Threshold Parameters for a Model with Households and Workplaces

Mathematical models for emerging infections in socially structured populations

Lorenzo Pellis

Department of Infectious Disease Epidemiology
Imperial College London

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Imperial College London

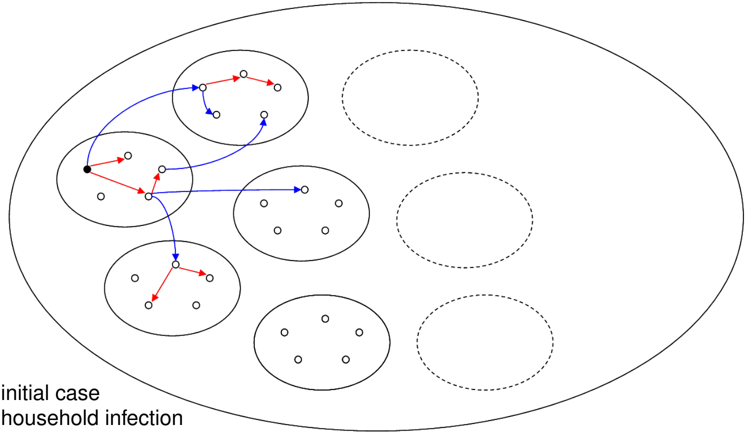
Aims of the PhD

- To develop an SIR model to describe the spread of an airborne disease in a population partitioned into households and schools/workplaces
- To determine one or more threshold parameters for the model
- To assess the effectiveness of the school/workplace closure as a control policy in the case of an emerging outbreak

Further restrictions:

- Single outbreak $\Rightarrow$ no demographic effects
- Analytically tractable model $\Rightarrow$ deep insight and quick real-time reaction

Households model and infections



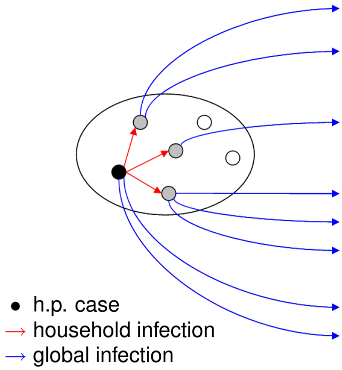
- ● initial case
- → household infection
- → global infection

R_*: the basic reproduction number for households

It is possible to prove (Wald's identity for epidemics) that

Formula for R_*

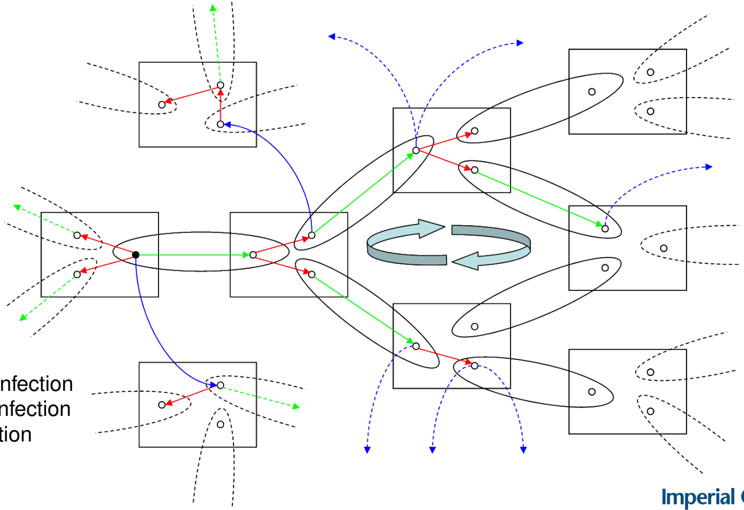
$$R_* = R_g\,(1 + \mu_H)$$



Note:

- R_* is linear in R_g
- The whole complexity of the local process is "squeezed" into μ_H

Households-workplaces model and infections



- ● initial case
- → household infection
- → workplace infection
- → global infection
- ⇌ cycle

The concept of clump

Definition of clump

A clump is a set of individuals infected through a chain of local epidemics

- Ball and Neal (2002) gave a condition under which chains of local epidemics stop (a.s.) after a finite number of steps
- In this case, the average size of a clump is finite Figure

A basic reproduction number for clumps

Let R_* be the average number of clumps infected by a “typical” clump in a totally susceptible population

A household perspective

Focus the attention on a household: it can be infected Figure

- locally: the h.p. case is infected in his or her workplace
- globally: the h.p. case is a d.p. case infected globally

The household can infect

- locally: through an infection occurring in a workplace
- globally: through a global infection

Define R_{ij}, for i and $j = L$ or G, as the average number of households infected through a contact of type i by a household which has been infected through a contact of type j

R_H: a basic reproduction number for households

Next generation matrix: Details

$$K = \begin{pmatrix} R_{GG} & R_{GL} \\ R_{LG} & R_{LL} \end{pmatrix} = \begin{pmatrix} R_g\,(1+\mu_H) & R_g\,(1+\mu_H) \\ \mu_W\,(1+\mu_H) & \mu_H\mu_W \end{pmatrix}$$

Formula for R_H

$$R_H = \frac{R_g(1+\mu_H)+\mu_H\mu_W}{2} + \\ + \frac{1}{2}\sqrt{[R_g(1+\mu_H)+\mu_H\mu_W]^2 + 4R_g\mu_W(1+\mu_H)}$$

Note:

- The formula is not symmetric in μ_H and μ_W
- R_H is not linear in R_g

Comparison between R_* and R_H

$$R_* = R_g \frac{(1+\mu_H)(1+\mu_W)}{1-\mu_H\mu_W}$$

$$R_H = \frac{R_g(1+\mu_H)+\mu_H\mu_W}{2} + \frac{1}{2}\sqrt{[R_g(1+\mu_H)+\mu_H\mu_W]^2 + 4R_g\mu_W(1+\mu_H)}$$

Comparison between R_* and R_H

$$R_* = R_g \frac{(1+\mu_H)(1+\mu_W)}{1-\mu_H\mu_W}$$

$$R_H = \frac{R_g(1+\mu_H)+\mu_H\mu_W}{2} + \frac{1}{2}\sqrt{[R_g(1+\mu_H)+\mu_H\mu_W]^2 + 4R_g\mu_W(1+\mu_H)}$$

Theorem

- $R_* = 1 \iff R_H = 1$
- $R_* > 1 \iff R_H > 1$
- $R_* < 1 \iff R_H < 1$

Critical vaccination coverage

As for the household model:

- Since R_* is linear in R_g, it is:

$$p^*_{crit} = 1 - \frac{1}{R_*}$$

- For R_H we conjecture: Reasons

$$p^H_{crit} \leq 1 - \frac{1}{R_H}, \quad \text{i.e.} \quad R^V_H \leq 1$$

School/workplace closure

$$R_* = R_g \frac{(1+\mu_H)(1+\mu_W)}{1-\mu_H\mu_W}$$

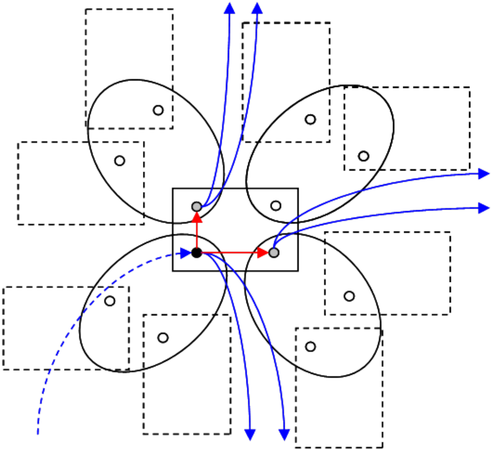
$$R_H = \frac{R_g(1+\mu_H)+\mu_H\mu_W}{2} + \frac{1}{2}\sqrt{[R_g(1+\mu_H)+\mu_H\mu_W]^2 + 4R_g\mu_W(1+\mu_H)}$$

- School/workplace closure can be modelled by setting $\mu_W = 0$:
$$R_H = R_* = R_g(1+\mu_H)$$
- If all the other parameters remain unaltered, we always reduce R_H and R_*
- If they change, we need to estimate them before and after school/workplace closure

Discussion topics

- R_H and the critical vaccination coverage. Are we loosing an important equation?
- I assumed a network with no loops.
  - Real social structures?
  - How do we define a workplace?
  - Does it matter?
- Is $R_\cdot$ a measure of the severity of the epidemic?

R_{GG}

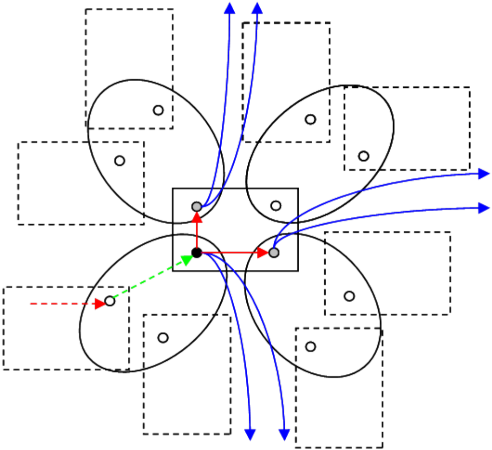


- ● primary case
- → household infection
- → workplace infection
- → global infection

Formula for R_{GG}

$$R_{GG} = R_g\,(1 + \mu_H)$$

R_{GL}



- ● primary case
- → household infection
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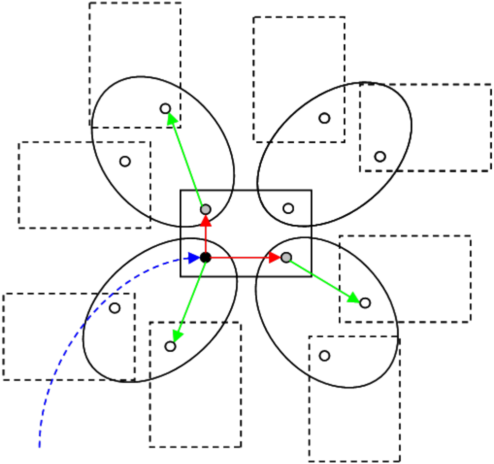
Formula for R_{GL}

$$R_{GL} = R_g\,(1 + \mu_H)$$

R_{LG}



- ● primary case
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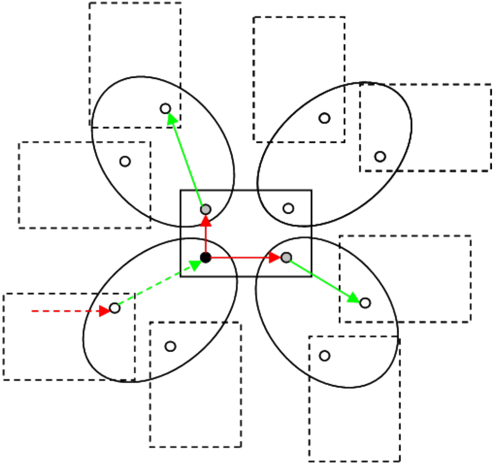
Formula for R_{LG}

$$R_{LG} = \mu_W \left(1 + \mu_H\right)$$

R_{LL}



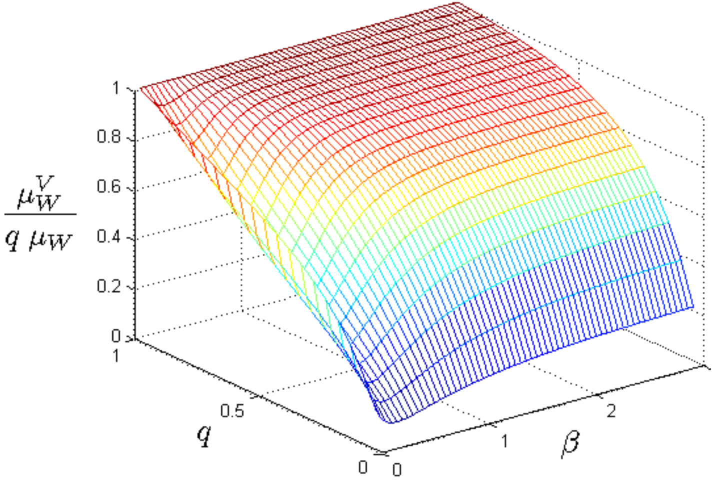
- ● primary case
- → household infection
- → workplace infection
- → global infection

Formula for R_{LL}

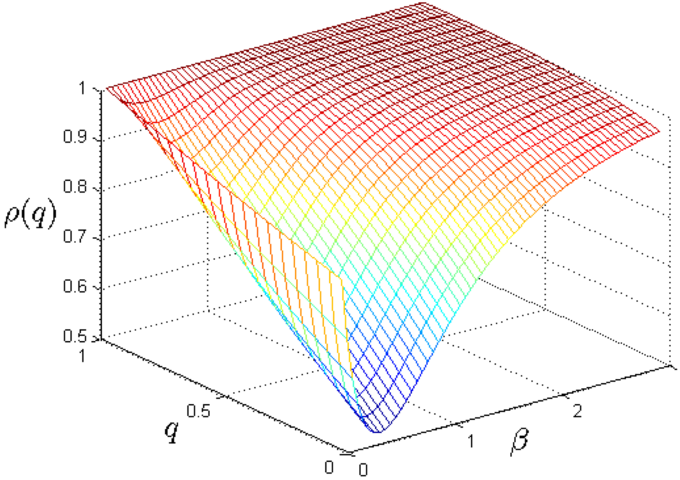
$$R_{LL} = \mu_H \mu_W$$

▸ Back

Reasons behind the conjecture (groups of equal size)



Reasons behind the conjecture (unequal group sizes)



Comparison between R_* and R_l

$$
\begin{aligned}
R_* &= R_g\left(1 + \mu_H\right) \\
R_l &= \frac{R_g}{2} + \frac{1}{2}\sqrt{R_g^2 + 4\mu_H R_g}
\end{aligned}
$$

Comparison between R_* and R_I

$$
\begin{aligned}
R_* &= R_g\,(1+\mu_H) \\
R_I &= \frac{R_g}{2} + \frac{1}{2}\sqrt{R_g^2 + 4\mu_H R_g}
\end{aligned}
$$

Theorem

- $R_* = 1 \iff R_I = 1$
- $R_* > 1 \iff R_I > 1$
- $R_* < 1 \iff R_I < 1$

Monotonic relationship

$$R_* = R_g\left(1 + \mu_H\right)$$
$$R_l = \frac{R_g}{2} + \frac{1}{2}\sqrt{R_g^2 + 4\mu_H R_g}$$