Measles and Rubella Transmission Modelling Workshop
NDMC, IIT-Bombay, 5-8 February 2024

Block 2: History and current understanding of measles and rubella-specific dynamics
2.1: Population-level dynamics

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By the end of this session you should …

❑ Know how to construct simple models of infectious disease transmission and express them in computer code.

❑ Understand how demographic processes can lead to cycles and express them in computer code.

❑ Understand basic concepts (force of infection, reproduction numbers) and how they relate to parameters in infectious disease models.

Static and dynamic models

Recap: In an infectious disease model, the **force of infection** is the rate at which people who are susceptible to an infection become infected.

Force of infection = 0.1/day

Day 0
0 infected
10 susceptible

Day 1
1 infected
9 susceptible
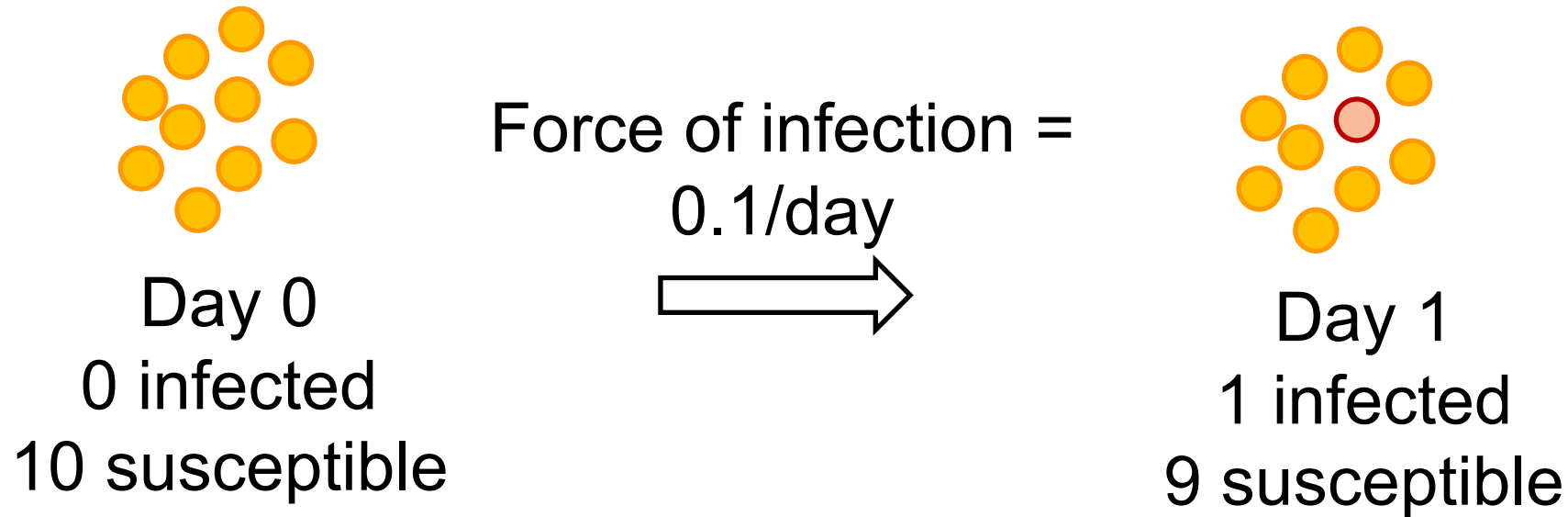
In a **static model**, the force of infection is fixed (unchanging).
In a **dynamic model**, the force of infection changes over time.

SIR compartmental model (e.g. measles)

COMPARTMENTS

S
Susceptible

I
Infected

R
Recovered
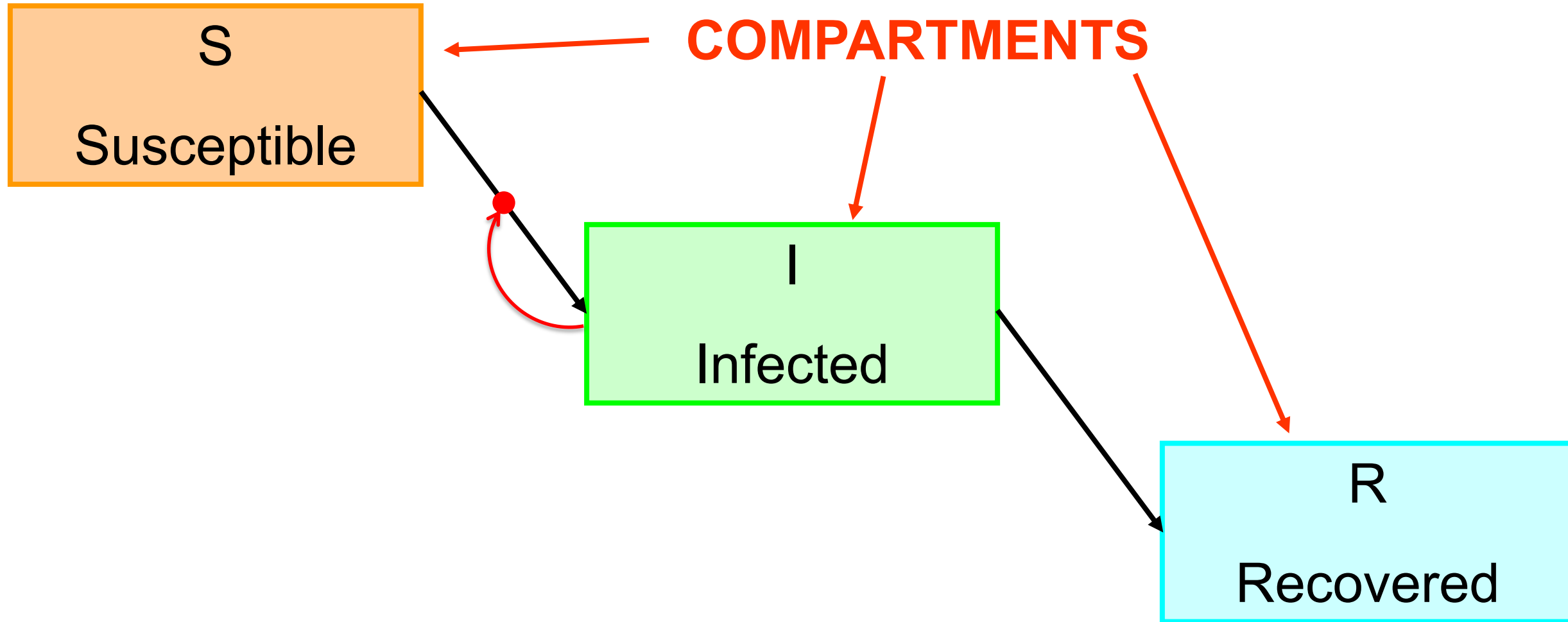
Exercise: Can you write this as a set of differential equations?

Mathematical representation

They can be written as a set of differential equations:

Rate of infection transmission

susceptible $\longrightarrow$ $$\frac{dS}{dt} = -\beta IS$$

force of infection

infectious $\longrightarrow$ $$\frac{dI}{dt} = \beta IS - \gamma I$$

recovered $\longrightarrow$ $$\frac{dR}{dt} = \gamma I$$

recovery rate

Tangent

β can be either frequency-dependent (independent of population density) or density-dependent (scales with population density. See Ferrari et al. https://doi.org/10.1155/2011/267049
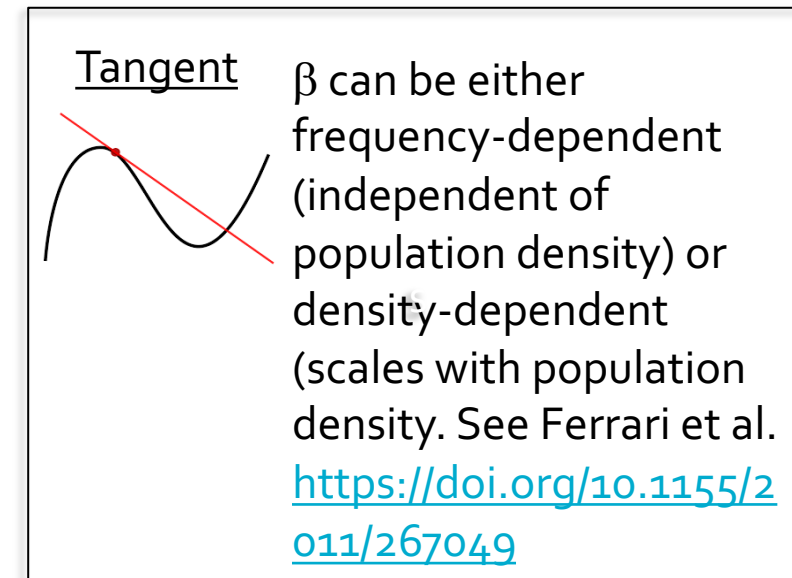
Notes:
1. Key assumption: homogenous mixing (each infectious individual is as likely to contact a susceptible person as an immune individual).
2. S, I and R can be expressed as either counts (number of individuals) or proportions (% of the total population).
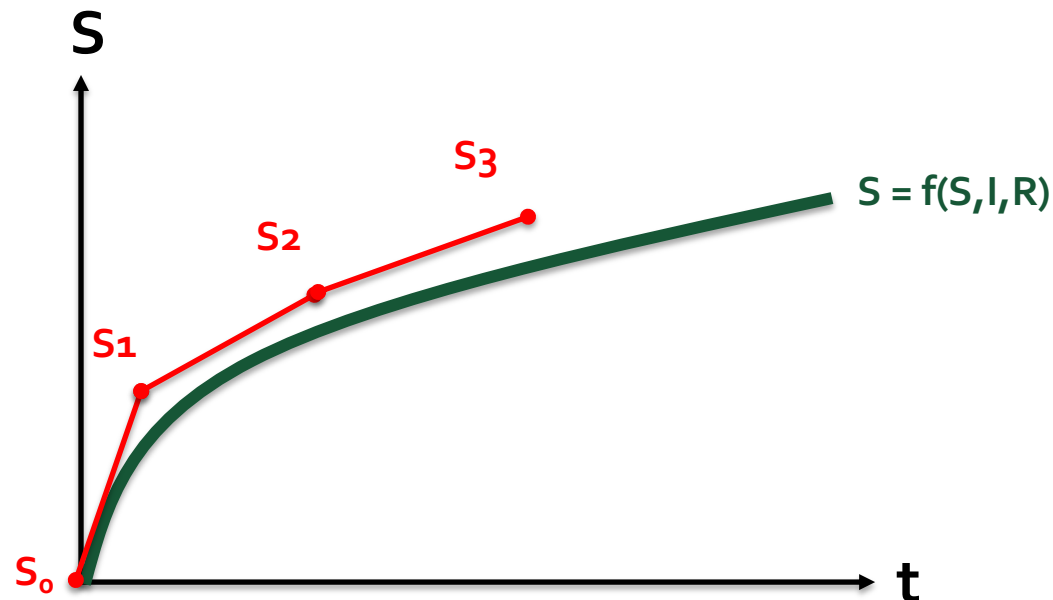
Mathematical representation

We can then integrate the differential equations e.g. using Euler's method

$$\frac{dS}{dt} = -\beta SI \qquad \Leftrightarrow \qquad S_{t+1} = S_t - \beta \, S_t \, I_t$$

This generates a set of difference equations:

Probability of transmission

susceptible → $S_{t+1} = S_t - \beta\, S_t\, I_t$

infected → $I_{t+1} = I_t + \beta\, S_t\, I_t - \gamma\, I_t$

recovered → $R_{t+1} = R_t + \gamma\, I_t$

recovery rate

Exercise: Can you write the equations above in pseudo-code or actual code in your preferred language?

function SIR_model

Define variables and parameters

tmax   =2000
S   =array[0,...tmax+1]
I   =array[0,...tmax+1]
R   =array[0,...tmax+1]
beta   =1
rec_rate =0.1

Run equations
 for(t in 1:tmax){
      S[t+1] =S[t]-beta*S[t]*I[t]
      I[t+1] =I[t]+beta*S[t]*I[t]-rec_rate*I[t]
      R[t+1]=R[t]+rec_rate*I[t]}
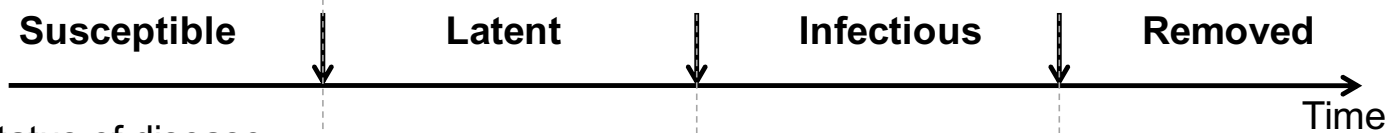
Look at the R code for an SIR model and understand it.
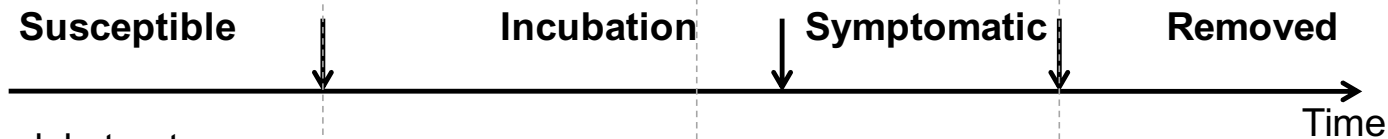
Run it with different values of β (beta) and γ (rec_rate). Do you notice anything?
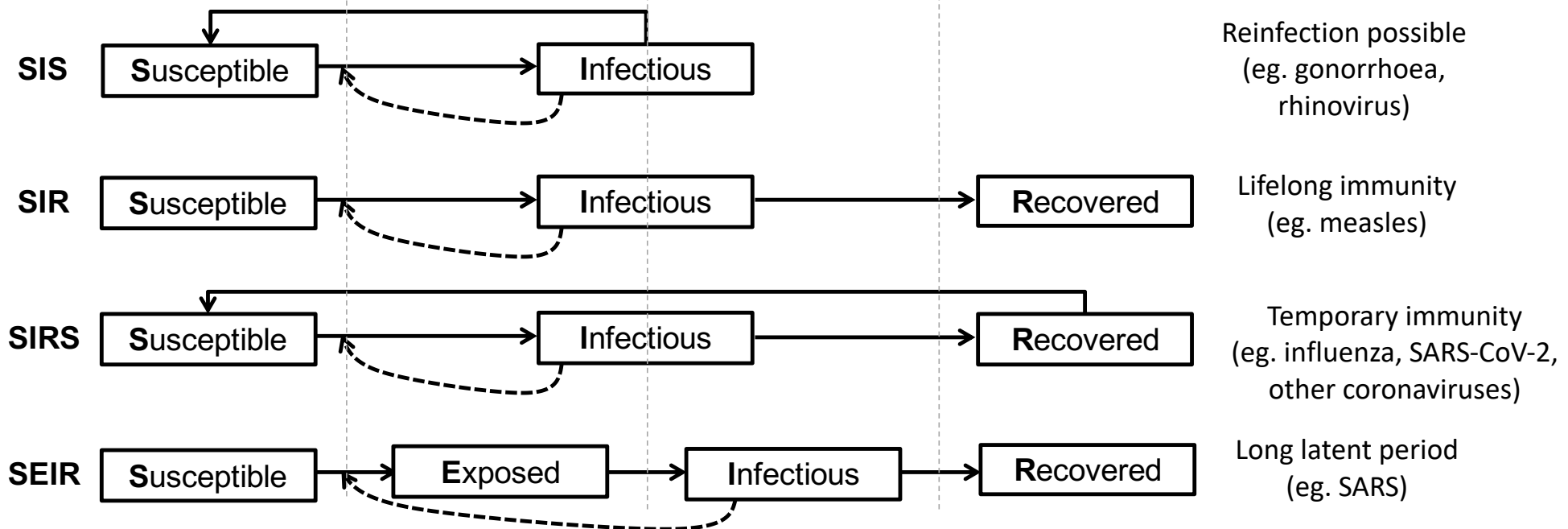
Other compartmental models

(a) Status of infection

Susceptible   **Latent**   **Infectious**   **Removed**

Time

(b) Status of disease

Susceptible   **Incubation**   **Symptomatic**   **Removed**

Time

(c) Model structures

SIS

Susceptible → Infectious

Reinfection possible
(eg. gonorrhoea, rhinovirus)

SIR

Susceptible → Infectious → Recovered

Lifelong immunity
(eg. measles)

SIRS

Susceptible → Infectious → Recovered

Temporary immunity
(eg. influenza, SARS-CoV-2, other coronaviruses)

SEIR

Susceptible → Exposed → Infectious → Recovered

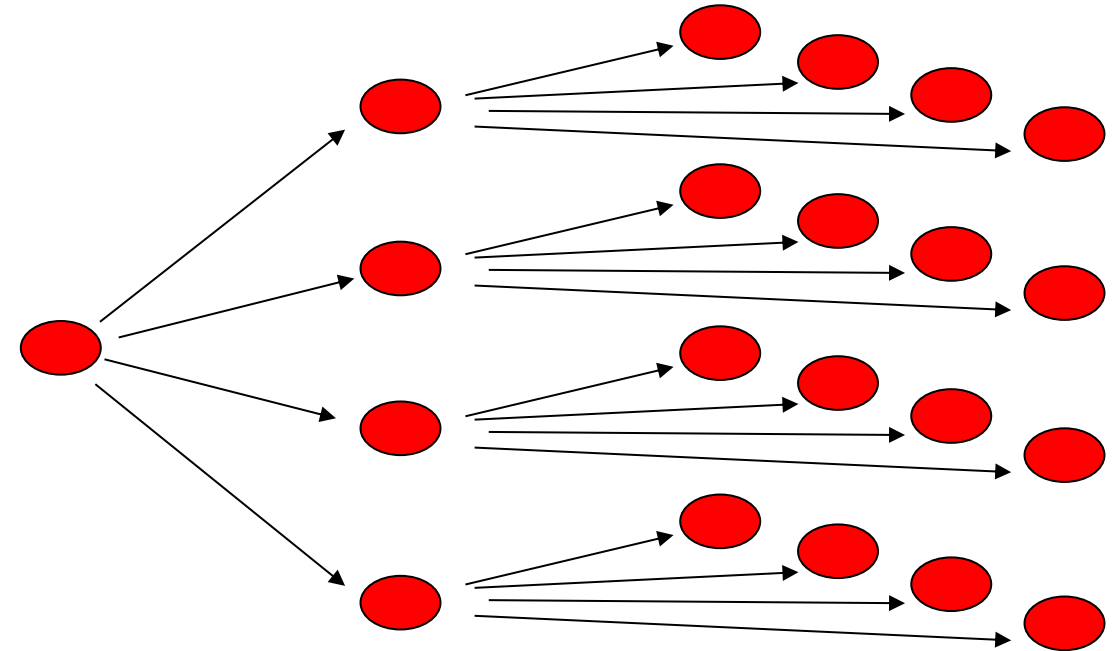Long latent period
(eg. SARS)

Jit and Brisson. *Pharmacoeconomics* 2011; 29:371.

R_0
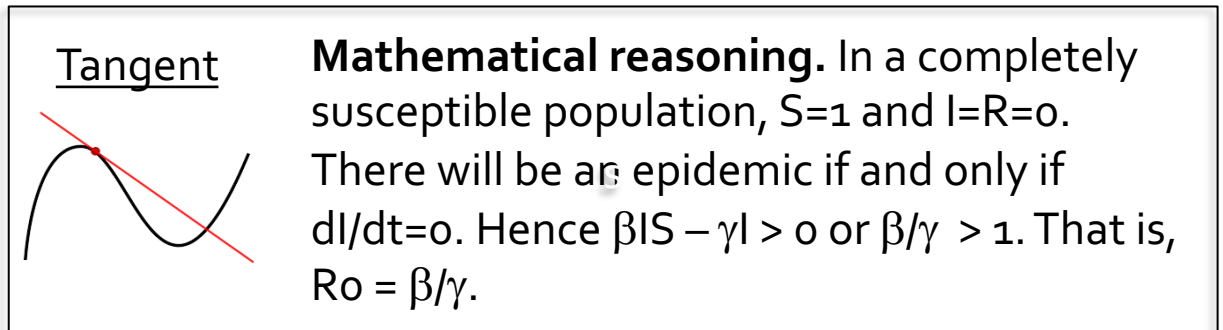
Basic reproduction number

The average number of secondary infectious cases resulting from the introduction of a single infectious case into a totally susceptible population
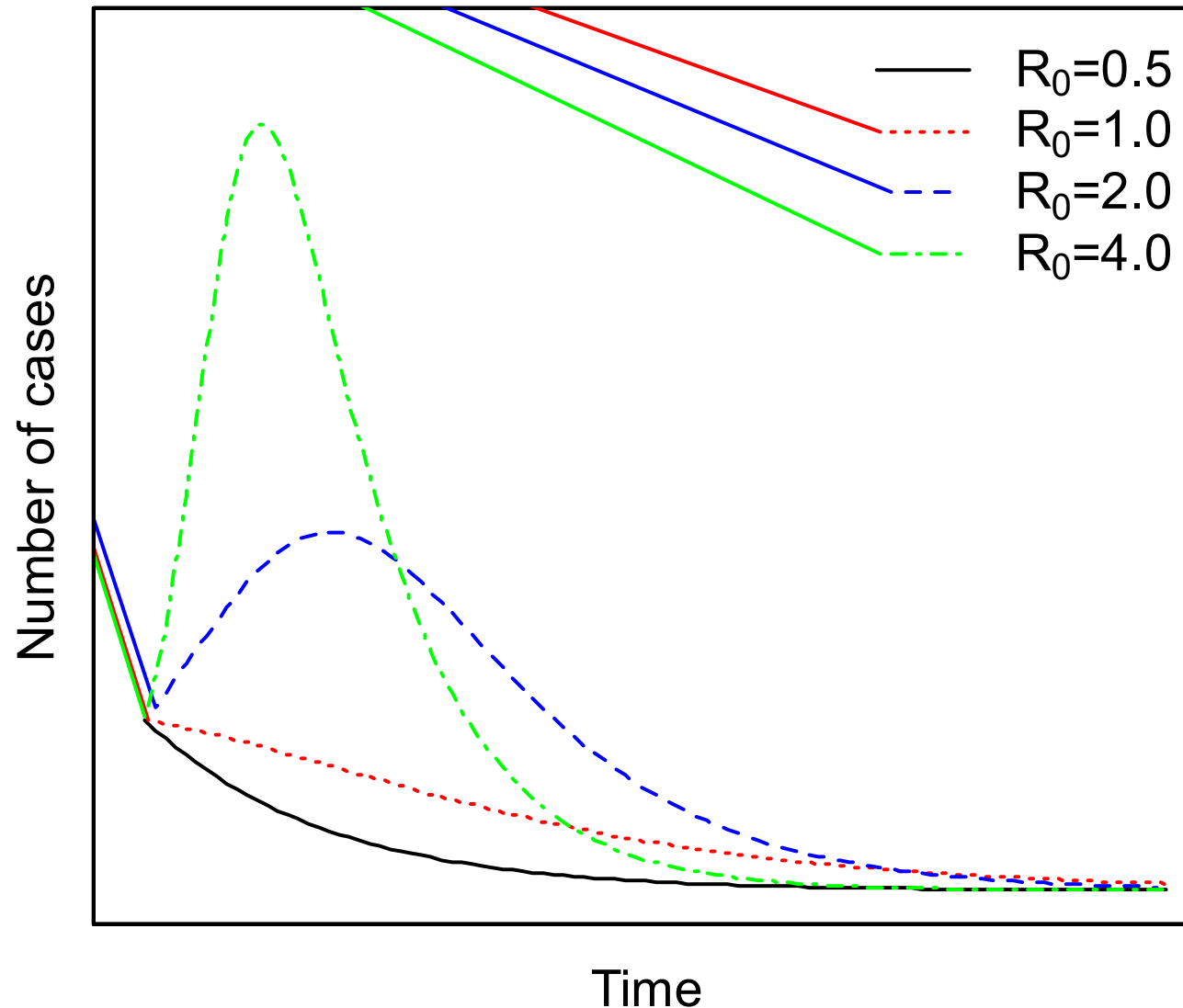
Population with R_0 of 4

Basic reproduction number

$R_0 =$ Number of people someone will come in contact with per unit time X Probability that contacts is with infectious individual X Probability contact will be infectious

$=$ Number of effective contacts per unit time X $1/$ Length of time someone is infectious (L)

$= \beta/\gamma$

Tangent

Mathematical reasoning. In a completely susceptible population, S=1 and I=R=0. There will be an epidemic if and only if dI/dt=0. Hence βIS – γI > 0 or β/γ > 1. That is, Ro = β/γ.

Basic reproduction number

Legend:
- $R_0=0.5$ (black solid line)
- $R_0=1.0$ (red dotted line)
- $R_0=2.0$ (blue dashed line)
- $R_0=4.0$ (green dash-dot line)

Y-axis: Number of cases
X-axis: Time

For an infection to persist in a population, it must have an $R_0 > 1$.

R_0 has limited use in practice:

- Hard to find a totally susceptible population!
- Once the disease spreads, a portion of the population will move into the infected and recovered compartments (if the infection is immunising).

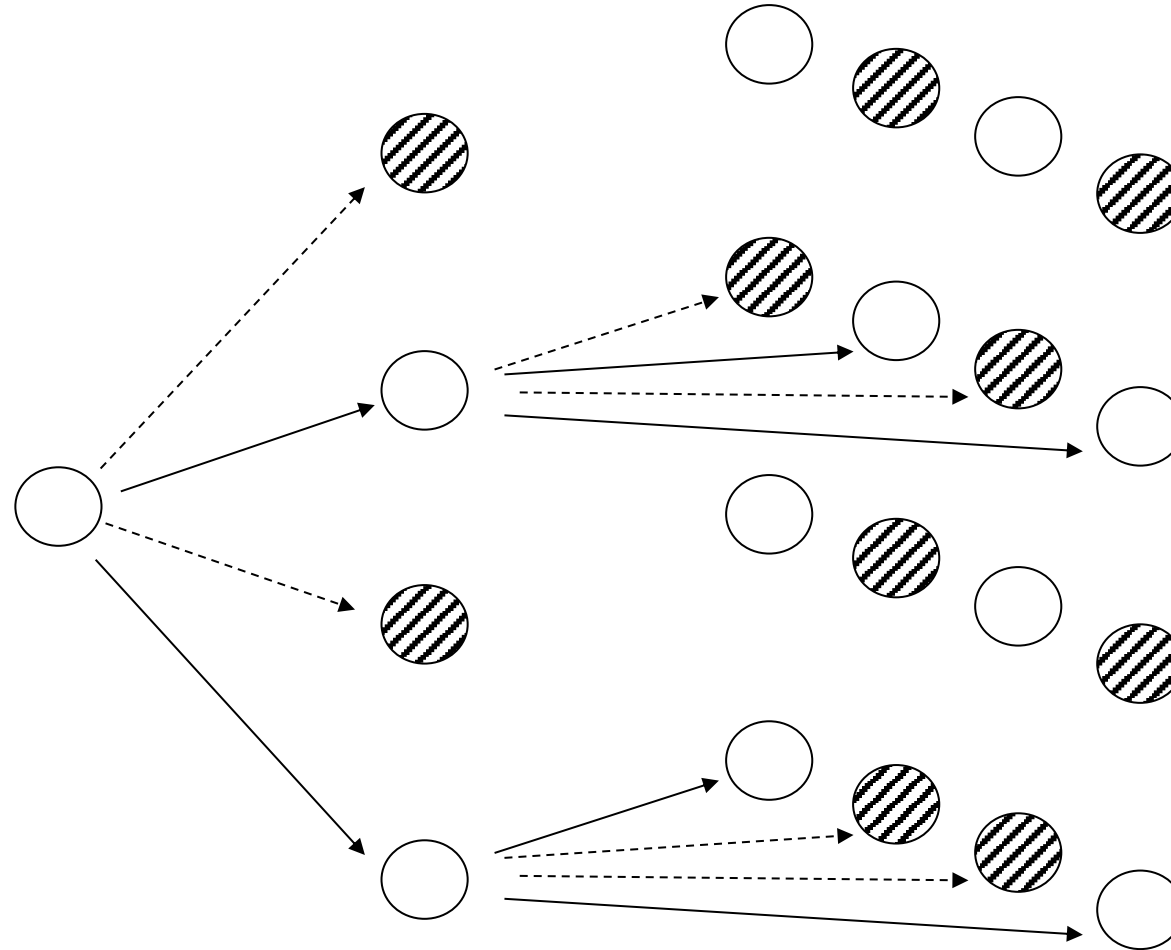Usually, it is more useful to talk about …

R_0

Basic reproduction number

The average number of secondary infectious cases resulting from the introduction of a single infectious case into a totally susceptible population

R_n

Net reproduction number

The average number of secondary infectious cases resulting from each infectious case in a given population
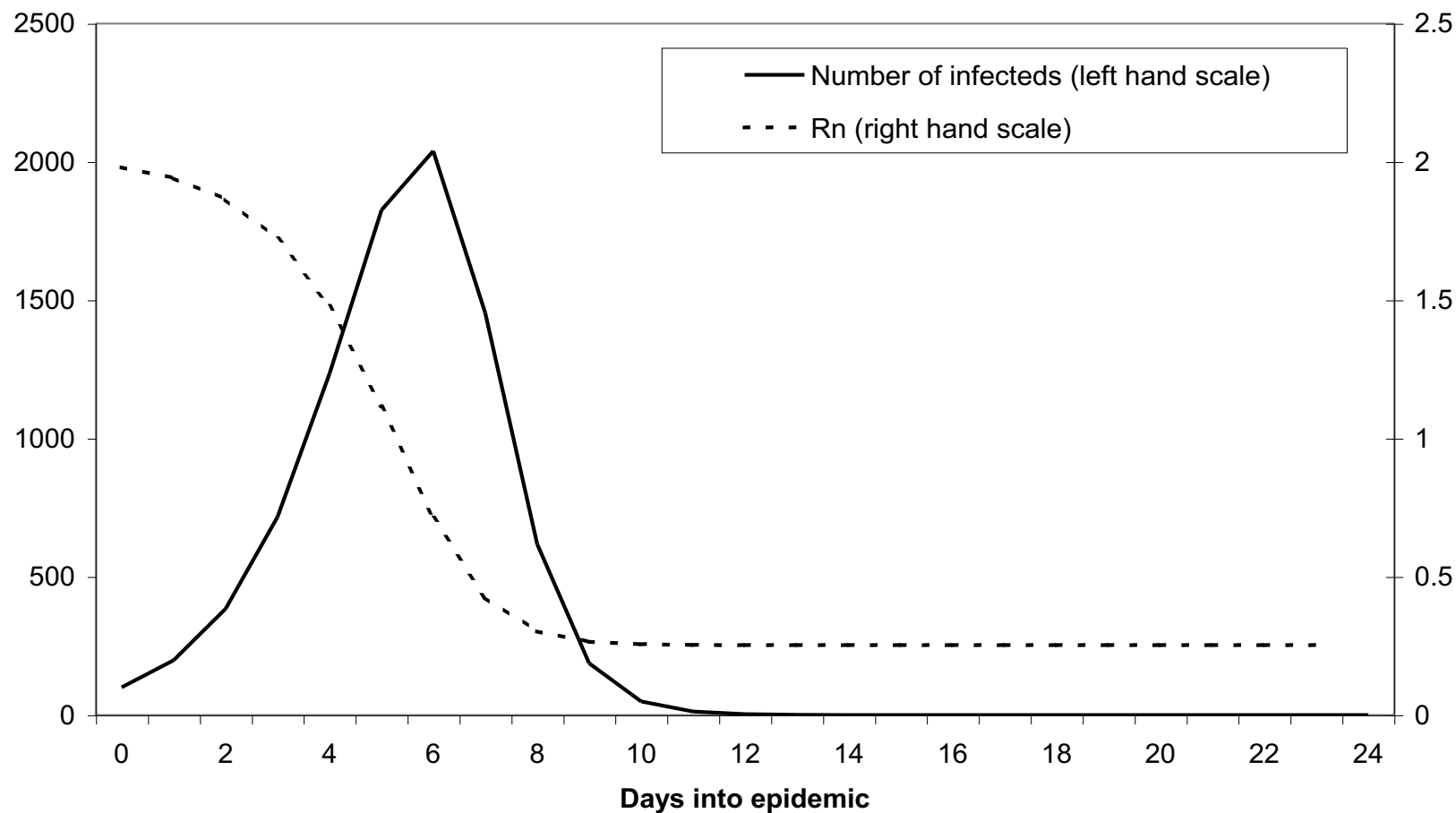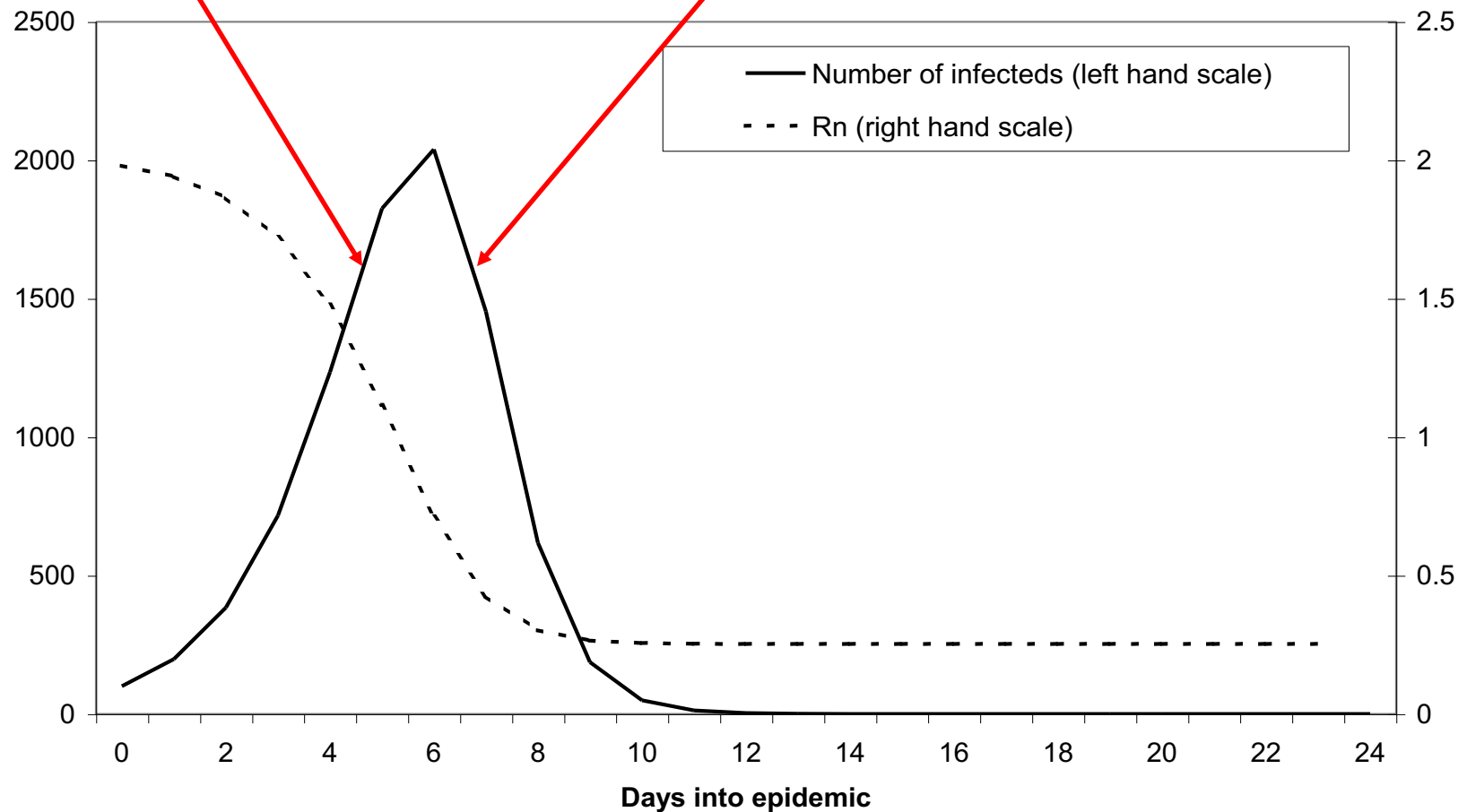
Population with R_0 of 4 but R_n of 2

The magnitude of R_n usually correlates with the trend in the disease incidence.

Net reproduction number
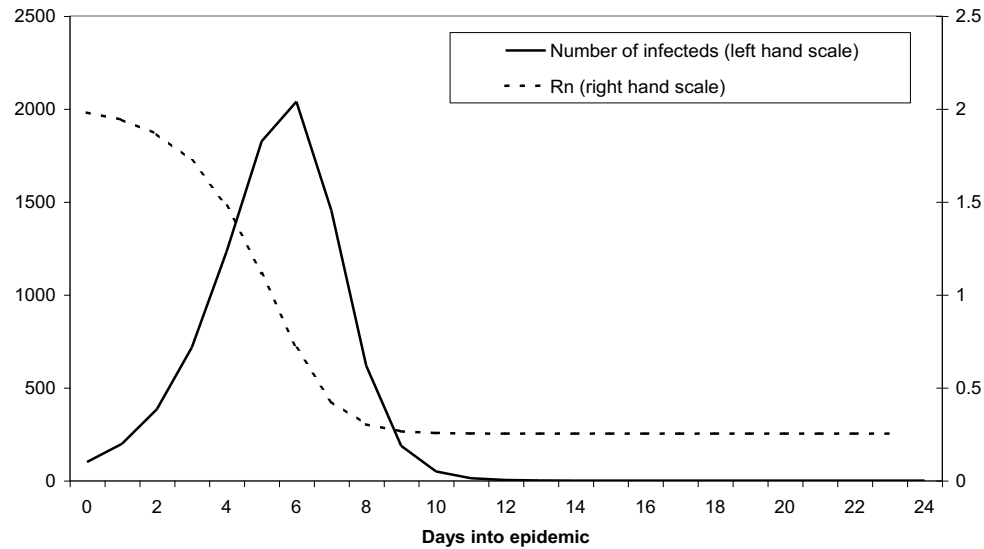

R_n>1. Disease incidence increases, number of susceptibles decreases.

R_n<1. Most susceptibles are immune, disease incidence decreases.

Number of infecteds (left hand scale)

Rn (right hand scale)

Days into epidemic

4-weekly notifications of measles, mumps, rubella and pertussis in Canada (pre-vaccination)

Do these model results match actual time-series data about the incidence of endemic diseases like measles? Why not?

Trottier *et al. Emerg Themes Epidemiol* 2006; 3:9.
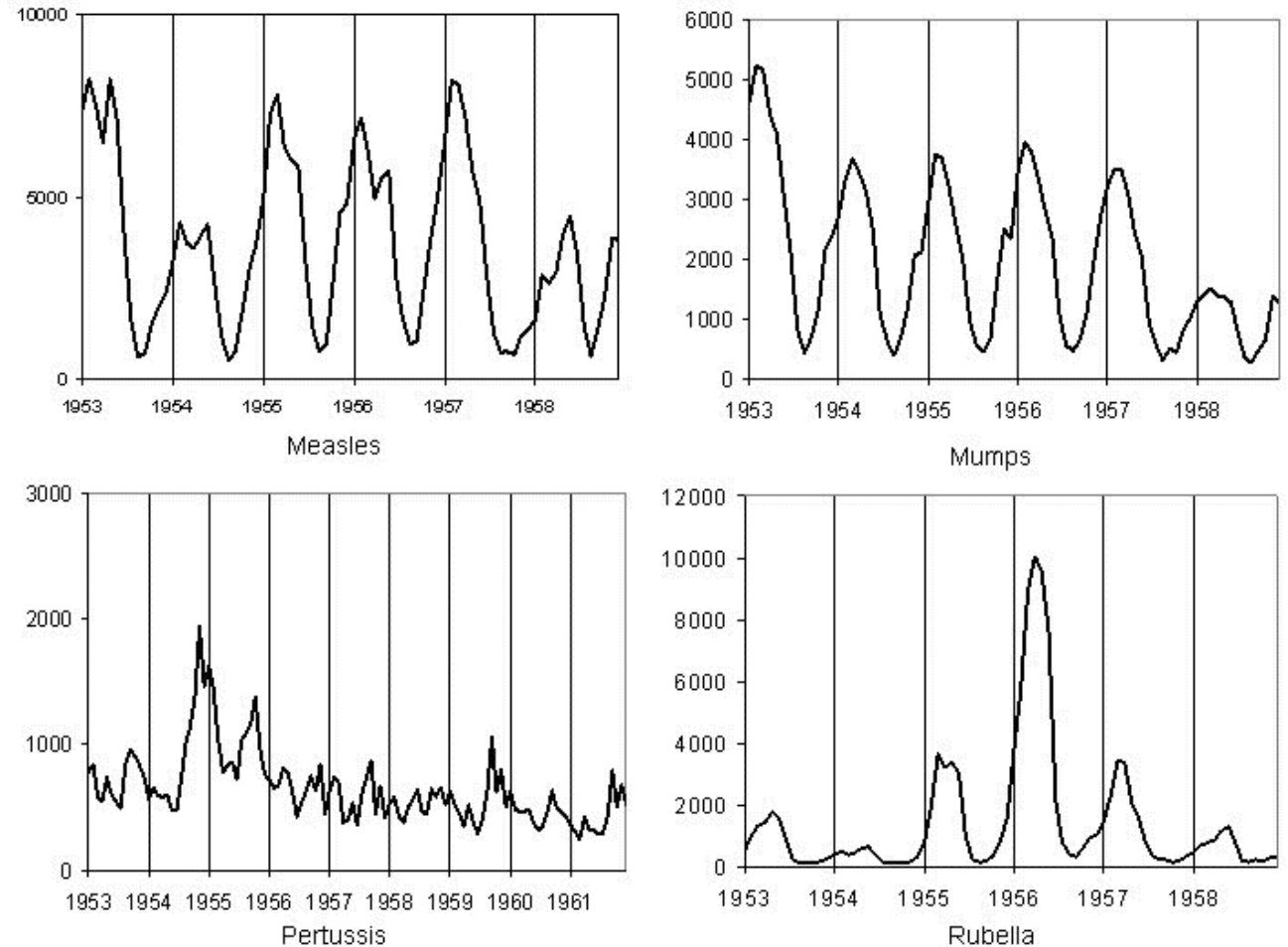
Why does disease incidence cycle?

Hamer (1906): Changes in the prevalence of susceptibles as a result of recovering from disease and new births (and waning vaccine protection).
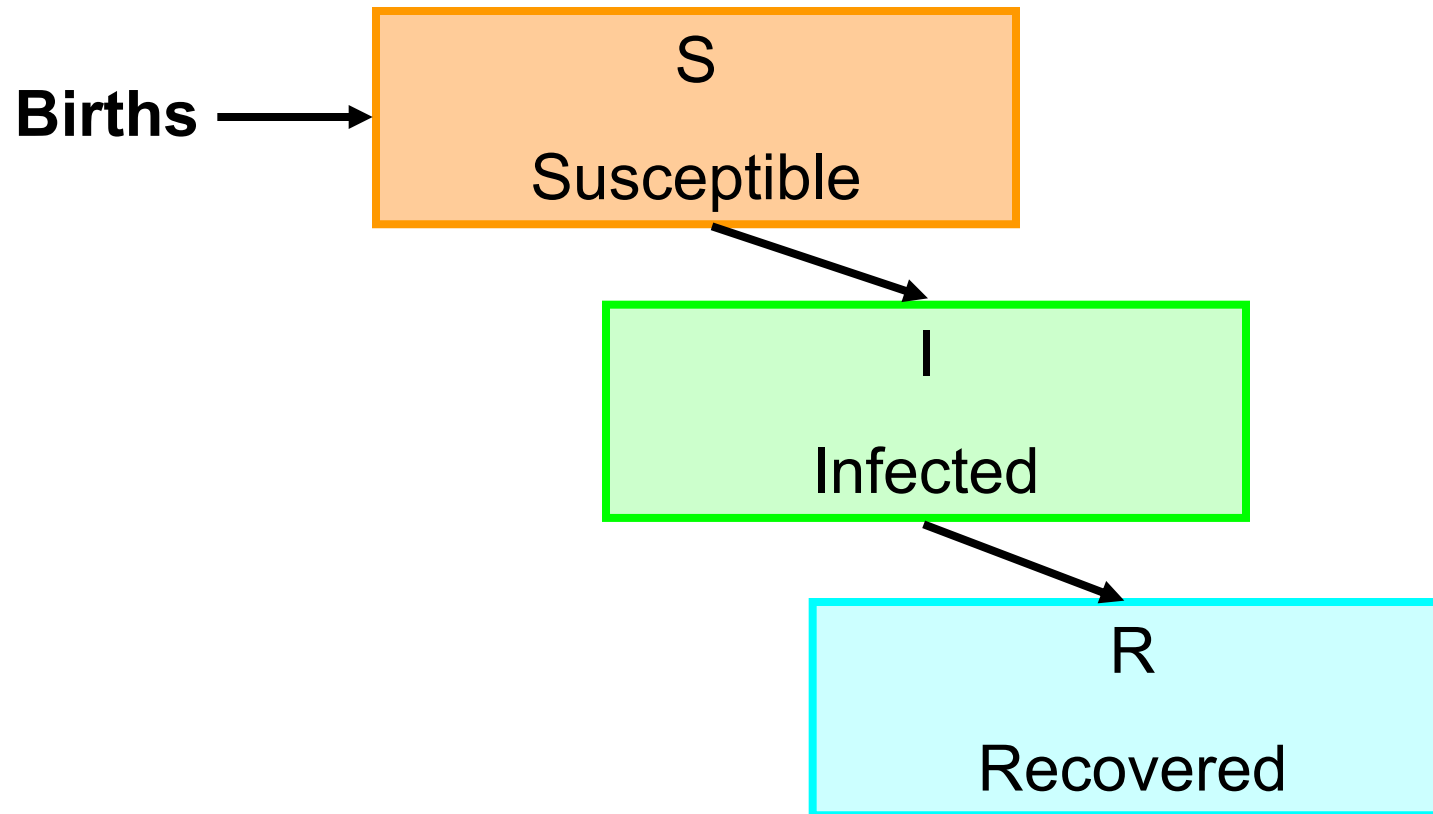
SIR equations with births and deaths

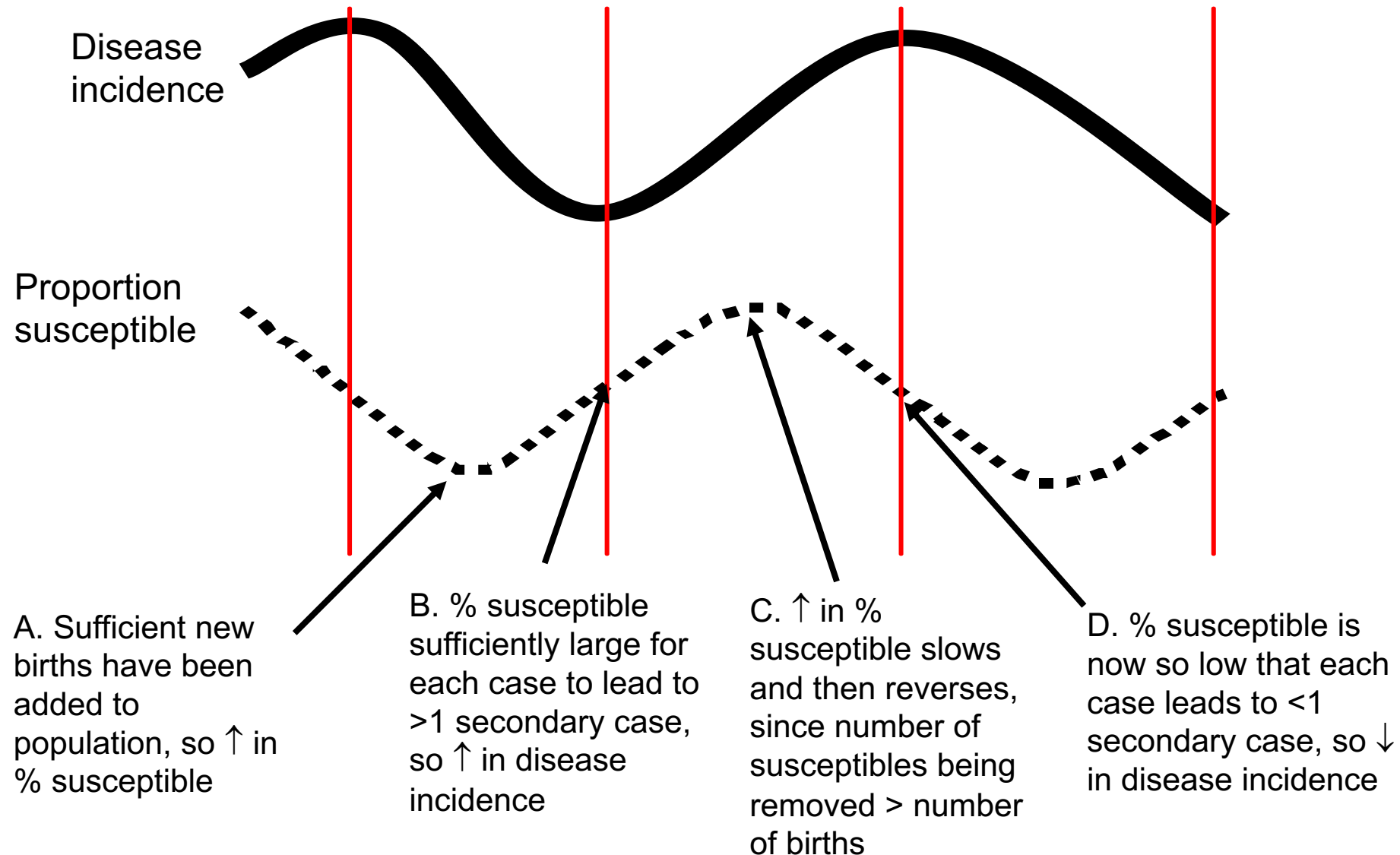$$S_{t+1} = b(S_t + I_t + R_t) + S_t - \beta\, I_t\, S_t - dS_t$$

$$I_{t+1} = I_t + \beta\, I_t\, S_t - \gamma\, I_t - dI_t$$

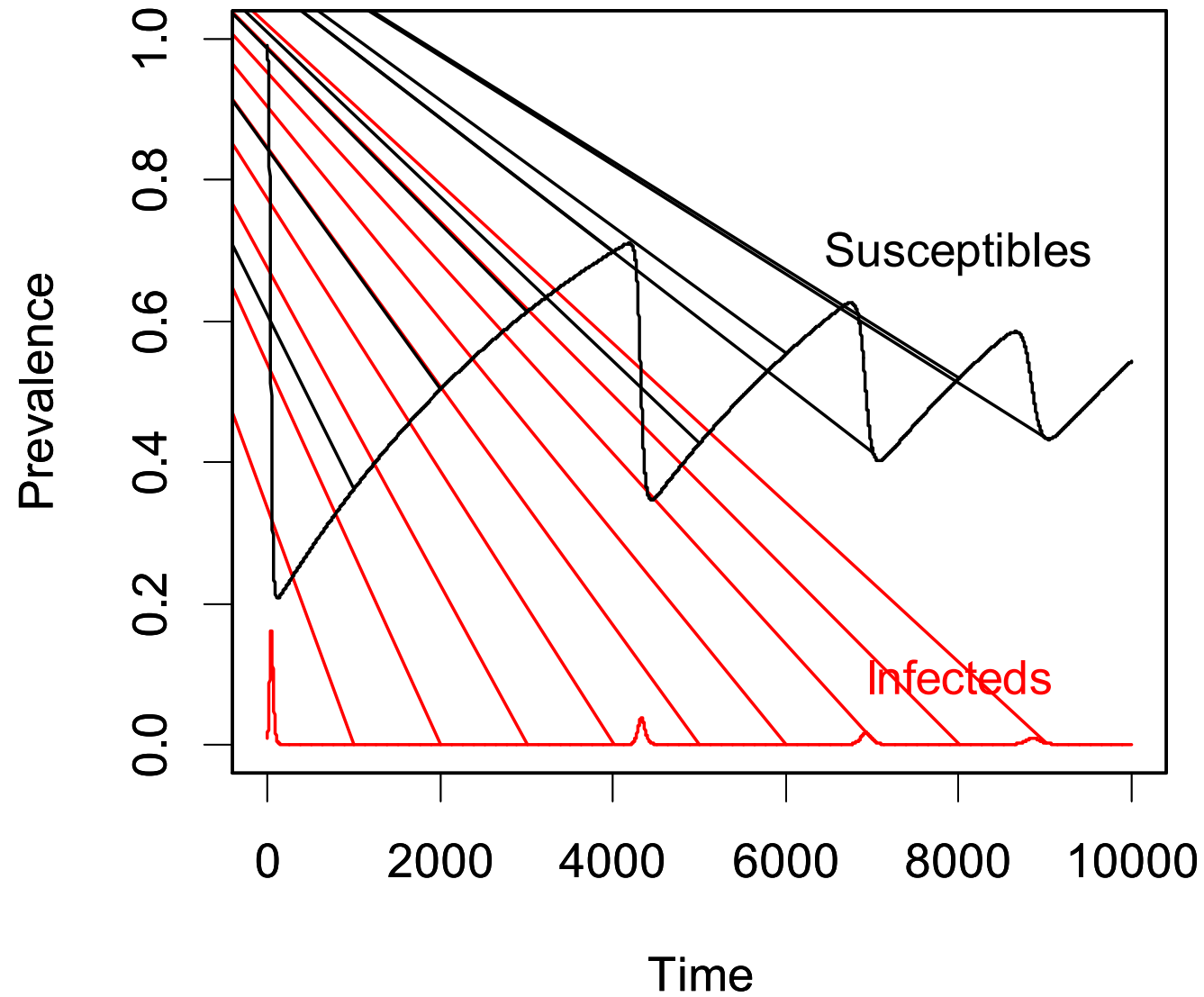$$R_{t+1} = R_t + \gamma\, I_t - dR_t$$

Notes:

1. Births occur in susceptibles but deaths can occur in any compartment.

2. This assumes that the infection itself does not increase the death rate.

Seasonal patterns

Disease incidence

Proportion susceptible

A. Sufficient new births have been added to population, so ↑ in % susceptible

B. % susceptible sufficiently large for each case to lead to >1 secondary case, so ↑ in disease incidence

C. ↑ in % susceptible slows and then reverses, since number of susceptibles being removed > number of births

D. % susceptible is now so low that each case leads to <1 secondary case, so ↓ in disease incidence

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