The effects of population heterogeneities on spread of infection

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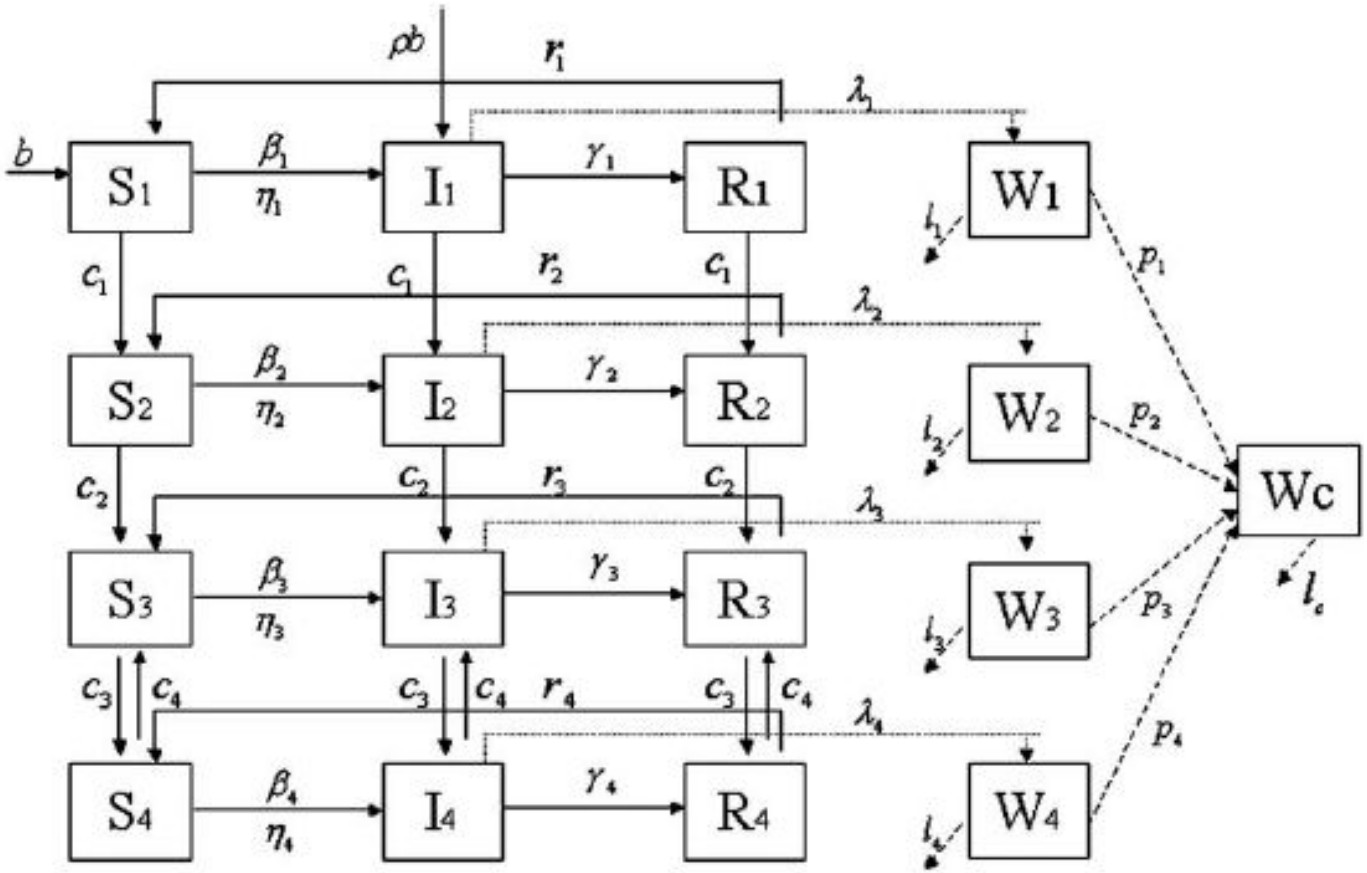
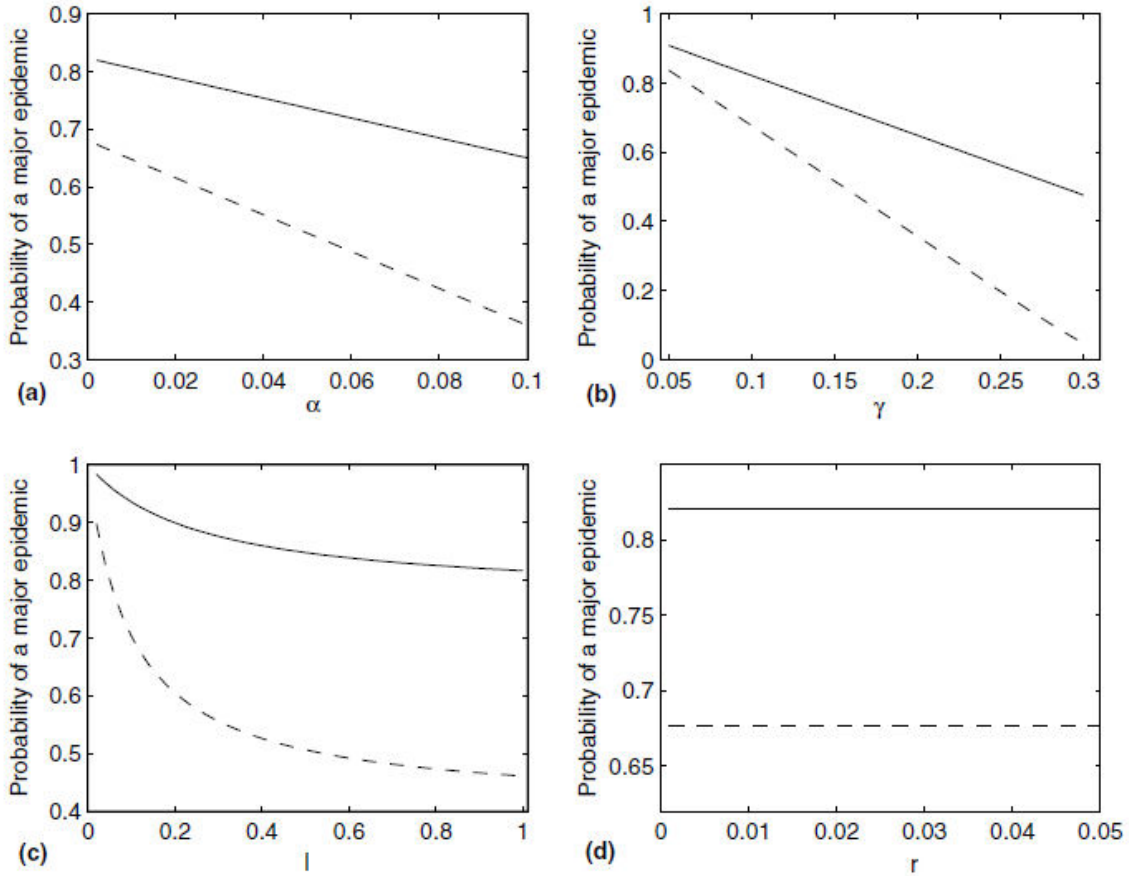
University of Liverpool

Background: Salmonella transmission in a dairy herd



Y. Xiao, D. Clancy, N.P. French, R.G. Bowers (2006), Math. Biosci.

Salmonella transmission in a dairy herd



Major outbreak probability versus various model parameters. Dashed line is for structured model, solid line for homogeneous model with R_0 matched.

A generic model

- Population partitioned into k groups
- Group i consists of N_i individuals, with $N_1 + \cdots + N_k = N$
- Each group i infective contacts each group j susceptible at rate

$$\beta_{ij} = \frac{\beta}{N} \times \lambda_i \times \pi_{ij} \times \mu_j \qquad \text{(irreducible)}$$

$$\begin{aligned} \beta &: \quad \text{overall scaling factor} \\ \lambda_i &: \quad \text{infectivity} \\ \mu_j &: \quad \text{susceptibility} \\ \pi_{ij} &: \quad \text{mixing matrix} \end{aligned}$$

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π_{ij} : mixing matrix

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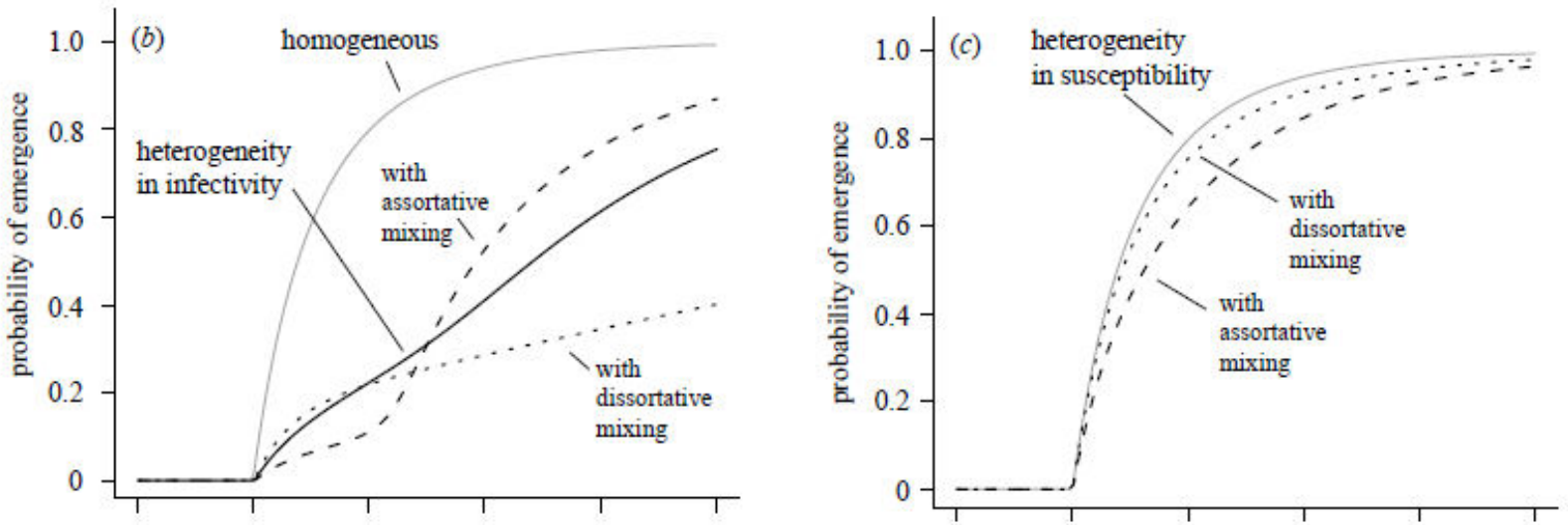
Separable model

- Model with $\beta_{ij} = \frac{\beta}{N} \lambda_i \mu_j$ is called separable, or sometimes proportionate mixing
- Model of E. Kenah, J.M. Robins (2007), J. Theo. Biol., 'Network-based analysis of stochastic SIR epidemic models with random and proportionate mixing'

Graphs from Yates et al.



Major outbreak probability versus R_0
(a) Hetero infectivity (combined with hetero mixing)
(b) Hetero susceptibility (combined with hetero mixing)

Initial conditions

- Cattle model: Initial infective in group 2 (weaned calves)
- Yates et al: Initial infective in group i with probability $\mu_i f_i$

  $f_i = N_i/N$, proportion of total population in group i
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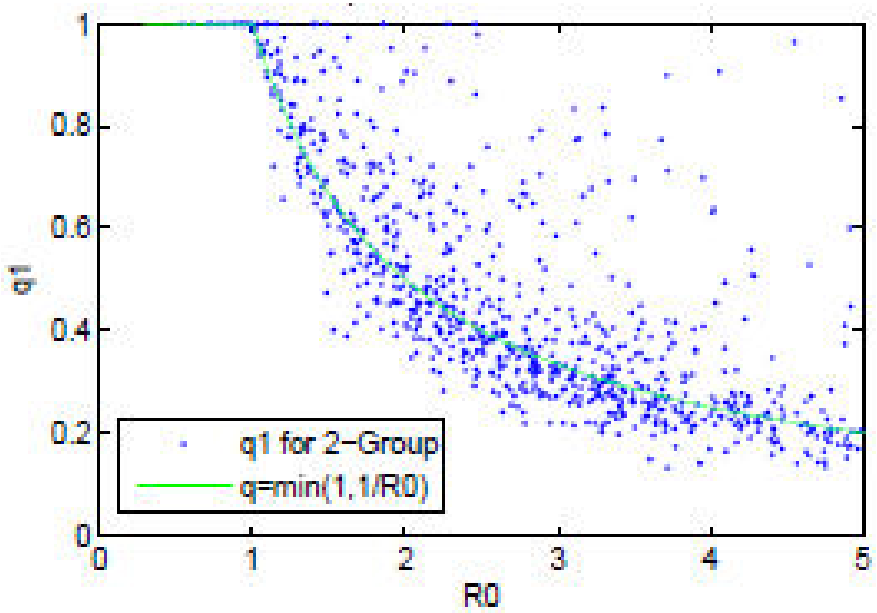
Separable model, randomly chosen parameter values



Minor outbreak probability versus R_0, with initial infective in group 1, with hetero infectivity and susceptibility
Green line for homogeneous model.

Major outbreak probability

Notation:

$$T = \text{infectious period}, \qquad \psi(\theta) = E\left[\exp(\theta T)\right]$$

$$G_{ij} = \text{Number of group } j \text{ offspring of group } i \text{ parent}$$

$$\phi_i(\mathbf{s}) = E\left[\prod_{j=1}^{k} s_j^{G_{ij}}\right] = \psi\left(-\beta \sum_{j=1}^{k} \lambda_i \pi_{ij} \mu_j f_j \left(1 - s_j\right)\right)$$

If the outbreak is started by 1 infective, belonging to group i with probability ν_i, then the major outbreak probability is $1 - \sum_i \nu_i q_i$, where

$$q_i = \phi_i\left(\mathbf{q}\right) \text{ for } i = 1, 2, \ldots, k$$

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Theorem

If the distribution $\boldsymbol{\nu}$, specifying the group of the initial infective, is a left-eigenvector of the next-generation-mean matrix, corresponding to the dominant eigenvalue R_0, then the major outbreak probability is bounded above by the homogeneous population (matched according to R_0 value).

(Similar to N. Becker, I. Marschner (1990), Lect. Notes Biomath.)

- Interpretation of the eigenvector: In the case of a major outbreak, with successive generations the proportion of all infectives which belong to group i converges to ν_i.

- So not a very natural initial condition, except in special cases.

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Special cases

In general: $\beta_{ij} = \frac{\beta}{N} \times \lambda_i \times \pi_{ij} \times \mu_j$ and $f_i = N_i/N$

1. Separable case: $\beta_{ij} = \frac{\beta}{N} \lambda_i \mu_j$. Then it's natural to assign the initial infective to group i with probability $\mu_i f_i$, and this is the appropriate eigenvector.

2. Hetero mixing: If $\beta_{ij} = \frac{\beta}{N} \pi_{ij}$ with $\sum_i \pi_{ij} = 1$ and $f_j = 1/k$ for all j, then the uniform distribution is the appropriate eigenvector.

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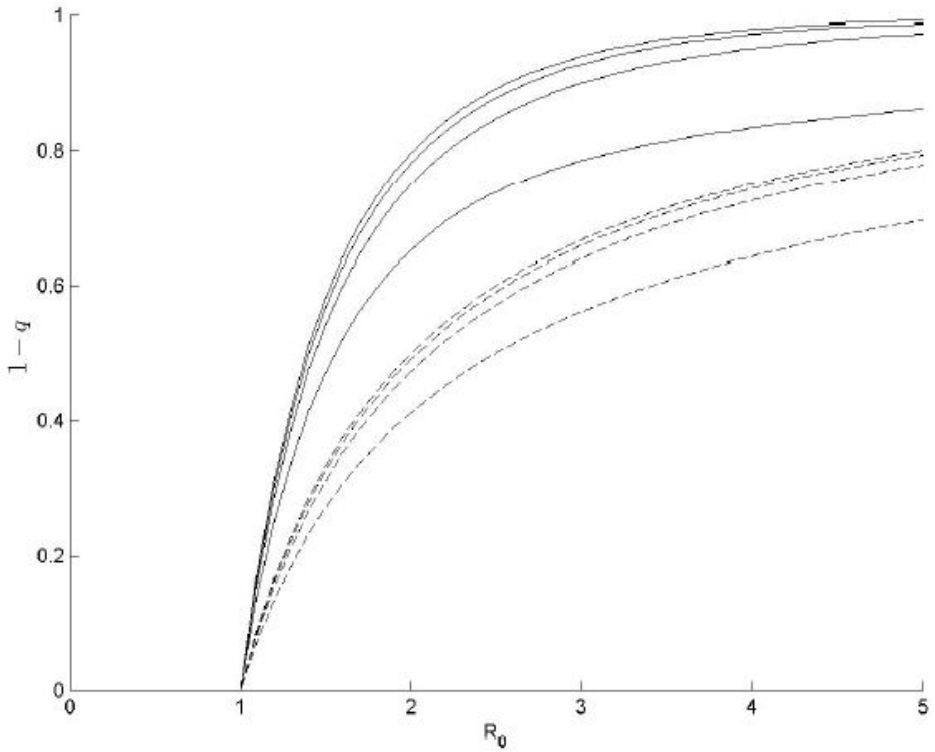
Separable model $\beta_{ij} = (\beta/N)\,\lambda_i\,\mu_j$



Major outbreak probability versus R_0
Two groups, hetero susceptibility, varying hetero infectivity.
Infectious period: Solid = Constant, Dashed = Exponential

Model assumptions

- Infectious period - any distribution
- Latent period
- Demographic processes
- Disease-induced immunity

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Outbreak size

SIR model, infection followed by lifelong immunity

- Final size: N_i^* = number of group i individuals ever infected
- Vector $(N_1^*, N_2^*, \ldots, N_k^*)$ is asymptotically multivariate normal
- Mean proportions $\tau_i = E\,[N_i^*/N_i]$ asymptotically satisfy

$$\tau_i \;=\; 1 - \exp\left(-\frac{\beta}{N}\sum_{j=1}^{k} \tau_j\, f_j\, \lambda_j\, \pi_{ji}\, \mu_i\right) \text{ for } i = 1, 2, \ldots, k$$

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For the separable model $\beta_{ij} = (\beta/N)\,\lambda_i\,\mu_j$, if Covariance $[\boldsymbol{\lambda},\, \boldsymbol{\mu}] \geq 0$ then total final size is maximised in the homogeneous case.

- Total final size $= N \sum_i \tau_i\, f_i$ (asymptotic mean)
- Covariance $[\boldsymbol{\lambda},\, \boldsymbol{\mu}] = \sum \lambda_i \mu_i f_i - (\sum \lambda_i f_i)\,(\sum \mu_i f_i)$
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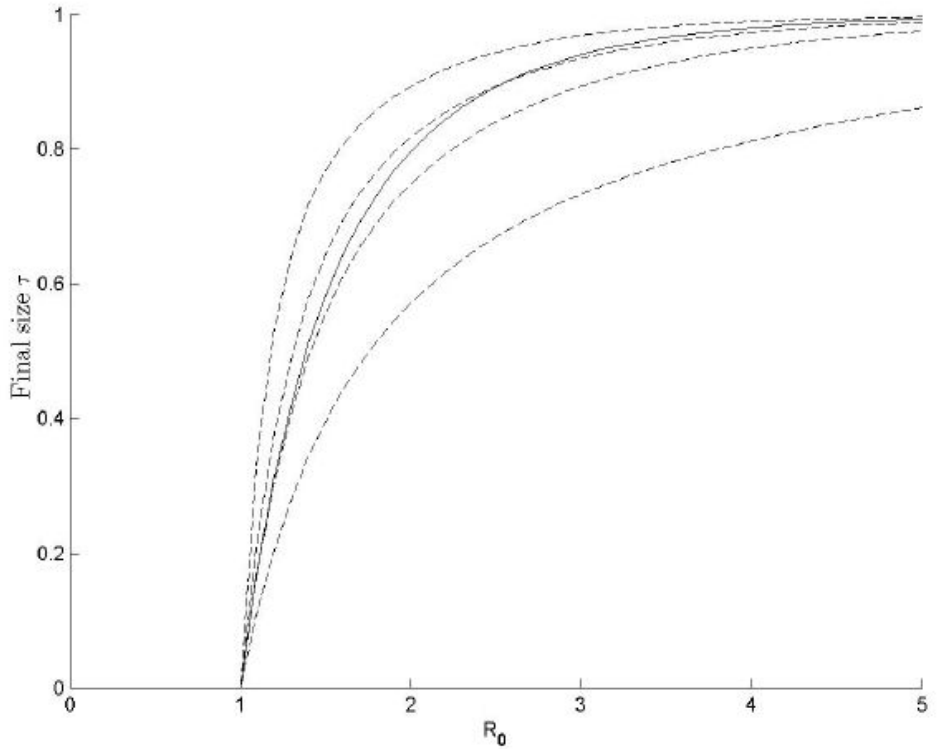

Total outbreak size versus R_0

Two groups, hetero susceptibility, varying hetero infectivity.

Solid line shows homogeneous case

Endemic prevalence level

SIS model, infection followed by immediate return to susceptibility

- Assume infectious periods exponentially distributed, then in large population limit can approximate Markov process with deterministic ODE system.
- x_i = proportion of group i infected
- Endemic equilibrium point $\mathbf{x}$ satisfies

$$x_i = \beta (1 - x_i) \sum_{j=1}^{k} x_j \, f_j \, \lambda_j \, \pi_{ji} \, \mu_i \text{ for } i = 1, 2, \ldots, k$$

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In the separable case,

$$x_i \quad = \quad \frac{D\mu_i}{1 + D\mu_i} \text{ for } i = 1, 2, \ldots, k$$

where D solves (uniquely for $R_0 > 1$)

$$\beta \sum_{j=1}^{k} \frac{\lambda_j\, \mu_j\, f_j}{1 + D\mu_j} \quad = \quad 1$$

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Theorem

For the separable model $\beta_{ij} = (\beta/N)\,\lambda_i\,\mu_j$, if Covariance $[\boldsymbol{\lambda}, \boldsymbol{\mu}] \geq 0$ then the overall endemic prevalence level is maximised in the homogeneous case.

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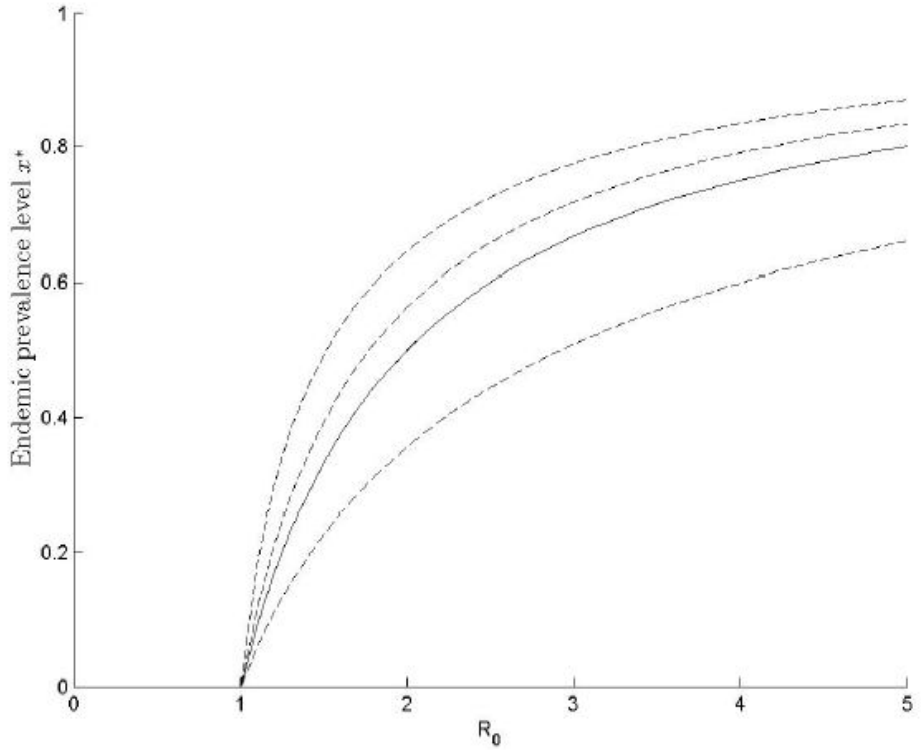

Endemic prevalence level versus R_0

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Time to fade-out

- For the above SIS model, disease extinction occurs within finite time with probability 1.
- Before extinction, state of process settles to a quasi-stationary distribution, which can be evaluated as eigenvector of truncated transition rate matrix.
- Mean time to extinction, starting from quasi-stationarity, is quasi-stationary probability that there is only 1 infective present multiplied by recovery rate of that 1 infective.

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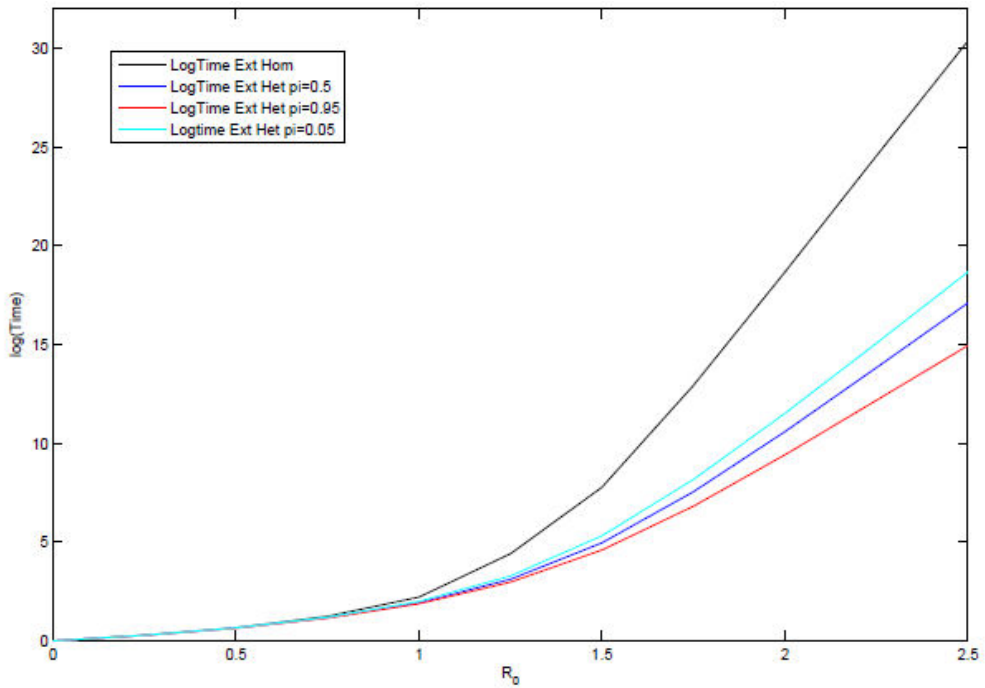
Log (expected persistence time) versus R_0



Hetero infectivity, combined with hetero mixing
Black = homogeneous, Blue = hetero infectivity only

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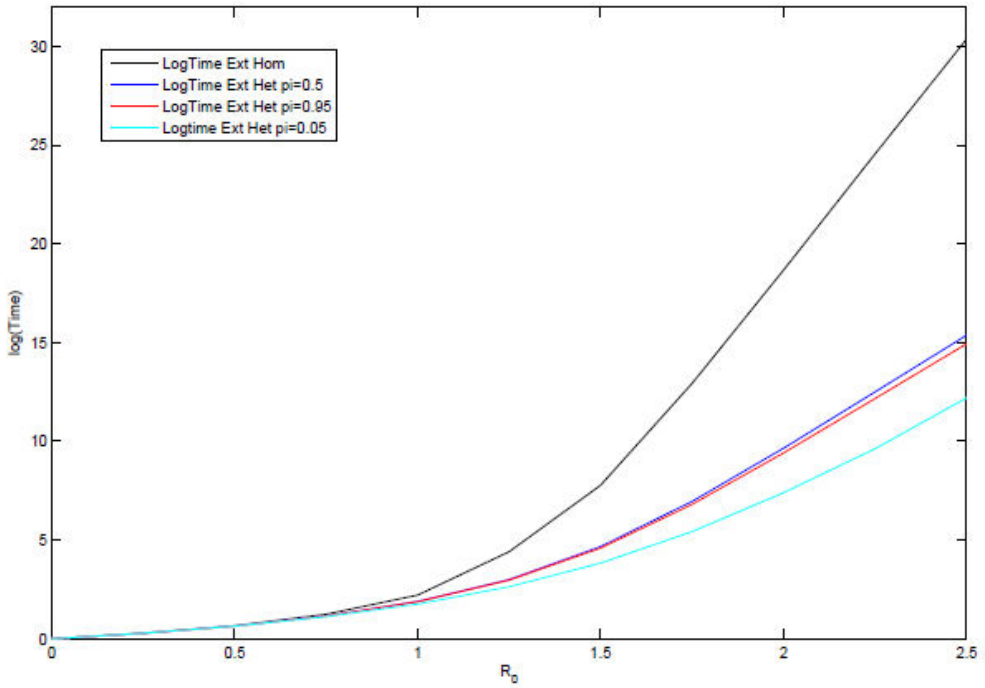

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- Variance matrix S is the $k \times k$ matrix satisfying

$$JS + SJ^T + G = 0$$

where J is Jacobian of the ODE system at endemic equilibrium and G is local variance matrix of approximating k-dimensional Ornstein-Uhlenbeck process.

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It appears that:

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- Sufficient conditions for this to be true depend on particular measure of spread
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Conclusions

- Heterogeneity often seems to reduce spread, whether measured by major outbreak probability; outbreak size; endemic prevalence; persistence time
- Sufficient conditions for this to be true depend on particular measure of spread
- Numerical work shows that the sufficient conditions obtained are very far from being necessary conditions

Related models

- Above results keep number of groups k fixed, and suppose each group is large.

  What happens if groups stay small (households), and consider limit $k \to \infty$?

- Compare with J.C. Miller (2007), Phys. Rev. E, SIR network model, homogeneous infectivity maximises probability of major outbreak, homogeneous susceptibility maximises outbreak size.

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