

Lecture 14: Estimating the basic reproduction number for non-randomly mixing populations

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Introduction to Infectious Disease Modelling and its Applications
LSHTM

Objectives

By the end of this session you should understand:

- Importance of accounting for heterogeneity in contact between individuals when calculating R_0 and critical vaccination coverage;
- How R_0 and herd immunity threshold are calculated for both randomly and non-randomly (“heterogeneously”) mixing populations.

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Revision: Basic reproduction number, R_0

Definition: R_0 is the number of secondary cases generated by one typical infectious person introduced into a totally susceptible population:

$$R_0 = \beta N D$$

If $R_0 > 1$, incidence increases following the introduction of an infectious person into a totally susceptible population.

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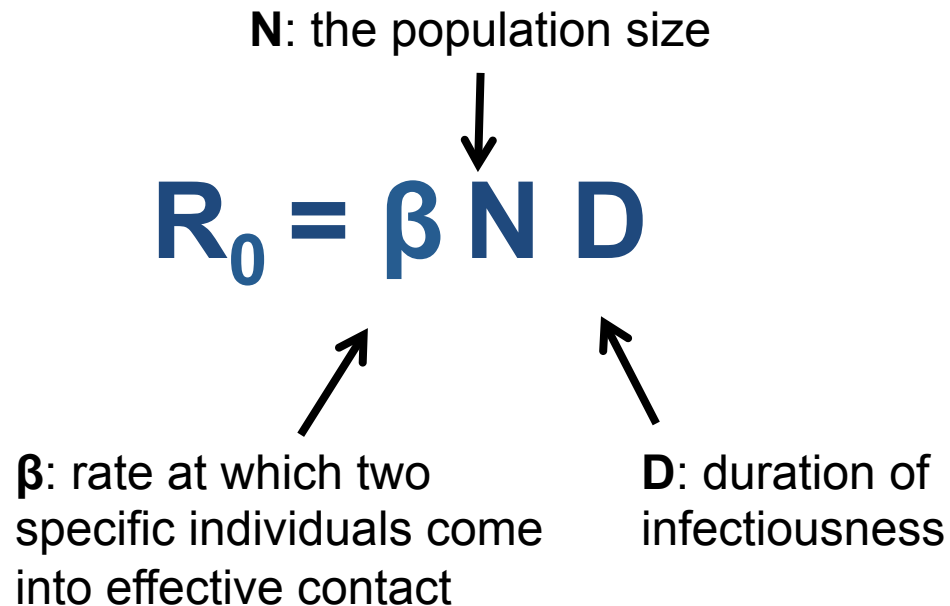
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D : duration of infectiousness



The diagram illustrates the formula for the basic reproduction number, $R_0 = \beta N D$. It features three definitions with arrows pointing to the corresponding variables in the formula: N (population size) points to N , β (rate of effective contact) points to β , and D (duration of infectiousness) points to D .

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In a randomly-mixing population: $R_n = R_0 s$

At equilibrium for an endemic infection:

$$s=s^* \text{ \& } R_n=1 \Rightarrow R_0 s^* =1$$

Rearranging this equation, we obtain the result:

$$R_0 = 1 / s^*$$

Note: this only applies in a randomly-mixing population

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Estimating R_0 in randomly mixing populations (1)

The expression $R_0 = 1/s^*$ leads to several expressions for R_0 :

For population with a rectangular age distribution:

$$R_0 = L/A$$

where L is the life expectancy, A is the average age at infection.

Example:

- Life expectancy = 70 years
- Average age of infection = 10 years $\Rightarrow R_0 = 7$

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Estimating R_0 in randomly mixing populations (2)

For any given population:

$$R_0 = \frac{N}{B (A-m)}$$

where

N: population size

B: number of surviving infants born each year

A: average age at infection (and is small)

m: duration of maternal antibody

Explanation:

- $(A-m)$ is the number of years for which individuals are susceptible.
- If A is small, then $B(A-m) \approx$ number of susceptible individuals.
- $B(A-m)/N$ is the proportion of the population that is susceptible.

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Revision: the herd immunity threshold

$1/R_0$ is the critical proportion susceptible or the **epidemic threshold**

Elimination requires maintaining $R_n < 1$ i.e. $s < 1/R_0$

This can be achieved by immunising a proportion H

$$H = 1 - 1/R_0$$

How much of this theory still applies when we do not assume that individuals mix randomly?

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Calculating R_0 for an endemic infection in a randomly mixing population

- Measure proportion seronegative.
- Calculate equilibrium proportion susceptible, s^* .
- Calculate R_0 using $R_0 = 1/s^*$.

Calculating R_0 for an endemic infection in a non-randomly mixing population

- Measure prevalence in serosurvey
- Estimate forces of infection in different subgroups (e.g. age strata)
- Choose WAIFW matrix structure
- Calculate WAIFW values
- Formulate “Next Generation Matrix” (NGM)
- Calculate R_0 from NGM

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Writing down the Next Generation Matrix

Number of secondary infections generated by one infectious person introduced into totally susceptible population depends on subgroup to which index case belongs

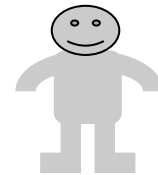
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Population A



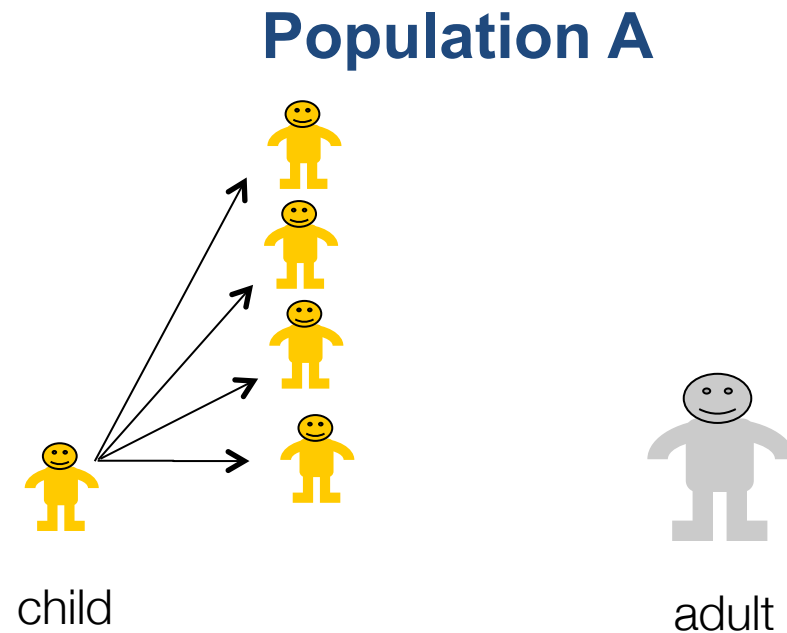
child



adult

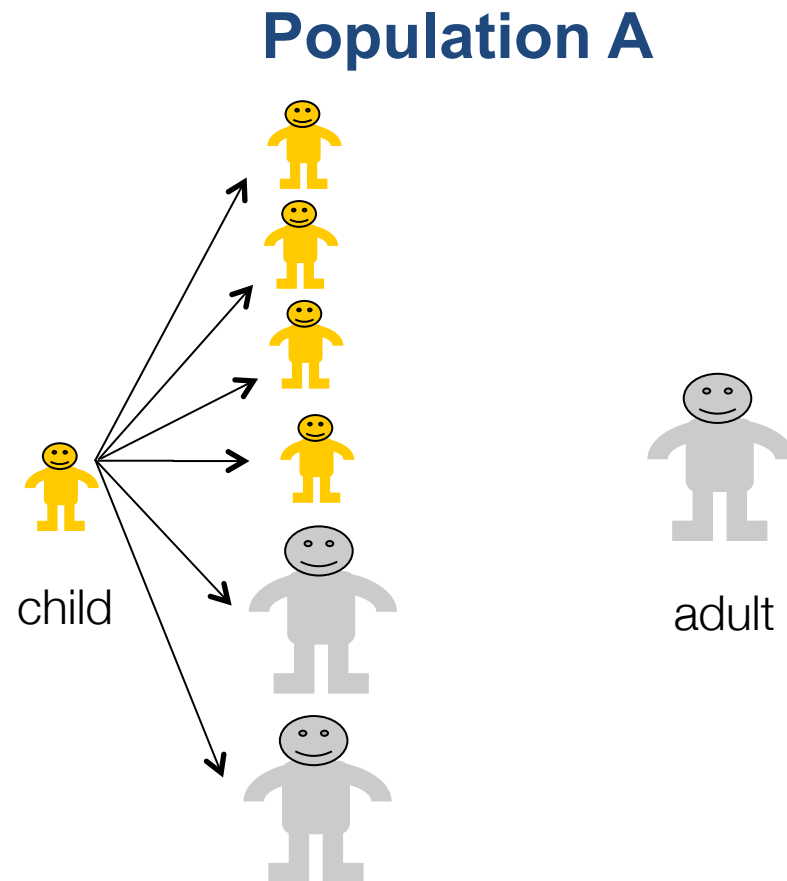
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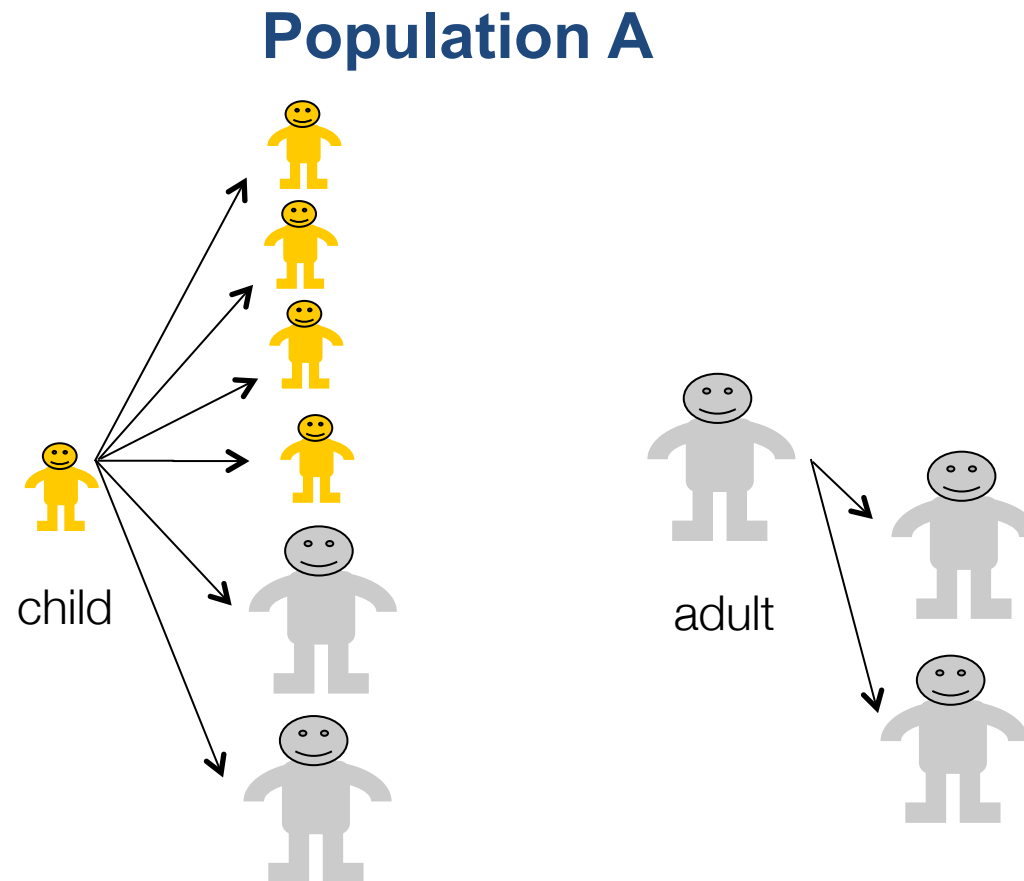
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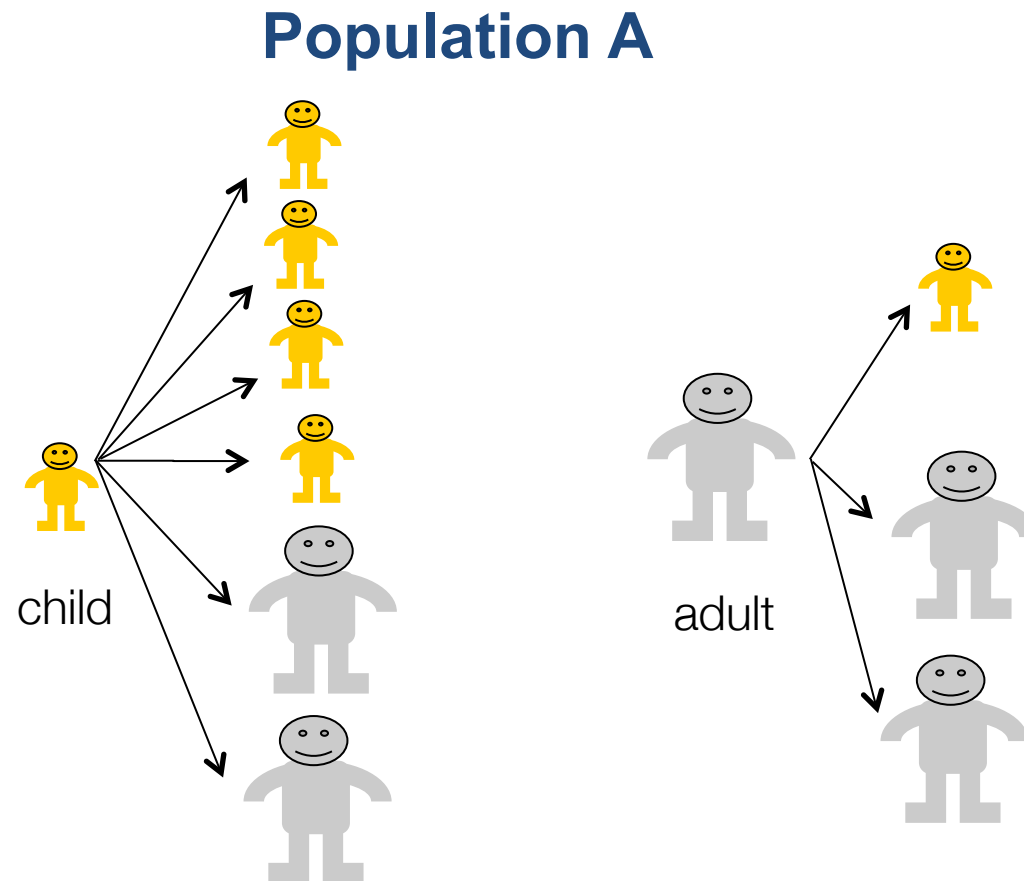
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Writing down the Next Generation Matrix

For a population containing several groups, the number of secondary infections in group **i** produced by an infectious person in group **j** in a totally susceptible population is denoted R_{ij}

$$R_{ij} = \beta_{ij} N_i D$$

- The Next Generation Matrix has these values as its entries, where R_{ij} is the value in the i^{th} row and the j^{th} column.
- We'll generally think about groups representing different age categories, but they can have all sorts of other interpretations.

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Example: writing down the Next Generation Matrix

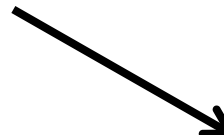
For populations stratified into young and old individuals, the Next Generation Matrix is given by:

$$\begin{pmatrix} R_{yy} & R_{yo} \\ R_{oy} & R_{oo} \end{pmatrix}$$

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For populations stratified into young and old individuals, the Next Generation Matrix is given by:

No. of *young* secondary infectious people generated by each *young* infectious person = $\beta_{yy} N_y D$

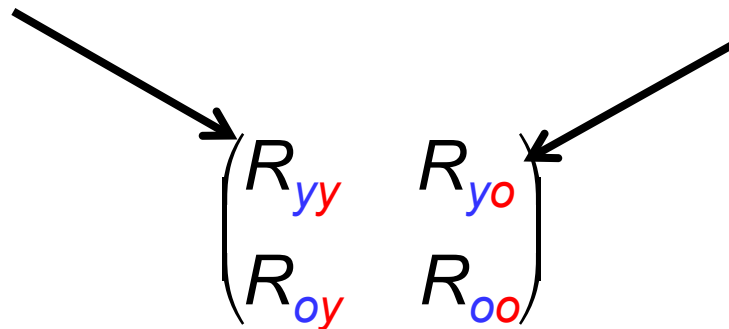

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No. of *young* secondary infectious people generated by each *old* infectious person = $\beta_{yo} N_y D$



The diagram shows two arrows pointing towards the Next Generation Matrix. The first arrow originates from the text 'No. of young secondary infectious people generated by each young infectious person' and points to the R_{yy} element in the matrix. The second arrow originates from the text 'No. of young secondary infectious people generated by each old infectious person' and points to the R_{yo} element in the matrix.

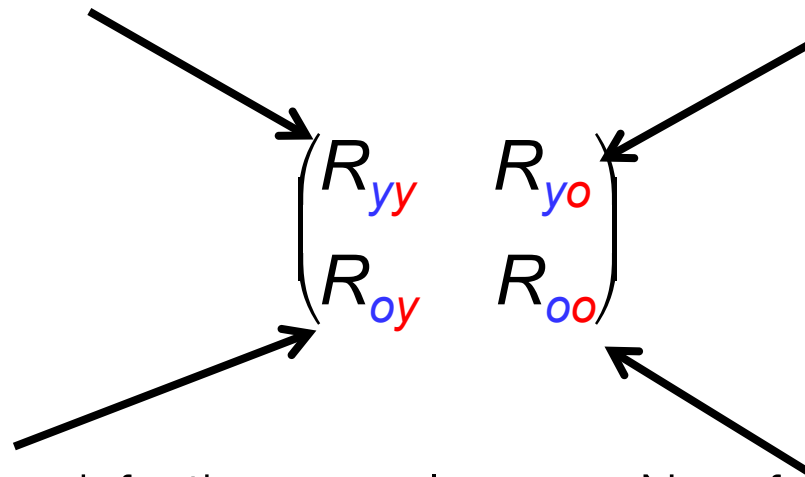
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No. of *old* secondary infectious people generated by each *young* infectious person = $\beta_{oy} N_o D$

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A note on notation (repeat)

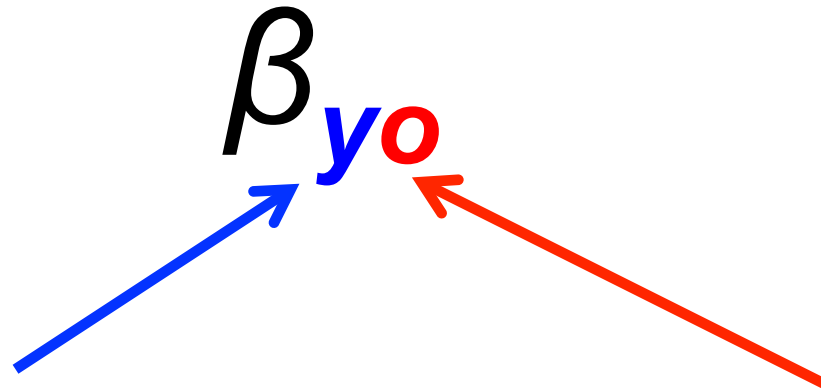
$$\beta_{yo}$$

Therefore:

β_{yo} = rate at which a specific young (susceptible) individual has contact with specific old (infectious) individual per unit time.

Note: we could have defined it the other way round if we had wanted, so long as we're clear about what we mean.

A note on notation (repeat)



Category of the susceptible person
(the recipient of the infection)

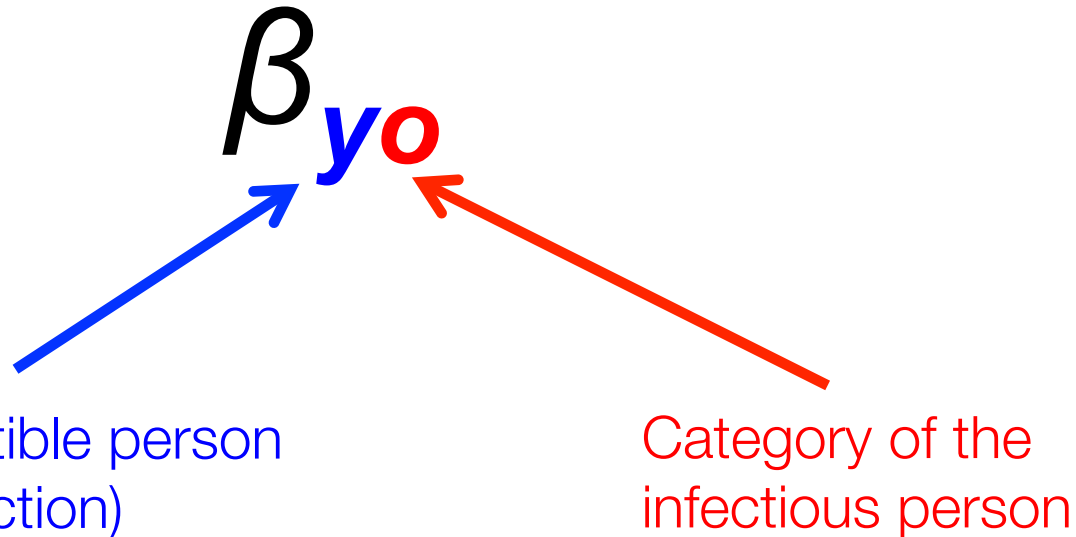
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Similarly,

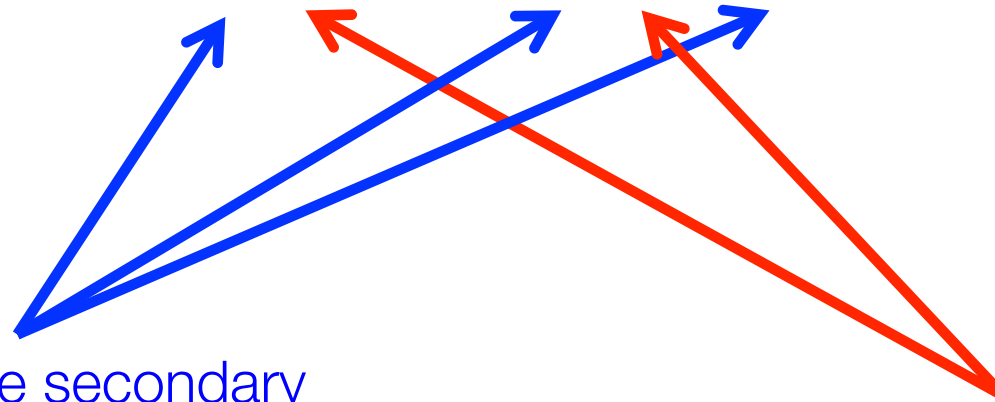
$$R_{yo} = \beta_{yo} N_y D$$

Therefore:

R_{yo} = number of secondary infectious young individuals resulting from one old (infectious) individual in a totally susceptible population

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Category of the secondary
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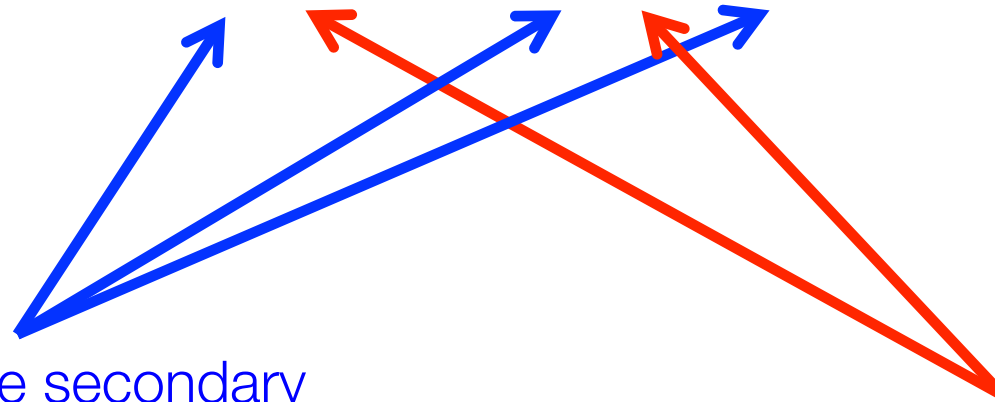
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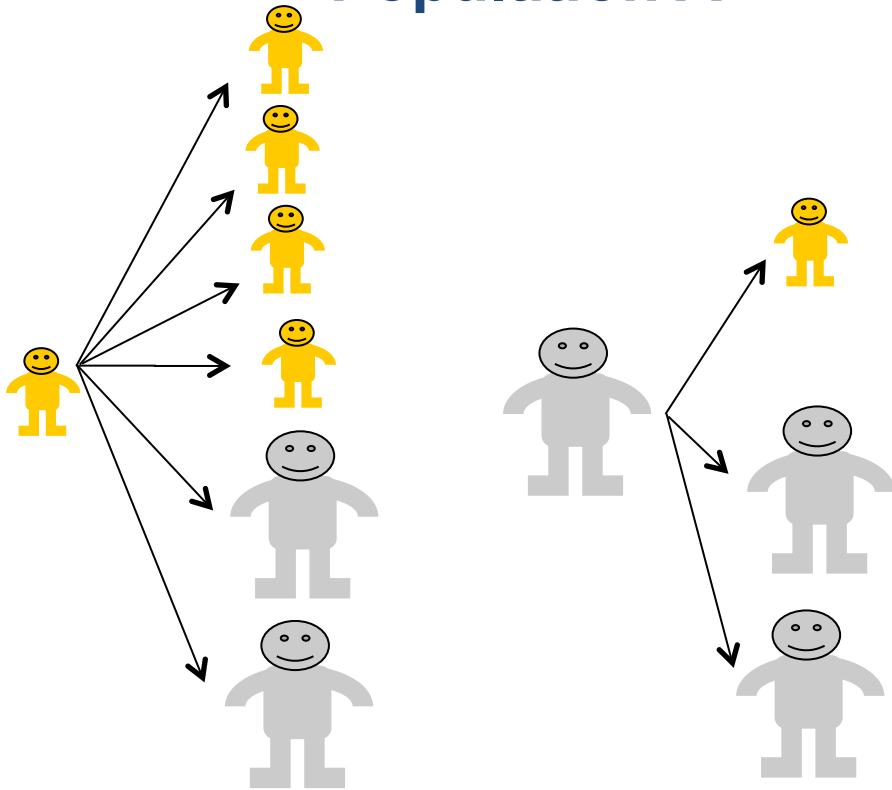
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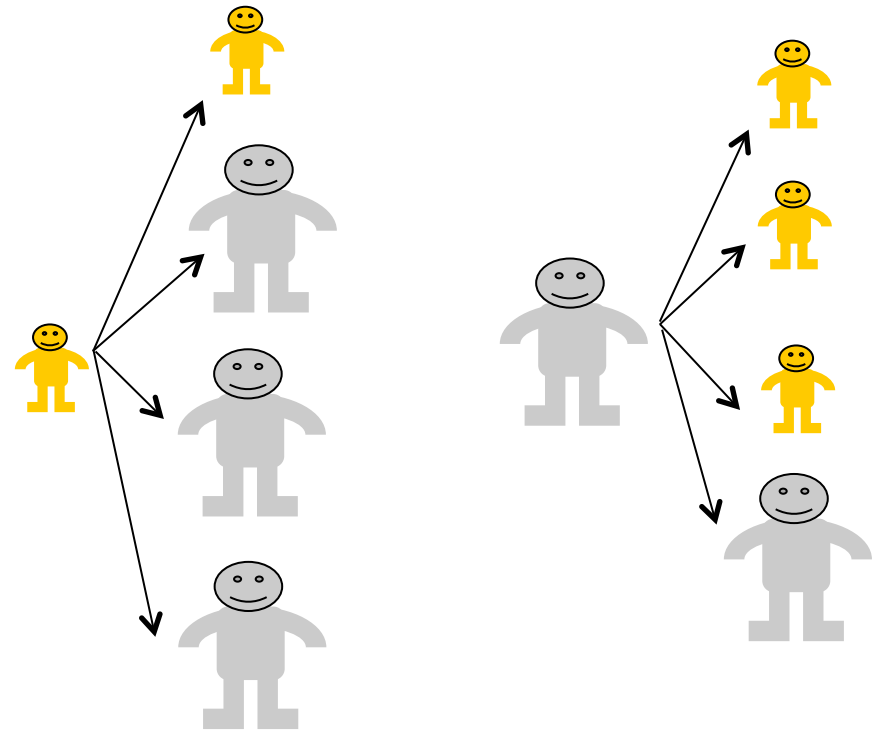
R_{yo} = number of secondary infectious **young individuals** resulting from one **old (infectious) individual** in a totally susceptible population

Exercise: write down Next Generation Matrix for these two populations

Population A



Population B



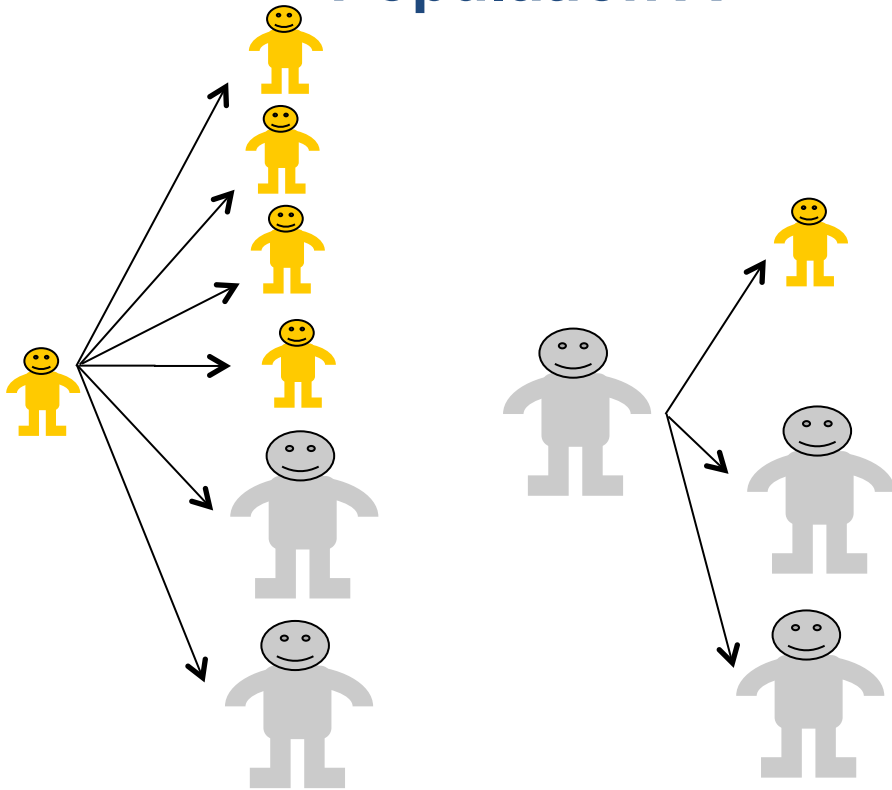
NGM:

child	child	adult
adult	$\left(\begin{array}{cc} & \end{array} \right)$	

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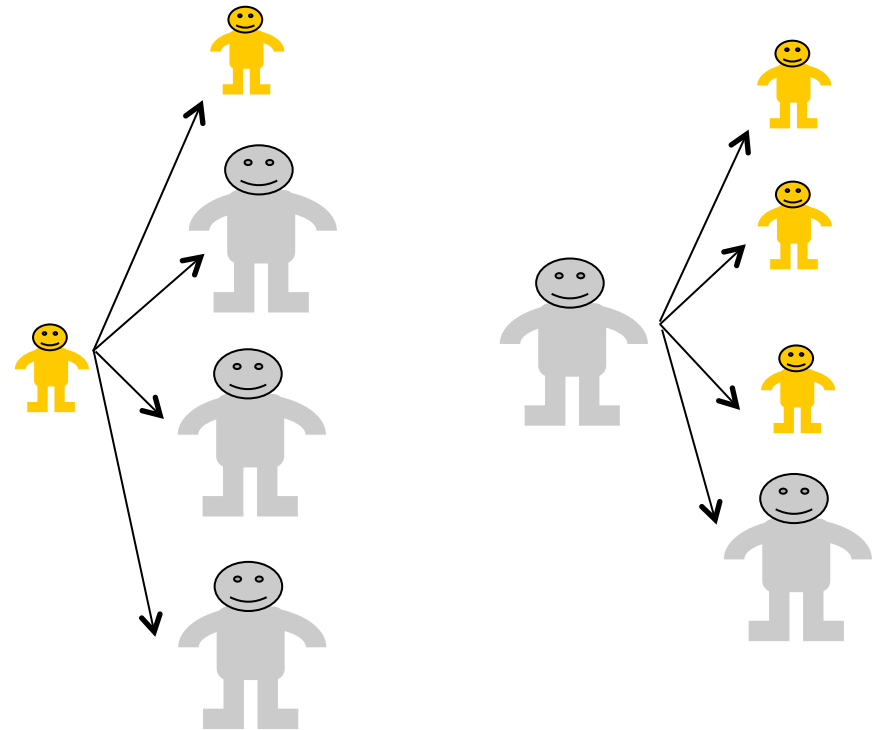
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	child	adult
child	4	1
adult	2	2

NGM

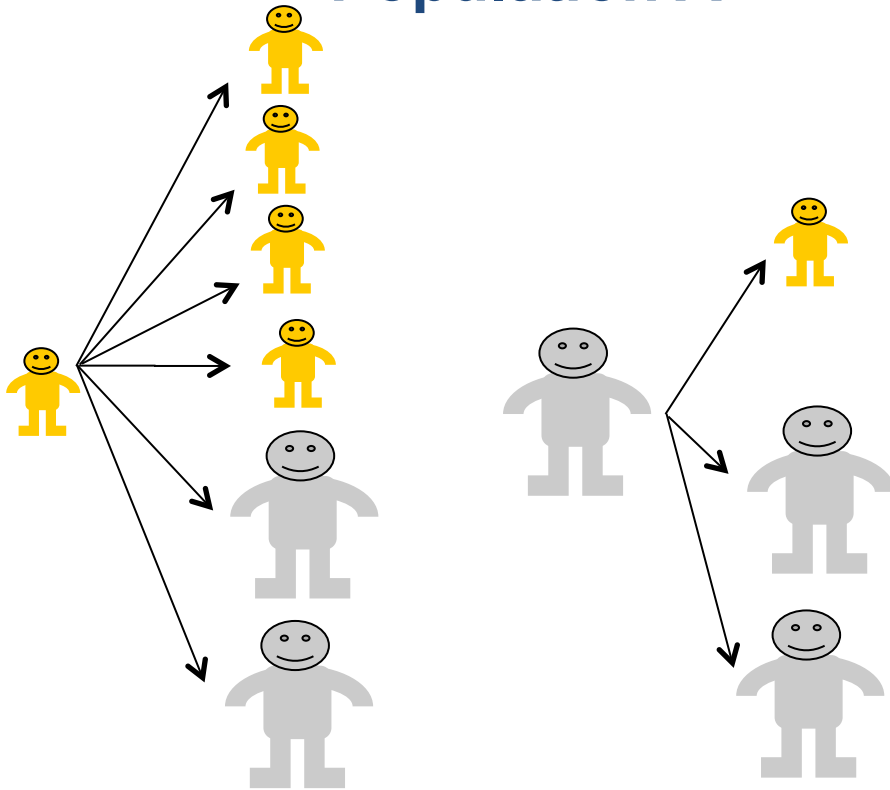
Population B



	child	adult
child		
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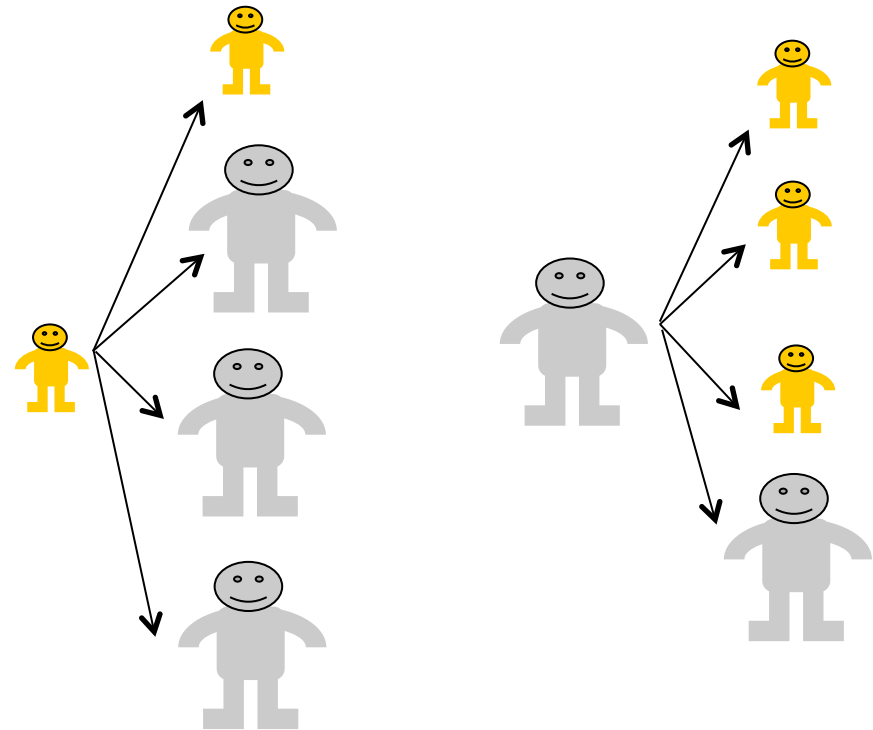


NGM

child
adult

$$\begin{matrix} & \text{child} & \text{adult} \\ \begin{matrix} \text{child} \\ \text{adult} \end{matrix} & \begin{pmatrix} 4 & 1 \\ 2 & 2 \end{pmatrix} \end{matrix}$$

Population B



child
adult

$$\begin{matrix} & \text{child} & \text{adult} \\ \begin{matrix} \text{child} \\ \text{adult} \end{matrix} & \begin{pmatrix} 1 & 3 \\ 3 & 1 \end{pmatrix} \end{matrix}$$

Calculating R_0 from the Next Generation Matrix

How many secondary infections does one infectious individual produce in a totally susceptible population?

- It depends on which group the infectious person is in.
- To calculate R_0 , need to define a “typical” infectious person as some suitable average across all groups.
- The true value for R_0 will be some average of the number of secondary cases caused by the different types of person.

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$$\text{NGM} = \begin{matrix} & \begin{matrix} c & a \end{matrix} \\ \begin{matrix} c \\ a \end{matrix} & \begin{pmatrix} 1 & 1 \\ 1 & 1 \end{pmatrix} \end{matrix}$$

An infectious person causes 1 secondary infection in their own group and 1 secondary infection in the other group

i.e. 2 secondary infections in total,

so $R_0 = 2$.

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An infectious child causes 1 secondary infectious adult

An infectious adult causes 4 secondary infectious children

What is R_0 ?

We must define a “typical” infectious person as being partly a child and partly an adult

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If a fraction x of the typical infectious person is a child, then a fraction $(1-x)$ is an adult.

We can describe this typical infectious person using vector notation:

$$\begin{pmatrix} x \\ 1-x \end{pmatrix}$$

To find R_0 , we simply calculate how many secondary cases this “typical” infectious person causes.

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$$\text{NGM} = \begin{matrix} & \begin{matrix} c & a \end{matrix} \\ \begin{matrix} c \\ a \end{matrix} & \begin{pmatrix} 0 & 4 \\ 1 & 0 \end{pmatrix} \end{matrix}$$

If a fraction x of the typical infectious person is a child, then a fraction $(1-x)$ is an adult.

We can describe this typical infectious person using vector notation:

$$\begin{pmatrix} x \\ 1-x \end{pmatrix}$$

To find R_0 , we simply calculate how many secondary cases this “typical” infectious person causes.

How to calculate R_0

According to theory:

If we repeatedly multiply a vector representing an initial infectious person introduced into a totally susceptible population by the Next Generation Matrix then (assuming that there is an unlimited supply of susceptibles):

1. the number of secondary infectious people resulting from each infectious person converges to R_0 .
2. The distribution of infectious people in each generation converges to a distribution that represents a “typical” infectious person.

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Example

Suppose we have a NGM=

$$\begin{matrix} & \begin{matrix} c & a \end{matrix} \\ \begin{matrix} c \\ a \end{matrix} & \begin{pmatrix} 1 & 1 \\ 1 & 4 \end{pmatrix} \end{matrix}$$

What happens when we repeatedly multiply the vector $\begin{pmatrix} 1 \\ 0 \end{pmatrix}$ by this NGM?

- This is equivalent to simulating the introduction of one infectious child into a totally susceptible population, assuming that there is an unlimited supply of susceptibles.
- In reality, as more cases are produced we begin to run out of susceptibles - this process is simply for the purpose of calculating R_0 , not a long-term prediction of disease behaviour.

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Calculating R_0

Generation 1

$$\begin{matrix} & c & a \\ c & \left(\begin{array}{cc} 1 & 1 \\ 1 & 4 \end{array} \right) \end{matrix} \begin{pmatrix} 1 \\ 0 \end{pmatrix} = \begin{pmatrix} 1 \times 1 + 1 \times 0 \\ 1 \times 1 + 4 \times 0 \end{pmatrix} = \begin{pmatrix} 1 \\ 1 \end{pmatrix}$$

Number of infectious

children adults total
(G_k)

1 1 2

G_k/G_{k-1}

2

Generation 2:

$$\begin{matrix} & c & a \\ c & \left(\begin{array}{cc} 1 & 1 \\ 1 & 4 \end{array} \right) \end{matrix} \begin{pmatrix} 1 \\ 1 \end{pmatrix} = \begin{pmatrix} 1 \times 1 + 1 \times 1 \\ 1 \times 1 + 4 \times 1 \end{pmatrix} = \begin{pmatrix} 2 \\ 5 \end{pmatrix}$$

2 5 7 3.5

Generation 3:

$$\begin{matrix} & c & a \\ c & \left(\begin{array}{cc} 1 & 1 \\ 1 & 4 \end{array} \right) \end{matrix} \begin{pmatrix} 2 \\ 5 \end{pmatrix} = \begin{pmatrix} 1 \times 2 + 1 \times 5 \\ 1 \times 2 + 4 \times 5 \end{pmatrix} = \begin{pmatrix} 7 \\ 22 \end{pmatrix}$$

7 22 29 4.1

Calculating R_0

Generation 1

c a

$$\begin{matrix} c \\ a \end{matrix} \begin{pmatrix} 1 & 1 \\ 1 & 4 \end{pmatrix} \begin{pmatrix} 1 \\ 0 \end{pmatrix} = \begin{pmatrix} 1 \times 1 + 1 \times 0 \\ 1 \times 1 + 4 \times 0 \end{pmatrix} = \begin{pmatrix} 1 \\ 1 \end{pmatrix}$$

Number of infectious
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Generation 2:

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4.1

Calculating R_0

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G_k/G_{k-1}

1

1

2

2

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c a

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7

22

29

4.1

Calculating R_0

Generation 4-7

Exercise...

Generation 8

$$\begin{matrix} & c & a \\ c & \begin{pmatrix} 1 & 1 \\ 1 & 4 \end{pmatrix} \end{matrix} \begin{pmatrix} 2293 \\ 7573 \end{pmatrix} = \begin{pmatrix} 9866 \\ 32585 \end{pmatrix}$$

Generation 9:

$$\begin{matrix} & c & a \\ c & \begin{pmatrix} 1 & 1 \\ 1 & 4 \end{pmatrix} \end{matrix} \begin{pmatrix} 9866 \\ 32585 \end{pmatrix} = \begin{pmatrix} 42451 \\ 140206 \end{pmatrix}$$

Number of infectious

children adults total G_k/G_{k-1}

(G_k)

9866

32585

42451

4.3

42451

140206

182657

4.3

Calculating R_0

Generation 4-7

Exercise...

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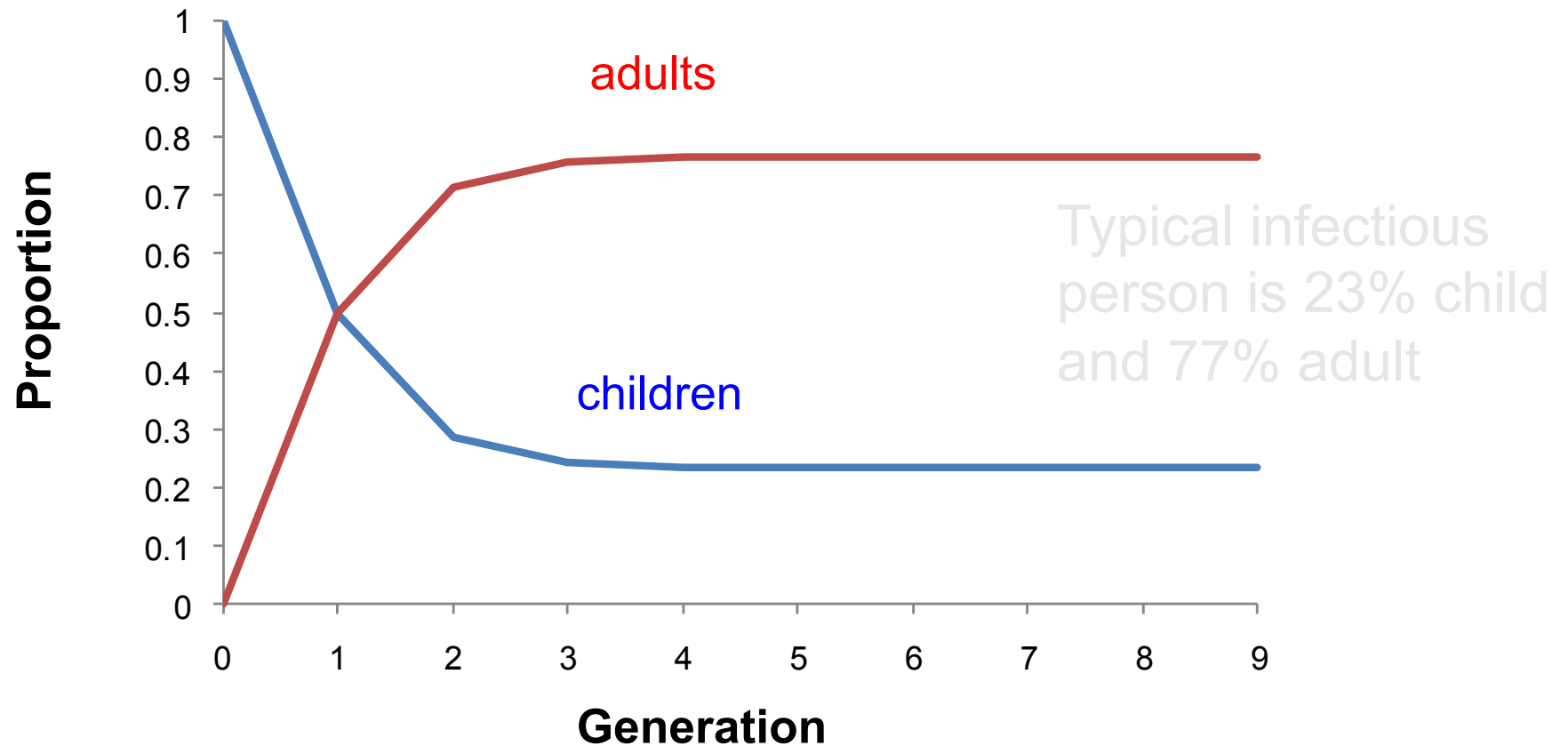
140206

182657

4.3

Example – defining the typical infectious person

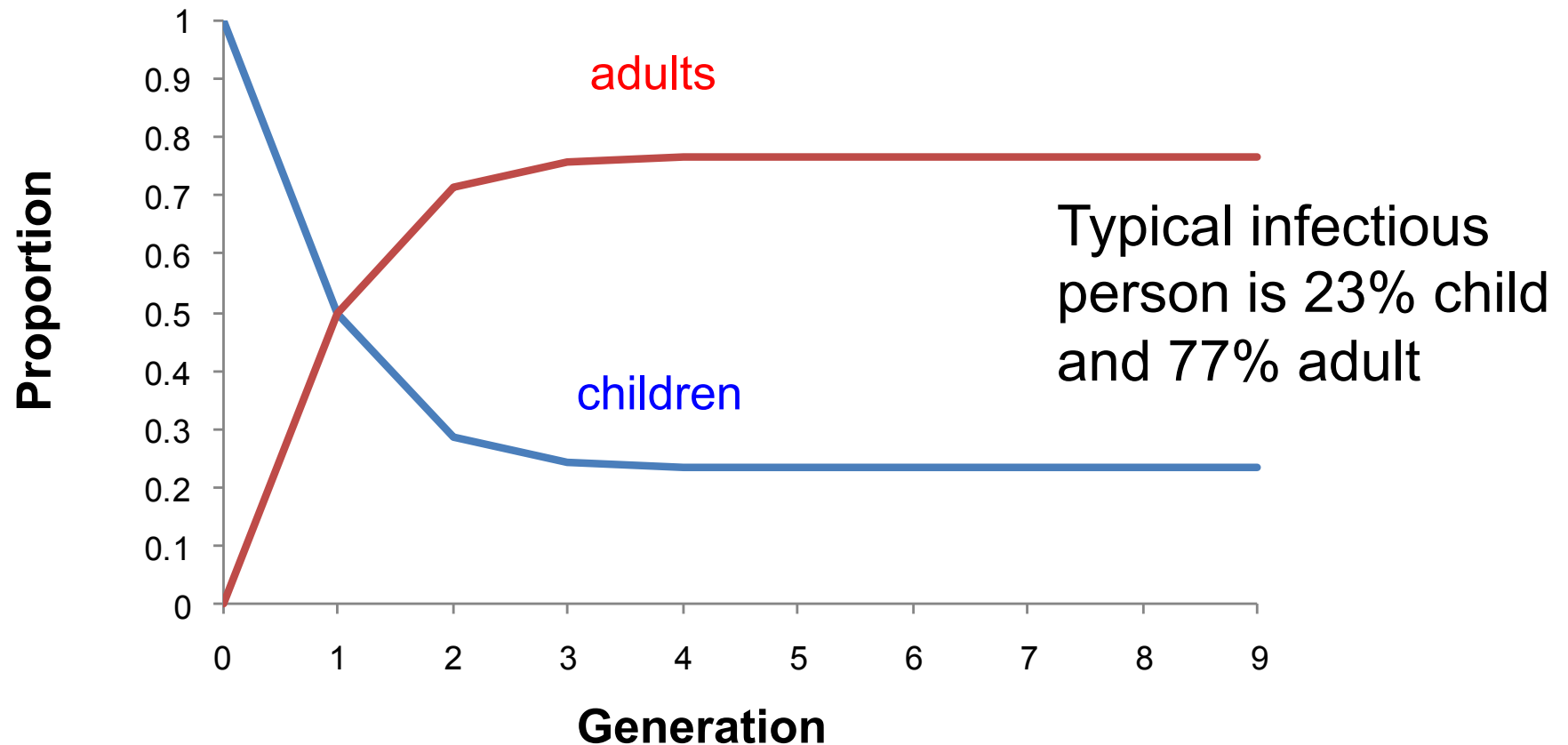
Proportion of individuals in each generation in each group



After several generations, the distribution of children and adults converges to represent a “typical infectious person”.

Example – defining the typical infectious person

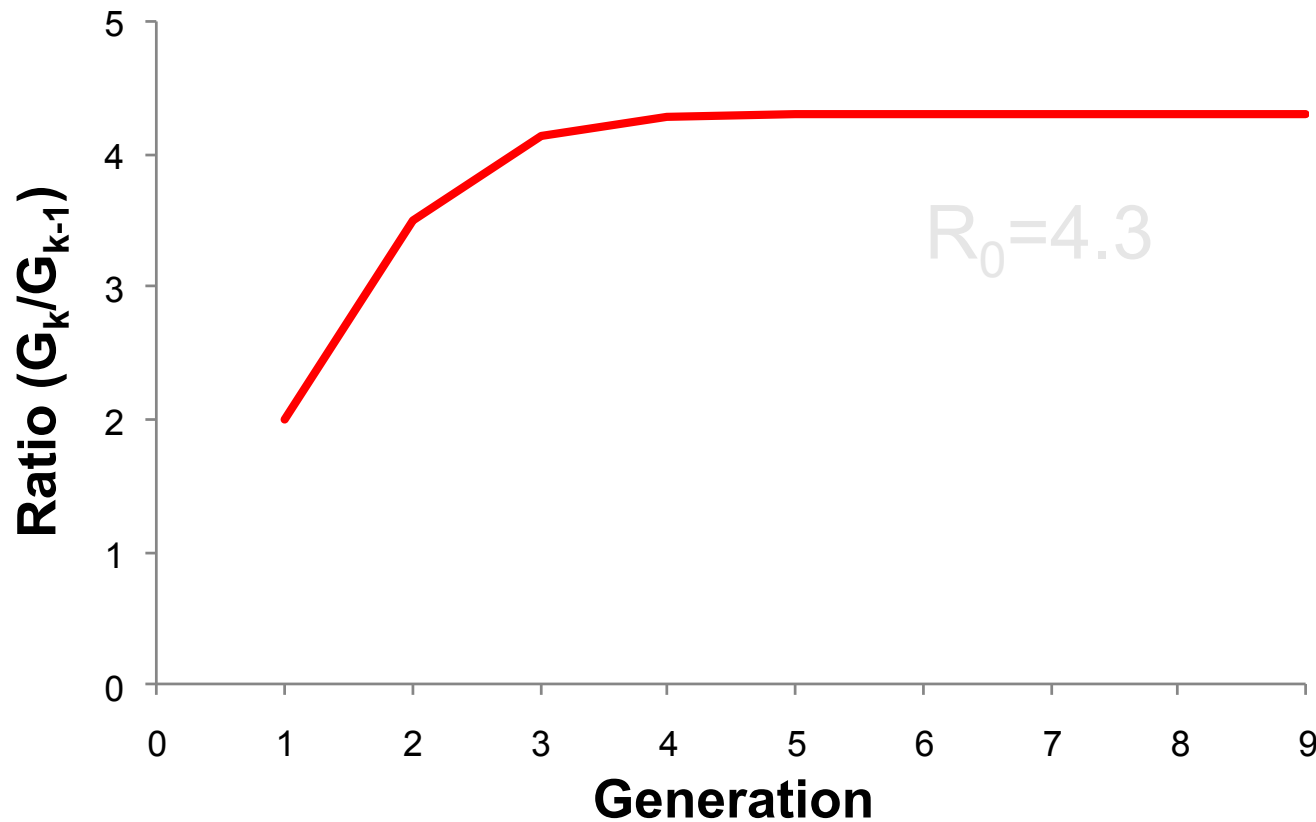
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Example – R_0

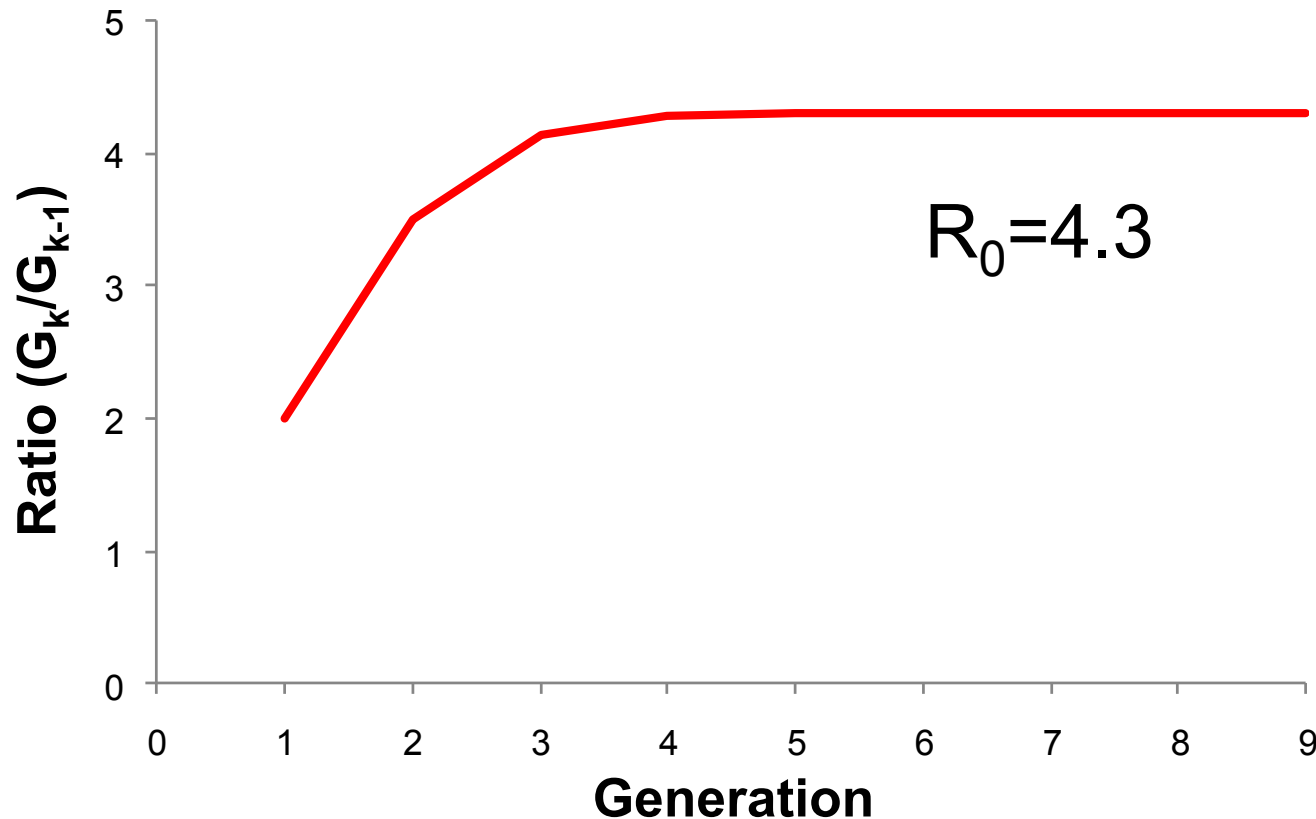
Ratio between the number of infectious people in successive generations



After several generations, the ratio between the number of infectious people in successive generations (G_k/G_{k-1}) converges to a value equal to R_0 .

Example – R_0

Ratio between the number of infectious people in successive generations



After several generations, the ratio between the number of infectious people in successive generations (G_k/G_{k-1}) converges to a value equal to R_0 .


Another method for calculating R_0

For a population comprising 2 groups, R_0 can be calculated by solving the equations (see Appendix):

$$R_{yy} x + R_{yo} (1-x) = R_0 x$$

$$R_{oy} x + R_{oo} (1-x) = R_0 (1-x)$$

The equations can also be written using the following matrix notation:

Next generation matrix 

$$\begin{pmatrix} R_{yy} & R_{yo} \\ R_{oy} & R_{oo} \end{pmatrix} \begin{pmatrix} x \\ 1-x \end{pmatrix} = R_0 \begin{pmatrix} x \\ 1-x \end{pmatrix}$$

- The formal (mathematical) definition of R_0 is that it is the **dominant eigenvalue of the Next Generation Matrix**, i.e. the largest value for R_0 which satisfies the above equations.
- NB There may be more than 1 value for “ R_0 ” that satisfies the above equations – R_0 is the largest such value.


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Example 3 revisited

$$\text{NGM} = \begin{matrix} & \begin{matrix} c & a \end{matrix} \\ \begin{matrix} c \\ a \end{matrix} & \begin{pmatrix} 0 & 4 \\ 1 & 0 \end{pmatrix} \end{matrix}$$

Number of secondary infectious children = $0.x + 4.(1-x) = 4 - 4x = R_0 x$

Number of secondary infectious adults = $1.x + 0.(1-x) = x = R_0 (1-x)$

Two simultaneous equations for x and R_0 :

$$4 - 4x = R_0 x$$

$$x = R_0 (1-x)$$

Solution is $x = 2/3$ and $R_0 = 2$.

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Note:

2 is the square root of 4×1 ,



Example 3 revisited

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$$x = R_0 (1-x)$$

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Note:

**2 is the square root of 4×1 ,
Both 4 and 1 are in the Next
Generation Matrix...**

**Could this reflect a short cut to
calculating R_0 for this matrix?**

A shortcut for calculating R_0 for “disassortative” matrices

$\begin{matrix} & \begin{matrix} c & a \end{matrix} \\ \begin{matrix} c \\ a \end{matrix} & \begin{pmatrix} 0 & 4 \\ 1 & 0 \end{pmatrix} \end{matrix}$ is an example of a “disassortative” matrix: people in a given group only contact others in a different group from their own

Possible kinds of populations: animal vectors and humans, males and females for a STI

In general, for the following type of Next Generation Matrix

$$\begin{matrix} & \begin{matrix} \text{Group 1} & \text{Group 2} \end{matrix} \\ \begin{matrix} \text{Group 1} \\ \text{Group 2} \end{matrix} & \begin{pmatrix} 0 & R_{12} \\ R_{21} & 0 \end{pmatrix} \end{matrix}$$

R_0 is given by:

$$R_0 = \sqrt{R_{12}R_{21}}$$

A shortcut for calculating R_0 for “disassortative” matrices

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$$R_0 = \sqrt{R_{12}R_{21}}$$

Example

The following is the Next Generation Matrix for a sexually-transmitted infection in a heterosexual population, i.e. it is transmitted from males to females and from females to males, but not between females or between males

$$\begin{array}{cc} & \begin{array}{cc} m & f \end{array} \\ \begin{array}{c} m \\ f \end{array} & \left(\begin{array}{cc} 0 & 1.6 \\ 0.9 & 0 \end{array} \right) \end{array}$$

R_0 is given by: $R_0 = \sqrt{R_{12}R_{21}}$

Substituting for $R_{12}=1.6$ and $R_{21}=0.9$ into this equation gives:

$$R_0 = \sqrt{1.6 \times 0.9} = \sqrt{1.44} = 1.2$$

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Obtaining the result $R_0 = \sqrt{R_{12}R_{21}}$ for “disassortative” matrices

Step 1: Substitute the Next Generation Matrix into the matrix equation relating R_0 and the fraction of the typical infectious person that is in group 1 (x):

i.e. equation
$$\begin{pmatrix} R_{yy} & R_{yo} \\ R_{oy} & R_{oo} \end{pmatrix} \begin{pmatrix} x \\ 1-x \end{pmatrix} = R_0 \begin{pmatrix} x \\ 1-x \end{pmatrix}$$

becomes:
$$\begin{pmatrix} 0 & R_{12} \\ R_{21} & 0 \end{pmatrix} \begin{pmatrix} x \\ 1-x \end{pmatrix} = R_0 \begin{pmatrix} x \\ 1-x \end{pmatrix}$$

Step 2: Rewrite this matrix equation using simultaneous equations:

$$0 \times x + R_{12} \times (1-x) = R_0 x$$

$$R_{21} \times x + 0 \times (1-x) = R_0 (1-x)$$

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Step 2: The equations simplify to the following:

$$R_{12}(1 - x) = R_0 x \quad \text{Eq1}$$

$$R_{21}x = R_0(1 - x) \quad \text{Eq2}$$

Step 3: Rearrange these two equations so that you have an expression which is just in terms of R_0

Rearranging option 1 (laborious): Rearrange equation 1 to get an expression for x in terms of R_0 and substitute that expression into equation 2 to get an expression for R_0 :

Exercise...

Obtaining the result $R_0 = \sqrt{R_{12}R_{21}}$ for “disassortative” matrices

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Exercise...

Obtaining the result $R_0 = \sqrt{R_{12}R_{21}}$ for “disassortative” matrices (2)

Rearranging option 2 (quick): Rearrange both equations to get an expression for $x/(1-x)$ in terms of R_0 , R_{12} and R_{21} and set them equal to each other

$$\text{Eq 1 } (R_{12}(1-x) = R_0 x) \text{ rearranges to: } \frac{R_{12}}{R_0} = \frac{x}{1-x}$$

$$\text{Eq 2 } R_{21}x = R_0(1-x) \text{ rearranges to } \frac{x}{1-x} = \frac{R_0}{R_{21}}$$

Setting these two equations equal to each other gives: $\frac{R_{12}}{R_0} = \frac{R_0}{R_{21}}$

Multiplying both sides of the equations by R_0 gives: $R_0^2 = R_{12}R_{21}$

Take the square root of this equation gives: $R_0 = \sqrt{R_{12}R_{21}}$

Obtaining the result $R_0 = \sqrt{R_{12}R_{21}}$ for “disassortative” matrices (2)

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Obtaining the result $R_0 = \sqrt{R_{12}R_{21}}$ for “disassortative” matrices (2)

Rearranging option 2 (quick): Rearrange both equations to get an expression for $x/(1-x)$ in terms of R_0 , R_{12} and R_{21} and set them equal to each other

$$\text{Eq 1 } (R_{12}(1-x) = R_0x) \text{ rearranges to: } \frac{R_{12}}{R_0} = \frac{x}{1-x}$$

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Setting these two equations equal to each other gives: $\frac{R_{12}}{R_0} = \frac{R_0}{R_{21}}$

Multiplying both sides of the equations by R_0 gives: $R_0^2 = R_{12}R_{21}$

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The net reproduction number

- The same approach can be used to calculate the net reproduction number for a population in which some individuals are immune.
- Here, the next generation matrix is written down using the number of susceptible individuals in each group.
- R_n is calculated using the resulting next generation matrix in exactly the same way that we calculated R_0 .

The net reproduction number

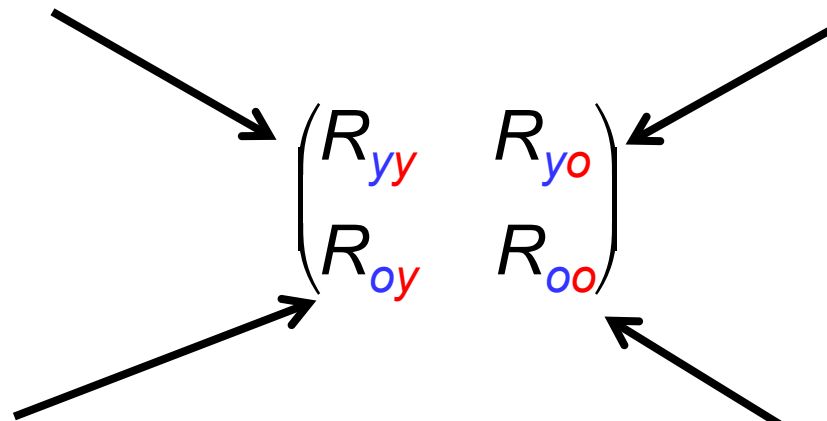
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Recall: writing down the Next Generation Matrix to calculate R_0

For populations stratified into young and old individuals, the Next Generation Matrix is given by:

No. of *young* secondary infectious people generated by each *young* infectious person = $\beta_{yy} N_y D$

No. of *young* secondary infectious people generated by each *old* infectious person = $\beta_{yo} N_y D$



No. of *old* secondary infectious people generated by each *young* infectious person = $\beta_{oy} N_o D$

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No. of *old* secondary infectious people generated by each *young* infectious person = $\beta_{oy} S_o D$

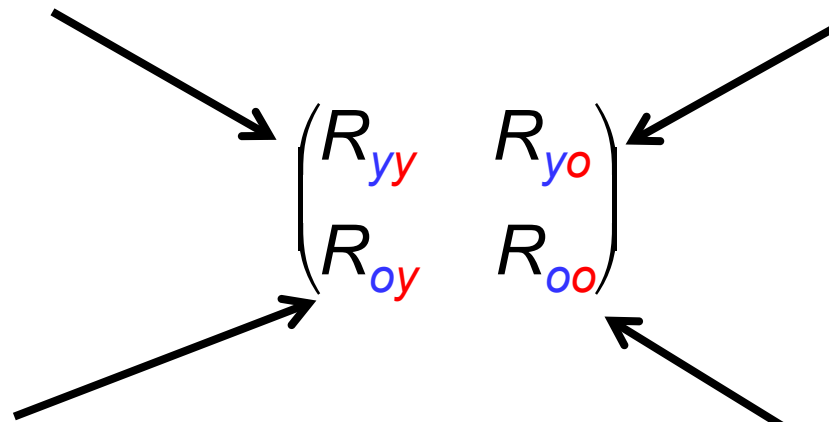
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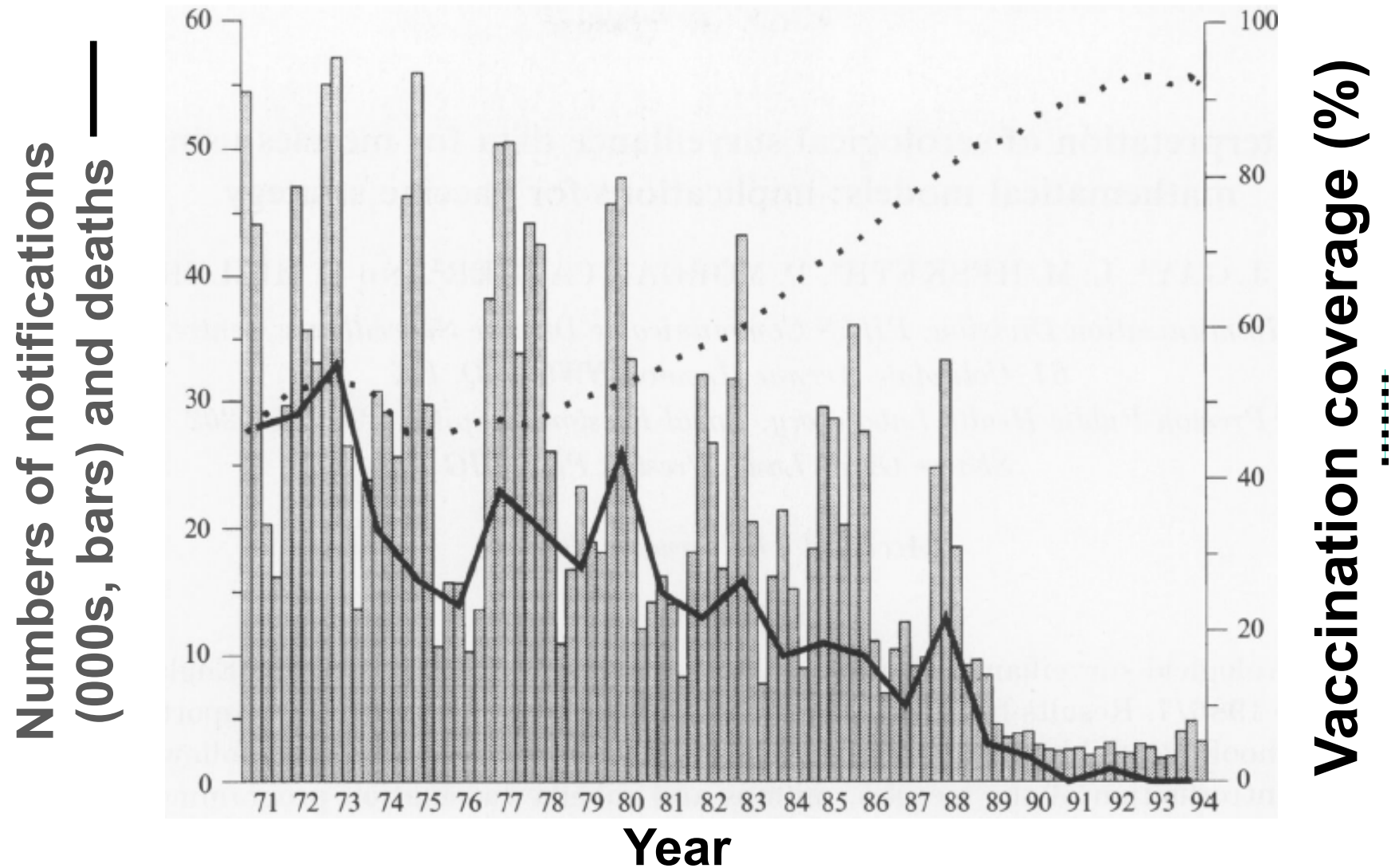
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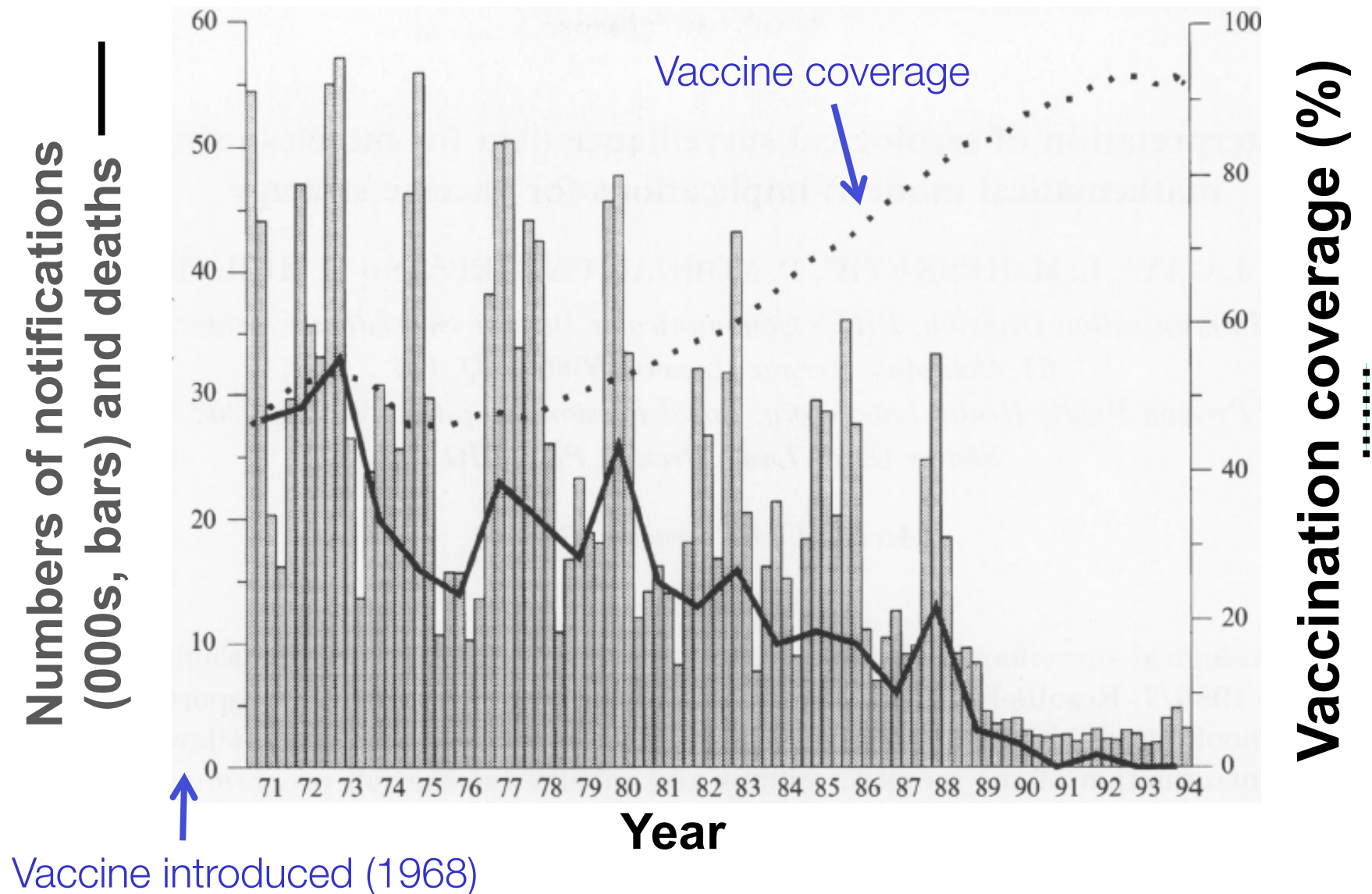
Steps for calculating R_n for an endemic infection in a non-randomly mixing population

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- Calculate R_n from NGM.

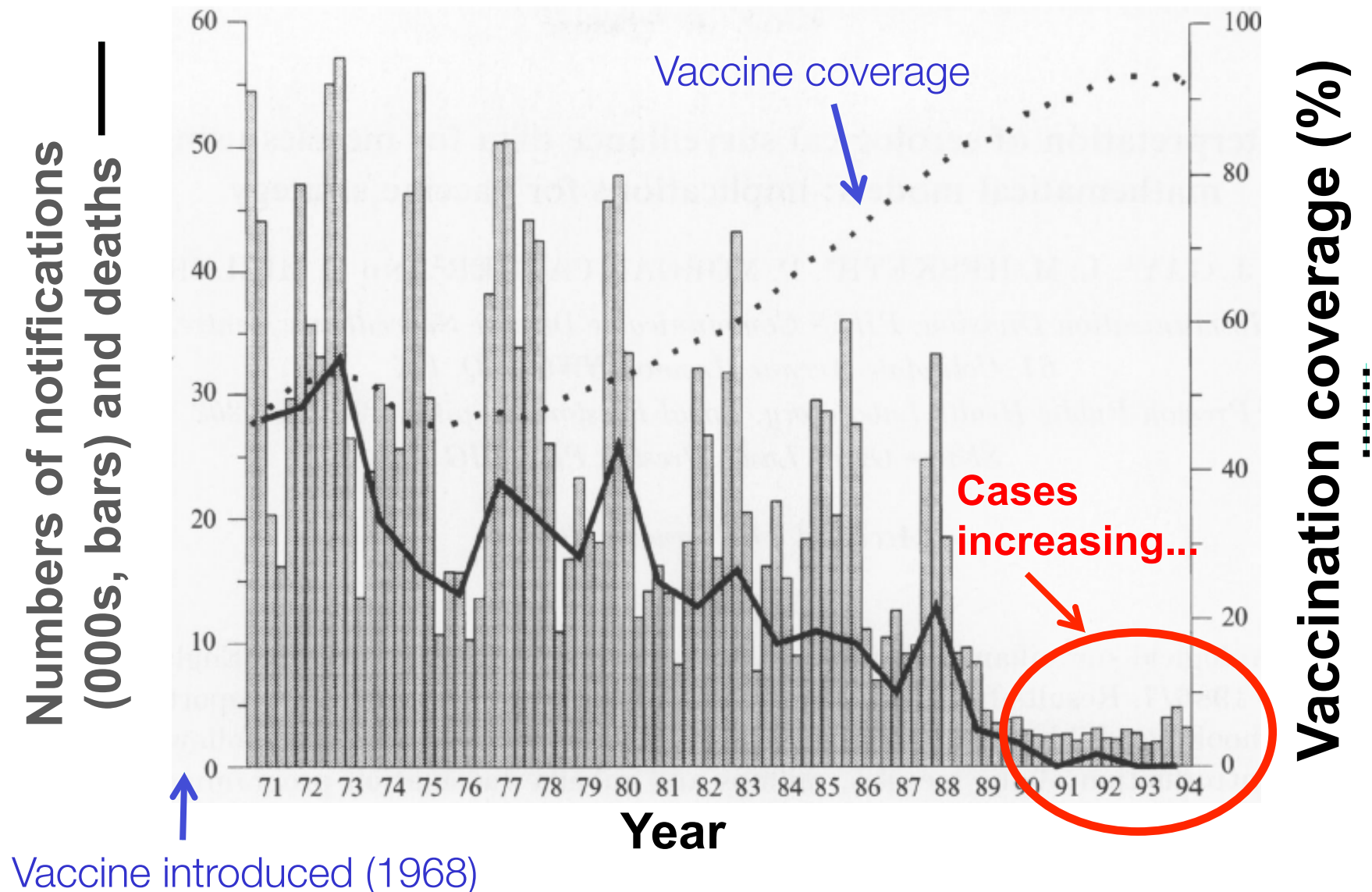
R_n calculations for measles in England and Wales
(Gay et al, 1995): notifications and deaths



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R_n calculations for measles in England and Wales: structure of WAIFW matrices

Model 1:

Age group	0–1	2–4	5–9	10–14	15+
0–1	β_1	β_1	β_1	β_4	β_5
2–4	β_1	β_2	β_2	β_4	β_5
5–9	β_1	β_2	β_3	β_4	β_5
10–14	β_4	β_4	β_4	β_4	β_5
15+	β_5	β_5	β_5	β_5	β_5

R_n calculations for measles in England and Wales: structure of WAIFW matrices

Model 1:

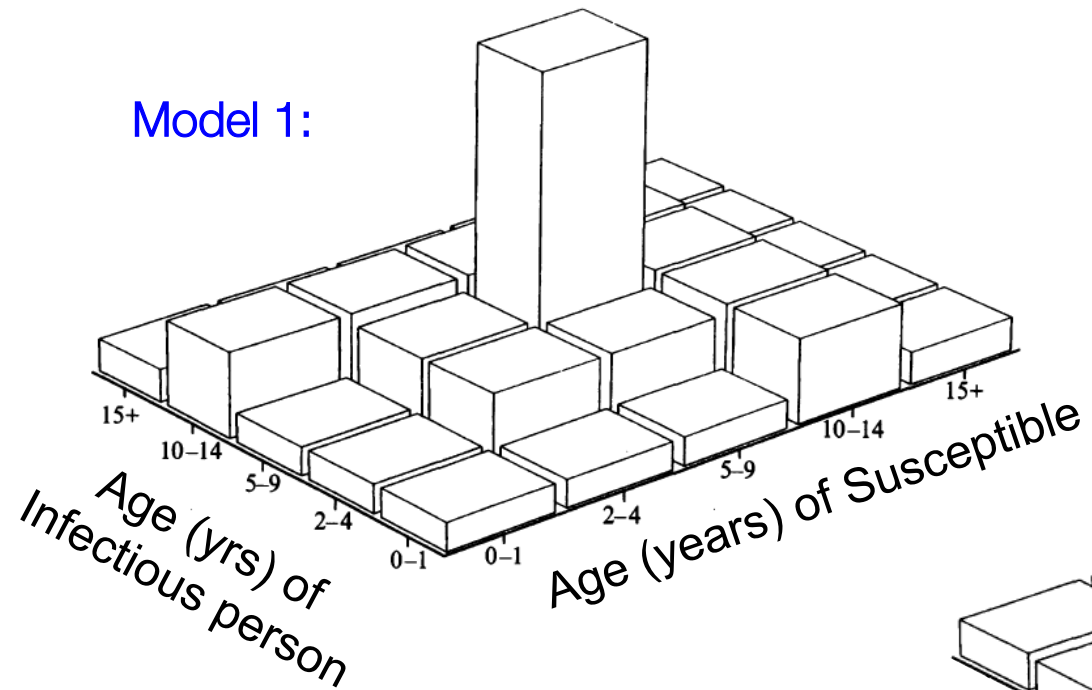
Age group	0–1	2–4	5–9	10–14	15+
0–1	β_1	β_1	β_1	β_4	β_5
2–4	β_1	β_2	β_2	β_4	β_5
5–9	β_1	β_2	β_3	β_4	β_5
10–14	β_4	β_4	β_4	β_4	β_5
15+	β_5	β_5	β_5	β_5	β_5

Model 2:

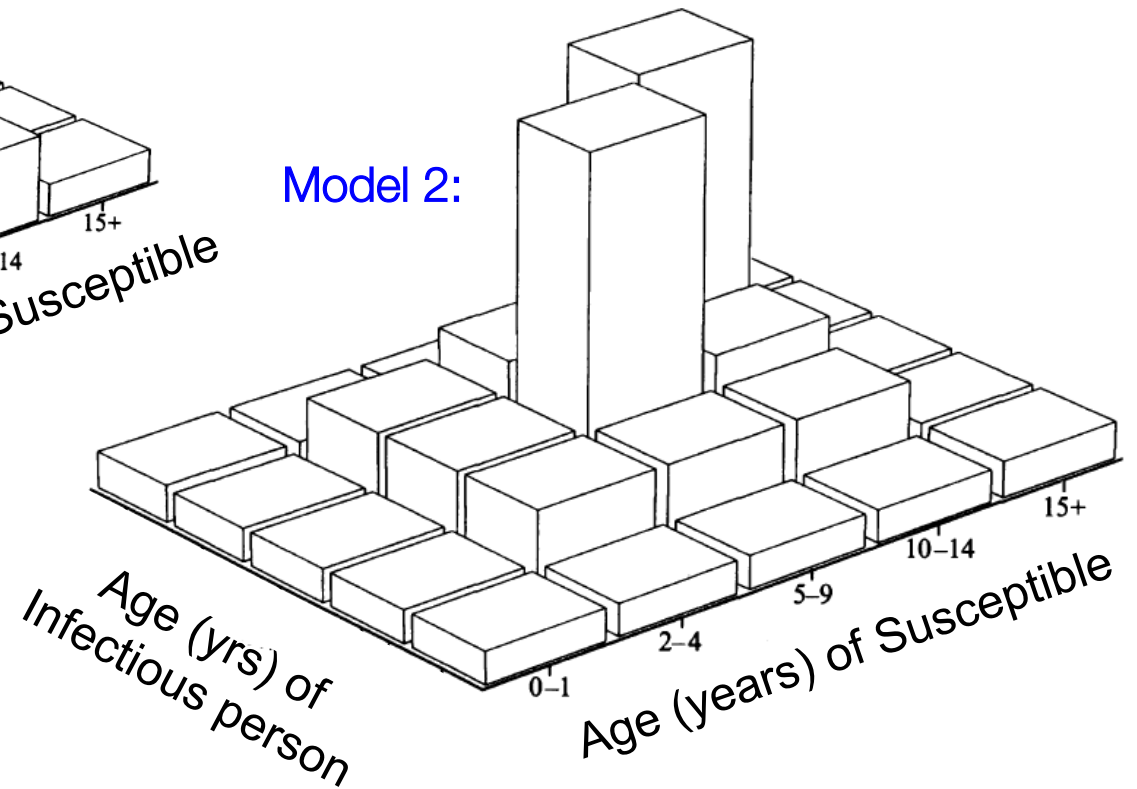
$$\begin{bmatrix} \beta_1 & \beta_1 & \beta_1 & \beta_1 & \beta_5 \\ \beta_1 & \beta_2 & \beta_2 & \beta_2 & \beta_5 \\ \beta_1 & \beta_2 & \beta_3 & \beta_4 & \beta_5 \\ \beta_1 & \beta_2 & \beta_4 & \alpha\beta_3 & \beta_5 \\ \beta_5 & \beta_5 & \beta_5 & \beta_5 & \beta_5 \end{bmatrix}$$

R_n calculations for measles in England and Wales: structure of WAIFW matrices

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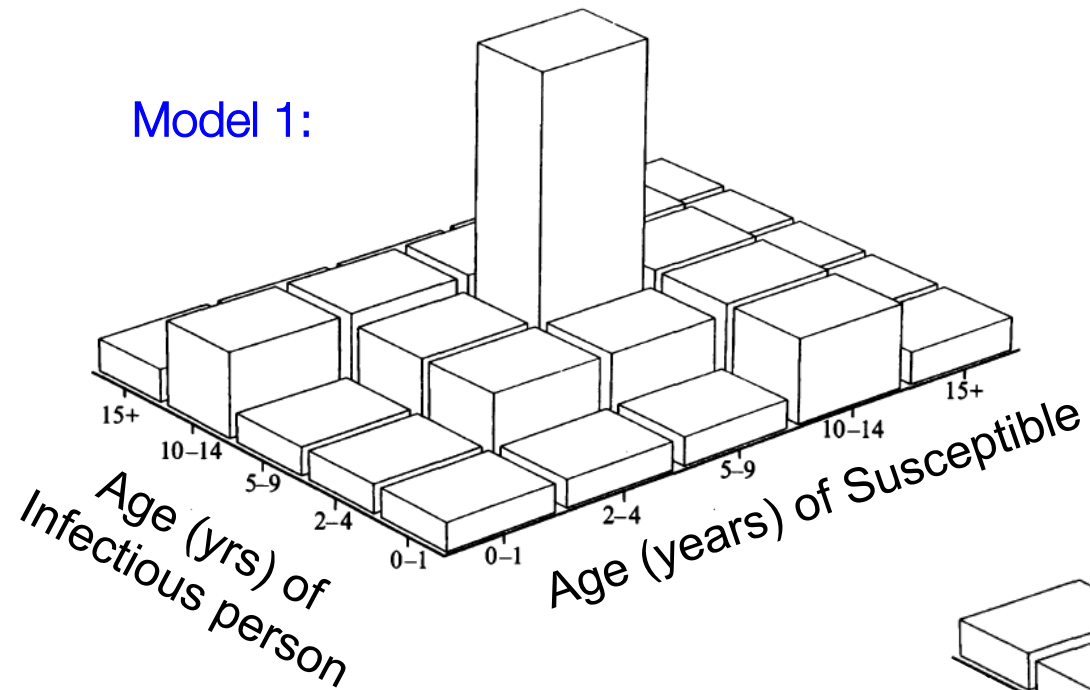


Model 2:

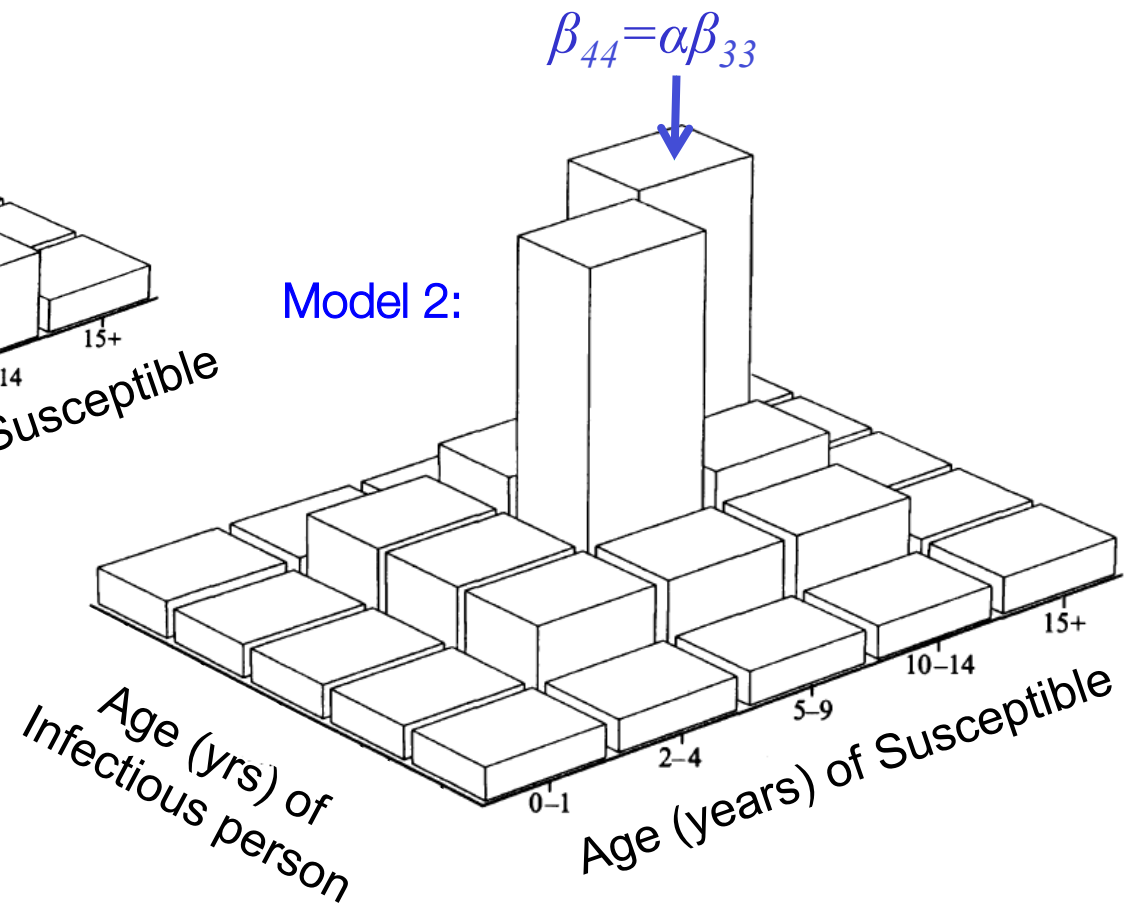


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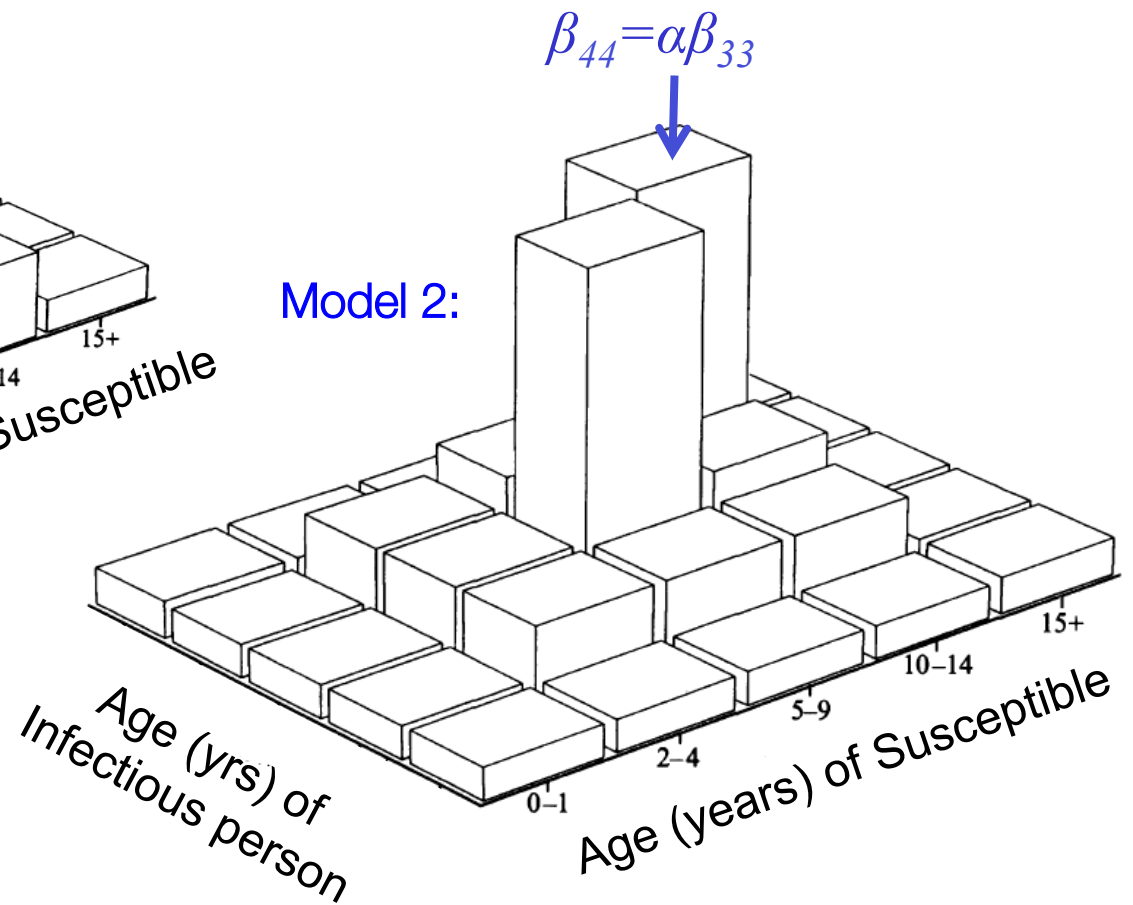
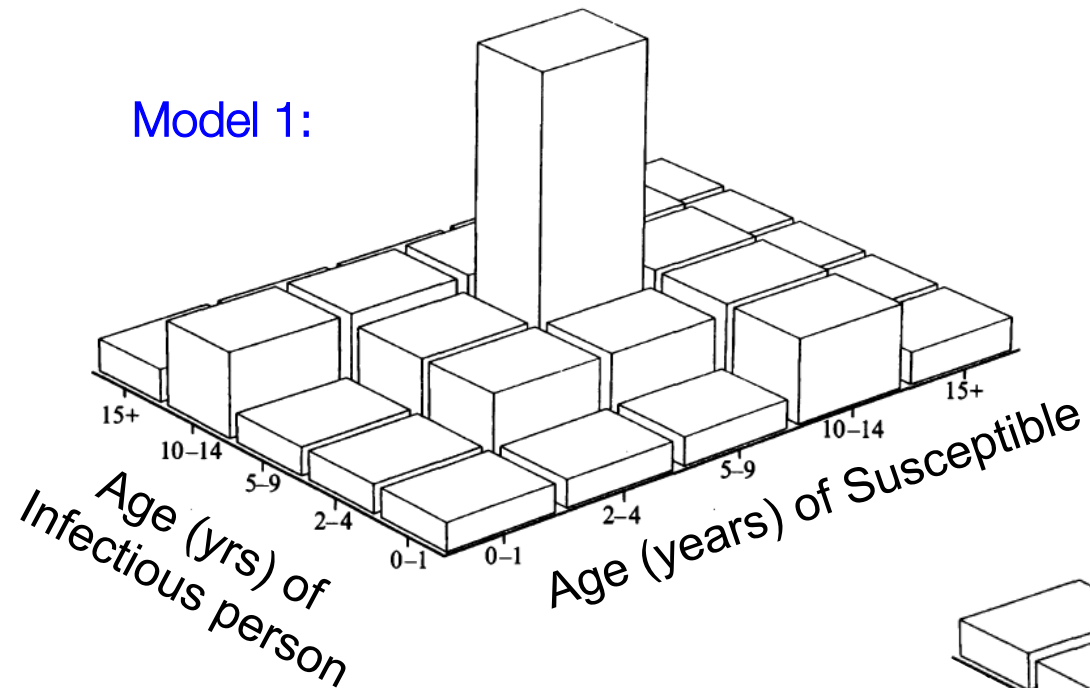
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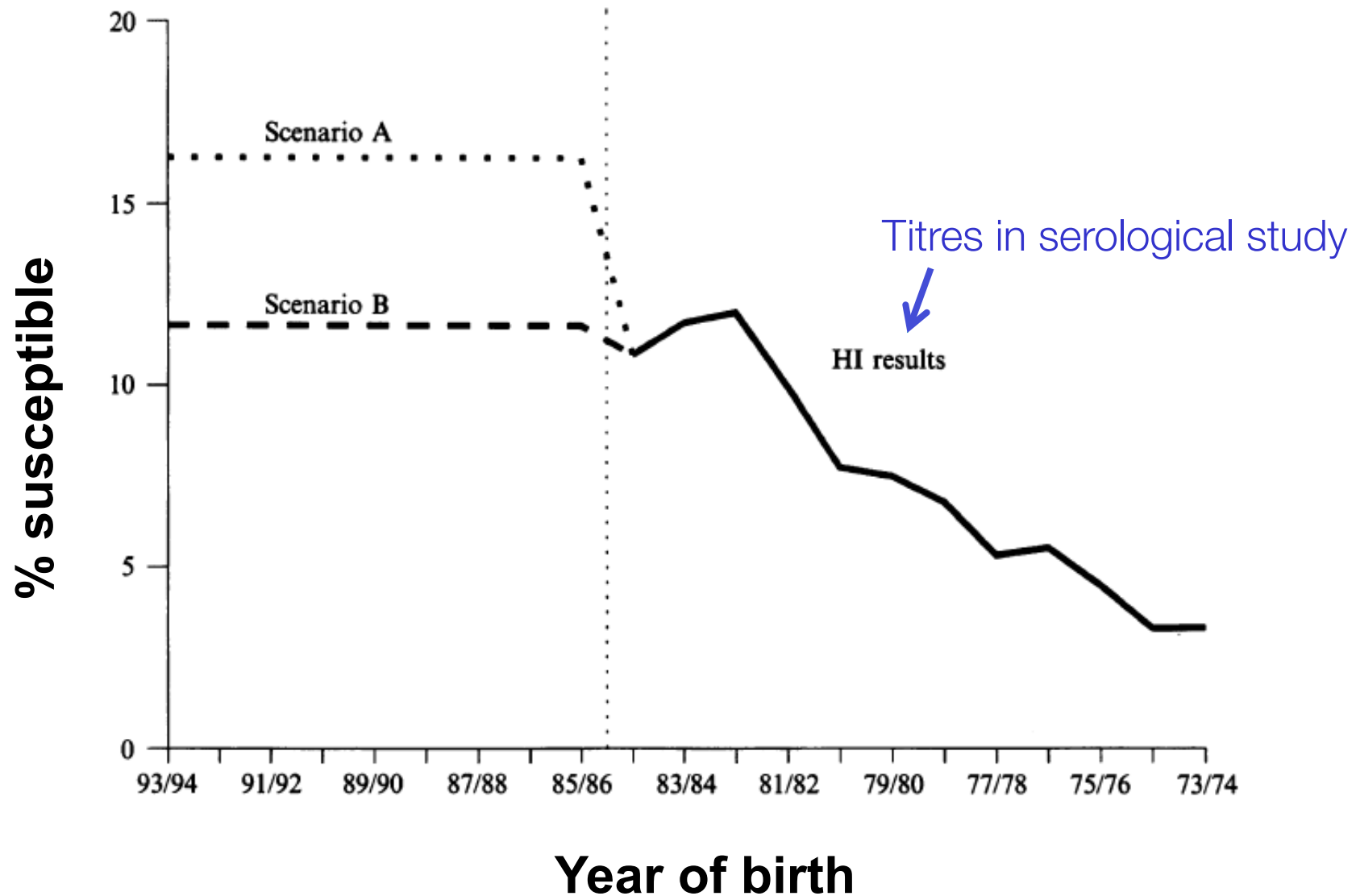


R_n calculations for measles in England and Wales: structure of WAIFW matrices

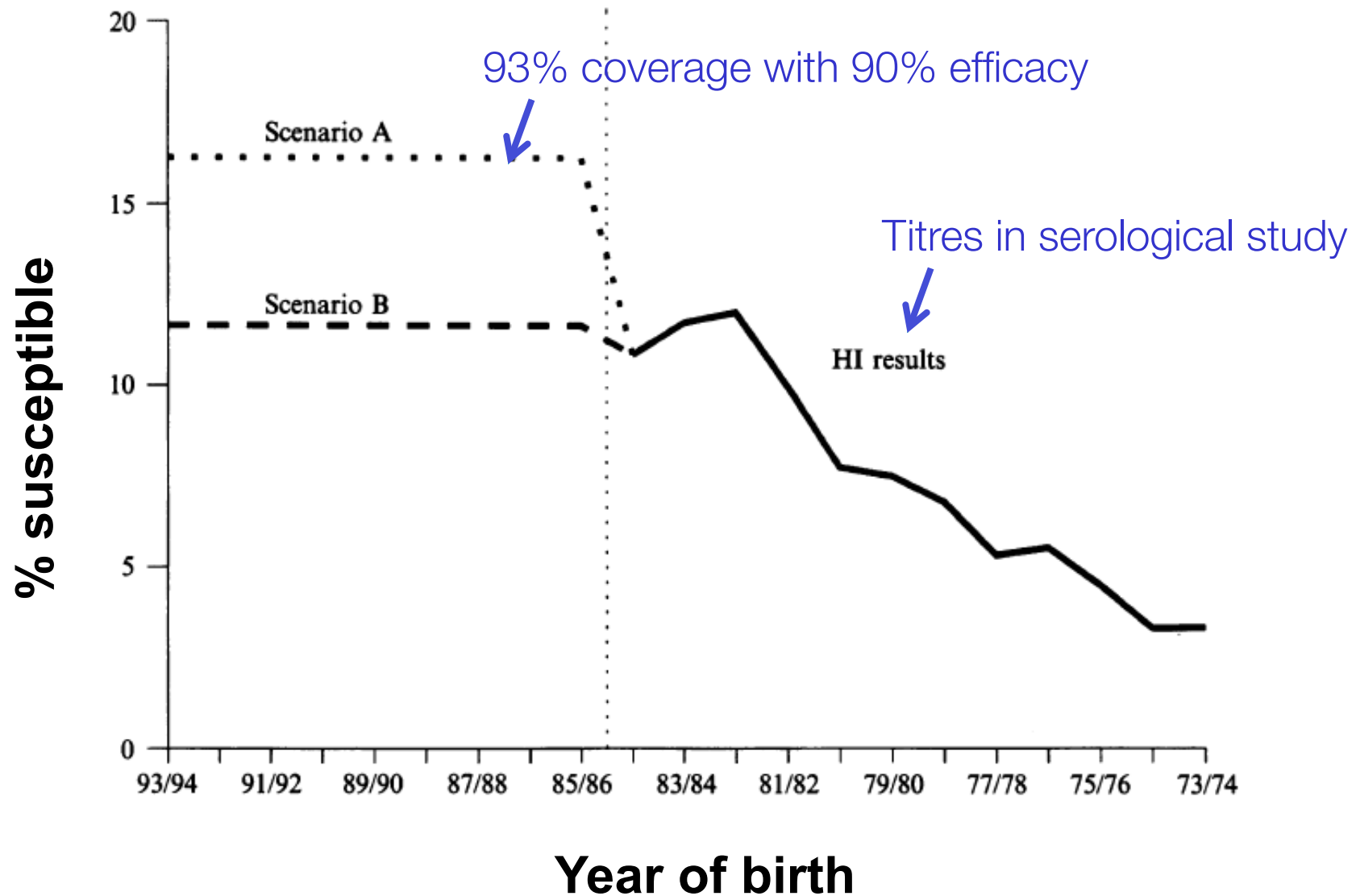


Thanks to recent studies, we can now do this step much better

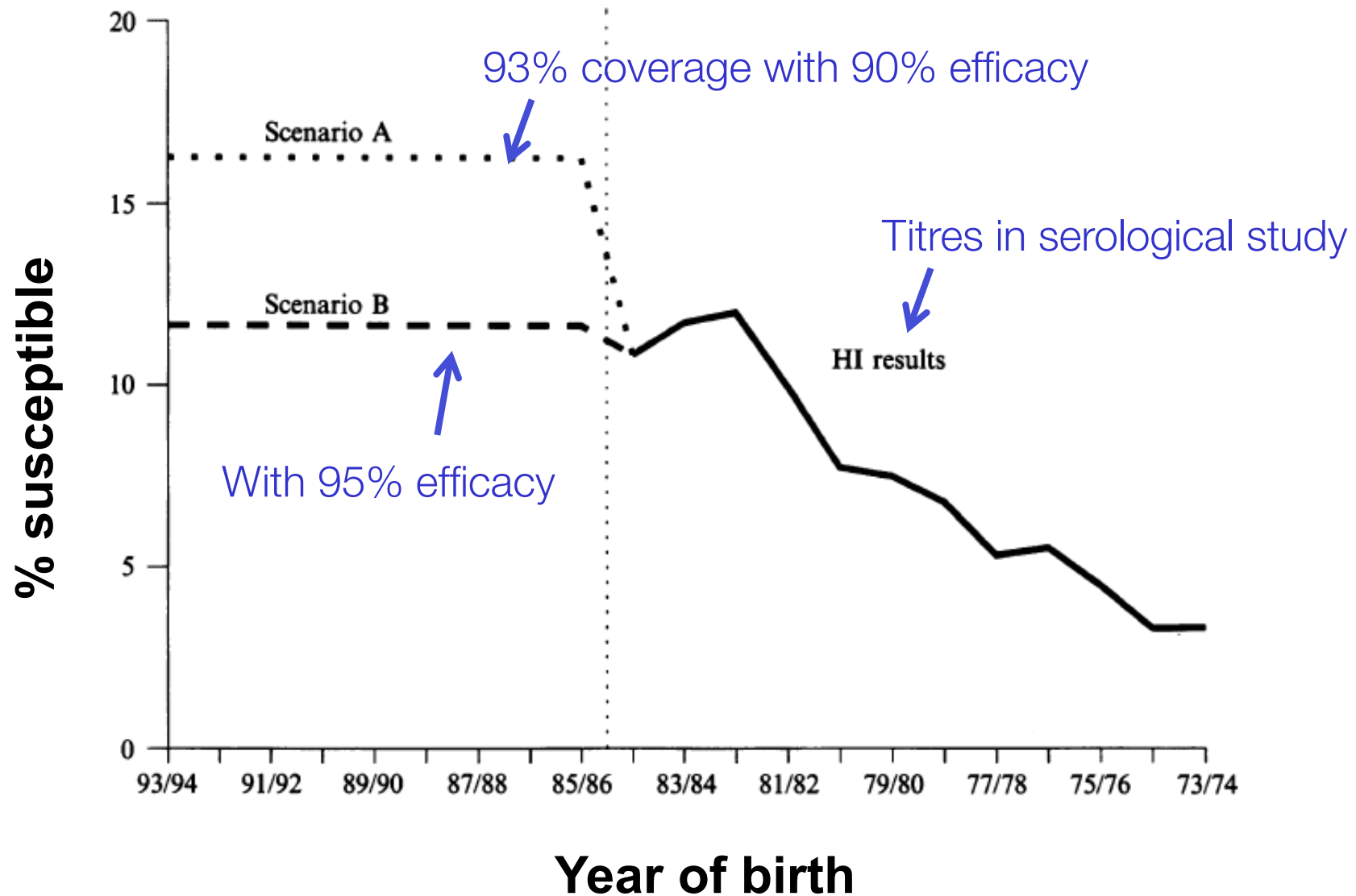
R_n calculations for measles in England and Wales: % susceptible by birth cohort



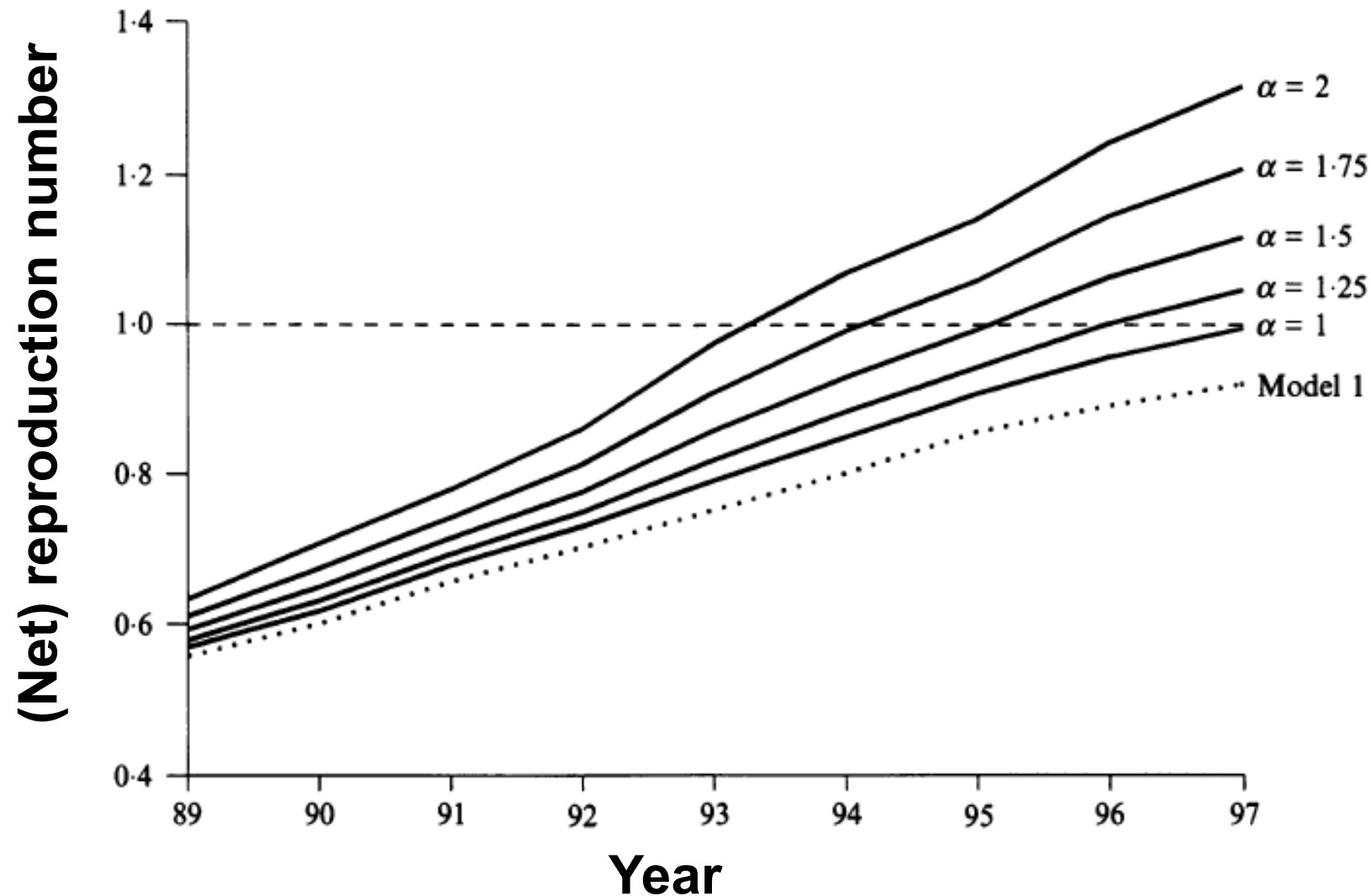
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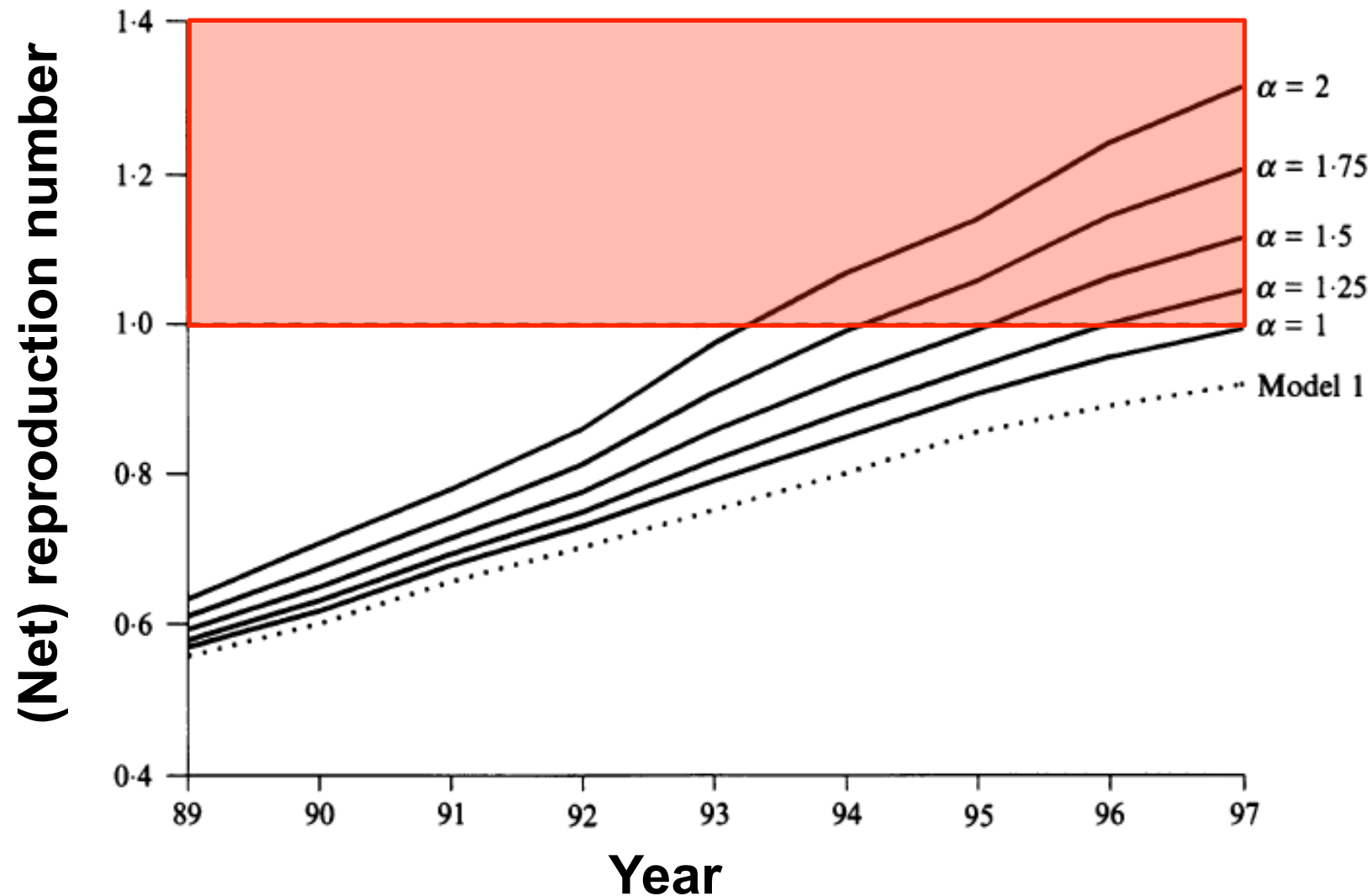
R_n calculations for measles in England and Wales: % susceptible by birth cohort



R_n calculations for measles in England and Wales: different assumptions about contact patterns (scenario A)



R_n calculations for measles in England and Wales: different assumptions about contact patterns (scenario A)



Conclusions and implications of the study by Gay et al (1997)

- Net reproduction number for measles very close to 1 during 1992-7.

“There was cause for concern over the levels of susceptibility to measles, with an epidemic of over 100,000 cases likely in 1995/6”

- The conclusions were supported by other studies using dynamic models (e.g. Babad et al, 1995).

⇒ A measles-rubella vaccination campaign was introduced in November 1994, targeting 95% of the 7 million 5-16 yr olds.

This was perhaps the first time that modelling was used to guide policy in the UK.

- Since then, the potential for a measles epidemic to occur continues to be evaluated in the same way (Choi et al, 2008).

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Summary - steps for calculating R_0 for an endemic infection in a non-randomly mixing population

- Measure prevalence in serosurvey.
- Estimate forces of infection in different subgroups (e.g. age strata).
- Choose WAIFW matrix structure.
- Calculate WAIFW values.
- Formulate “Next Generation Matrix” (NGM).
- Calculate R_0 from NGM.
- Herd immunity threshold can be calculated via $1-1/R_0$.

Appendix: Why is method 2 for calculating the R_0 equivalent to method 1?

If 1 infectious individual is introduced into a population in which individuals mix according to a WAIFW matrix and there is an “infinite” supply of susceptible individuals, then after several generations of infection:

A. the age distribution of the infectious people in each generation converges to some distribution

- e.g. A fraction x are young and a fraction $1-x$ are old

B. the number of secondary infectious people from each infectious person equals R_0

These statements can be written as:

$$R_{yy}x + R_{yo}(1-x) = R_0x$$

$$R_{oy}x + R_{oo}(1-x) = R_0(1-x)$$

Appendix: Derivation of method 2 for obtaining R_0

Note: If there are R_0 cases in a generation, then there are R_0x young infectious people and $R_0(1-x)$ old infectious people in that generation.

The Next Generation Matrix, tells us that the number of young infectious people in that generation equals $R_{yy}x + R_{yo}(1-x)$

So
$$R_{yy}x + R_{yo}(1-x) = R_0x$$

Similarly, using the NGM, the number of old infectious people in that generation equals $R_{oy}x + R_{oo}(1-x)$

So
$$R_{oy}x + R_{oo}(1-x) = R_0(1-x)$$

Appendix: Summary of the matrix equation for R_0

The equations

$$R_{yy} x + R_{yo} (1-x) = R_0 x$$
$$R_{oy} x + R_{oo} (1-x) = R_0 (1-x)$$

can be summarized using matrix notation:

$$\begin{pmatrix} R_{yy} & R_{yo} \\ R_{oy} & R_{oo} \end{pmatrix} \begin{pmatrix} x \\ 1-x \end{pmatrix} = R_0 \begin{pmatrix} x \\ 1-x \end{pmatrix}$$

NB There may be more than 1 value for “ R_0 ” which satisfies the above equation...

The formal (mathematical) definition of R_0 is that it is the “**dominant eigenvalue of the Next Generation Matrix**”, i.e. the largest value for R_0 which satisfies the above equation.

Estimating R_0 in randomly mixing populations (3)

For infections not conferring immunity (SIS), $R_0 = 1/(1-i^*)$

i^* : proportion infectious at equilibrium

Recall, for an SIS infection, proportion susceptible
= $1 - \text{proportion in the currently infectious category}$

