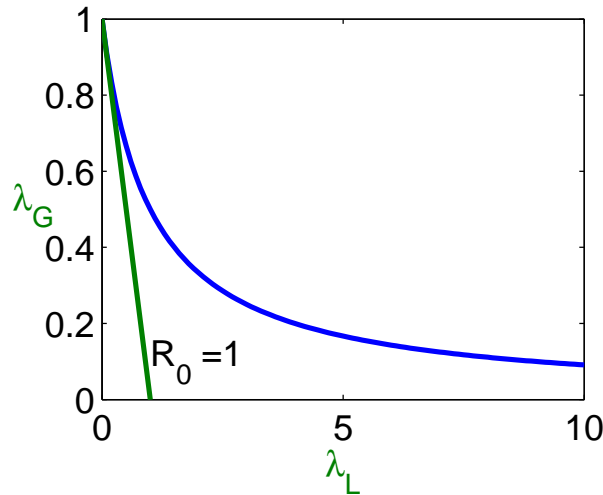
Households,  $R_* = 1$ .



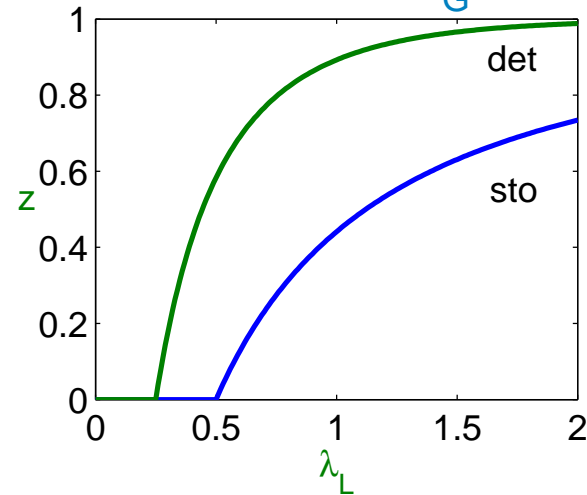
Households,  $z, \lambda_G = 0.75$ .



Great circle,  $R_* = 1$ .



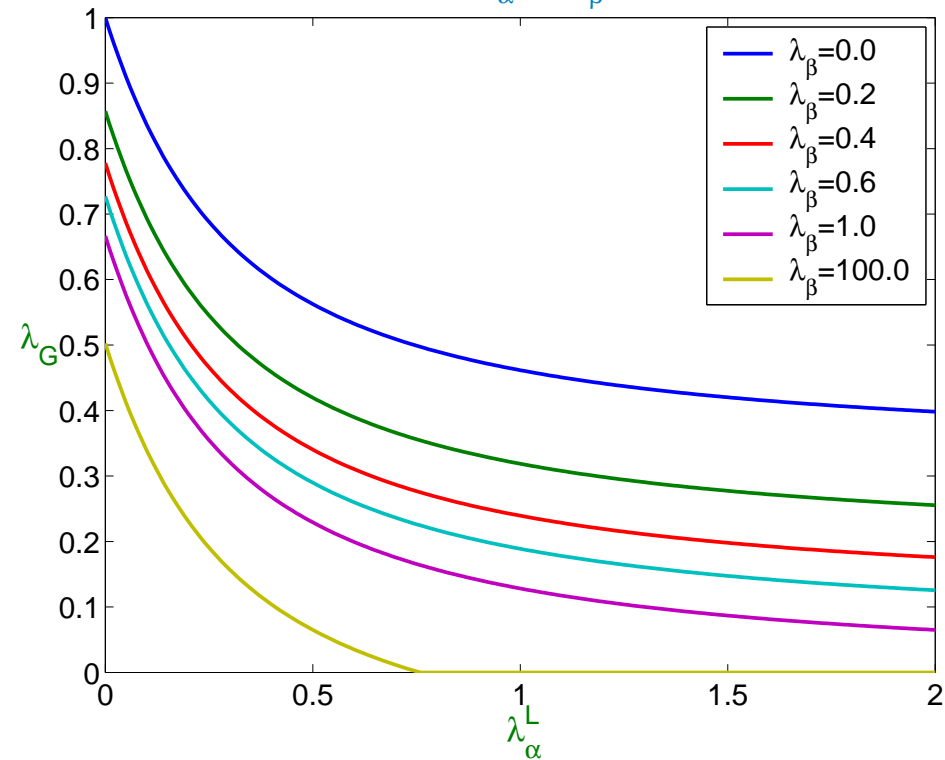
Great circle,  $z, \lambda_G = 0.5$



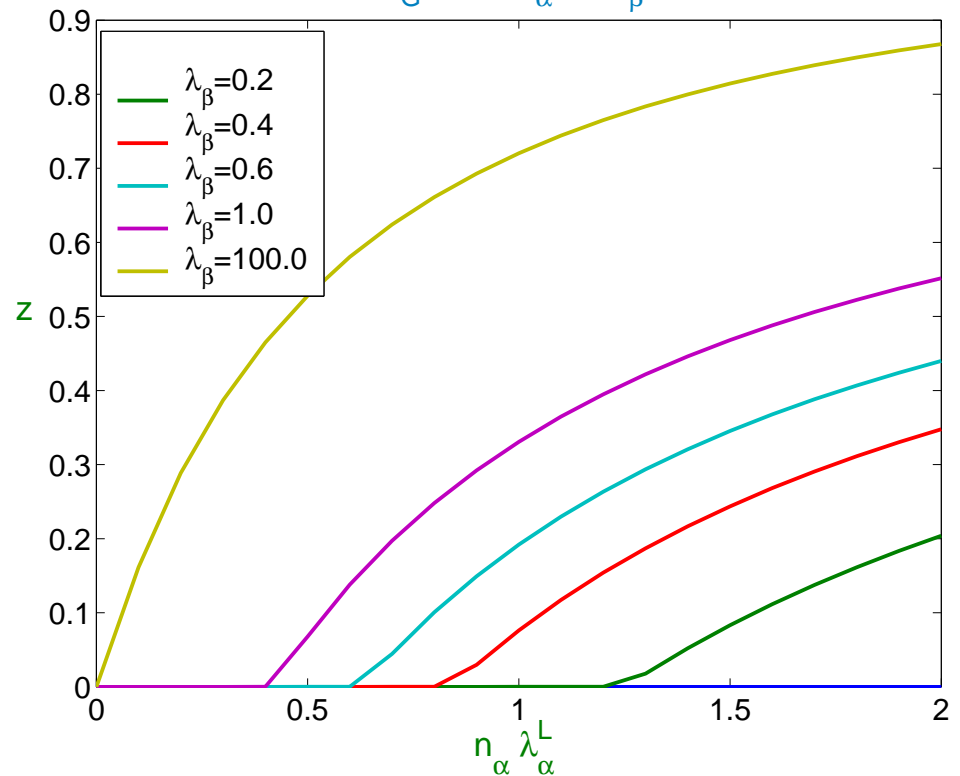
Critical values of  $(\lambda_L, \lambda_G)$  so that  $R_* = 1$  and final outcome  $\hat{z}$  when  $I \sim \text{Exp}(1)$ .

# Overlapping groups model, varying $\lambda_\beta^L$

$R_* = 1, n_\alpha = 3, n_\beta = 2$

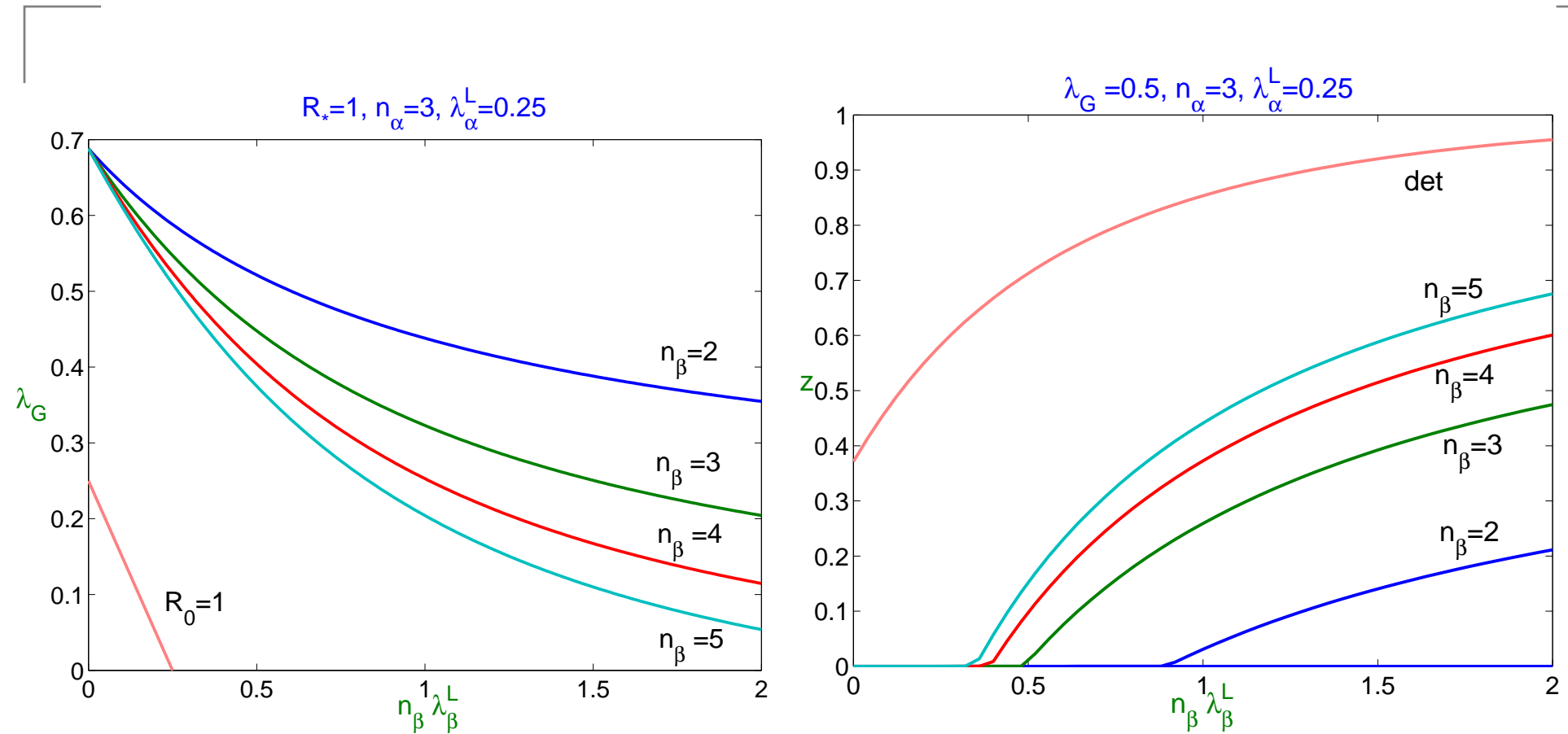


$z, \lambda_G = 0.5, n_\alpha = 3, n_\beta = 2$



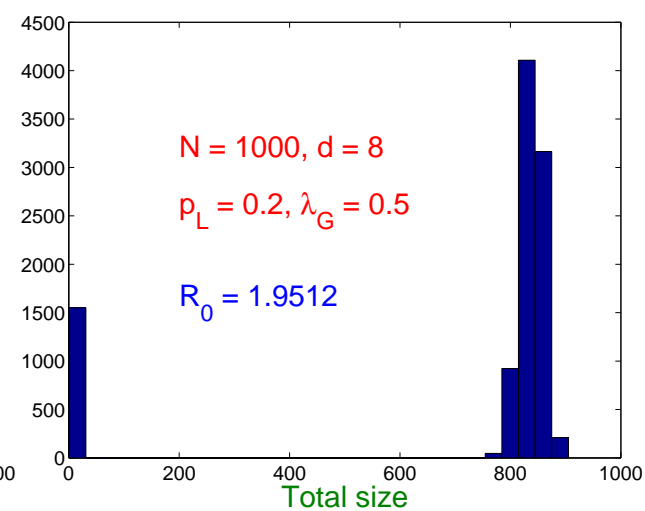
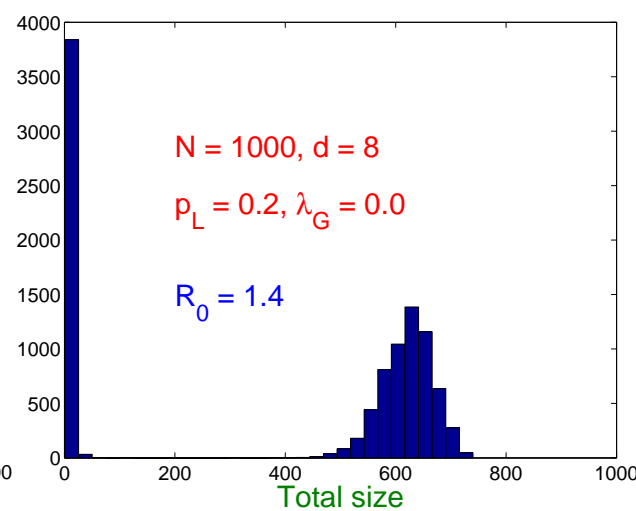
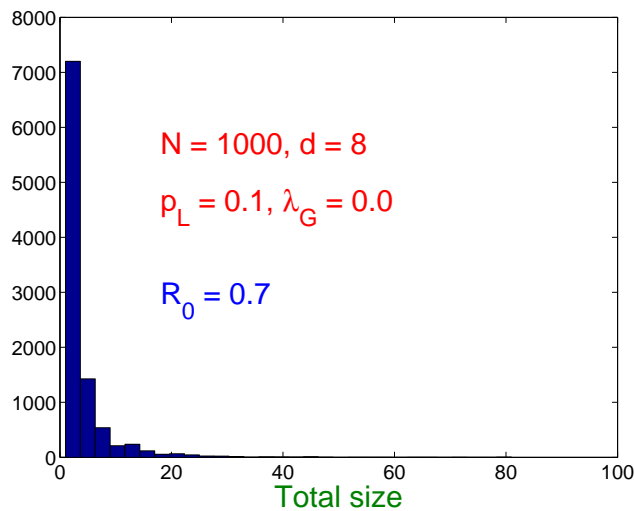
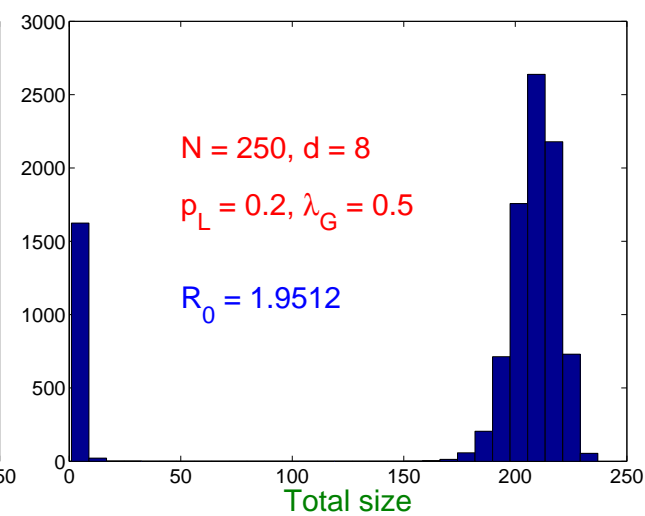
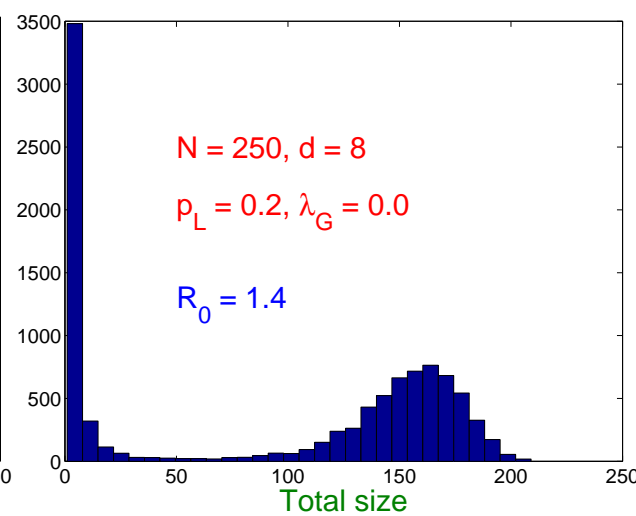
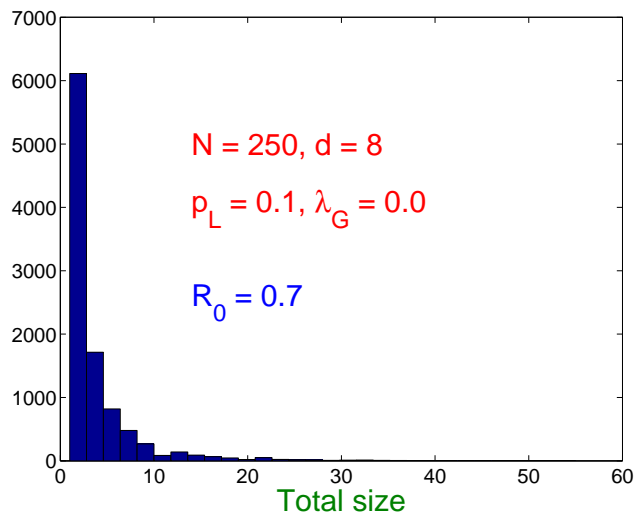
Critical values of  $(\lambda_\alpha^L, \lambda_G)$  so that  $R_* = 1$  and final outcome  $\hat{z}$  when  $I \sim \text{Exp}(1)$

# Overlapping groups model, varying $n_\beta$



Critical values of  $(\lambda_\beta^L, \lambda_G)$  so that  $R_* = 1$  and final outcome  $\hat{z}$  when  $I \sim \text{Exp}(1)$

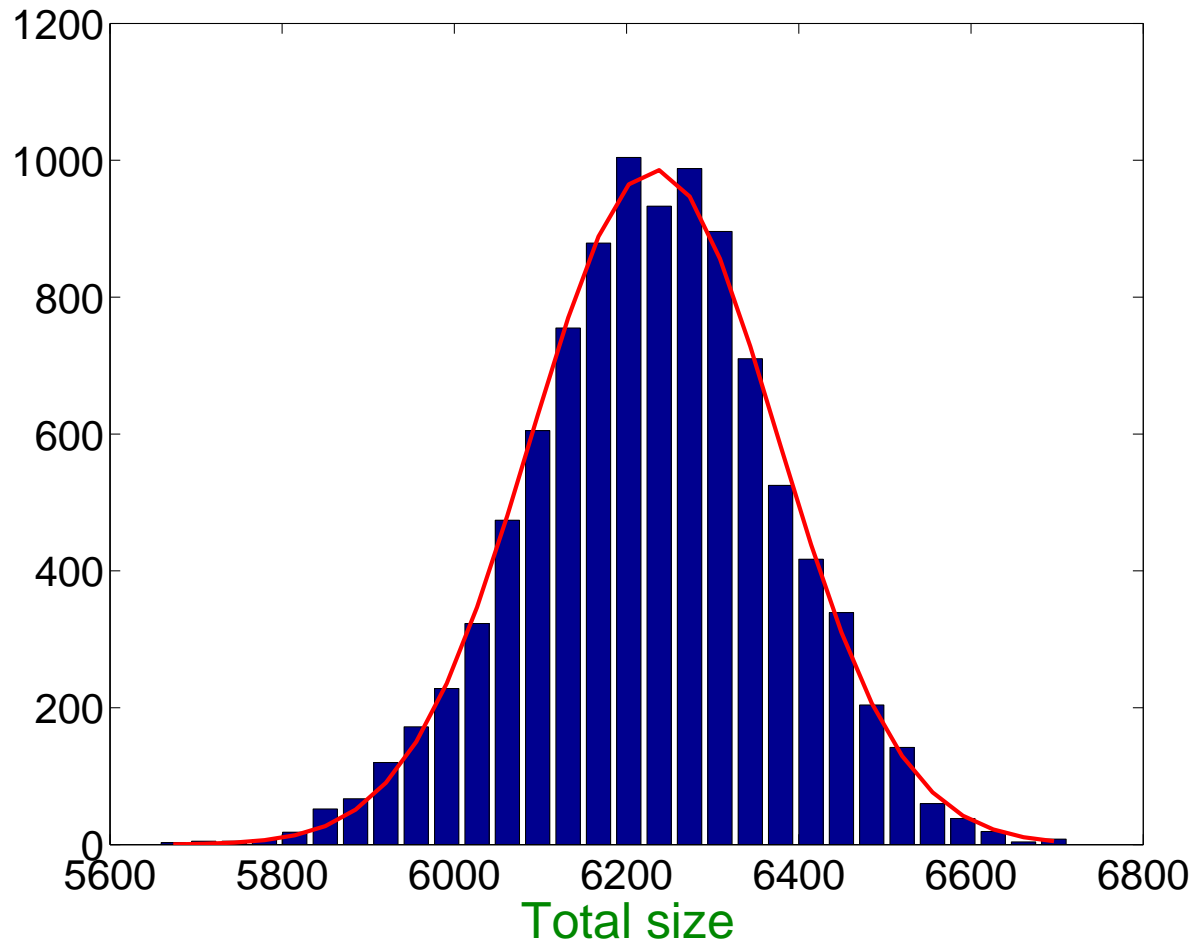
# Networks with casual contacts



Histograms of size of **10,000** simulated epidemics per parameter combination, for a **constant-degree** network with  $D \equiv d, I \equiv 1$  and other parameters as shown.

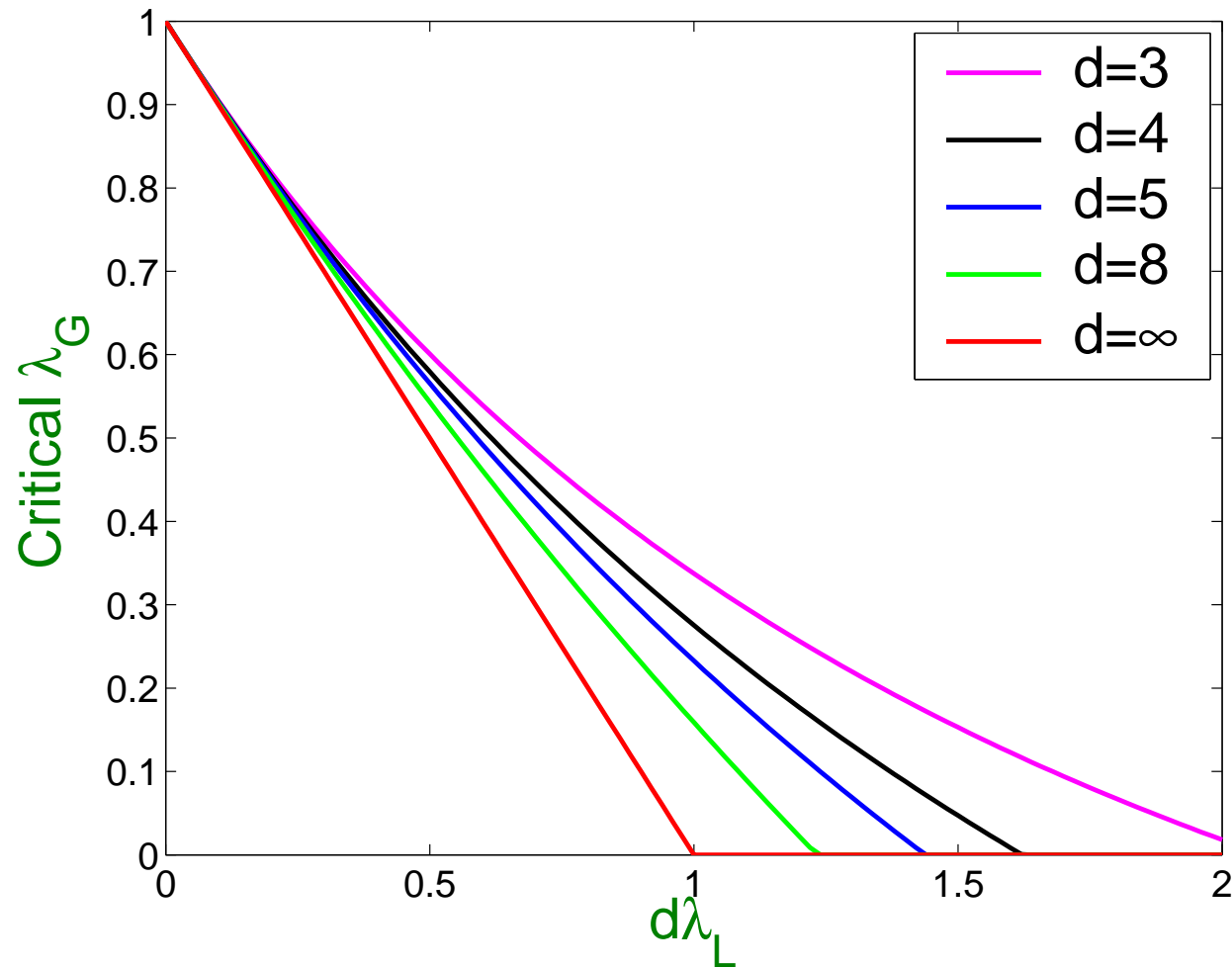


# Illustration of CLT



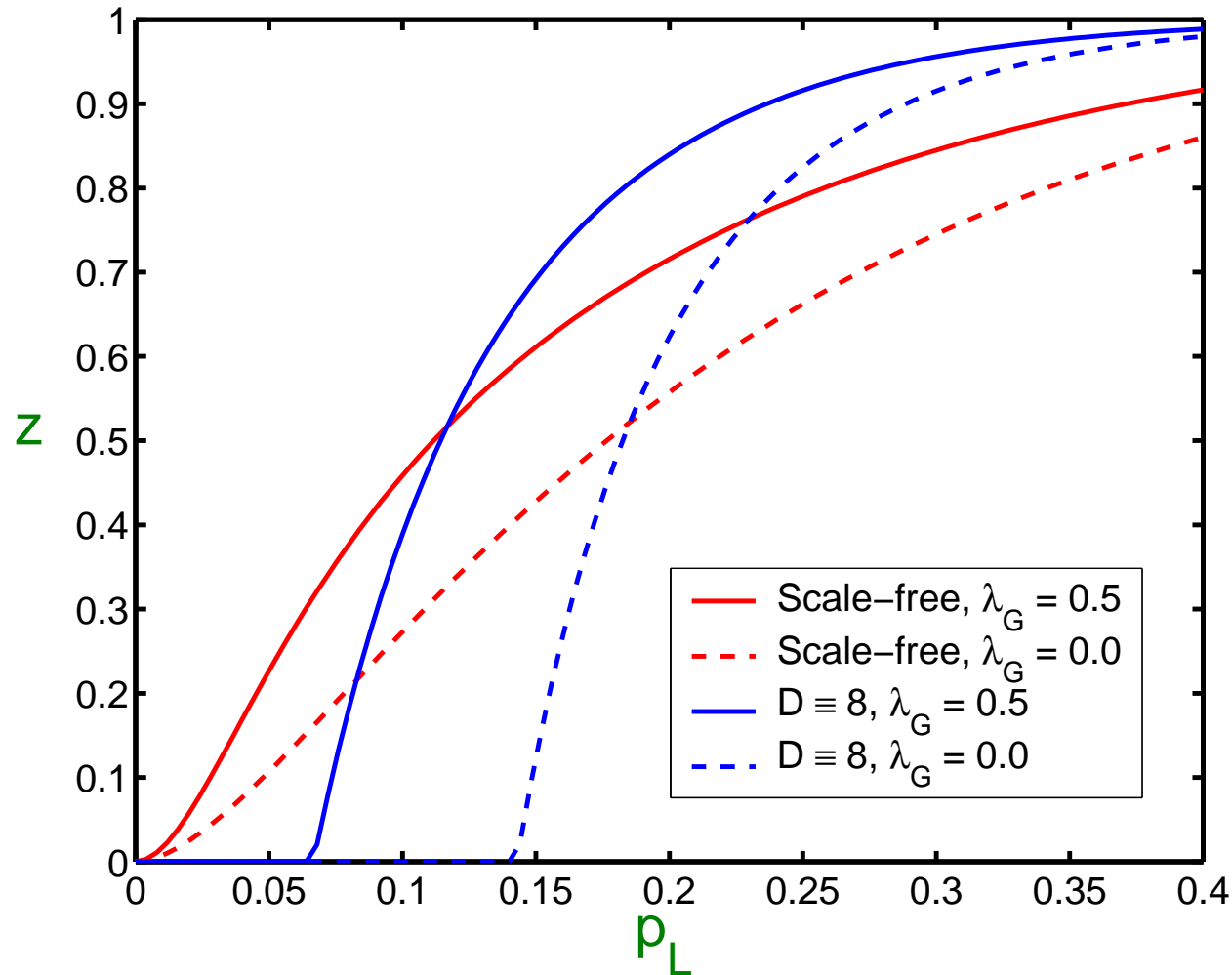
Histogram of size of **10,000** simulated **global epidemics** in a population of size  $N = 10,000$  when  $D \equiv 8$ ,  $\lambda_G = 0$  and  $p_L = 0.2$  ( $I \equiv 1$  and  $\lambda_L = -\log 0.8$ ), with **asymptotic normal approximation** superimposed.

# Networks with casual contacts



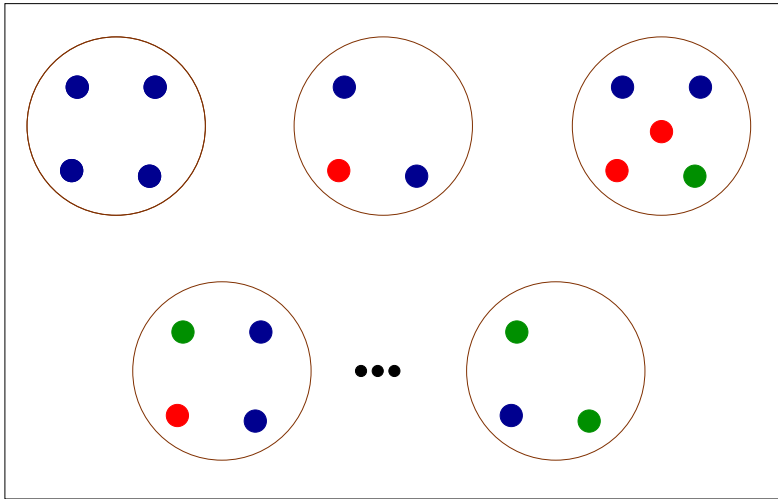
Critical values of  $(\lambda_L, \lambda_G)$  so that  $R_* = 1$  when  $I \equiv 1$ . [Expected number of potentially infectious contacts made by an infective is  $\lambda_G + d\lambda_L$ .]

# Networks with casual contacts



Asymptotic proportion of population infected by global epidemic,  $\hat{z}$ , for **constant-degree** and **scale-free** ( $P(D = k) \propto k^{-2.466956}$  ( $k = 3, 4, \dots$ )) networks with  $\mu_D = 8$  when  $I \equiv 1$ .

# Households SIR epidemic model



$m_n$  households of size  $n$  ( $n = 1, 2, \dots$ )

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

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

● SIR (susceptible  $\rightarrow$  infective  $\rightarrow$  removed)

● Infectious period  $\sim T_I$ , having an arbitrary but specified distribution

● Infection rates (individual  $\rightarrow$  individual)

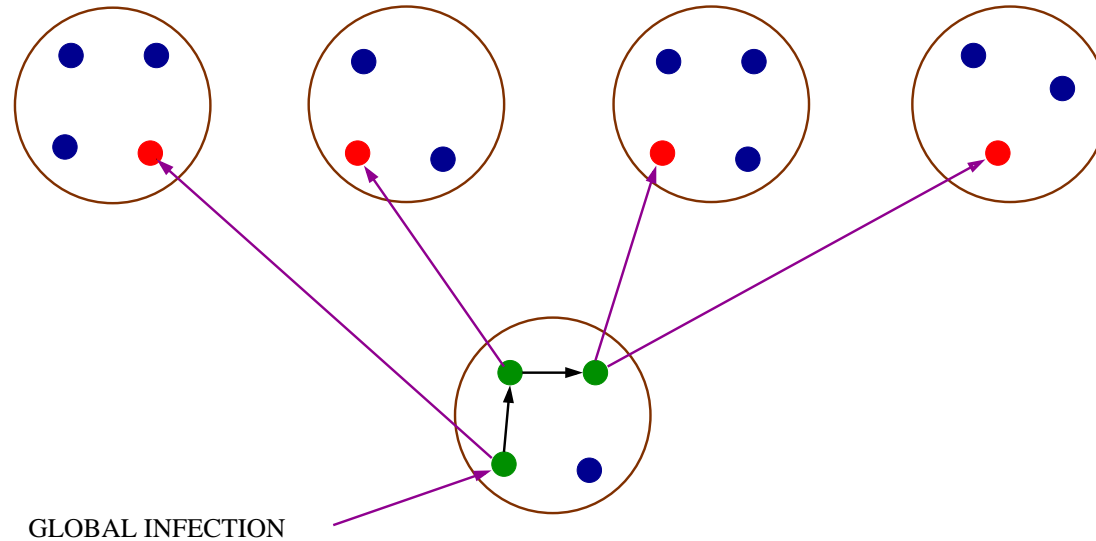
(i) local (within-household)  $\lambda_L$

(ii) global (between-household)  $\lambda_G/N$

● Latent period

(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

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

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))

# Vaccination

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

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

$\mu_{nv}$  = mean number of **global** contacts emanating from a **single-household** epidemic in a household in state  $(n, v)$ , initiated by an individual chosen **uniformly at randomly** being contacted **globally**

- Post-vaccination

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

- Vaccination coverage

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

- 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))

# Calculation of $\mu_{nv}$

●  $x_{nv}$  = proportion of size- $n$  households that have  $v$  members vaccinated  
 $\mu_{nv}$  = mean number of **global** contacts emanating from a **single-household** epidemic in a household in state  $(n, v)$ , initiated by an individual chosen **uniformly at randomly** being contacted **globally**

●  $\mu_{nv}$  depends on model for **vaccine action**.

● For an **all-or-nothing** model, in which vaccinees are rendered **immune** independently with probability  $\epsilon$ , otherwise the vaccine has **no effect**

$$\mu_{nv} = \sum_{k=0}^v \underbrace{\binom{v}{k} \epsilon^k (1 - \epsilon)^{v-k}}_{(1)} \underbrace{\frac{n-k}{n}}_{(2)} \underbrace{\mu_{n-k}(\lambda_L)}_{(3)} \lambda_G \mathbb{E}[T_I]$$

- (1) P( $k$  vaccinations are successful)
- (2) P(globally contacted individual is susceptible)
- (3) Mean size of single-household epidemic

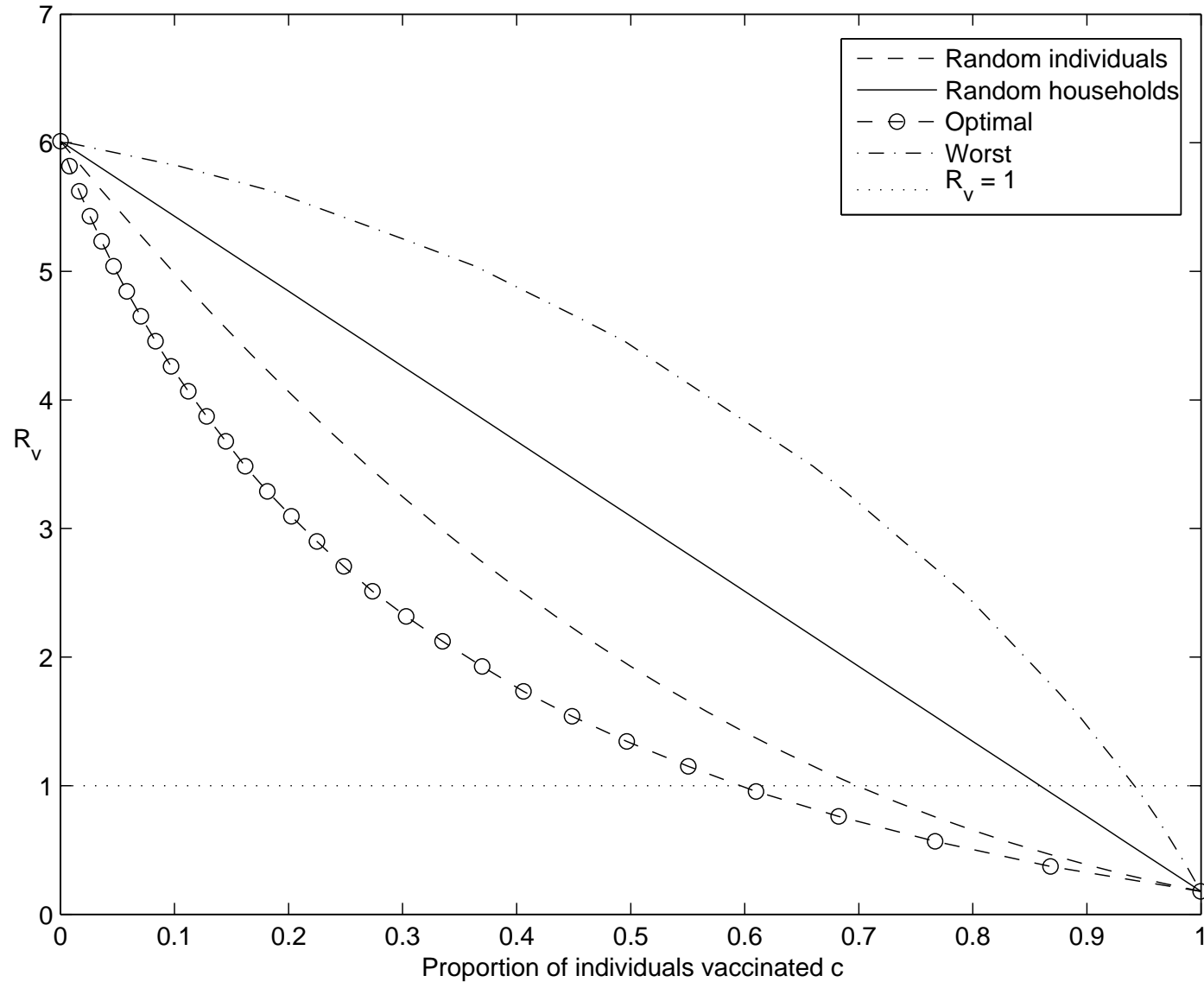
# *Variola Minor, Sao Paulo, 1956*

- 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



# Concluding comments

- General framework for determining **threshold behaviour** and **final outcome** of stochastic SIR epidemics with **two levels of mixing**.
- **Local** (e.g. **household**) structure matters!
  - Significant impact on **threshold** and **final outcome**.
  - Consequent impact on performance of **vaccination schemes**.
- **Explicit calculation** is possible only in a few special cases — need to find other **local structures** which are both **practically relevant** and **mathematically tractable**.
- Can relax **symmetries** and/or consider **multitype** epidemics.
- Non-**SIR** models
  - **SIS households** and **great circle**
  - SIR households with **demography**? **FADE OUT**

# References

- Andersson, H. (1999) Epidemic models and social networks. *Math. Scientist.* **24**, 128–147.
- Ball, F. G. and Lyne, O. D. (2002) Optimal vaccination policies for stochastic epidemics among a population of households. *Math. Biosci.* **177-178**, 333–354.
- Ball, F. G. and Lyne, O. D. (2006) Optimal vaccination schemes for epidemics among a population of households, with application to variola minor in Brazil. *Stat. Method Med. Res.* **15**, 481–497.
- Ball, F. G. and Lyne, O. D. (2010) Statistical inference for epidemics among a population of households. *J. R. Statist. Soc. B*, under revision.
- Ball, F. G., Mollison, D. and Scalia-Tomba, G. (1997) Epidemics with two levels of mixing. *Ann. Appl. Probab.* **7**, 46–89.
- Ball, F. G. and Neal, P. J. (2002) A general model for stochastic SIR epidemics with two levels of mixing. *Math. Biosci.* **180**, 73–102.
- Ball, F. G. and Neal, P. J. (2003) The great circle epidemic model. *Stoch. Proc. Appl.* **107**, 233–268.
- Ball, F. G. and Neal, P. J. (2008) Network epidemic models with two levels of mixing. *Math. Biosci.* **212**, 69–87.

# References

- Bartoszyński, R. (1972) On a certain model of an epidemic. *Appl. Math.* **13**, 139–151.
- Becker, N. G. and Dietz, K. (1995) The effect of household distribution on transmission and control of highly infectious diseases. *Math. Biosci.* **127**, 207–219.
- Becker, N. G. and Starczak. (1997) Optimal vaccination strategies for a community of households. *Math. Biosci.* **139**, 117–132.
- Becker, N. G. and Starczak. (1998) The effect of random vaccine response on the vaccination coverage required to prevent epidemics. *Math. Biosci.* **154**, 117–135.
- Bollobás, B. (2001) *Random graphs*. Cambridge University Press.
- Diekmann, O., De Jong, M. C. M. and Metz, J. A. J. (1998) A deterministic epidemic model taking account of repeated contacts between the same individuals. *J. Appl. Prob.* **35**, 448–462.
- Kiss, I., Green, D. and Kao, R. (2006) The effect of contact heterogeneity and multiple routes of transmission on final epidemic size. *Math. Biosci.* **203**, 124–136.
- Newman, M. (2002) Spread of epidemic disease on networks. *Phys. Rev. E* **66**, 016128.
- Scalia-Tomba, G. (1985) Asymptotic final size distribution for some chain-binomial processes. *Adv. Appl. Prob.* **17**, 477–495.