Day 2
Lecture 2: Understanding the phases of an epidemic

Short course on modelling infectious disease dynamics in R

Ankara, Türkiye, September 2025

Dr Juan F Vesga

Aims of the session

- Understand why epidemics rise
- Understand why epidemics peak
- Understand why epidemics fade out
- Examine the concept of heard immunity
- Understand R_0 and R_{eff}

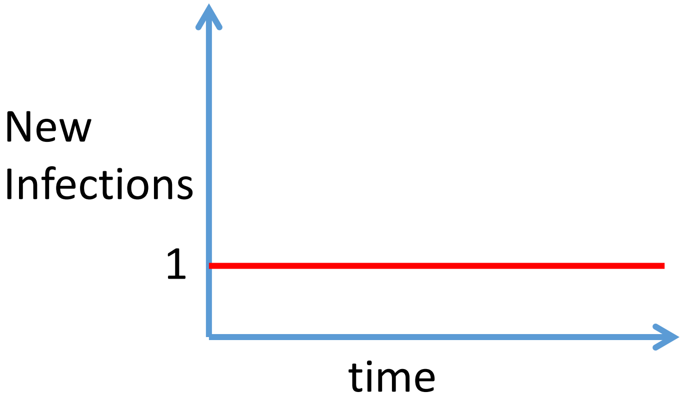
What it takes for an epidemic to rise?

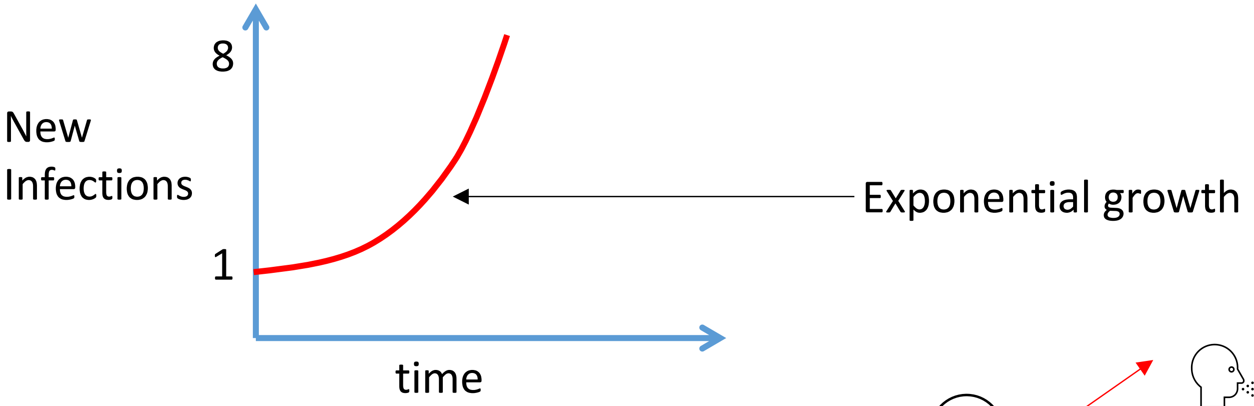
- A rate of infection -> transmission!
- A window of opportunity -> infectious period !

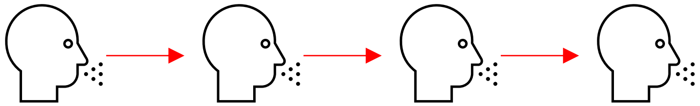
In general an epidemic starts if a pathogen is able to transmit quickly enough in that window of opportunity

- Other factors play a role too, like virulence behaviours etc.

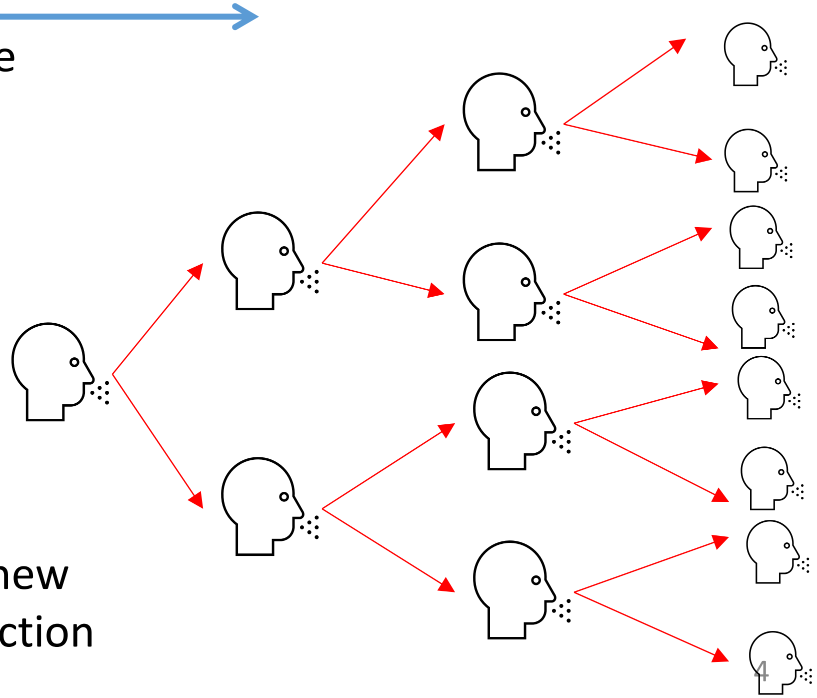
What it takes for an epidemic to rise?







Average of 1 new case
per infection



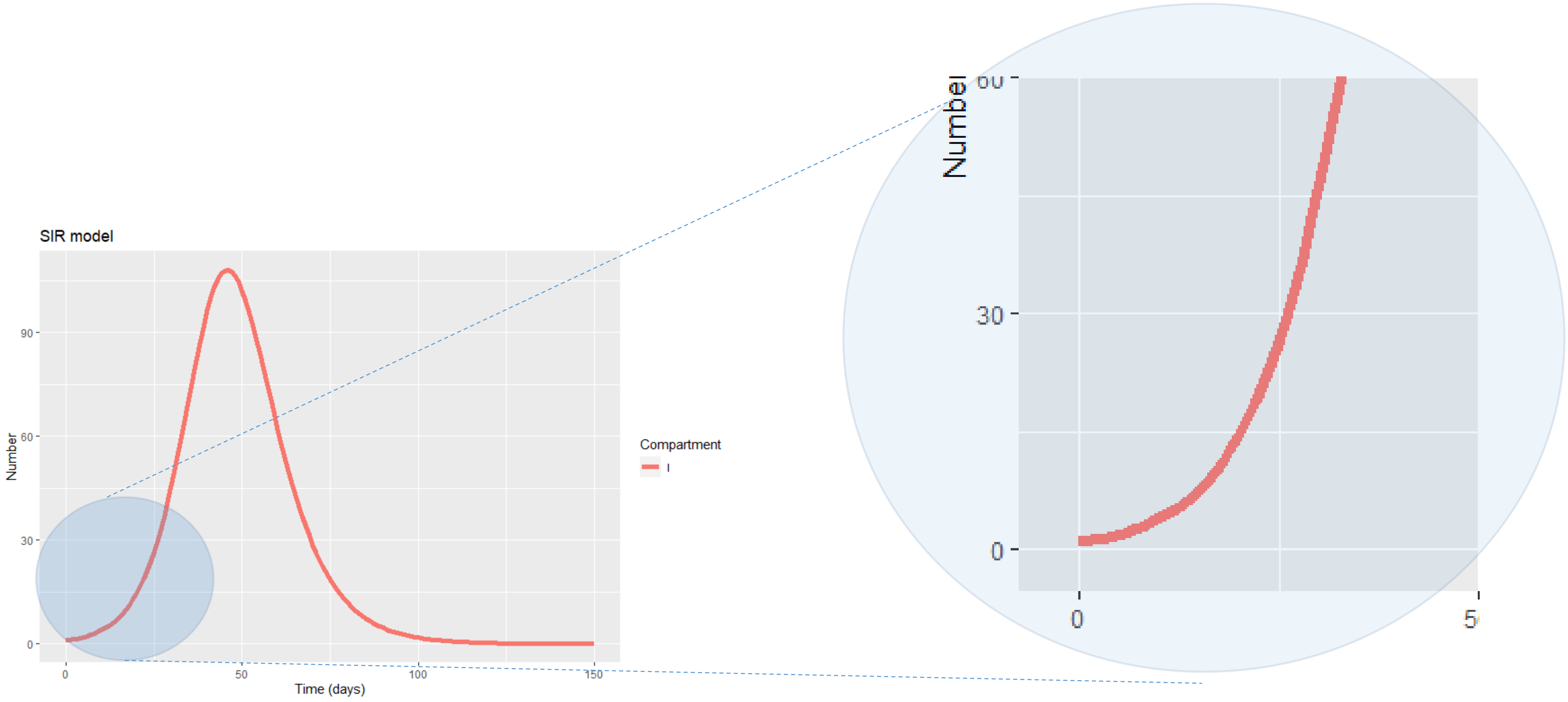
Average of 2 new
cases per infection

R_0 (basic reproduction number)

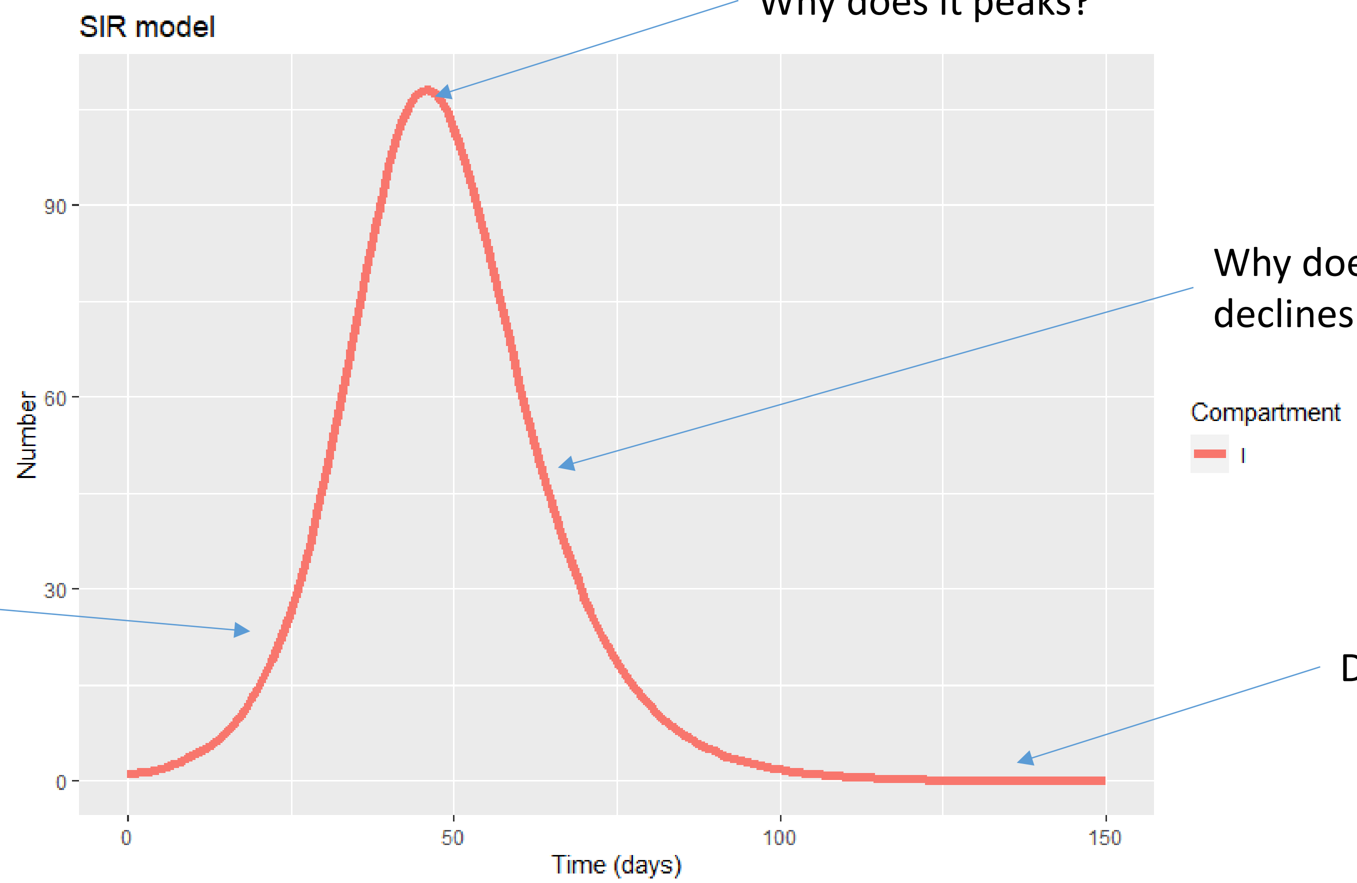
Average number of secondary infections caused by a single infectious case in a fully susceptible population

- If $R_0 > 1$, an epidemic start
- If $R_0 < 1$, an epidemic fails

Exponential growth of an epidemic



What are the phases?



Why does it peaks?

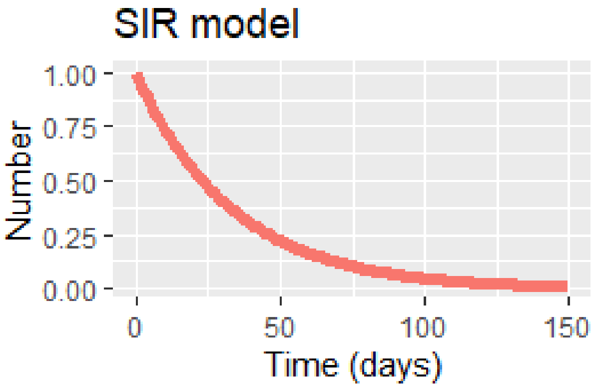
Why does it declines?

R0 > 1 means an epidemic grows exponentially

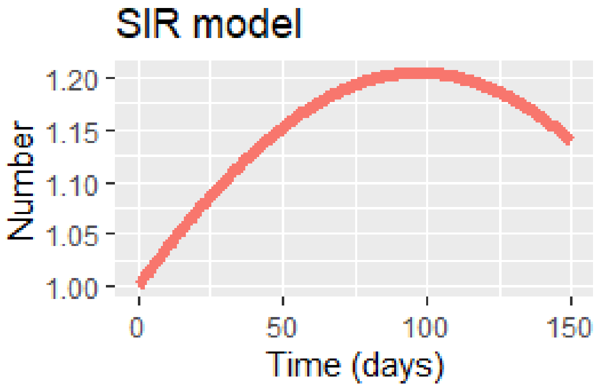
Does it reach zero?

Epidemic growth and R_0

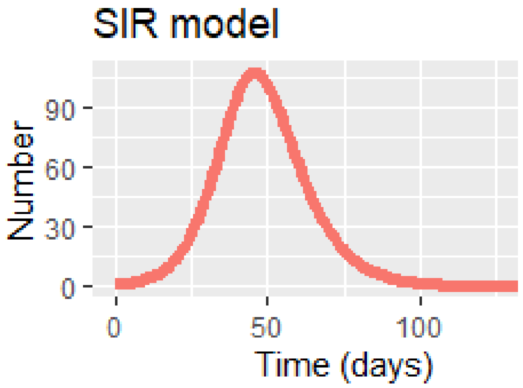
R0 = 1



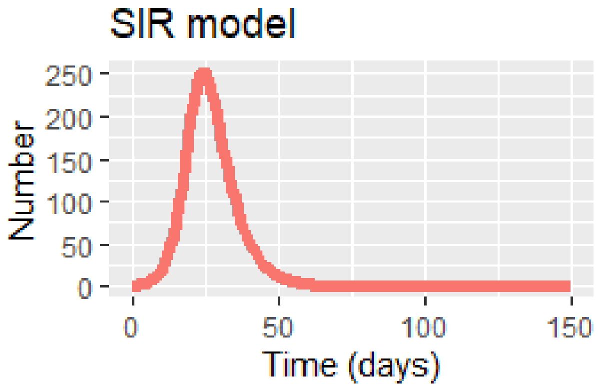
R0 = 1.2



R0 = 2

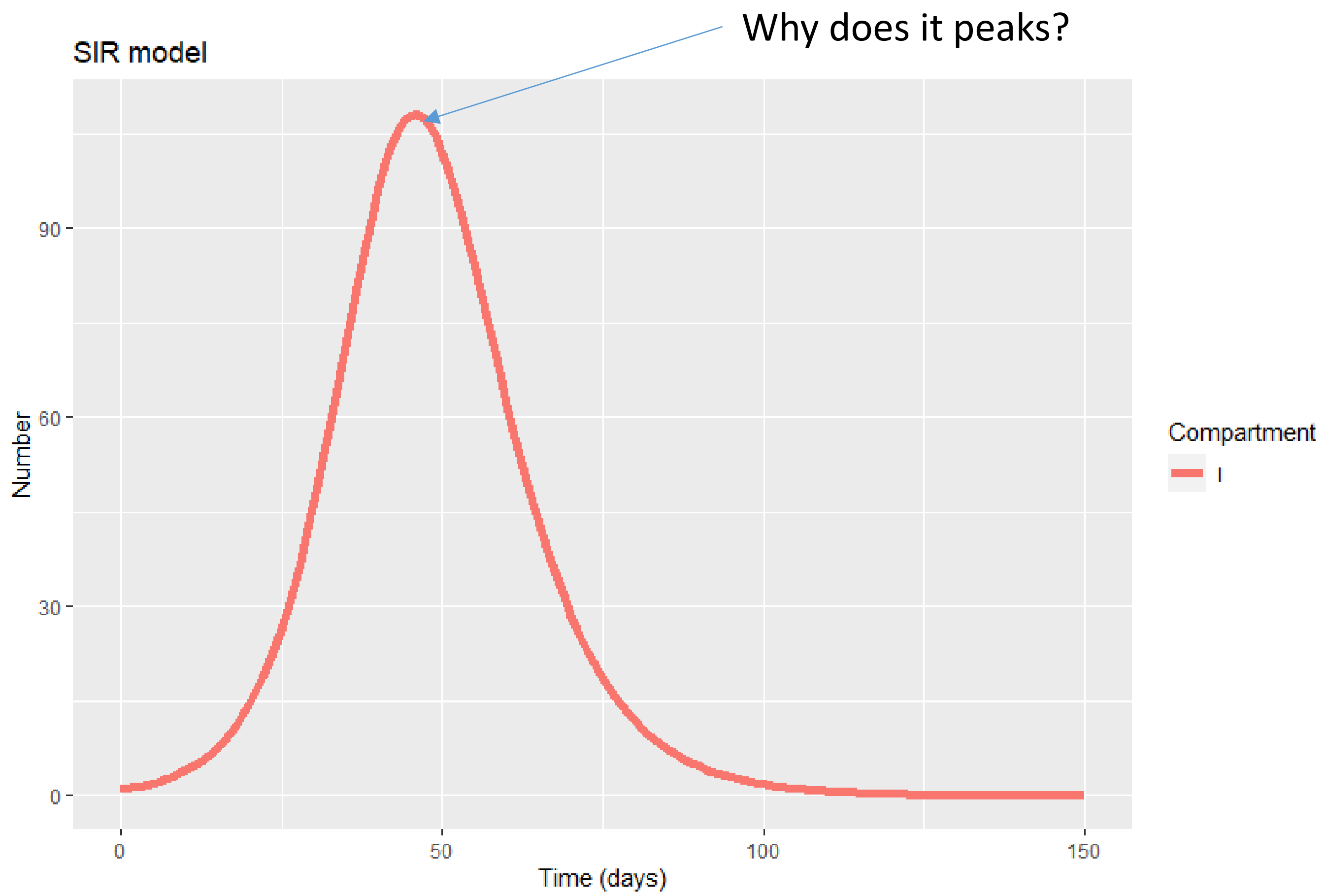


R0 = 3



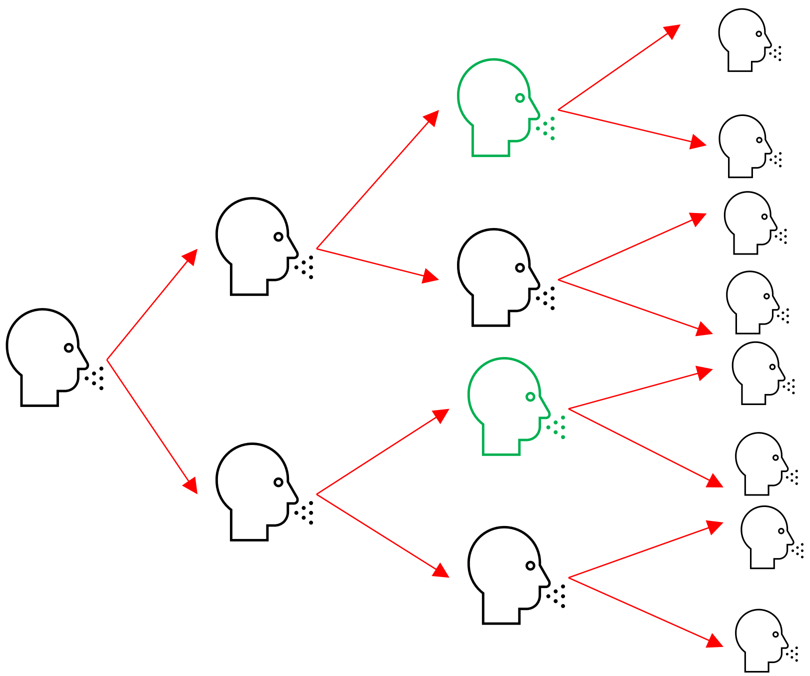
Behaviour of the number infected under different assumptions of R0 for an SIR model with a close population

Epidemic peak



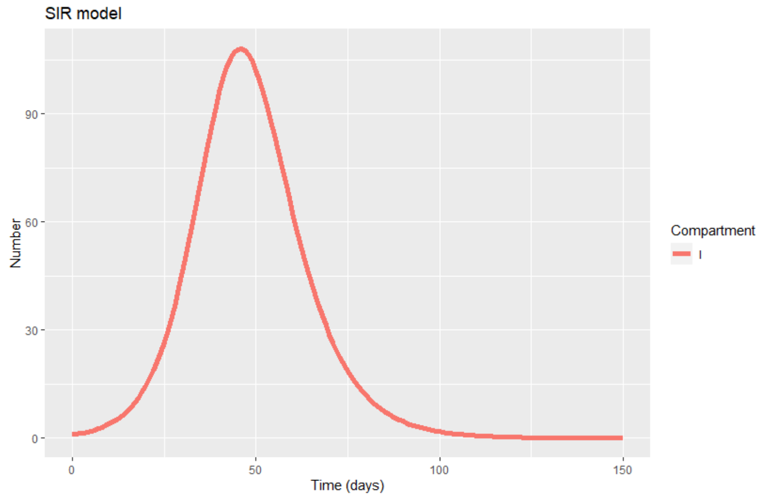
Epidemic peak

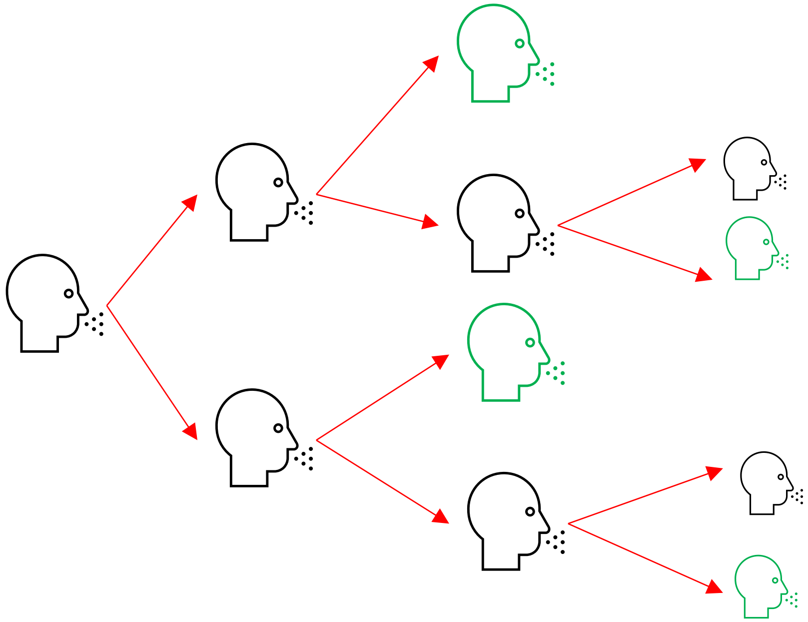
- We know that R0 plays a role in the epidemic rise.
- A second actor is immunity



Epidemic peak

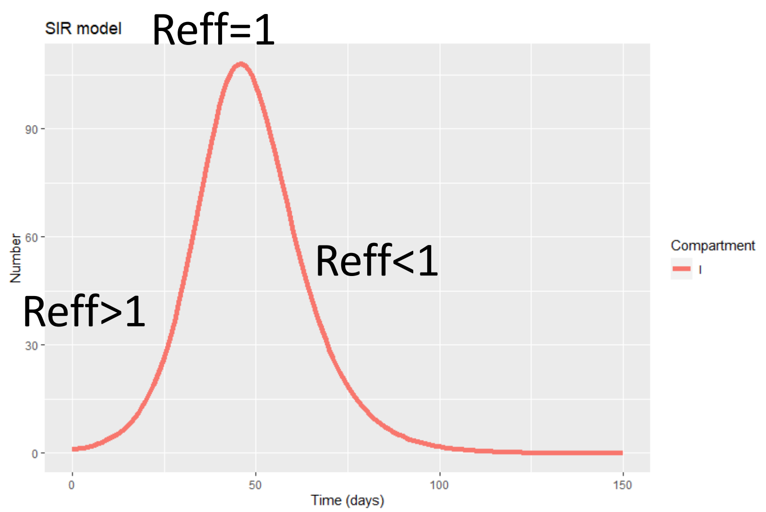
- We know that R0 plays a role in the epidemic rise.
- A second actor is immunity
- At the peak, the fraction susceptible in the population is insufficient to satisfy R0 for each infected case

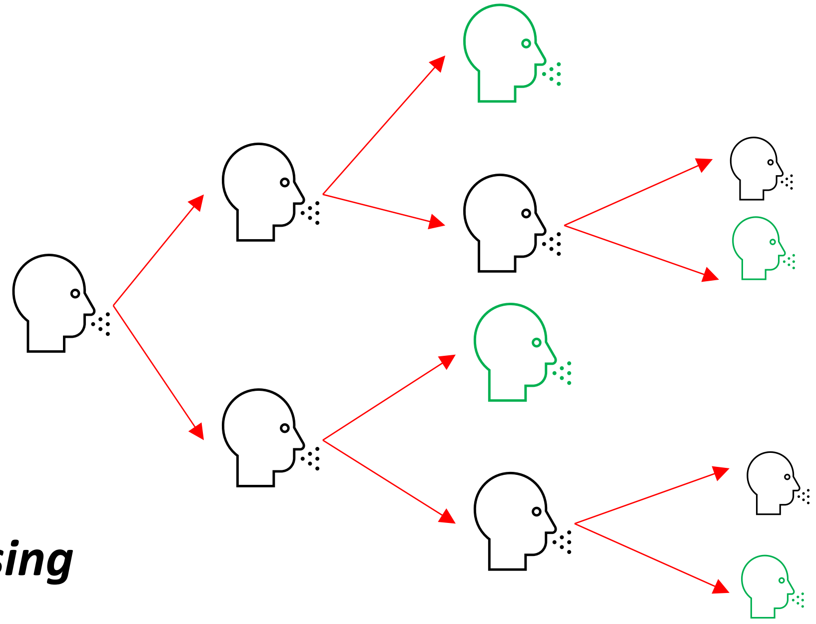




Epidemic peak

- R0 is defined for a fully susceptible population
- When immunity plays a role, we can define R_{eff}
- A depletion of Susceptible drives the epidemic down

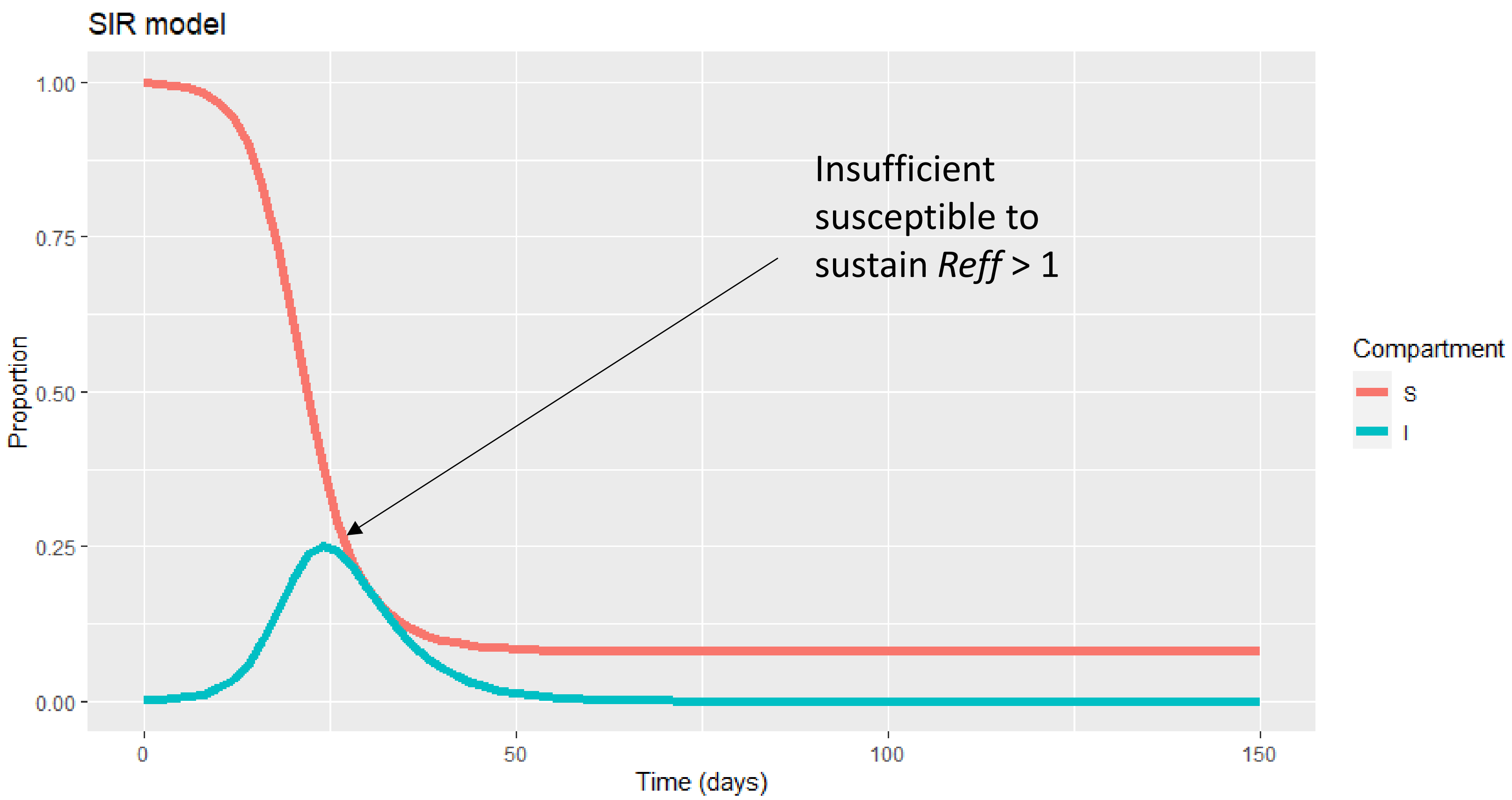




R_{eff} is the average number of secondary cases arising from an infected case at a given point in time

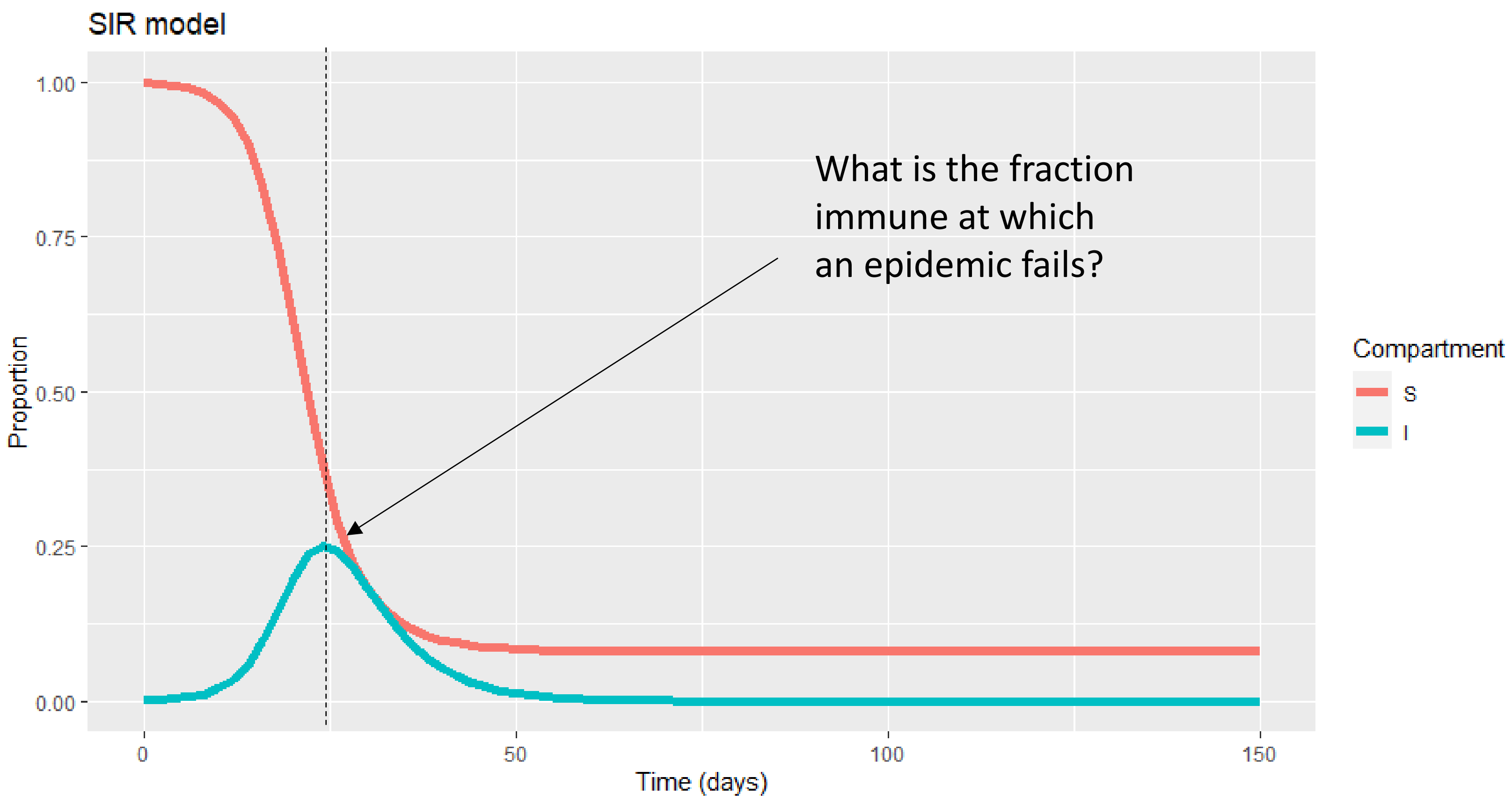
Epidemic peak

- Does everybody gets infected?
- No!

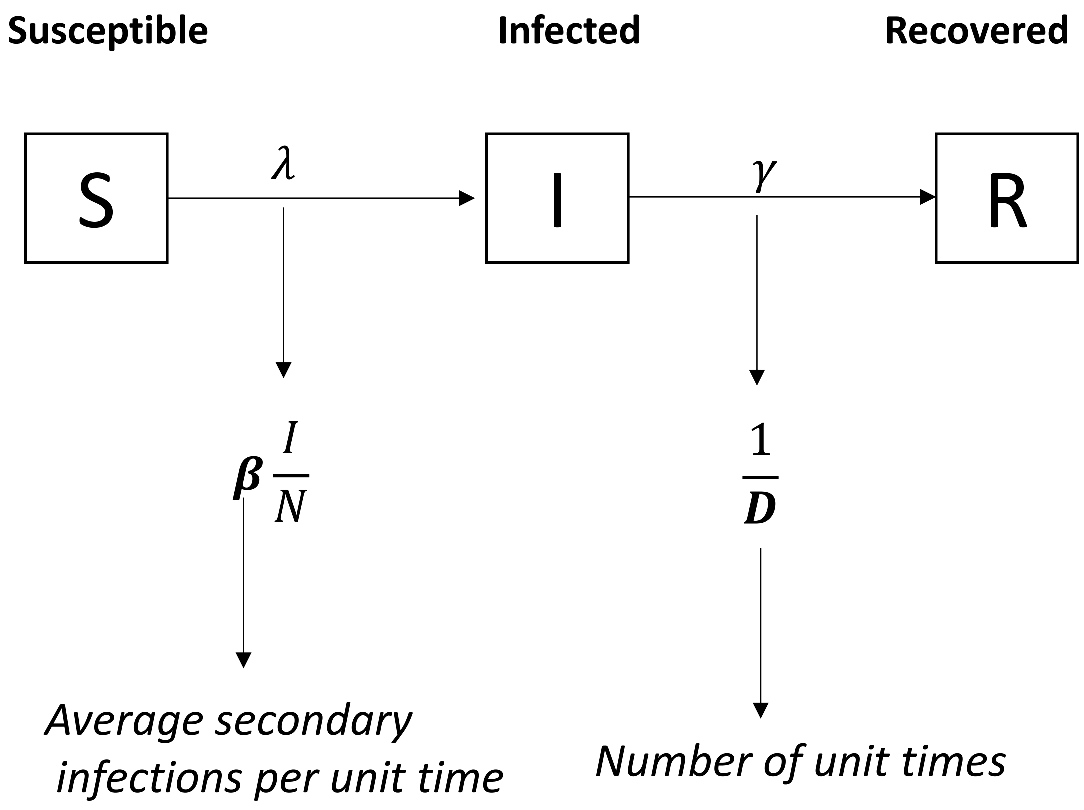


Herd immunity

- Reff =1
- Can be raised artificially with vaccination



How can this be explained in terms of SIR



At t=0

$$R_0 = \beta D = \beta \frac{1}{\gamma} = \frac{\beta}{\gamma}$$

Average number of secondary infections in the total duration of the infectious period

D= duration of infectious period

And R_{eff} ?

- If we said that the depletion of the susceptible compartment is what drives down an epidemic. Then R_{eff} is proportional to the fraction that remains susceptible at each time *t*

$$R_{eff} = R_0 \frac{S(t)}{N}$$

- Herd immunity
- Fraction immune necessary to bring epidemic down

$$R_{eff} = 1$$

$$R_0 \frac{S(t)}{N} = 1$$

$$\frac{S(t)}{N} = \frac{1}{R_0}$$

Fraction susceptible below which epidemic declines

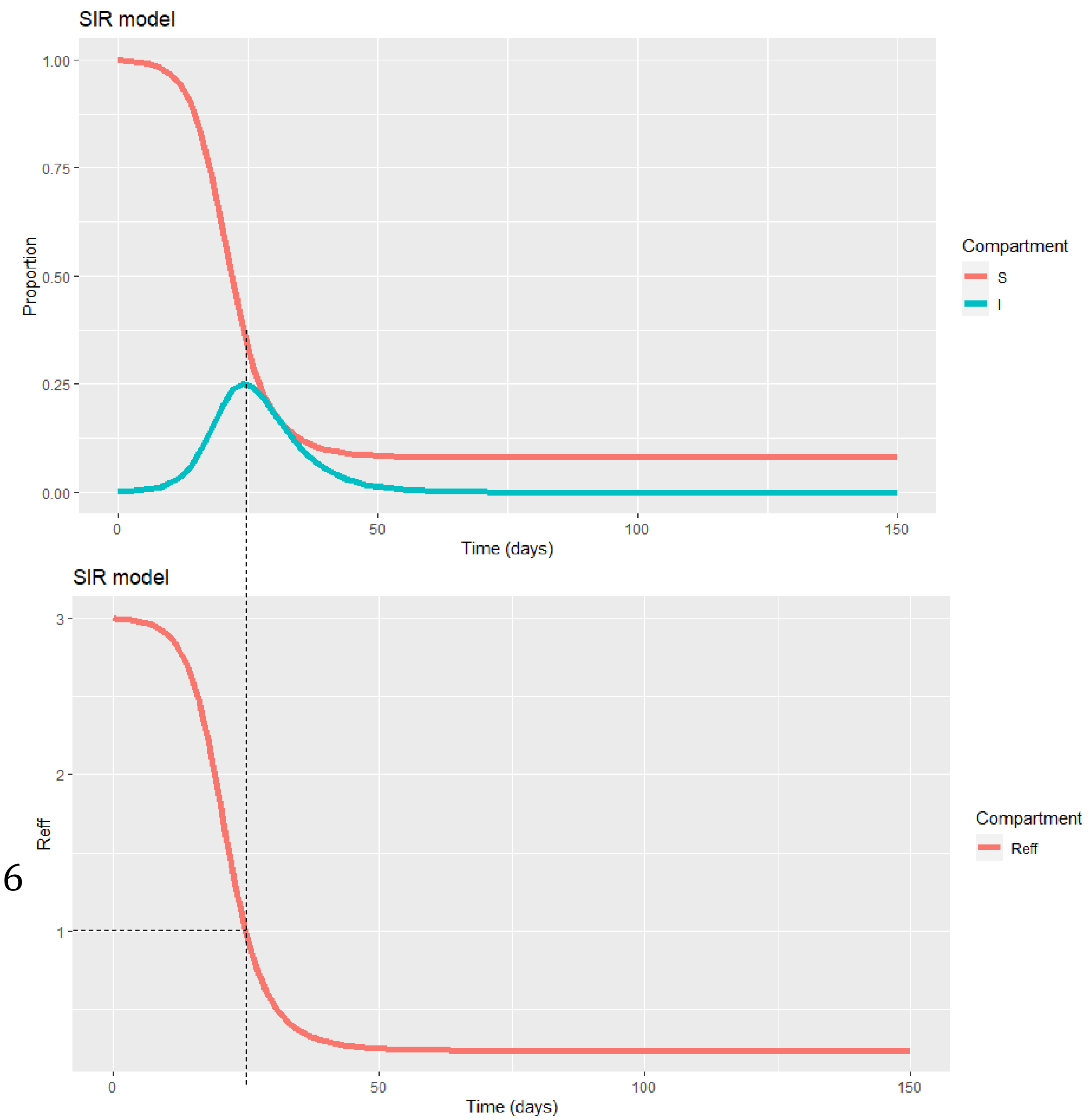
Example for R0=3

$$\frac{S(t)}{N} = \frac{1}{R_0}$$

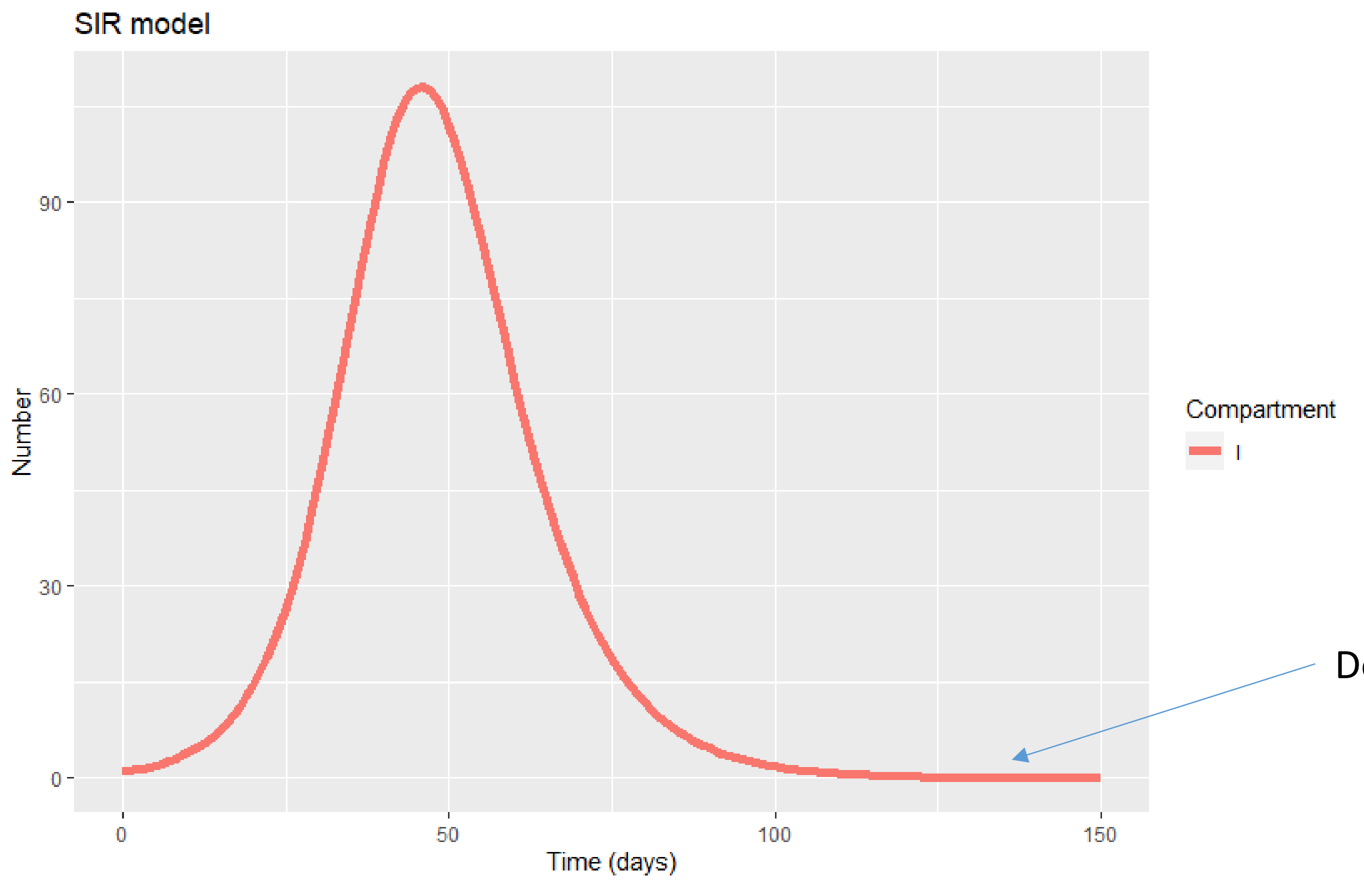
$$\frac{S(t)}{N} = \frac{1}{3} = 0.33$$

$$\boldsymbol{HIT} = 1 - 0.33 = 0.66$$

Herd immunity threshold

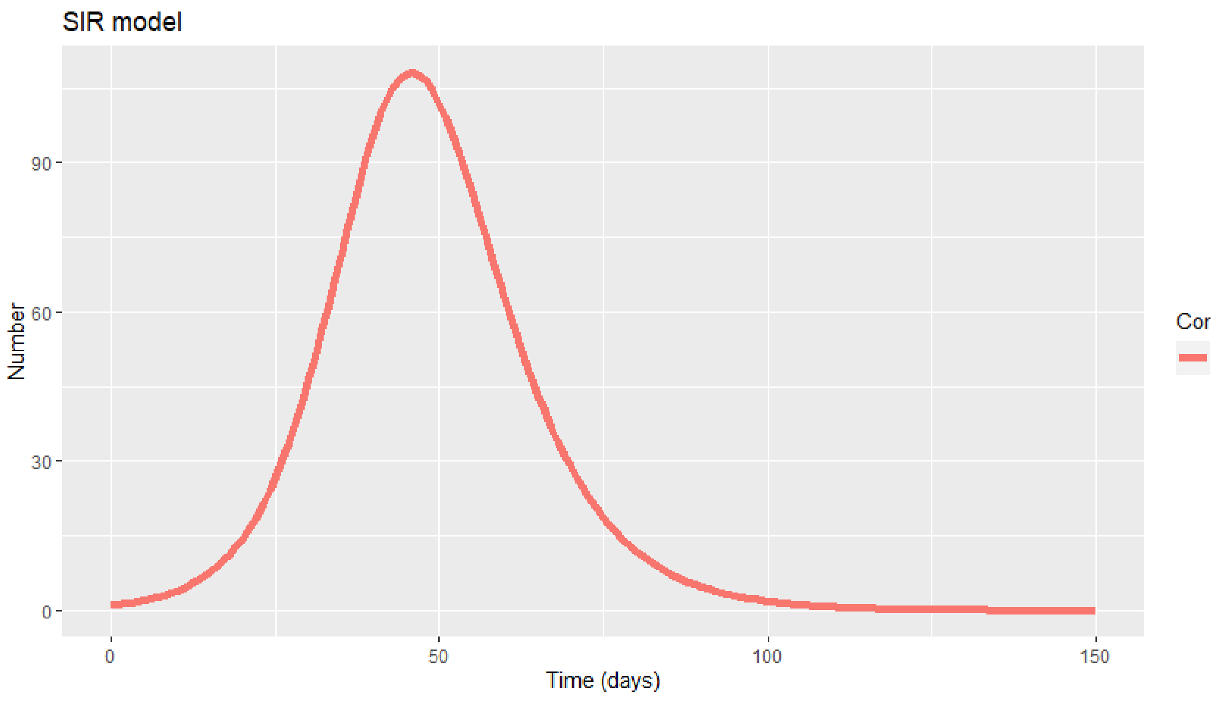


What if we have susceptible renewal?

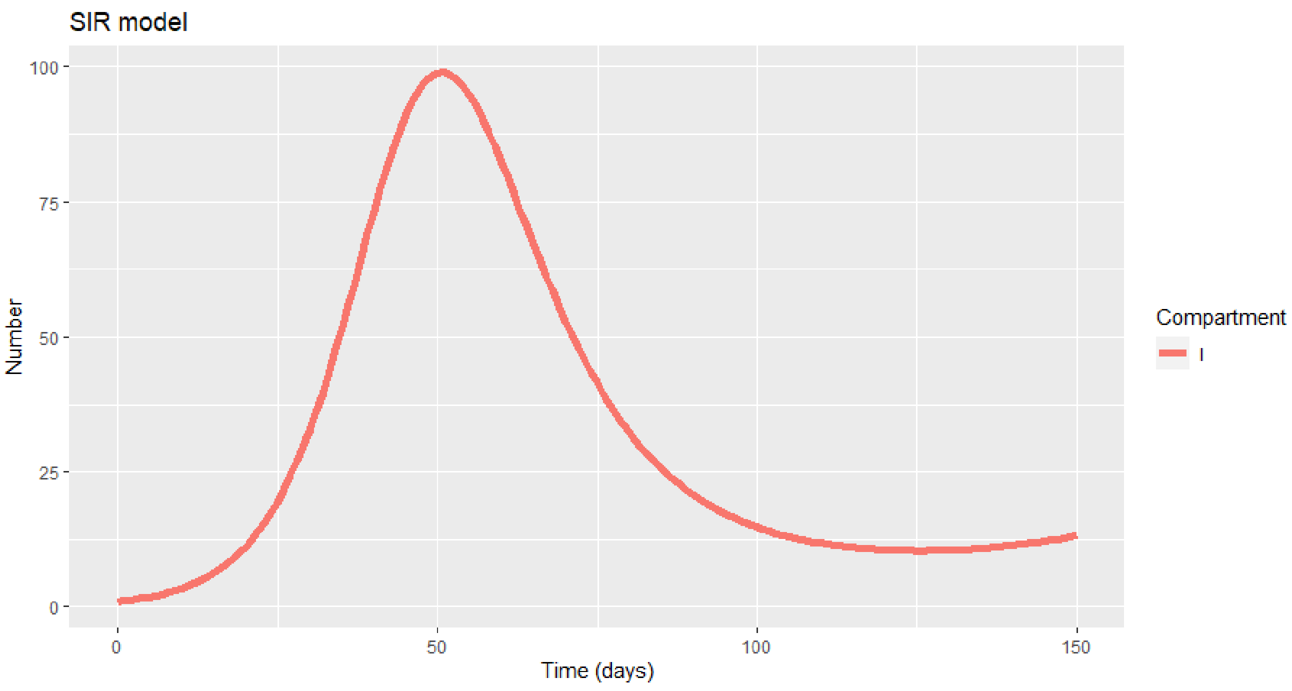


Does it reach zero?

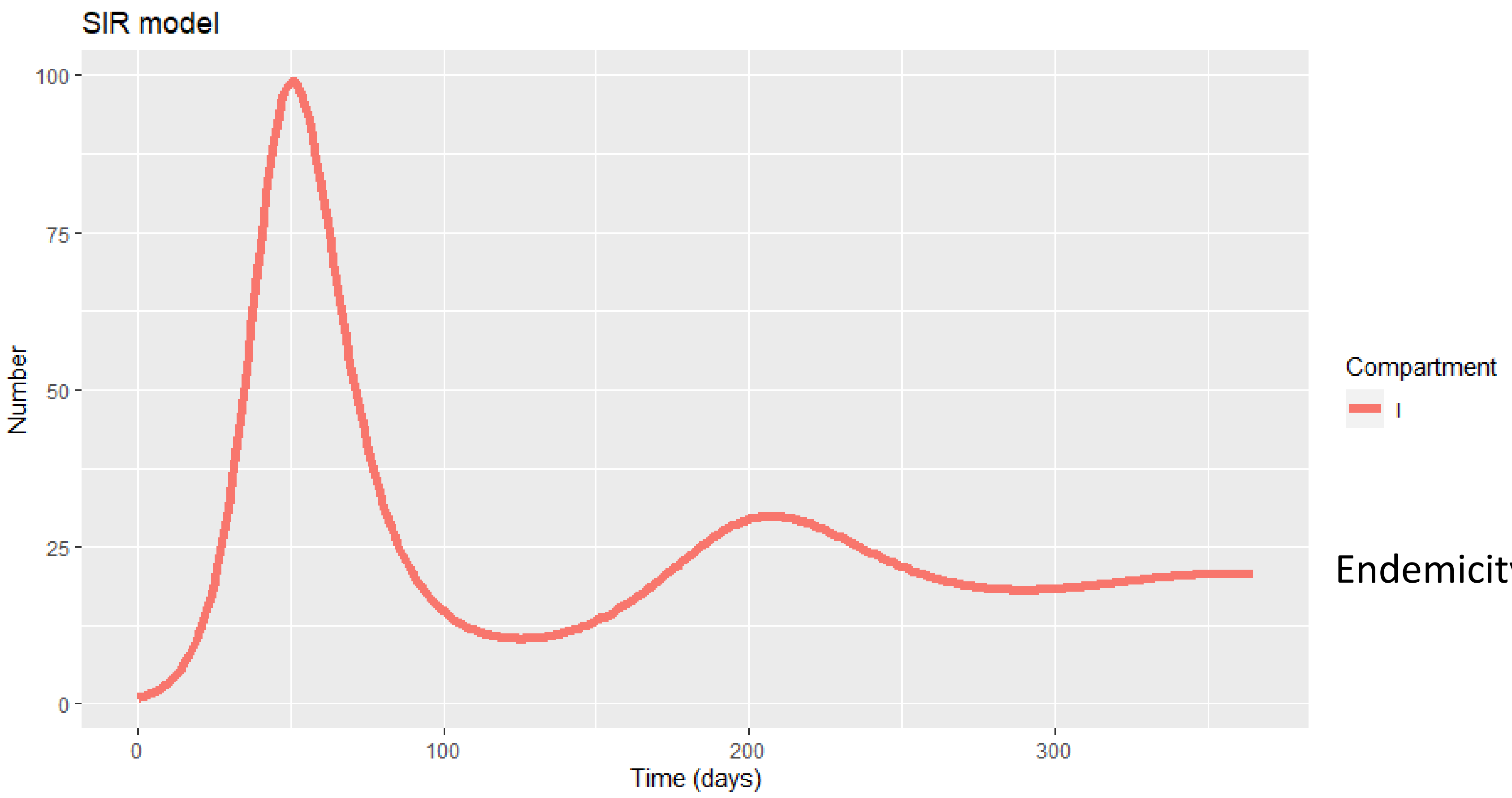
Close population



Susceptible
renewal (birth rate)



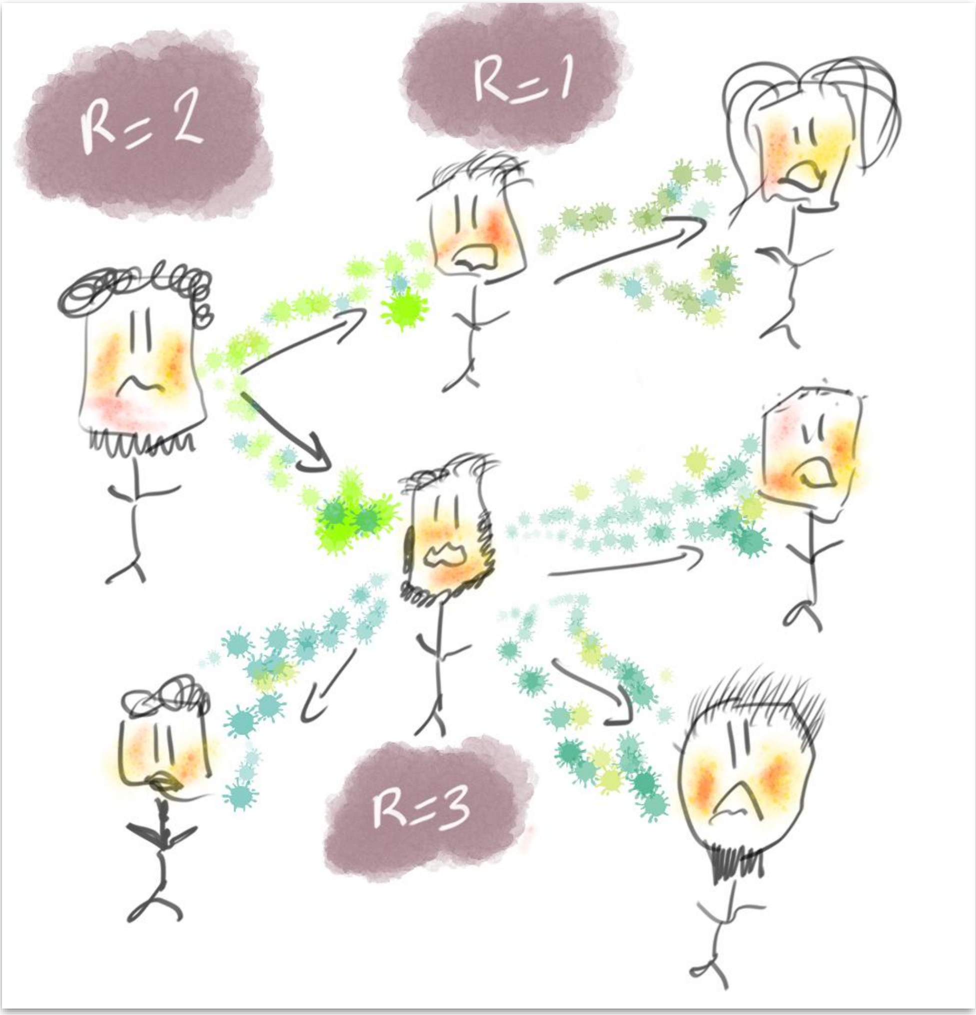
Long term dynamics



Endemicity

Some added complexity when understanding reproduction numbers

The reproduction number(s)

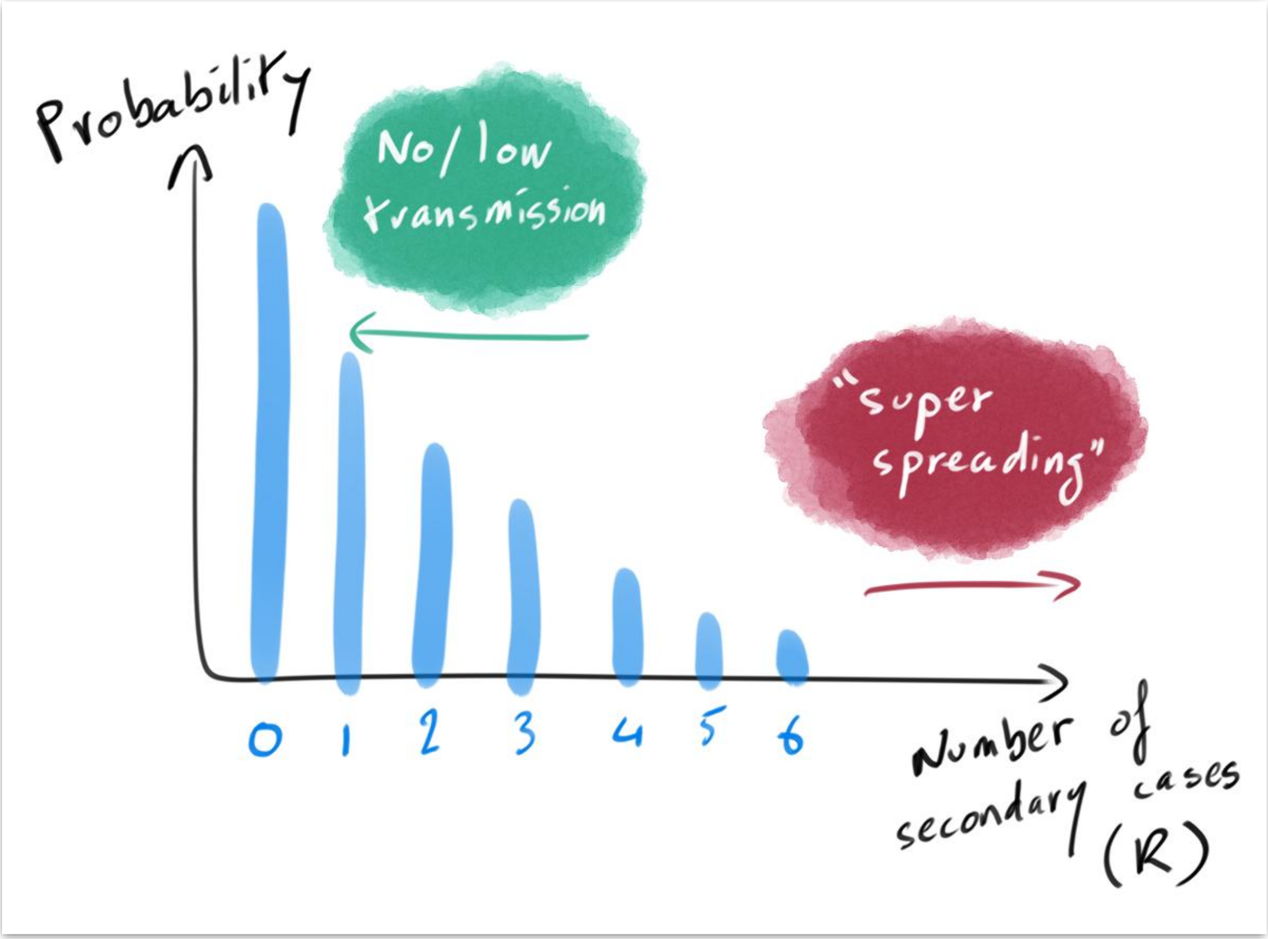


- Generalities
  - number of secondary cases by infected individual
  - R > 1 = exponential growth
  - R < 1 = exponential decline

- Basic reproduction number (R_0): R in a fully susceptible population
- Effective / case reproduction number (R_c): actually realised R
- Instantaneous reproduction number ($R_i(t)$): average R_c of infectors with symptoms at time t if transmissibility remains the same

With thanks to Thibaut Jombart

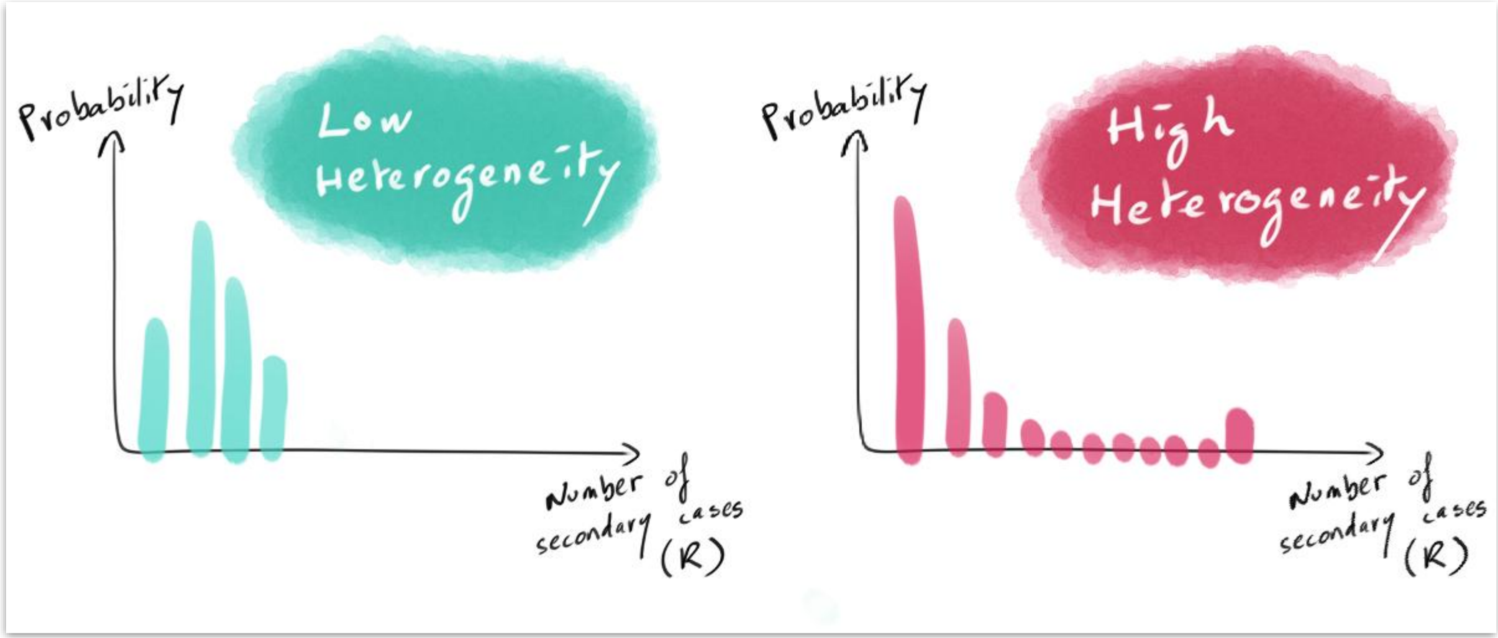
The offspring distribution



- Distribution of the number of secondary cases per infected case
- Its average is *R*
- Further indications of how transmission occurs:
  - Do all individuals transmit?
  - Are there super-spreading events?

With thanks to Thibaut Jombart

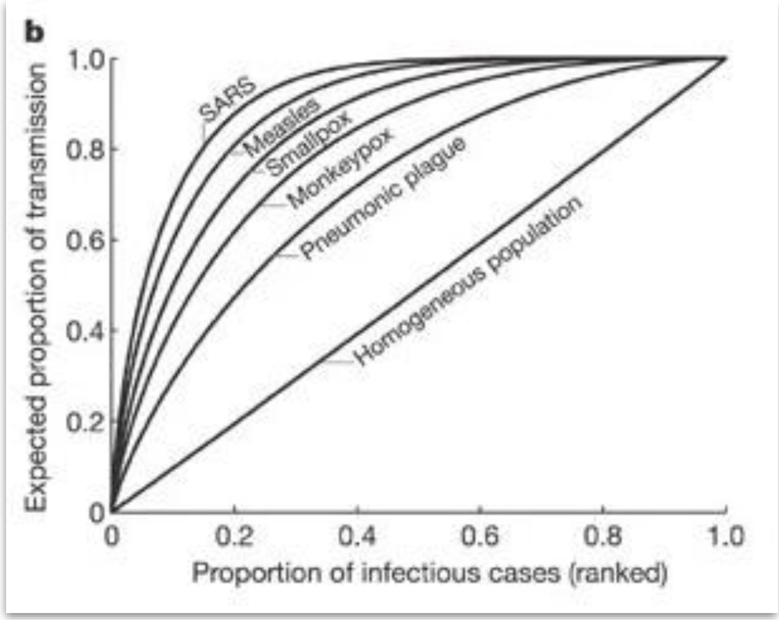
Heterogeneity in *R*

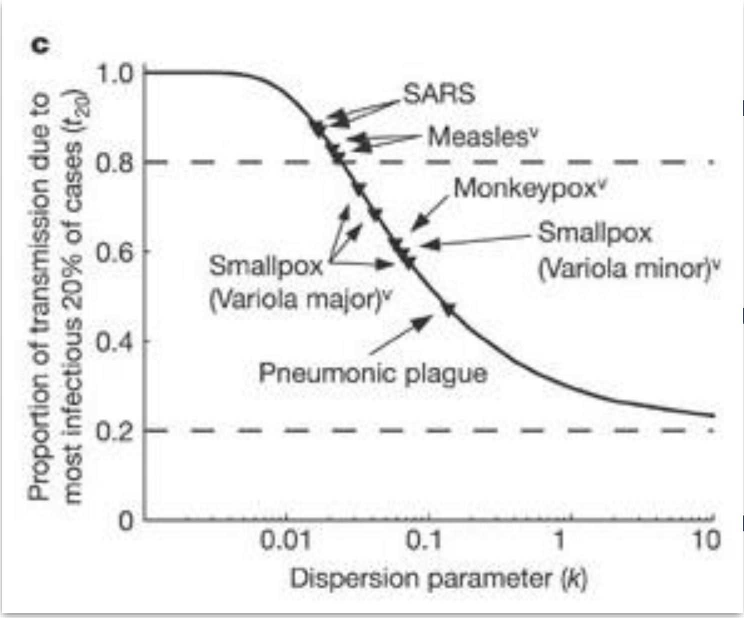


- Heterogeneity in *R* reflects differences in infectiousness between cases
- Higher heterogeneity
  - A smaller fraction of the population drives transmission
  - Presence of super-spreading events
  - Skewed offspring distribution

With thanks to Thibaut Jombart

Impact of heterogeneity in *R* for epidemic control





- Higher heterogeneity in *R*
  - Stochastic extinction more likely
  - Rarer, more 'explosive' outbreaks
  - Individual-based interventions better suited than population-wide
  - Targeted interventions require investigation of predictors of infectiousness
  - May need contact tracing, genetic data, etc. to reconstruct transmission chains

Source: [Lloyd-Smith *et al.* (2005)]

With thanks to Thibaut Jombart

What we should know by now

- Why epidemics rise
- What is R0 and Reff and how it relates to the SIR model
- What is herd immunity
- How we calculate HIT if we know R0
- How introducing demographics can change the picture of the long term dynamics
- In simple models we assess the population infectiousness, but in a real outbreak , estimation of R becomes more complex