Week 1: SIR Models

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University of Cambridge

Week 1 Overview

- ~~Monday, July 26:~~
  - ~~Introductory material, history of mathematical modeling~~
  - ~~Introduction to R~~
- ~~Tuesday, July 27:~~
  - ~~Epidemic determinants & parameters~~
  - ~~Guided practice in R~~
- Wednesday. July 28:
  - Model structures
  - Plots & compartmental models in R

Objectives

- Learn the structure and assumptions of a basic SIR model
- Understand how a graphic representation can be expressed mathematically

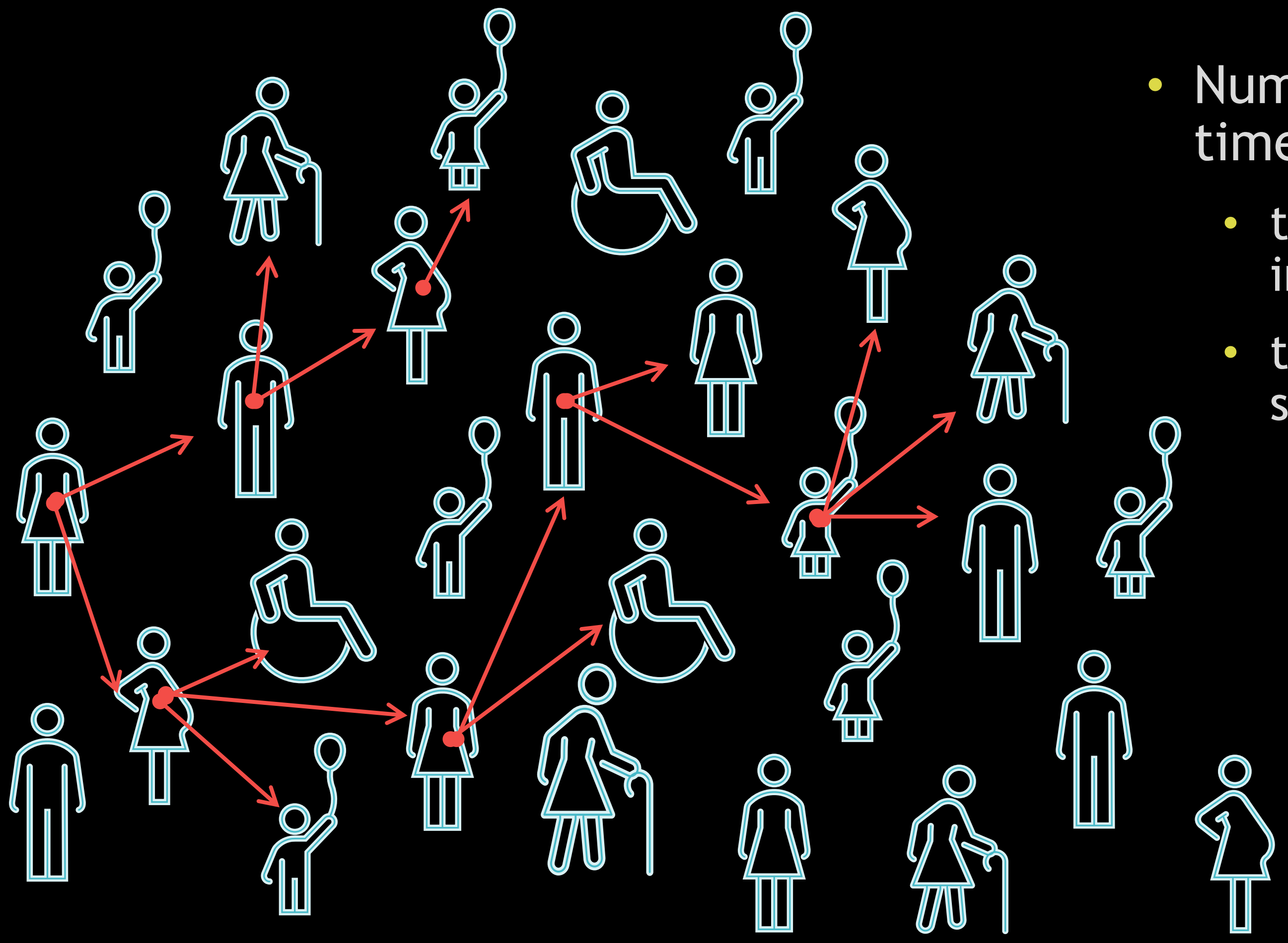
Post Questions in the Chat!

(we will have breaks to answer these during the workshop)

Workshop Schedule

Time	Topics
2:00—2:10 pm	~~Greetings~~
2:10—3:00 pm	SIR Model & Differential Equations
3:00—3:10 pm	Break
3:10—3:30 pm	SIR Model & Time Steps
3:30—3:40 pm	Break
3:40—5:00 pm	R Session

Core Concept



- Number of new infections per unit time is a function of:
  - the number of people who are infectious in a population
  - the number of people who are susceptible

SIR Model

- We want to build a model of transmission (scenario) for a completely immunizing infection
- We are going to develop a mechanistic (compartmental) model where individuals can be classified as:
  - susceptible
  - infected
  - recovered

SIR Model

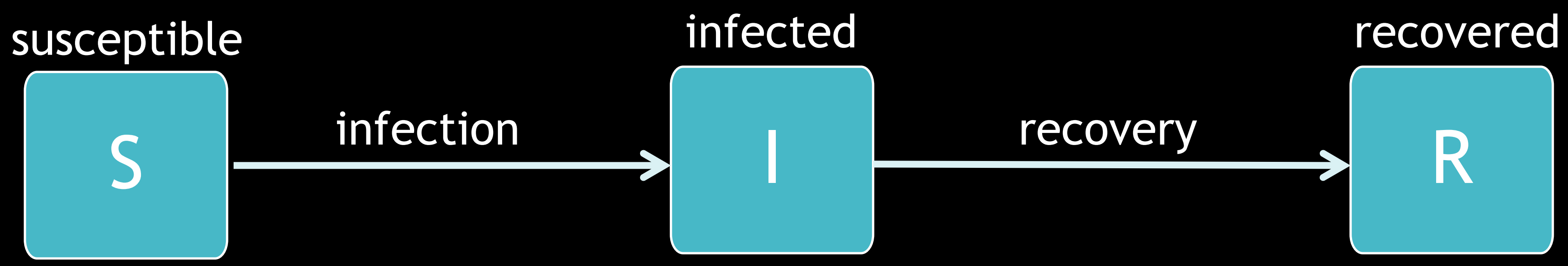
- Compartmental/mechanistic models
    1. Populations are divided into compartments
    2. Compartments and transition rates are determined by biological systems
    3. Transition rates between compartments are expressed mathematically

SIR Model

- What are the major assumptions?

SIR Model

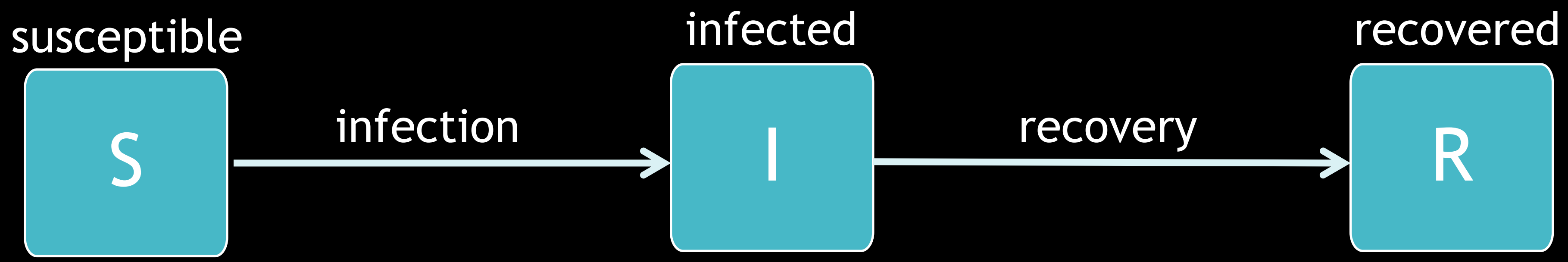
- Everyone is either:



- Population size is constant
  - no births
  - no deaths
  - no migrations

SIR Model

- Everyone is either:



- Recovery is permanent

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SIR Model

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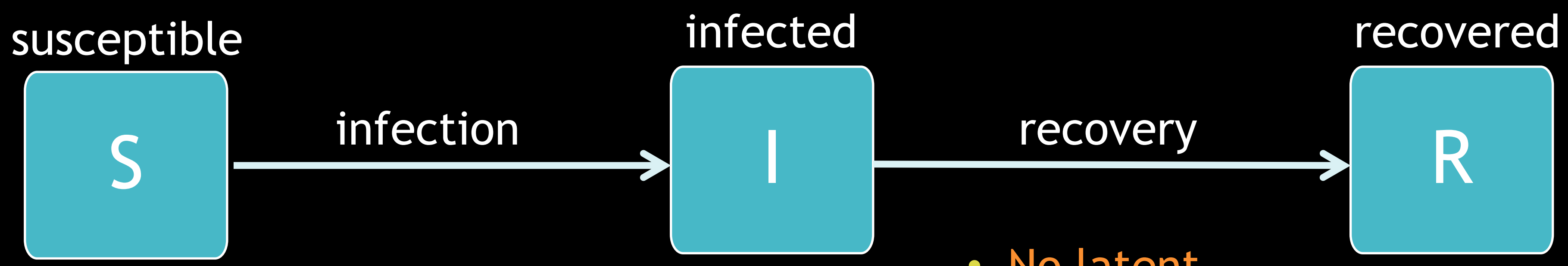

- Recovery is permanent
- No latent period
  - if you are infected, you are infectious
- Population size is constant
  - no births
  - no deaths
  - no migrations

SIR Model

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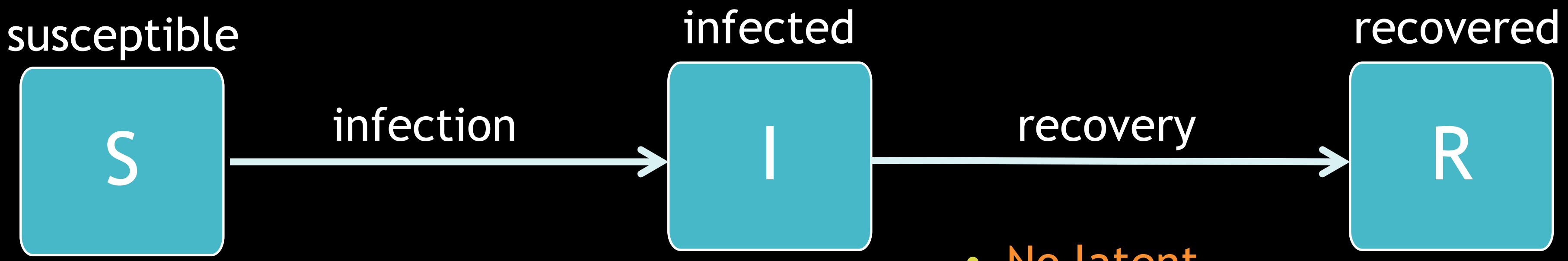

- Recovery is permanent

- No latent period
  - if you are infected, you are infectious

- Population size is constant
  - no births
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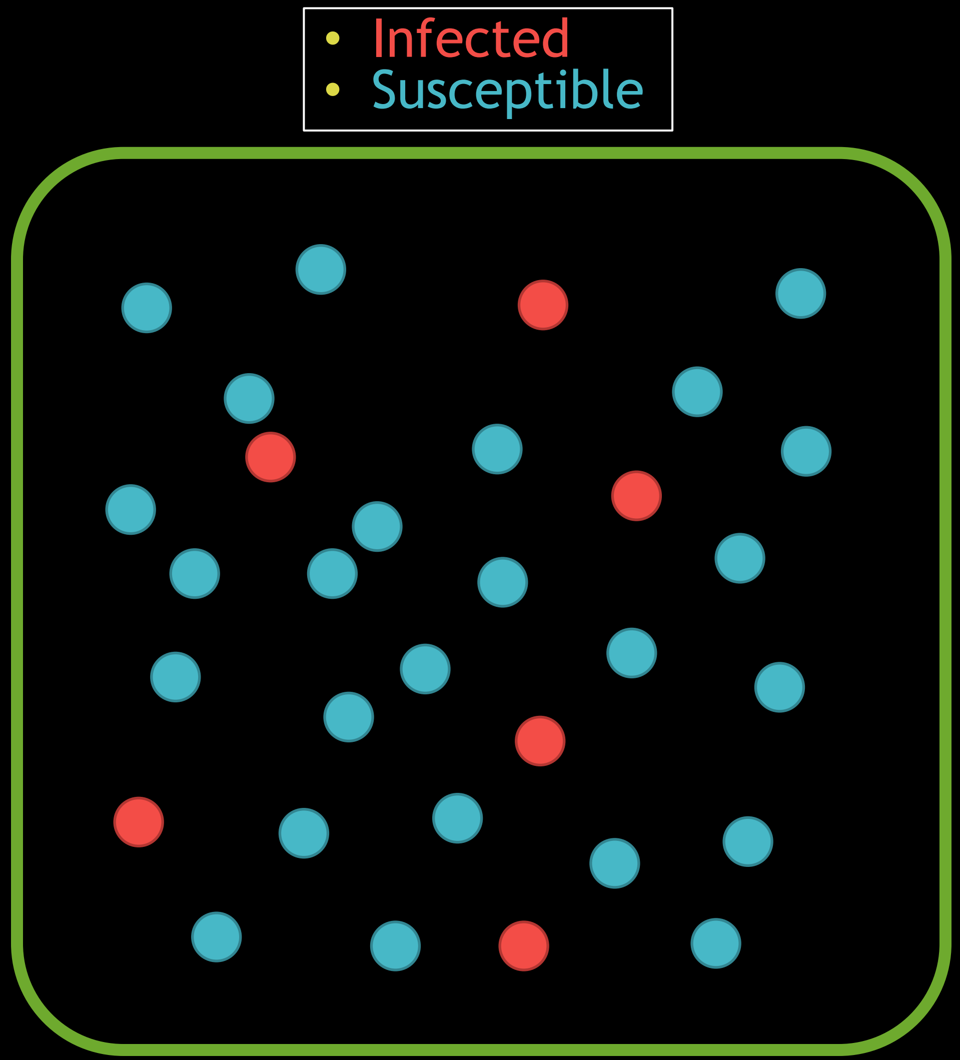
  - no migrations

- People mix uniformly
  - homogeneous mixing
  - random mixing
  - mass action

Law of Mass Action

- The rate at which individuals of two types contact one another in a population is proportional to the product of their densities



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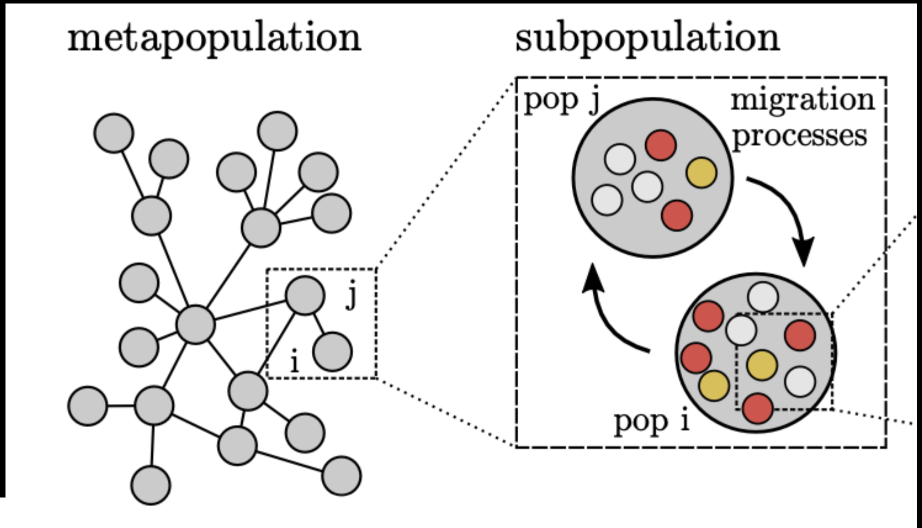
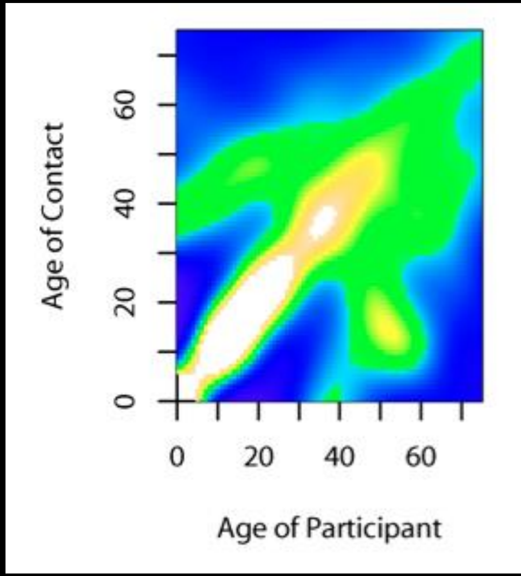


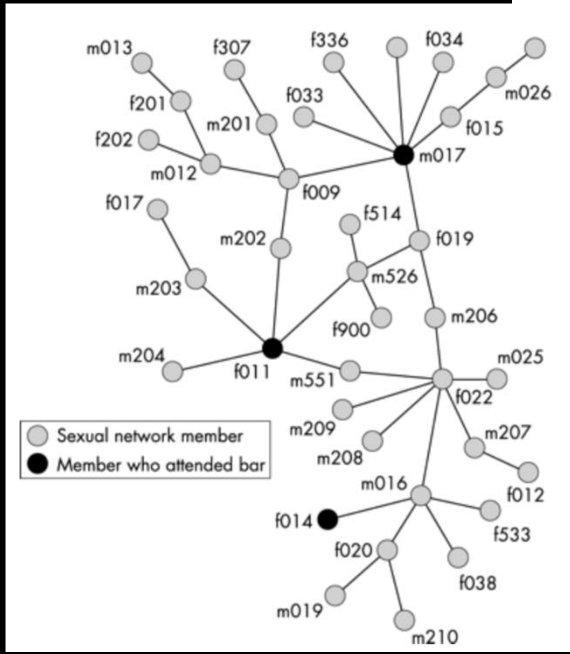
Hackl, et al (2019)

Metapopulations (spatial)



Mossong, et al. (2008)

Age Mixing

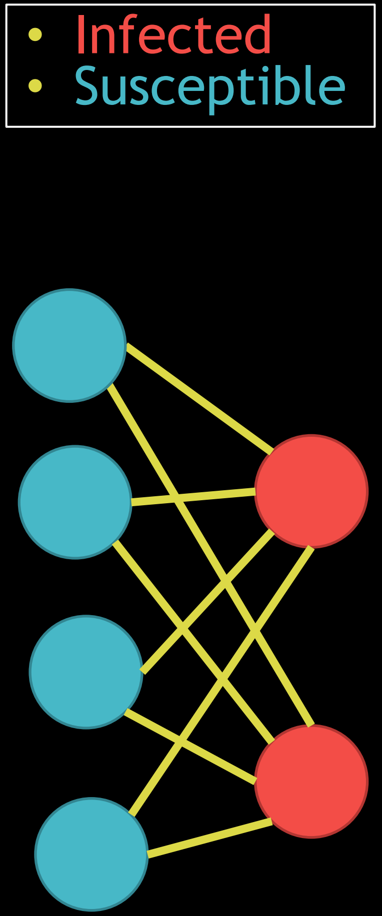


De, et al. (2004)

Network Contacts

Law of Mass Action

- Random mixing
- S x I is the number of unique contacts between the susceptible and infectious individuals
  - 2 infected
  - 4 susceptible
  - 8 unique contacts



$$\beta SI$$

Law of Mass Action

- Random mixing
- S x I is the number of unique contacts between the susceptible and infectious individuals
  - 2 infected
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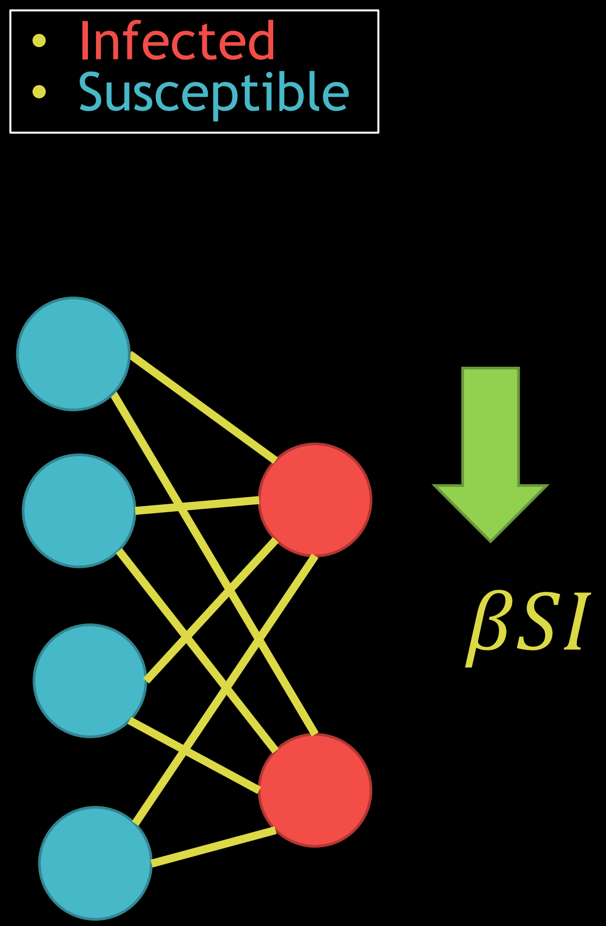
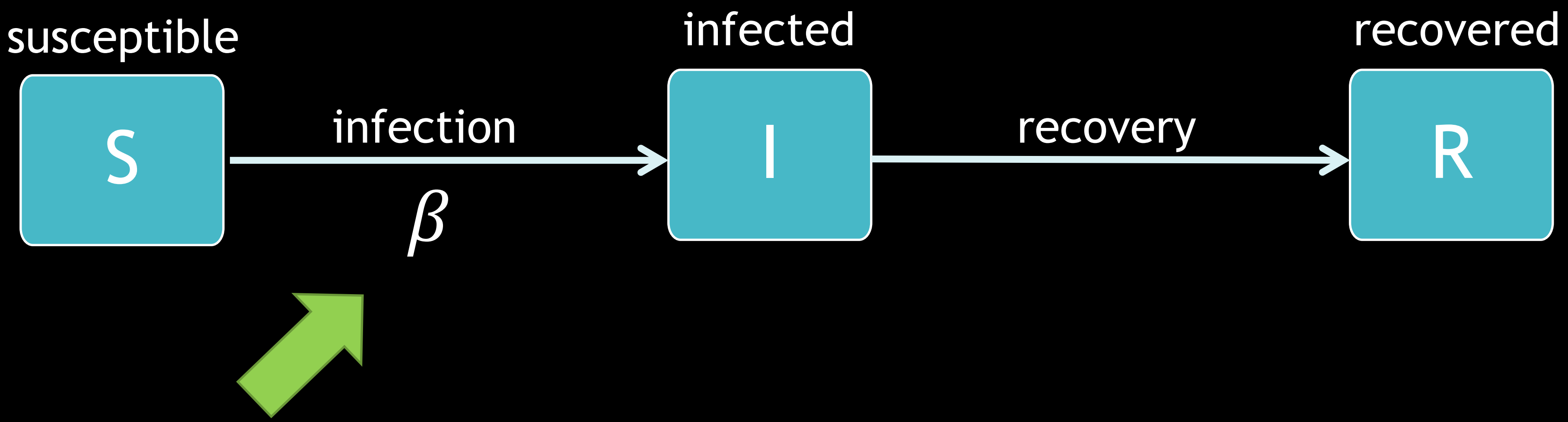
  - 8 unique contacts
- ß is a transmission coefficient
  - it is the probability of a susceptible becoming infected if they contact an infected person



SIR Model: Kermack & McKendrick



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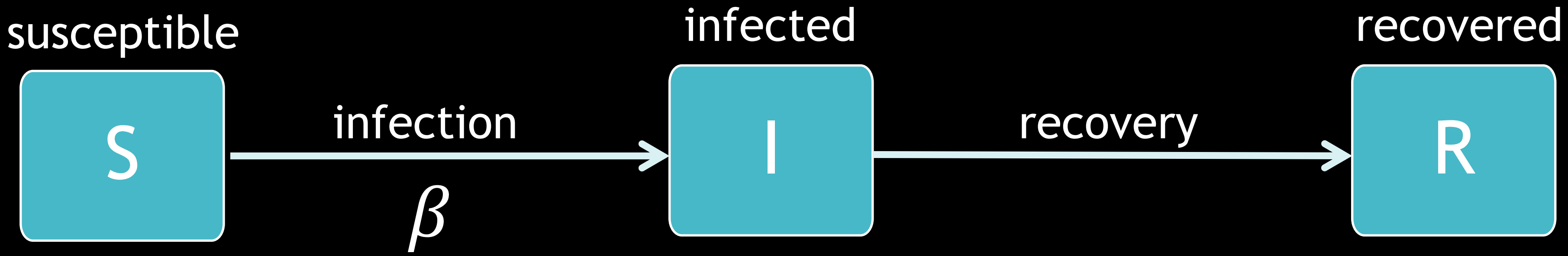
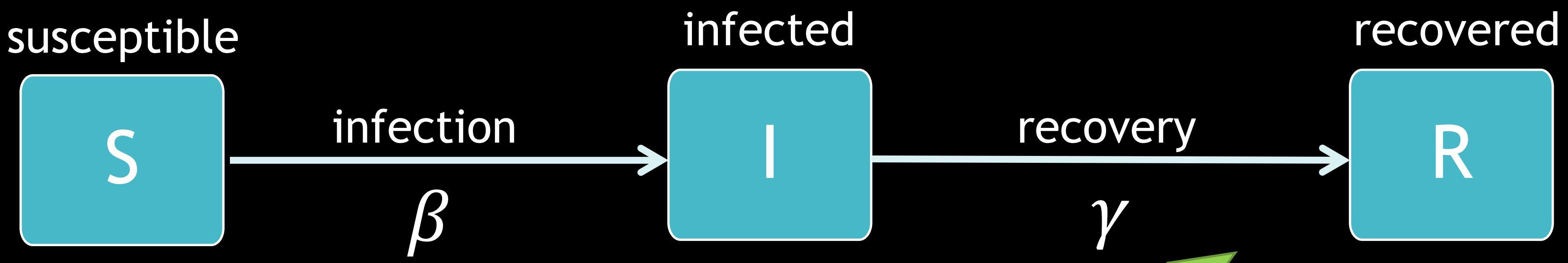


$$\frac{dS(t)}{dt} = -\beta S(t) I(t)$$

SIR Model: Kermack & McKendrick

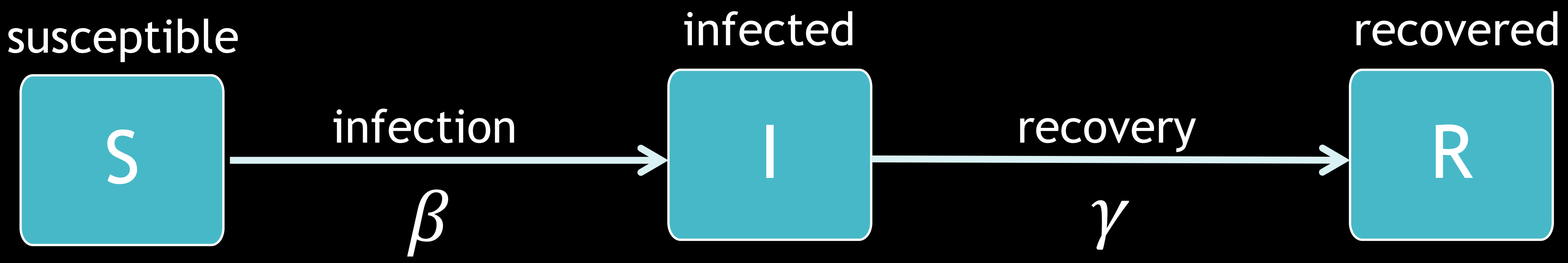


$$\frac{dS(t)}{dt} = -\beta S(t)I(t)$$

$$\frac{dI(t)}{dt} = \beta S(t)I(t) - \gamma I(t)$$

$$\frac{dR(t)}{dt} = \gamma I(t)$$

SIR Model: Kermack & McKendrick



- β is a transmission coefficient
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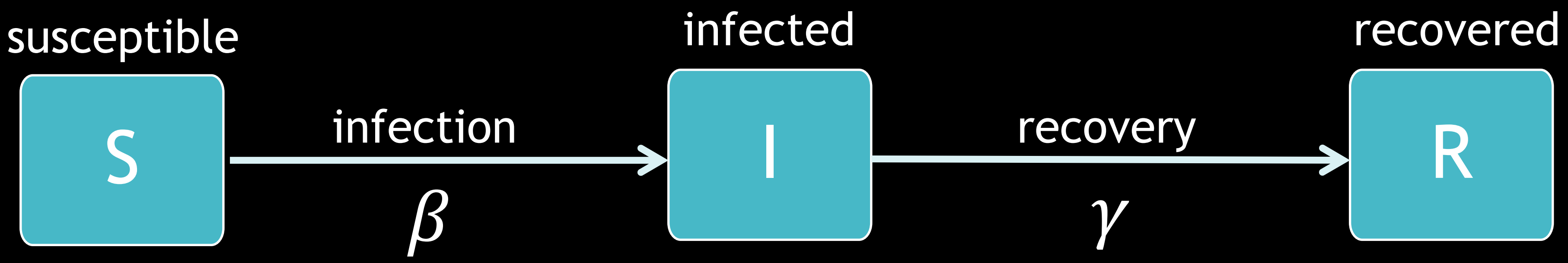
$$\frac{dR(t)}{dt} = \gamma I(t)$$

- γ is the recovery rate
  - 1/ γ is the duration of infectiousness

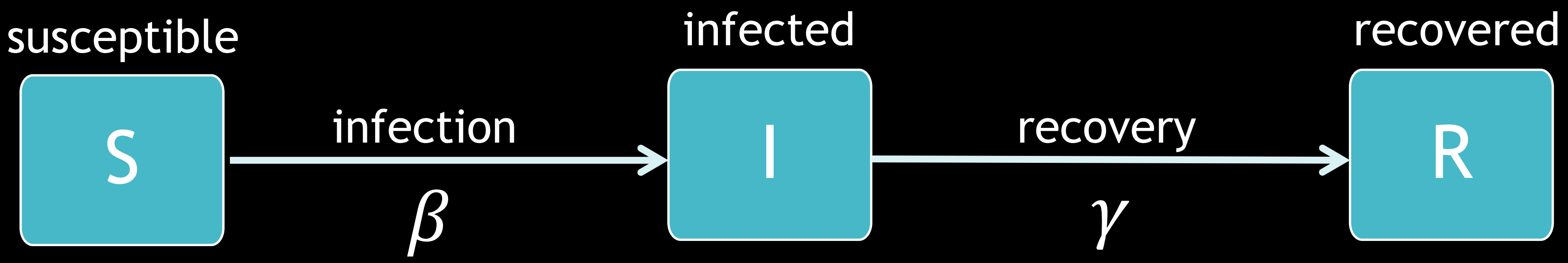
SIR Model: Kermack & McKendrick



- system of ordinary differential equations
  - ODE
  - mathematical expression of transition rates between compartments

$$
\begin{cases}
\dfrac{dS(t)}{dt} = -\beta S(t) I(t) \\[2ex]
\dfrac{dI(t)}{dt} = \beta S(t) I(t) - \gamma I(t) \\[2ex]
\dfrac{dR(t)}{dt} = \gamma I(t)
\end{cases}
$$

SIR Model: Kermack & McKendrick



- system of ordinary differential equations
    - multiply compartments by transition rates to express change

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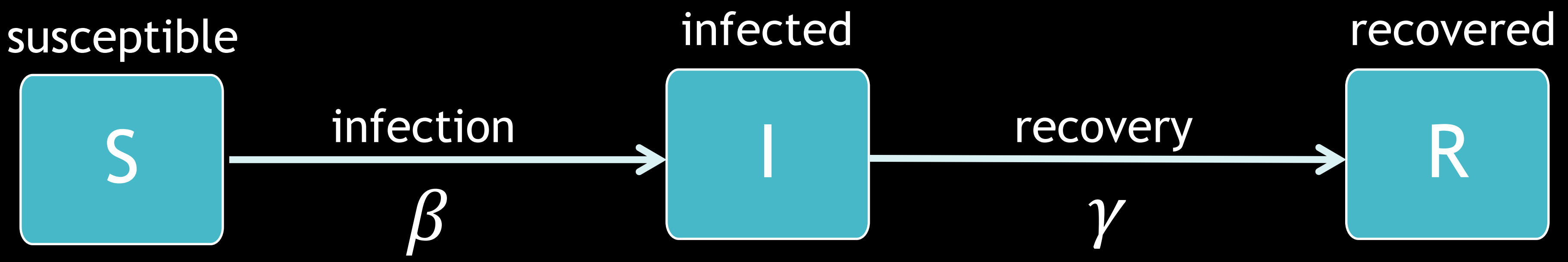


- rate of change in number of **susceptible** individuals at time t

$$\frac{dS(t)}{dt} = -\beta S(t) I(t)$$

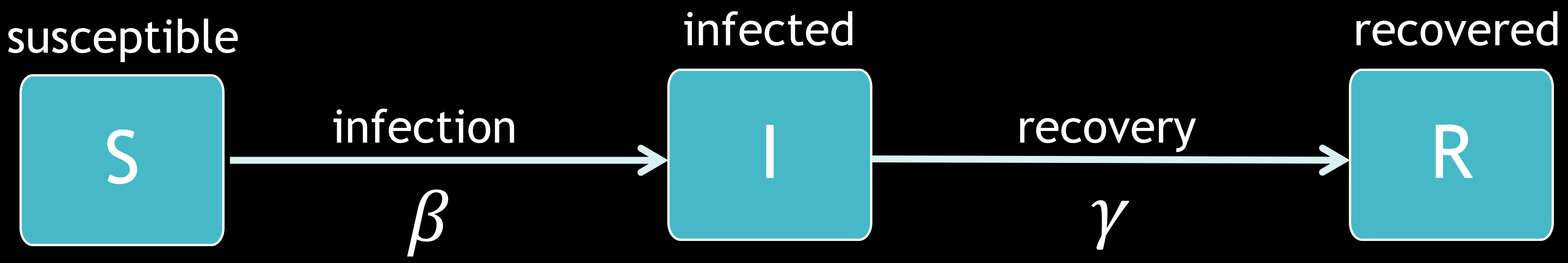
- rate of change in number of **infected** individuals at time t

$$\frac{dI(t)}{dt} = \beta S(t) I(t) - \gamma I(t)$$

- rate of change in number of **recovered** individuals at time t

$$\frac{dR(t)}{dt} = \gamma I(t)$$

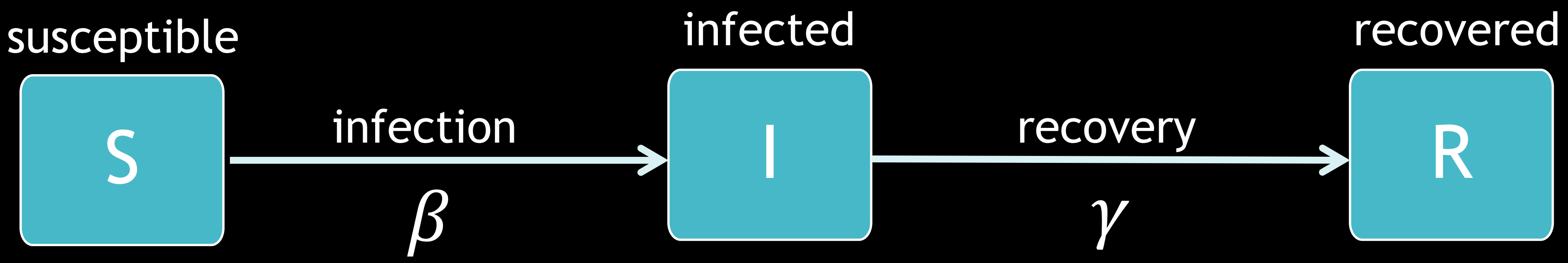
SIR Model: Kermack & McKendrick



- How do we calculate the rate of change for a compartment?
- For each compartment:
  - \+ number of individuals entering per unit time
  - \- number of individuals leaving per unit time

$$\frac{dS(t)}{dt} = -\beta S(t) I(t)$$

SIR Model: Kermack & McKendrick



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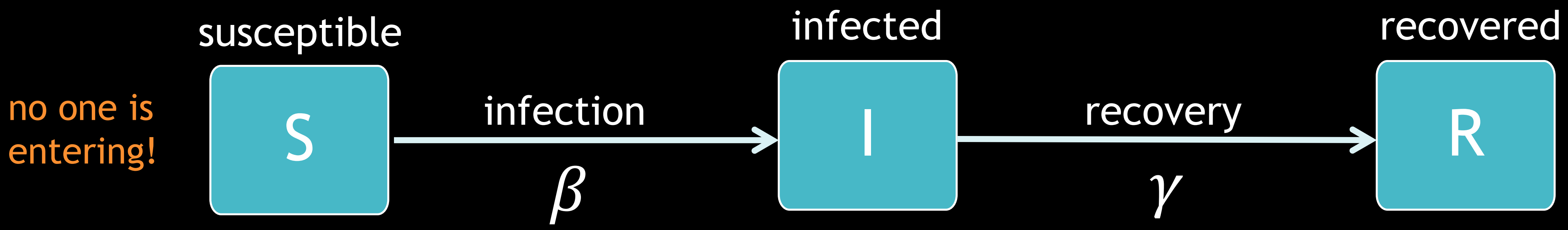
rate of change

SIR Model: Kermack & McKendrick



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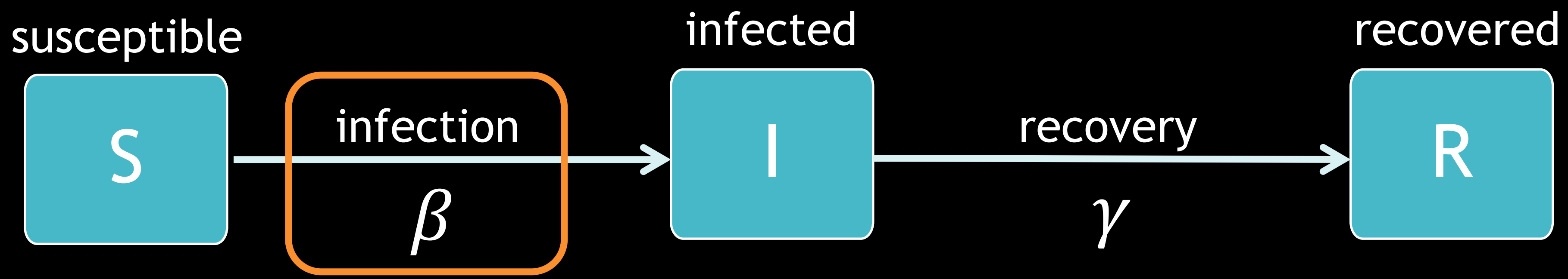
rate of change

no one to add

SIR Model: Kermack & McKendrick

no one is entering!



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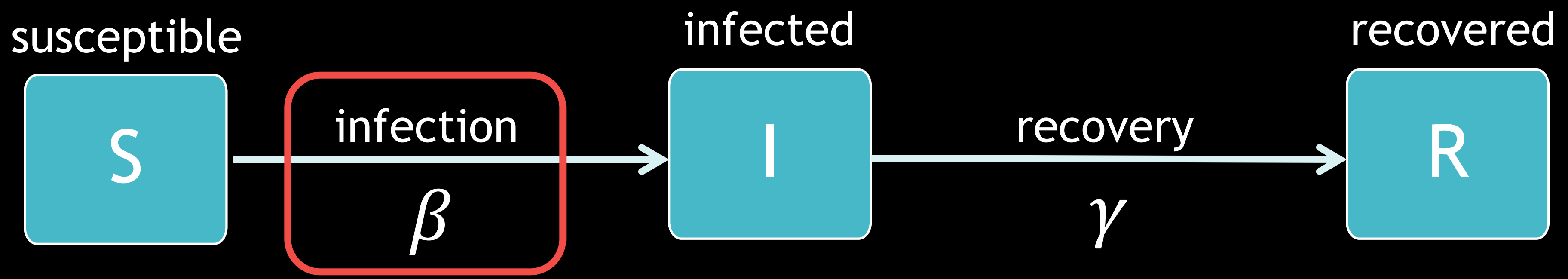
$$\frac{dS(t)}{dt} = -\underline{\beta S(t) I(t)}$$

rate of change

no one to add

the number infected depends on contact between S and I, and the probability of transmission

SIR Model: Kermack & McKendrick



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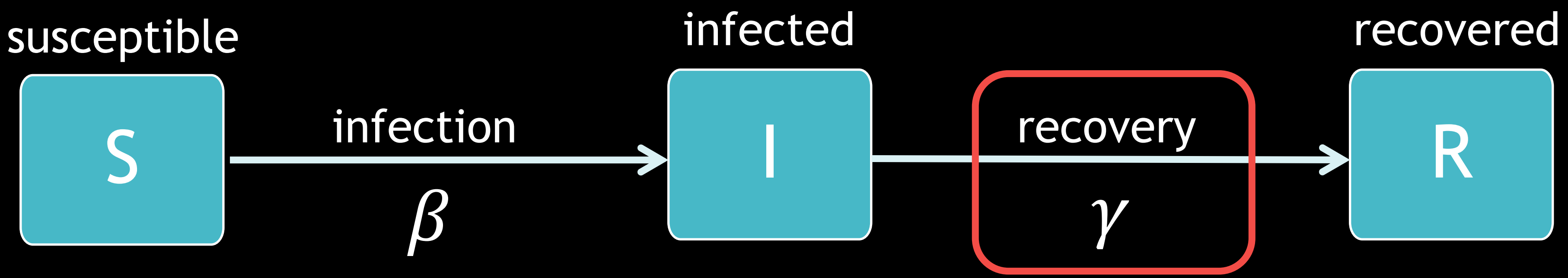

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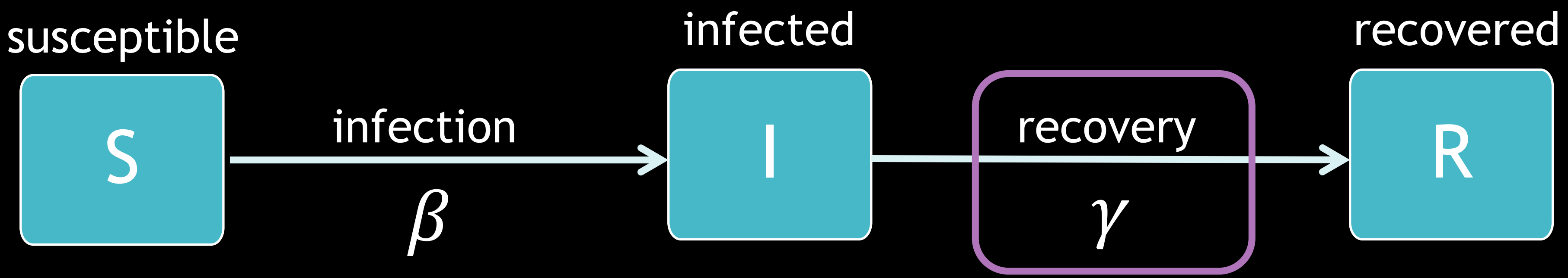
the number who recover only depends on I and the recovery rate

SIR Model: Kermack & McKendrick



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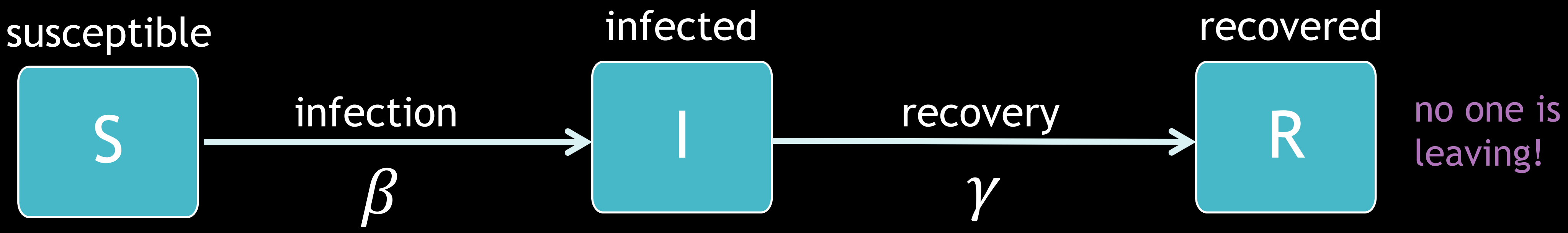
SIR Model: Kermack & McKendrick



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no one to subtract

Questions & Break

Workshop Schedule

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3:40–5:00 pm	R Session

SIR Model

- ODEs are solved to give us the rate of change for each compartment for each unit of time
- Units of time are meant to be infinitesimally small
  - larger time units have more inaccurate results
  - we want to model continuous time or instantaneous time units

$$\frac{dS(t)}{dt} = -\beta S(t)I(t)$$

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SIR Model

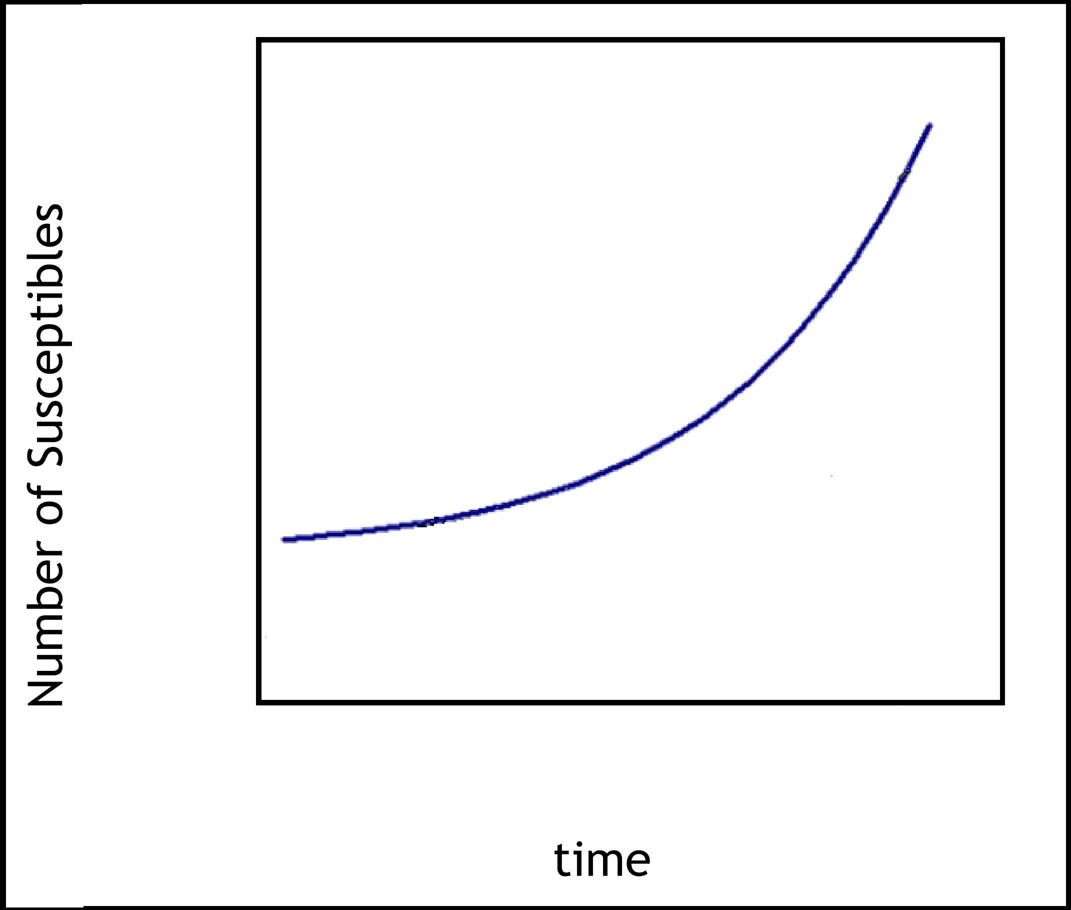
$$\frac{dS(t)}{dt} = -\beta S(t)I(t)$$

$$\frac{dS(t)}{dt} = \frac{S(t+\delta t) - S(t)}{\delta t}$$

$$as\ \delta t \rightarrow 0$$

- rate of change can be expressed another way
  - δt is our unit time

SIR Model



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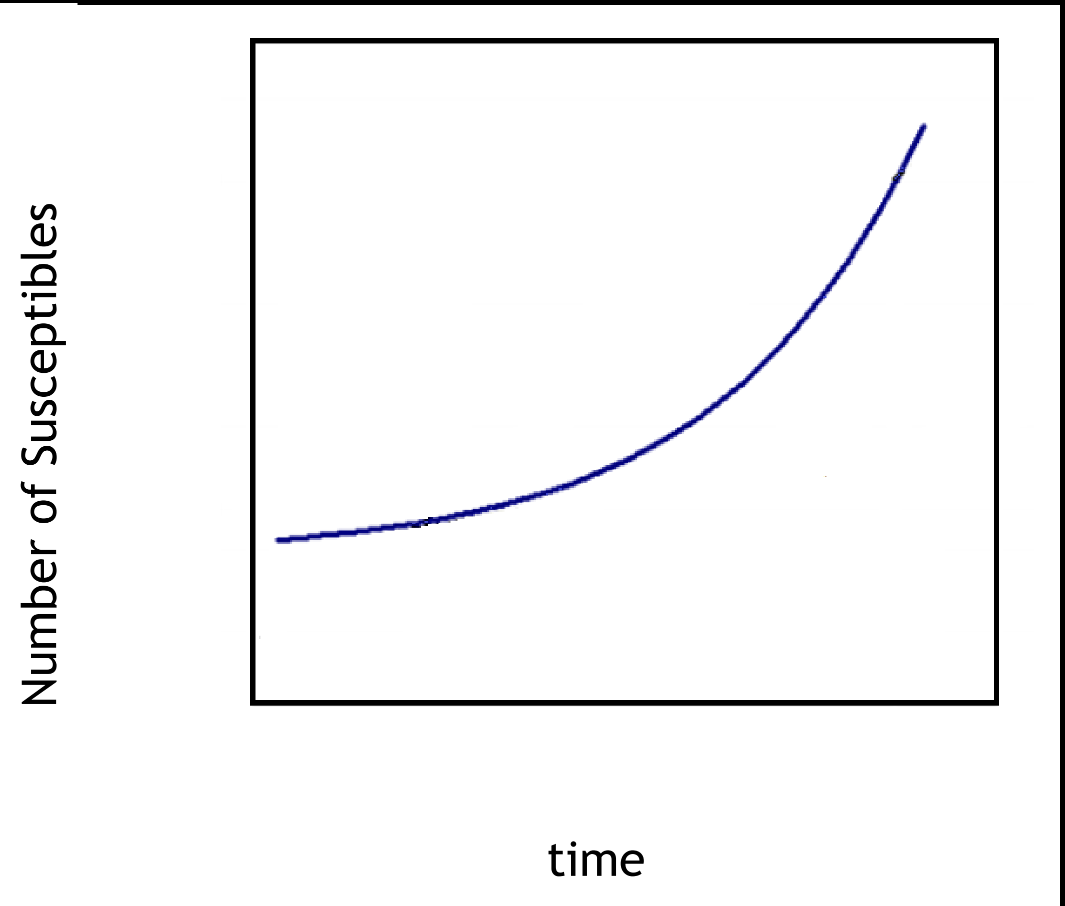

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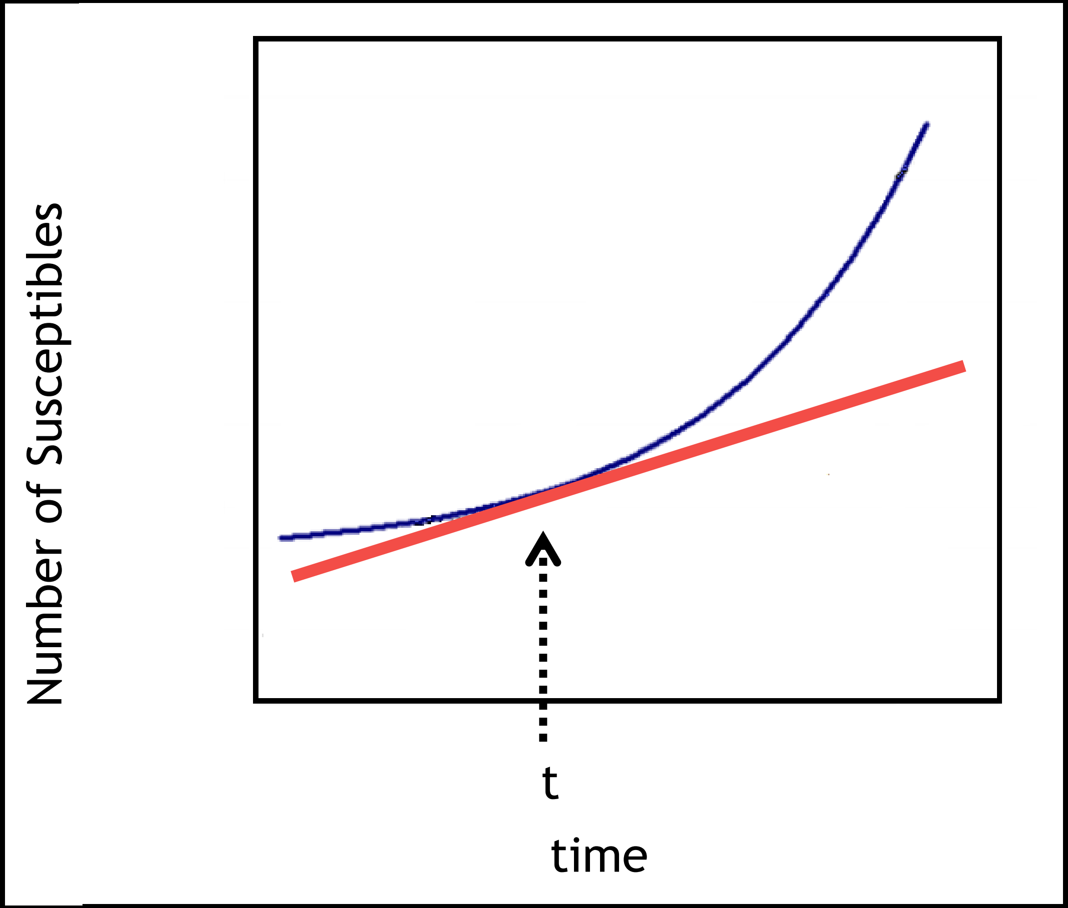
$$as\ \delta t \to 0$$

- δt is our unit time
- tangent of curve is rate for instantaneous time

SIR Model



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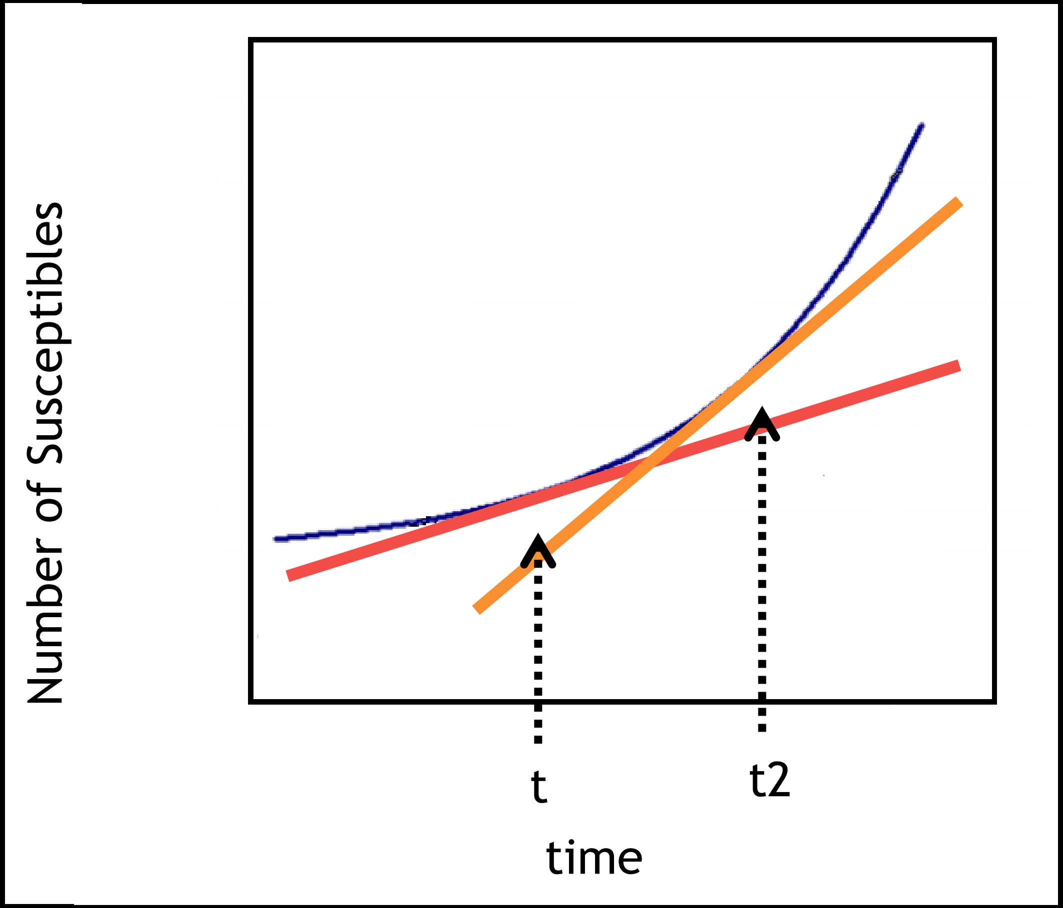

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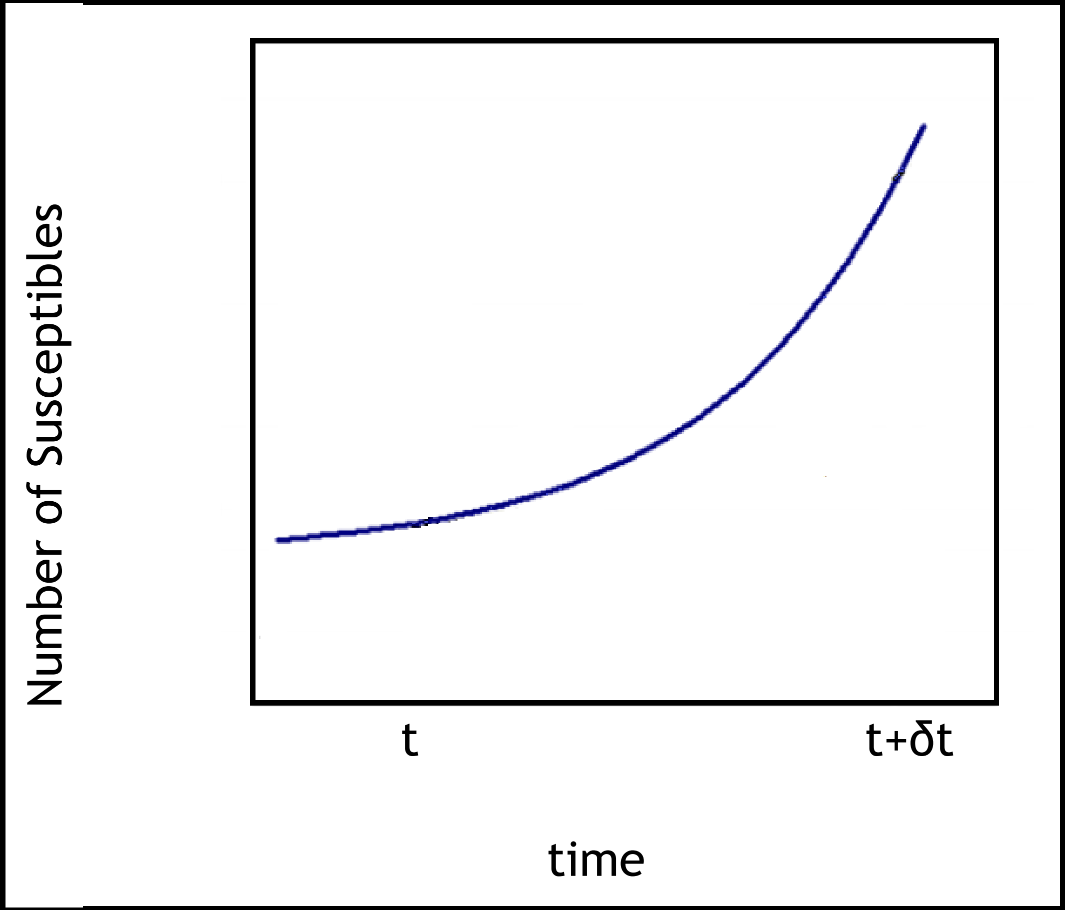

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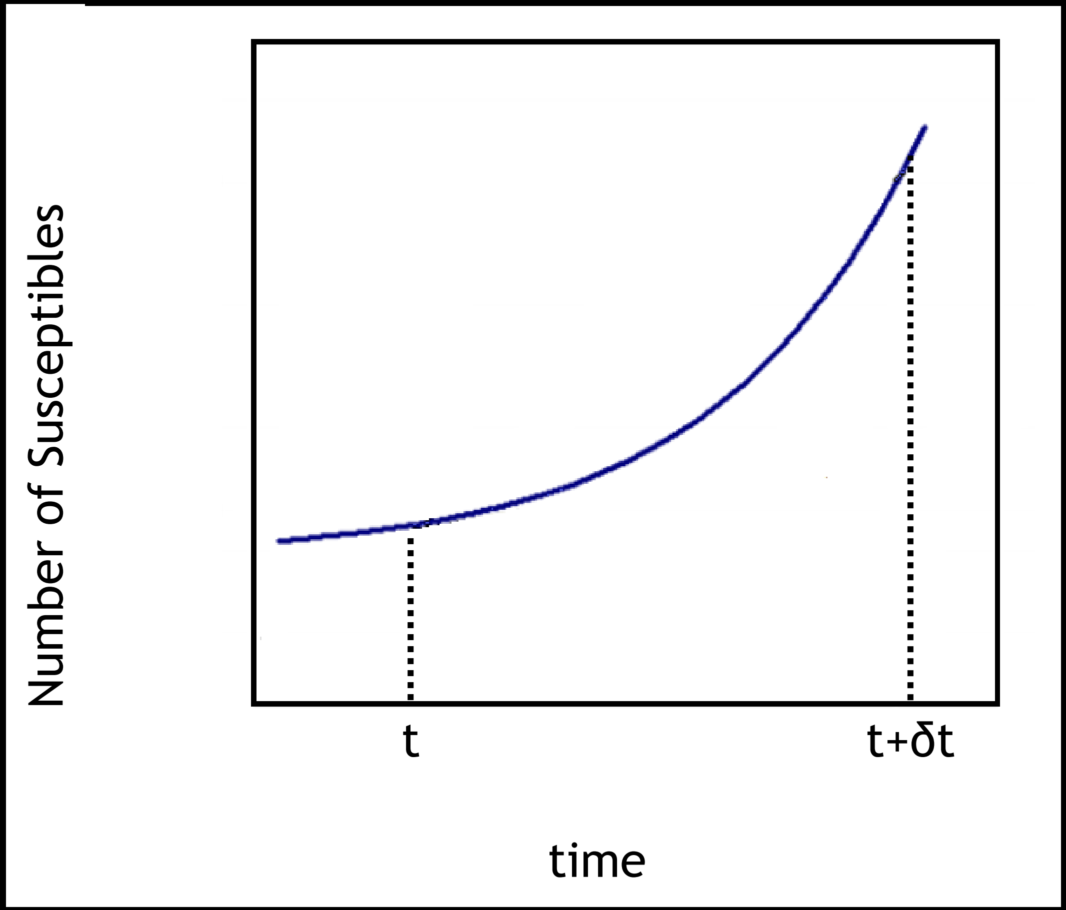
SIR Model



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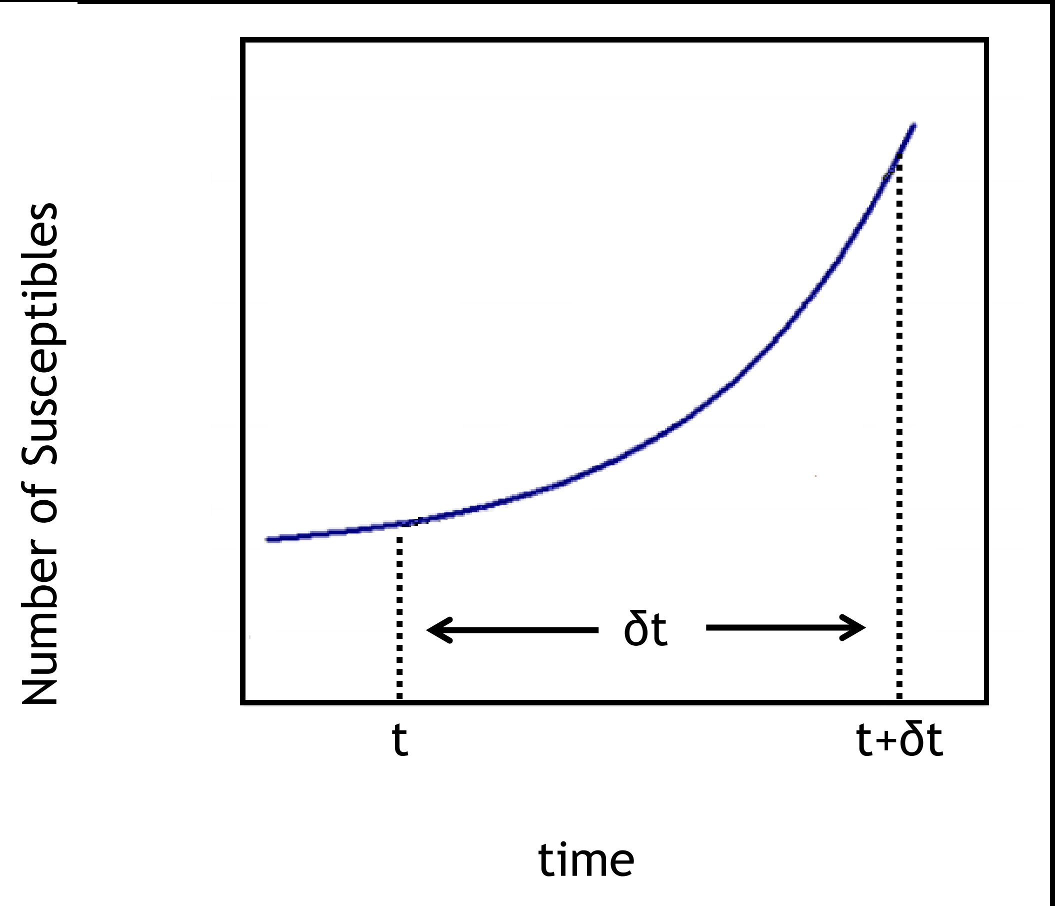

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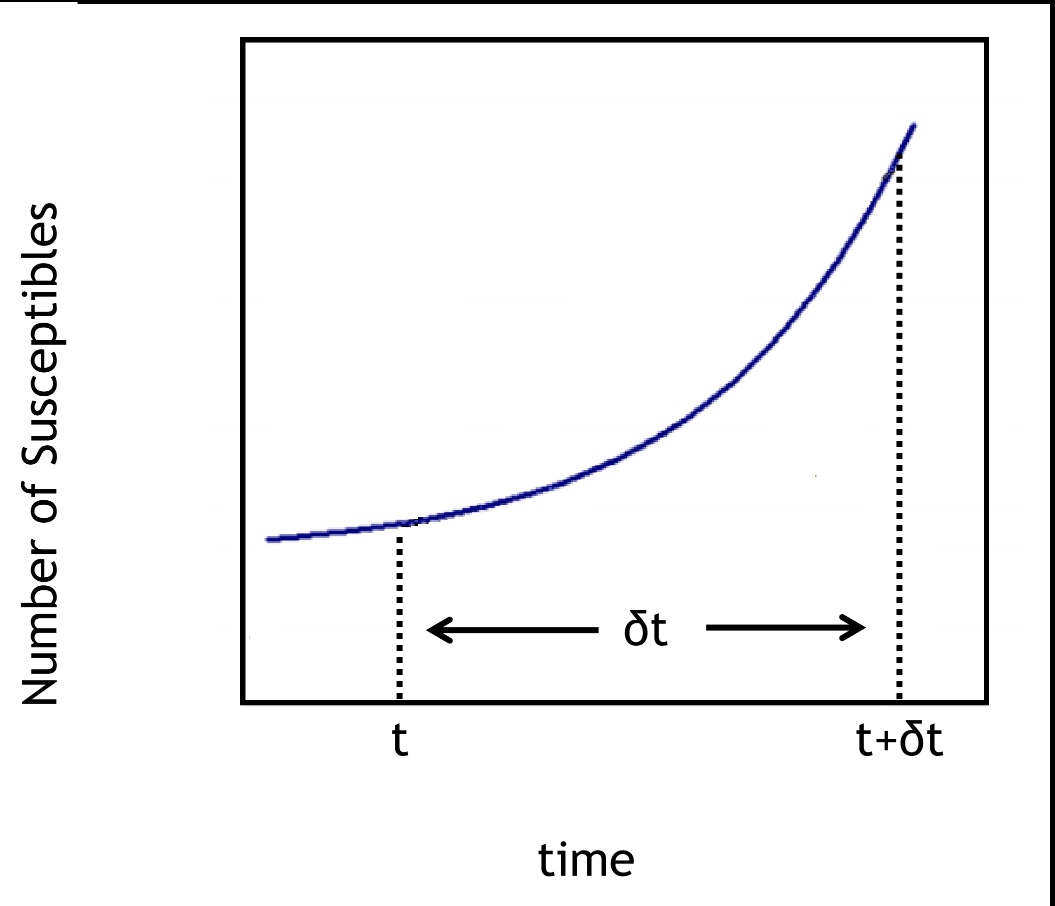

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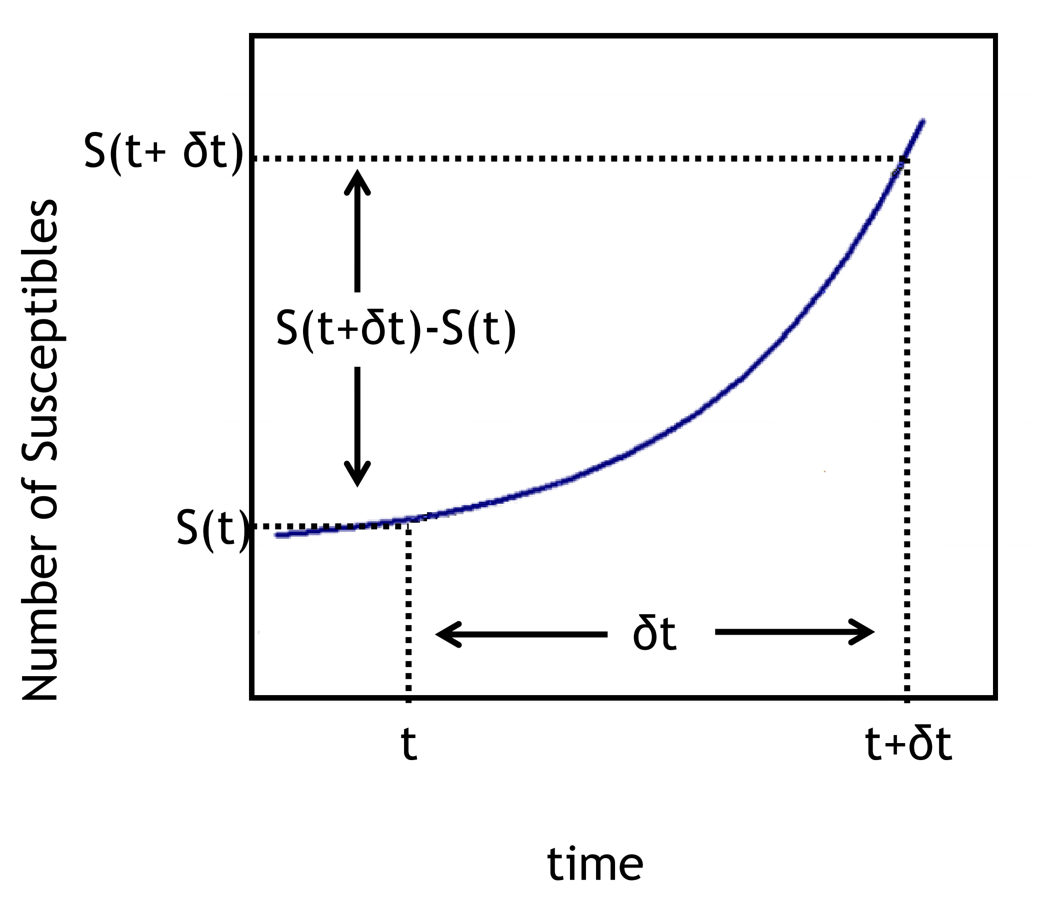

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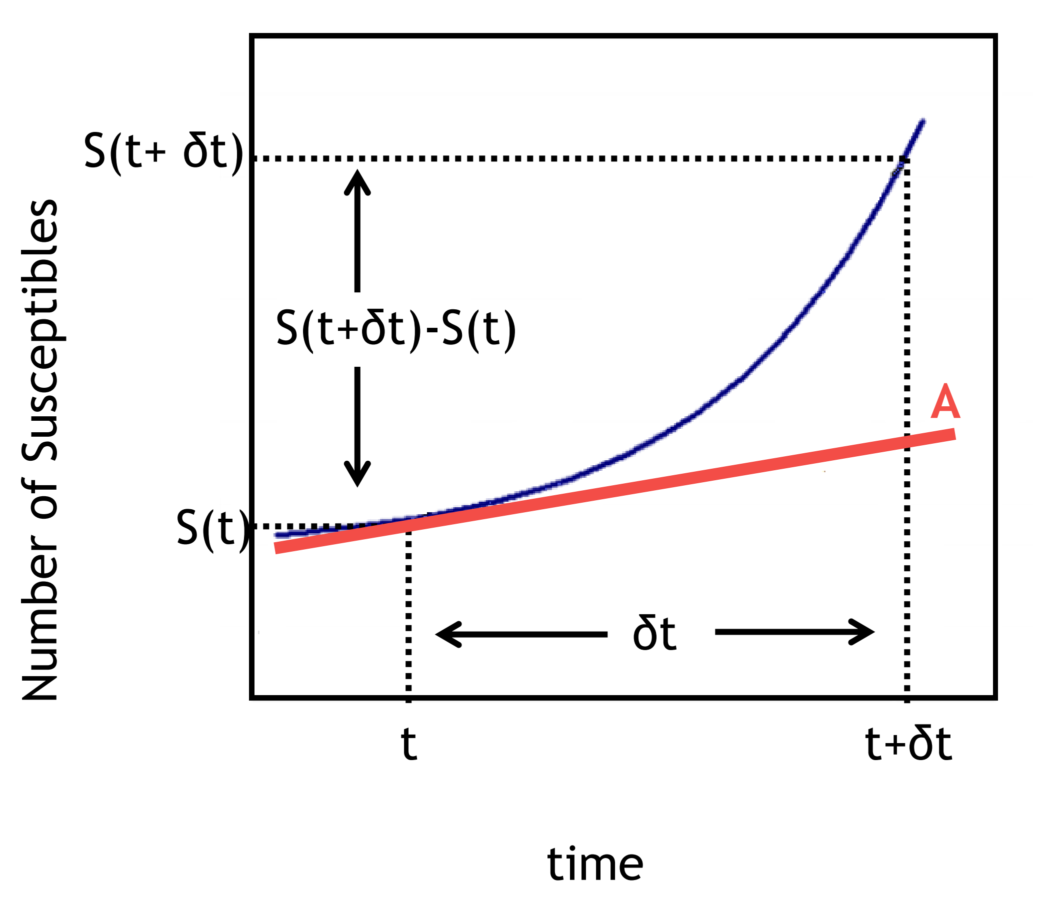
SIR Model



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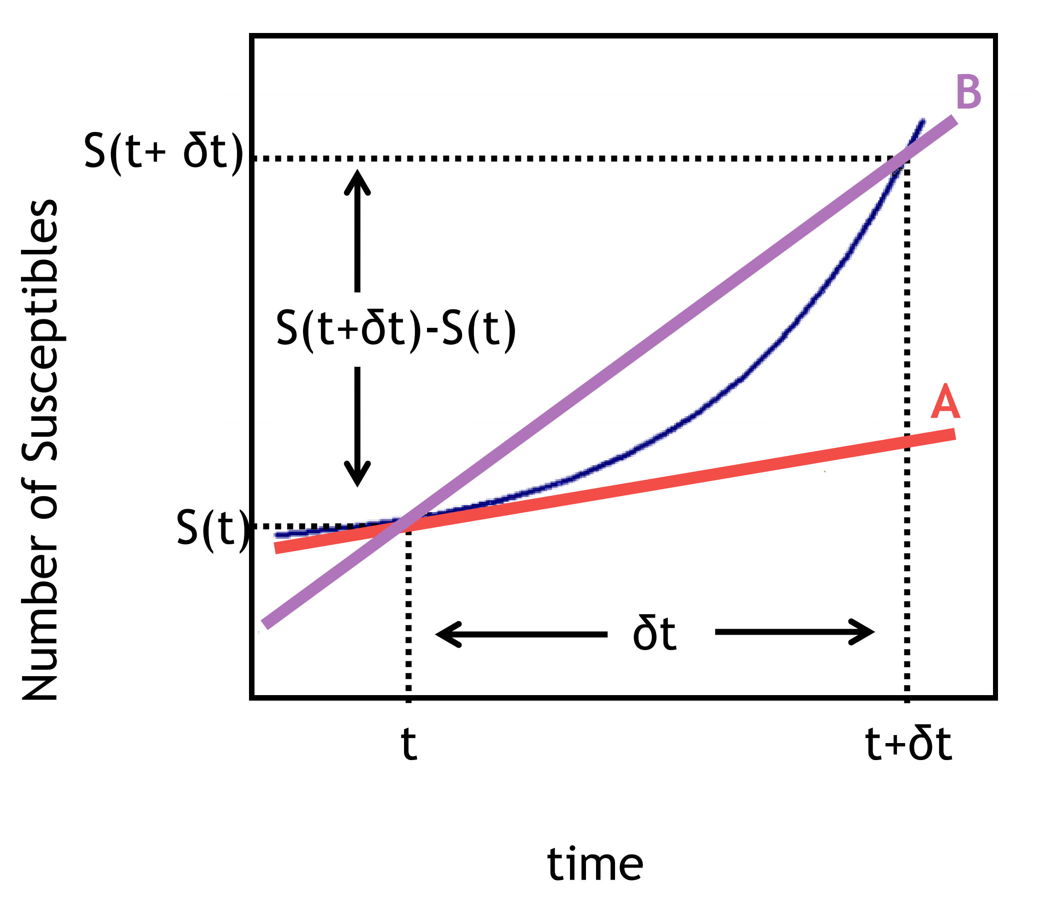
$$\frac{dS(t)}{dt} = \frac{S(t+\delta t) - S(t)}{\delta t}$$

$$as\ \delta t \rightarrow 0$$

- tangent of curve is rate for instantaneous time
- we want to know slope A

SIR Model



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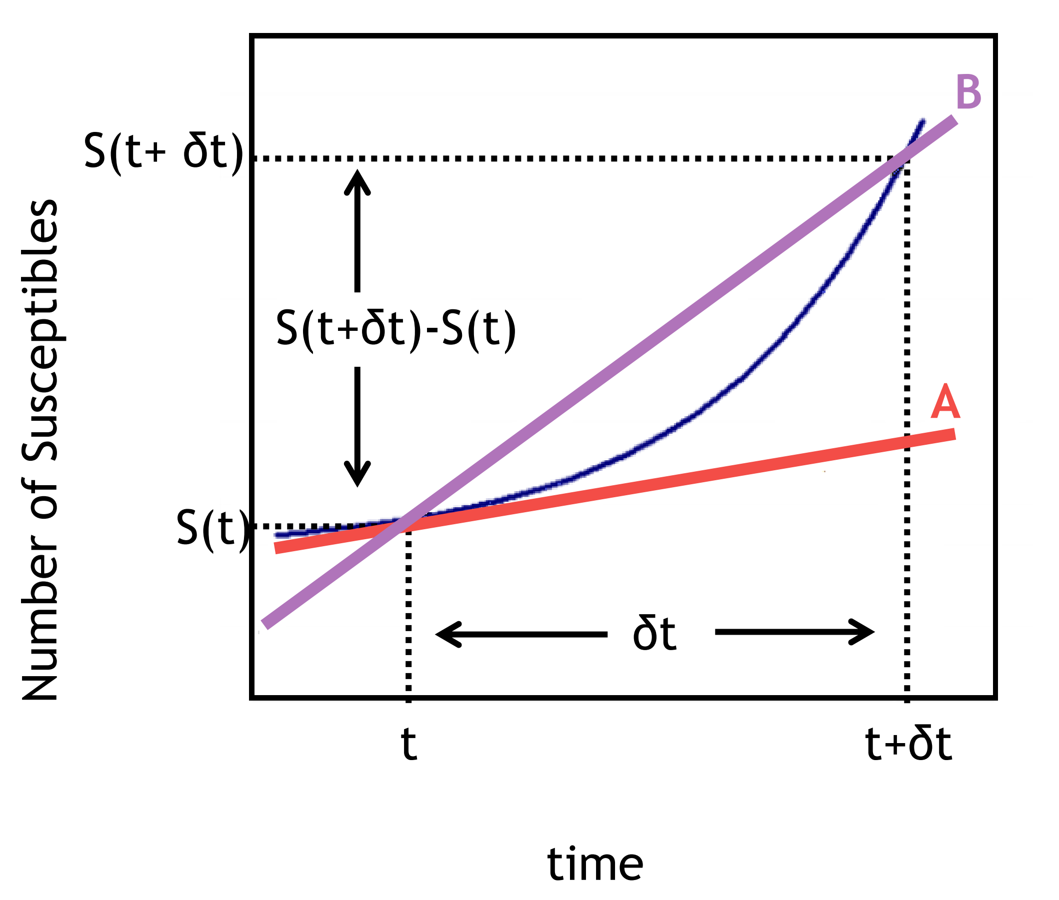
$$as\ \delta t \rightarrow 0$$

- we want to know slope A
- we can calculate slope B

SIR Model



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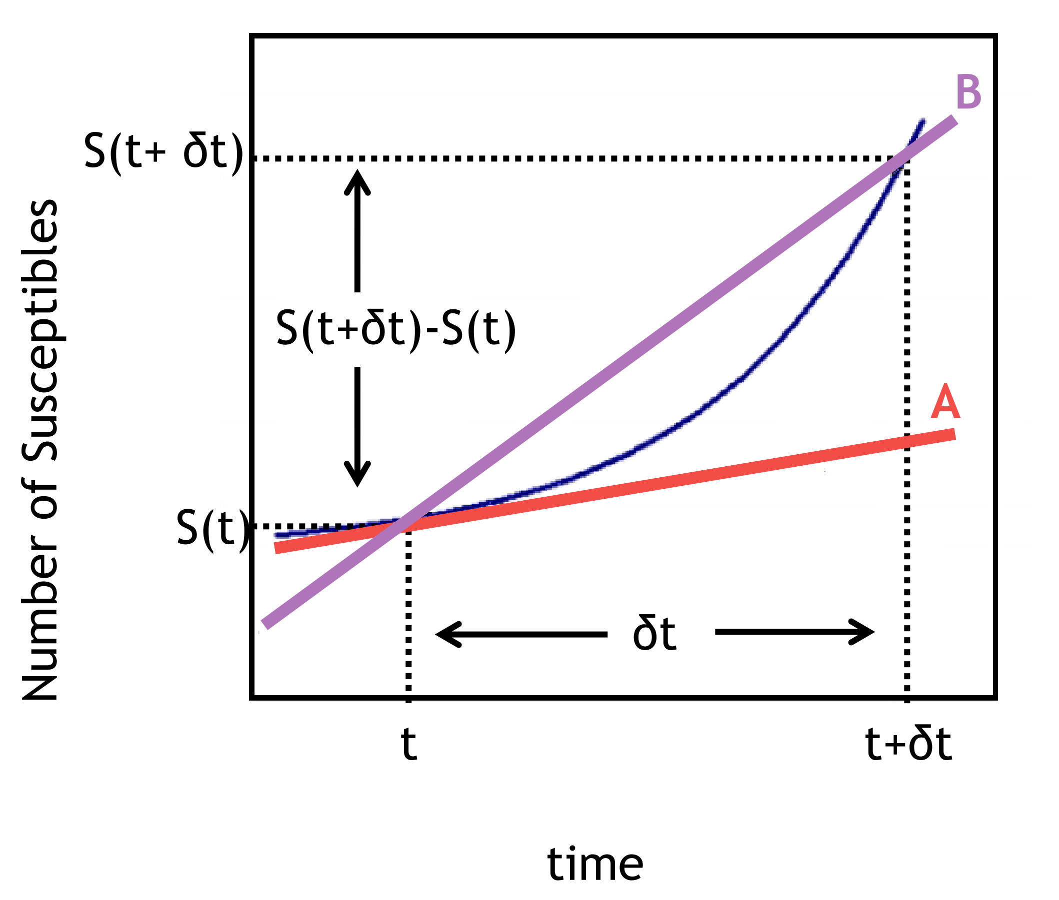
$$as\ \delta t \rightarrow 0$$

- A and B look very far apart

SIR Model



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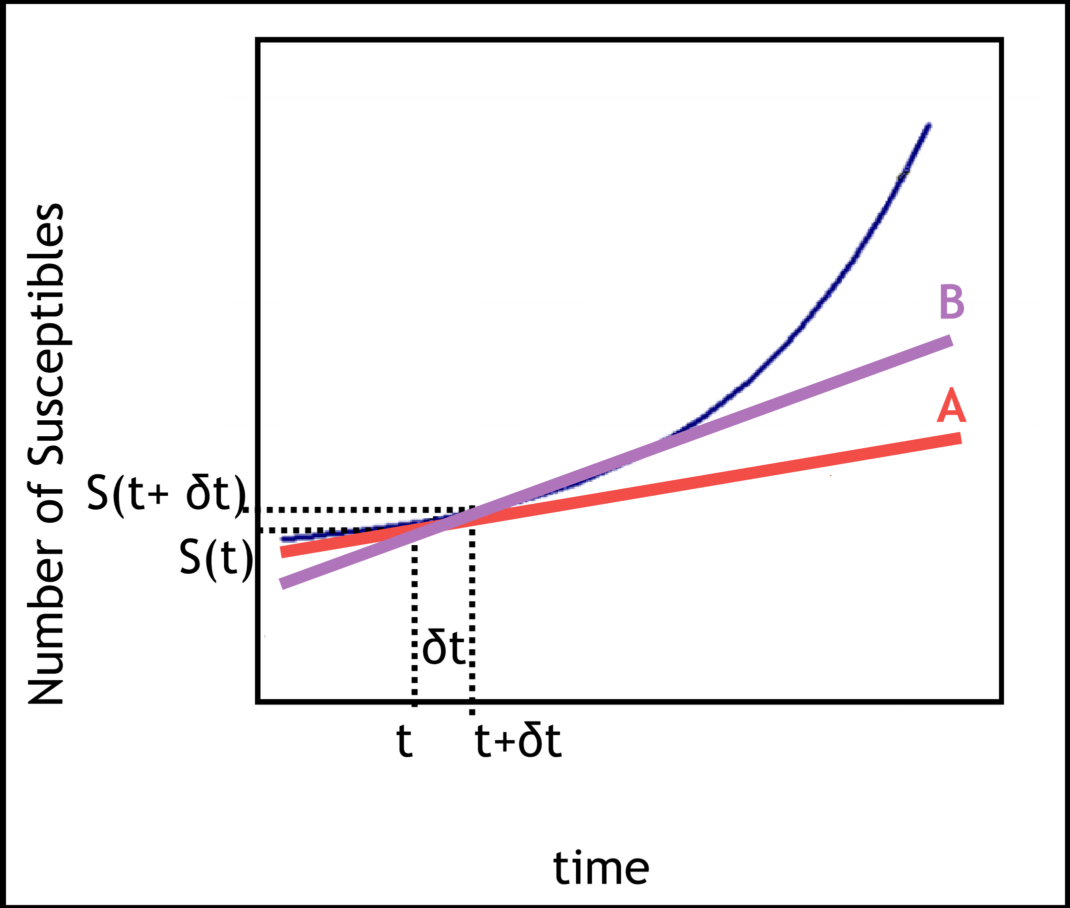
SIR Model



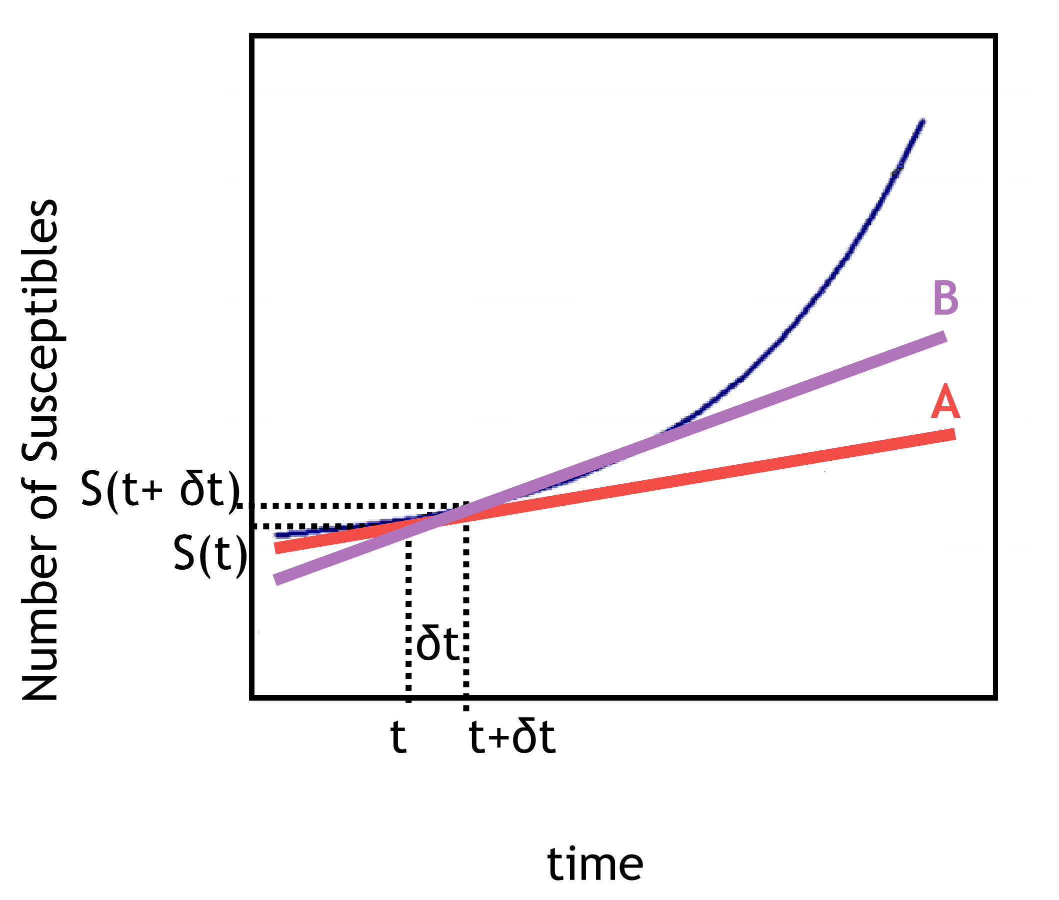
$$\frac{dS(t)}{dt} = -\beta S(t)I(t)$$

$$\frac{dS(t)}{dt} = \frac{S(t+\delta t) - S(t)}{\delta t}$$

$$\boxed{as\ \delta t \rightarrow 0}$$

- A and B look very far apart
- unless δt is very small!

SIR Model



$$\frac{dS(t)}{dt} = -\beta S(t)I(t)$$

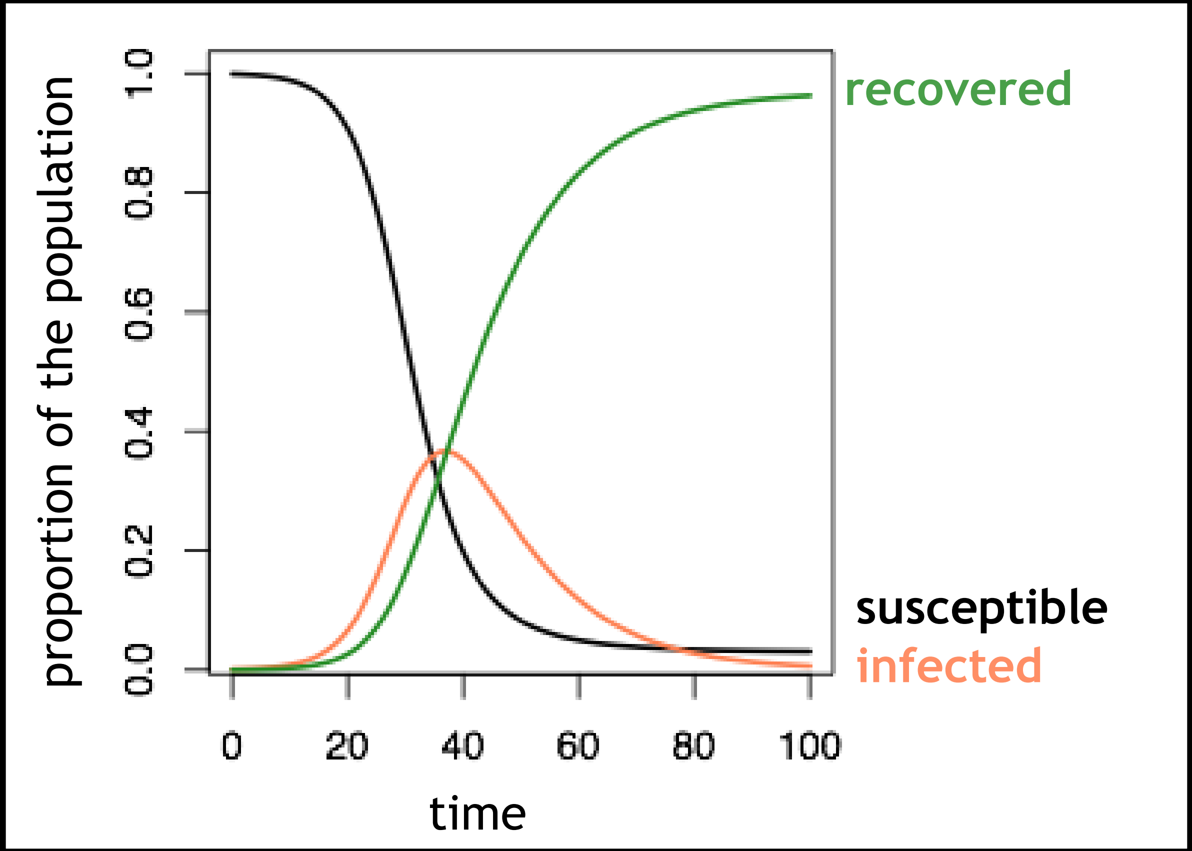
$$\frac{dS(t)}{dt} = \boxed{\frac{S(t+\delta t) - S(t)}{\delta t} \quad as\ \delta t \to 0}$$

- we can only solve for B, and B is only a good approximation for A if δt is very small

Solving Differential Equations

- Specialized software/programs
  - Berkeley Madonna
  - Stella
  - MatLab
  - Mathematica
  - Maple
  - R
- Software solves differential equations with different techniques (Euler, Runge-Kutta, Burlirsch-Stoer, etc.)
  - numerical integration

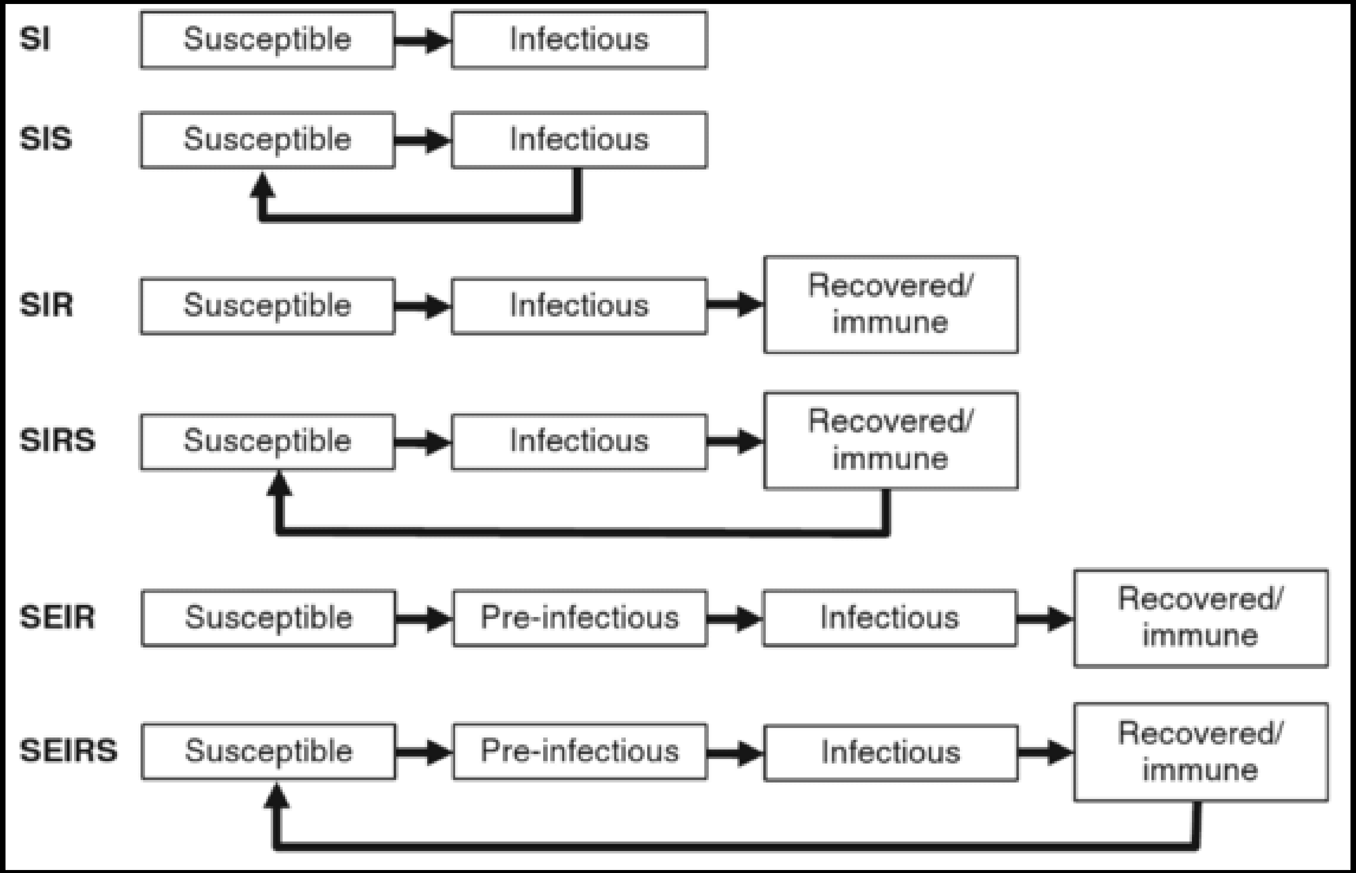
SIR Model Output



- We can examine the epidemic dynamics
- We will have values for S(t), I(t), and R(t) for each time step t
    - these can be expressed as population proportions and plotted
    - we can also find totals for each compartment at the end of the epidemic

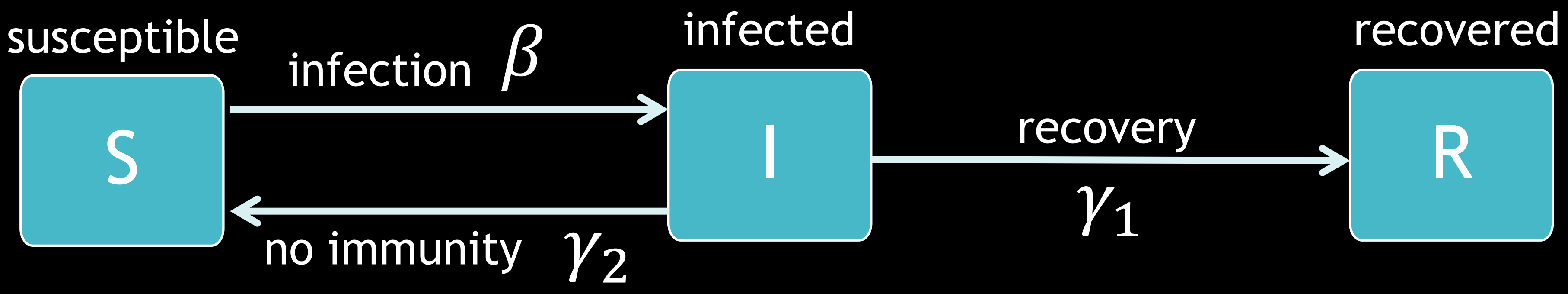
SIR Model Key Points

- Basic SIR model is the most commonly discussed compartmental/mechanistic model
- Models can be built to represent many disease systems, pathogen dynamics, and scenarios
  - Model building requires you to make assumptions – consider if the assumptions are valid for your situation
- Models are translated to mathematical expressions (ODEs) that are solved using numerical integration
- Output from models helps us understand dynamics of an epidemic



More Compartmental Models

Example: Hookworm Infection



$$\frac{dS(t)}{dt} = \gamma_2 I(t) - \beta S(t) I(t)$$

$$\frac{dR(t)}{dt} = \gamma_1 I(t)$$

$$\frac{dI(t)}{dt} = \beta S(t) I(t) - \gamma_1 I(t) - \gamma_2 I(t)$$

Workshop Schedule

Time	Topics
2:00–2:10 pm	~~Greetings~~
2:10–3:00 pm	~~SIR Model & Differential Equations~~
3:00–3:10 pm	~~Break~~
3:10–3:30 pm	~~SIR Model & Time Steps~~
3:30–3:40 pm	Break
3:40–5:00 pm	R Session