

# An introduction to infectious disease modelling and its applications

Sebastian Funk, Gwen Knight, Anton Camacho

Centre for the Mathematical Modelling of Infectious Diseases  
London School of Hygiene & Tropical Medicine

LONDON  
SCHOOL OF  
HYGIENE  
& TROPICAL  
MEDICINE



centre for the  
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# 1. Introduction

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# Overview of the course

## Day 1

- Introduction to infectious disease modelling

## Day 2

- PRACTICAL – Deterministic models in R
- Introduction to stochastic models

## Day 3

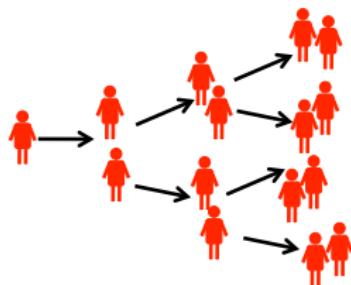
- Applications of modelling
- PRACTICAL – stochastic models in R

## Day 4

- Model fitting and inference (+ PRACTICAL)

## The reproduction number $R$

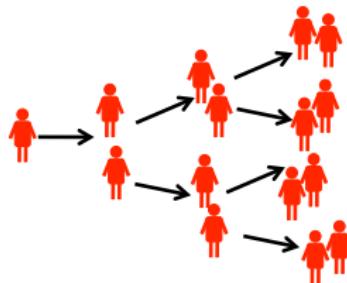
The number of secondary cases an infectious person generates.



What does this depend on?

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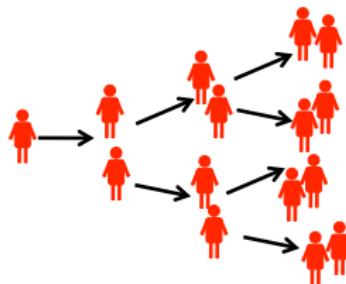


What does this depend on?

1. The **number of contacts** a person has per time,  $c$
2. The **probability of transmission** given contact,  $p$
3. The **duration of infectiousness**,  $D$
4. The **proportion of contacts that are susceptible**,  $s$

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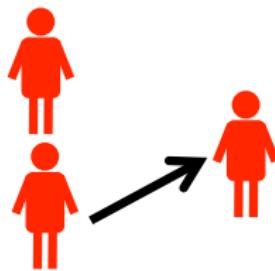
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2. The **probability of transmission** given contact,  $p$
3. The **duration of infectiousness**,  $D$
4. The **proportion of contacts that are susceptible**,  $s$

A simple model would suggest:  $R = c \times p \times D \times s$

## The basic reproduction number $R_0$

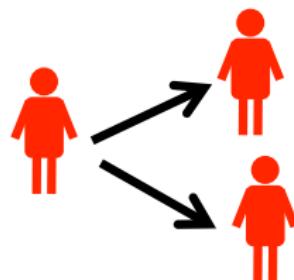
The average number of secondary infectious cases resulting from the introduction of a single infectious case into a totally susceptible population

$$R_0 < 1$$



Number of cases decreases

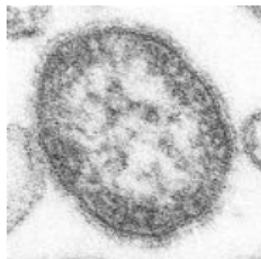
$$R_0 > 1$$



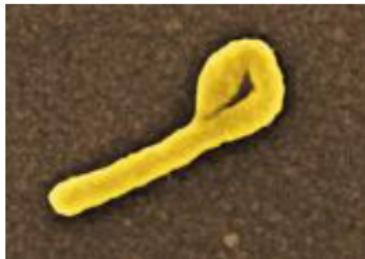
Number of cases increases

## $R_0$ of infectious diseases

Can you arrange these diseases according to their value of  $R_0$ ?



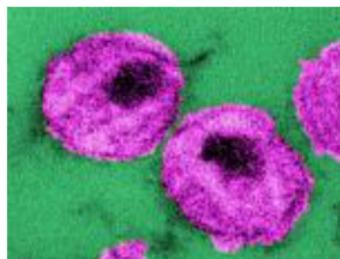
Measles



Ebola

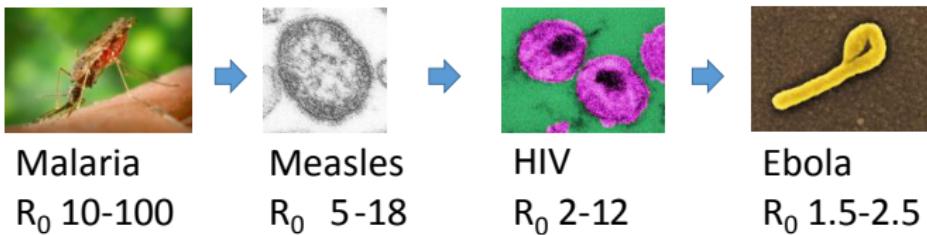


Malaria



HIV

## Empirical values of $R_0$



DEATHS

8

FLU - 1  
SMALLPOX - 3  
POLIO - 4/6



## More empirical values of $R_0$

Infection	Geographical location	Time period	$R_0$
Measles	Cirencester, England	1947–50	13–14
	England and Wales	1950–68	16–18
	Kansas, USA	1918–21	5–6
	Ontario, Canada	1912–13	11–12
	Willesden, England	1912–13	11–12
	Ghana	1960–8	14–15
	Eastern Nigeria	1960–8	16–17
Pertussis	England and Wales	1944–78	16–18
	Maryland, USA	1943	16–17
	Ontario, Canada	1912–13	10–11
	Maryland, USA	1913–17	7–8
Chicken pox	New Jersey, USA	1912–21	7–8
	Baltimore, USA	1943	10–11
	England and Wales	1944–68	10–12
	New York, USA	1918–19	4–5
Diphtheria	Maryland, USA	1908–17	4–5
	Maryland, USA	1908–17	7–8
	New York, USA	1918–19	5–6
	Pennsylvania, USA	1910–16	6–7
Mumps	Baltimore, USA	1943	7–8
	England and Wales	1960–80	11–14
	Netherlands	1970–80	11–14
	England and Wales	1960–70	6–7
Rubella	West Germany	1970–7	6–7
	Czechoslovakia	1970–7	8–9
	Poland	1970–7	11–12
	Gambia	1976	15–16
	USA	1955	5–6
Poliomyelitis	Netherlands	1960	6–7
	England and Wales (male homosexuals)	1981–5	2–5
	Nairobi, Kenya (female prostitutes)	1981–5	11–12
	Kampala, Uganda (heterosexuals)	1985–7	10–11
Human Immunodeficiency Virus (Type I)			

## Different $R_0$ values for a given diseases

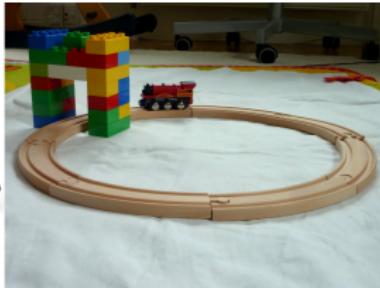
$R_0$  for a disease can have different values depending on factors such as:

- Population density and contact patterns
- Host factors (e.g., immunity)
- Seasonality
- Control measures

## 2. Mathematical models

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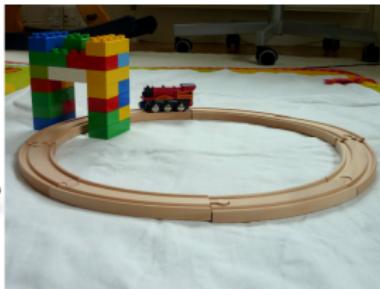
# What is a (mathematical) model?



*A simplified description, especially a mathematical one, of a system or process, to assist calculations and predictions*

Oxford English Dictionary

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Infectious disease model

- a set of equations describing transmission in a population
- an attempt to capture key processes, ignoring unnecessary detail

## Why model?

### 1. understand transmission dynamics

- Examples:
  - who are the risk groups?
  - where are the hotspots?
  - what is the impact of asymptomatic infection?
- highlight gaps in knowledge, data needs, etc

### 2. assess control strategies

- Examples
  - limited vaccine supply, how should it be distributed?
  - travel restrictions, etc.
  - school closures?

### 3. predict future course

- Examples
  - how many cases do we expect next week?
  - are we approaching the peak of an outbreak?
  - what is the impact of a changing climate?

## Purpose of mathematical models

*All models are wrong but some are useful*

George P. Box

### 3. Compartmental models

## Compartmental models

- Divide a population of  $N$  people into compartments, depending on infection status

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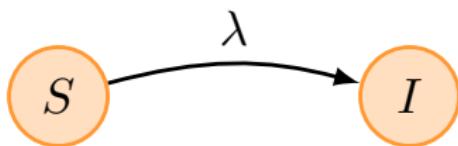


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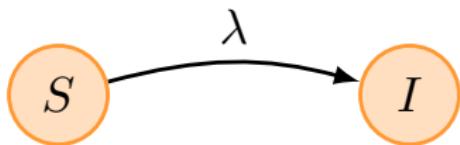


- $S$ : Number of susceptibles
- $I$ : Number of infectious
- $S$  and  $I$  are the compartments. They are state variables, i.e. they change over time.
- $N = S + I$  is the population size.  $N$  is a parameter, i.e. it does not change.

## The force of infection in the SI model



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- $\lambda$  is called the **force of infection**
- It is the **probability** that a **susceptible** person gets **infected** per unit time (i.e., per day, week, month year, ...)
- What is this probability?

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(Number of contacts per unit time)  $\times$

$c$

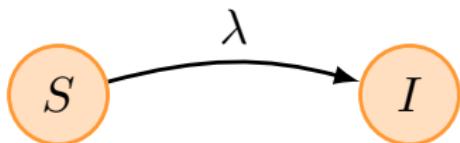
(Probability of transmission)  $\times$

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(Probability that contact is infectious)

$I/N$

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(Number of contacts per unit time)  $\times$   $c$   
(Probability of transmission)  $\times$   $p$   
(Probability that contact is infectious)  $I/N$

- We often write  $\beta = c \times p$ , so that  $\lambda = \beta I/N$
- $\beta$  is called the **infection rate**, a parameter

## The principle of mass action



$$\lambda = \beta \frac{I}{N}$$

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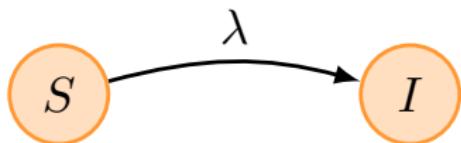
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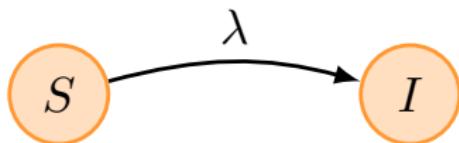
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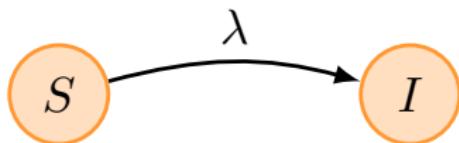
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- Is this realistic?
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  - **But:** sometimes it is a good **model**

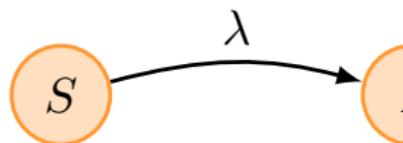
## Writing the SI model as differential equations



$$\lambda = \beta \frac{I}{N}$$

- $S$ : Number of people susceptible

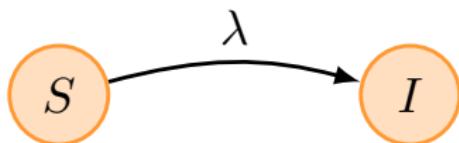
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If we replace  $\lambda$  as above:

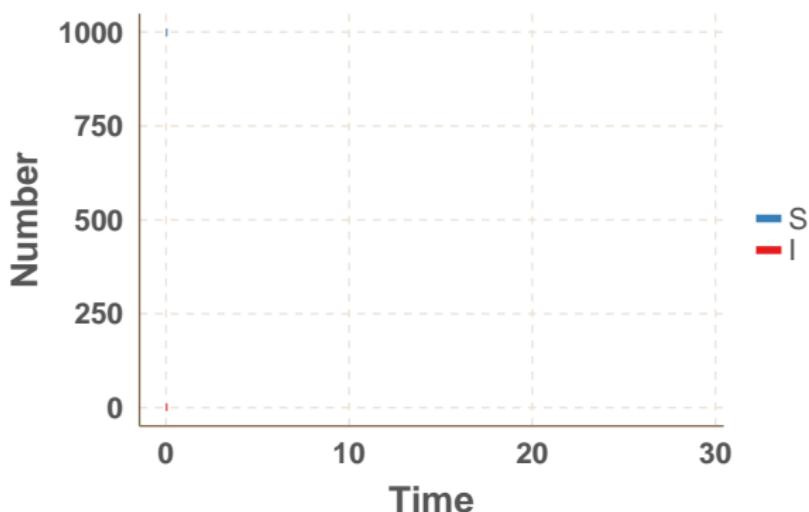
$$dS/dt = -\beta \frac{I}{N} S$$

$$dI/dt = +\beta \frac{I}{N} S$$

## Simulating the SI model using differential equations

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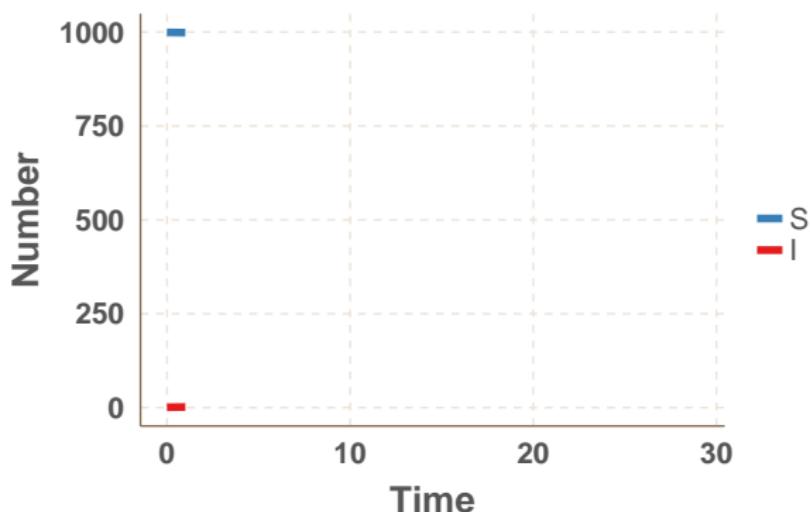
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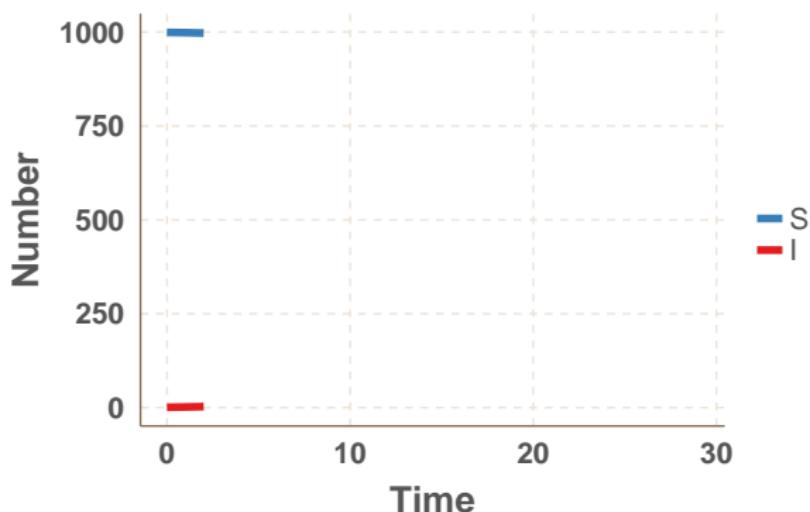
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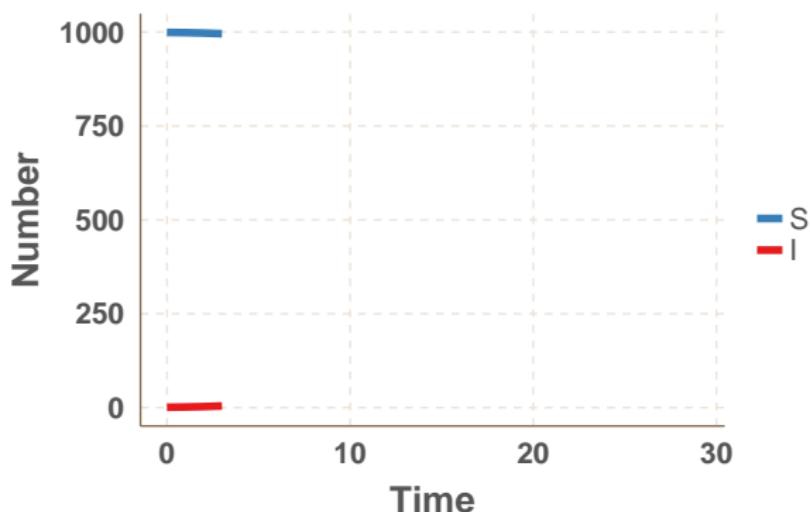
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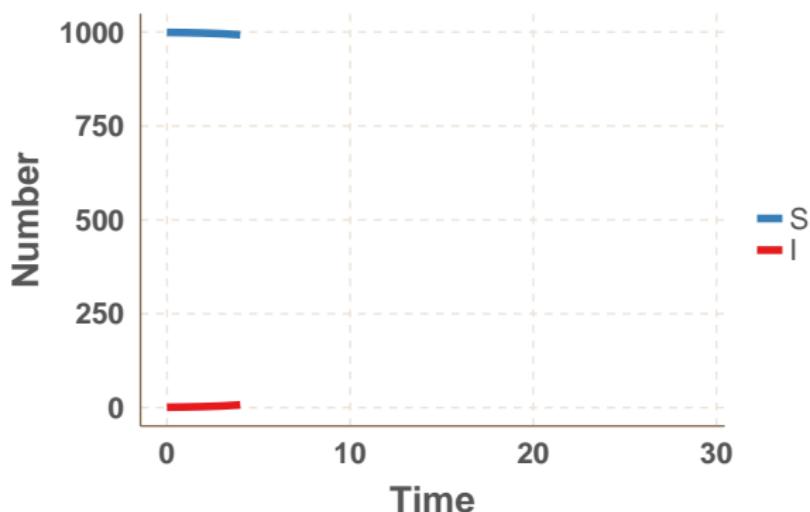
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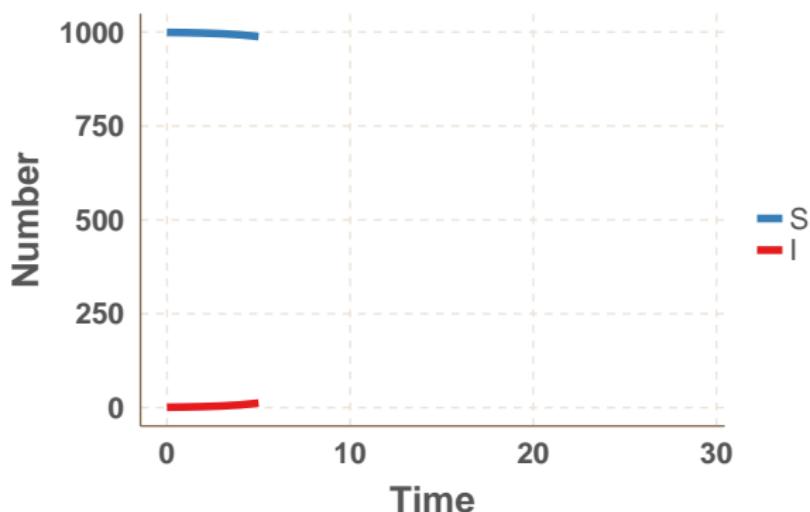
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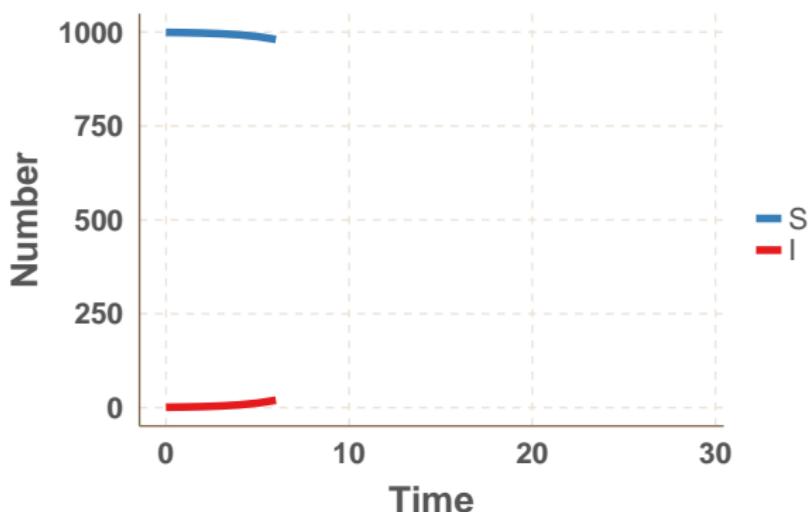
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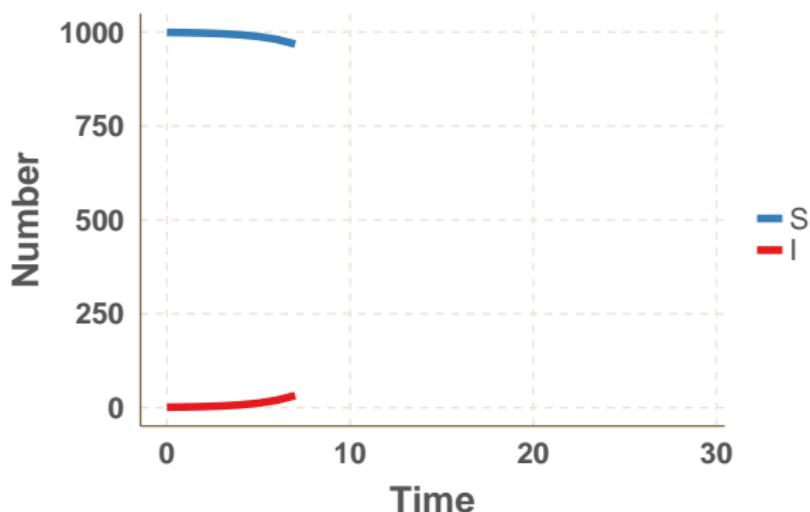
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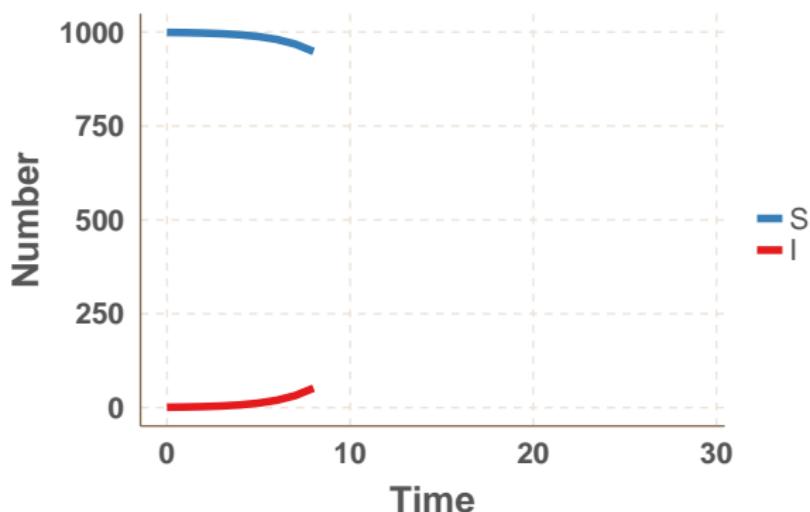
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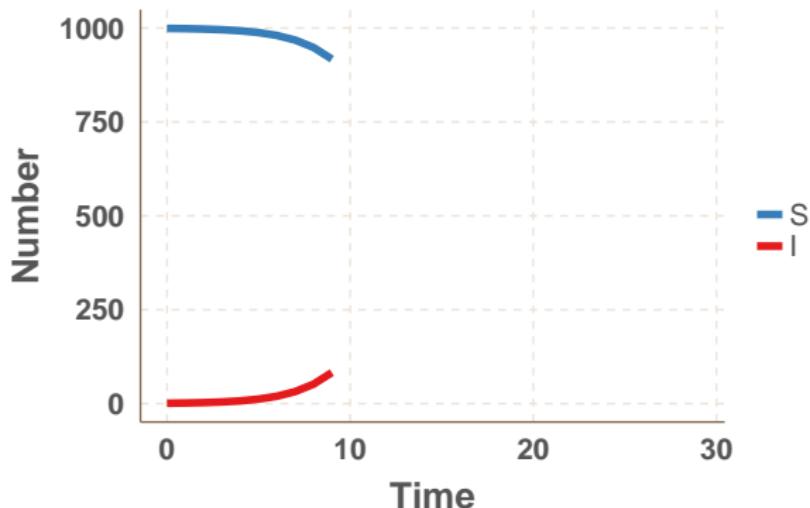
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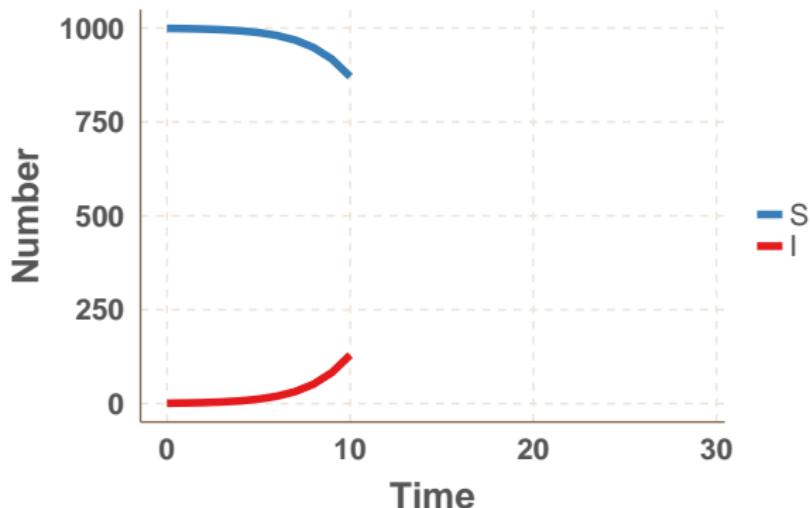
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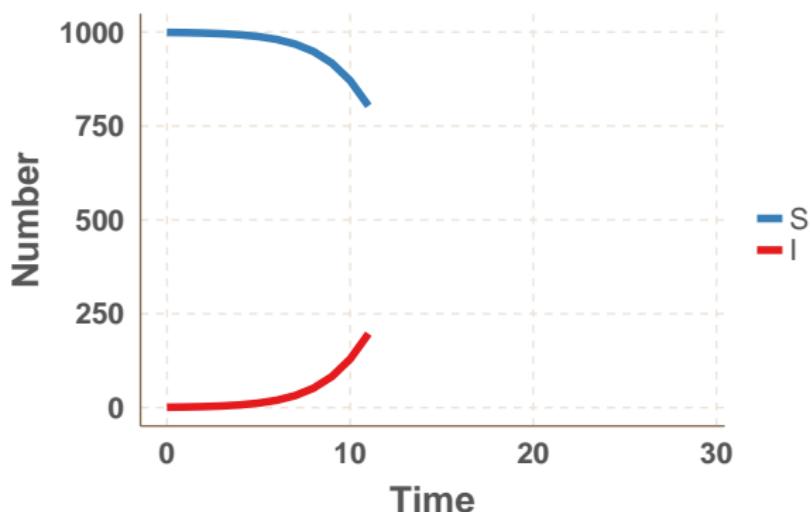
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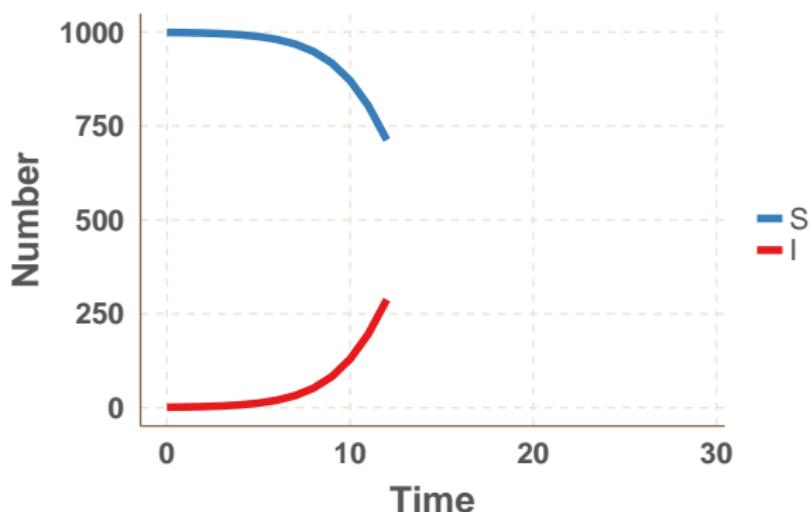
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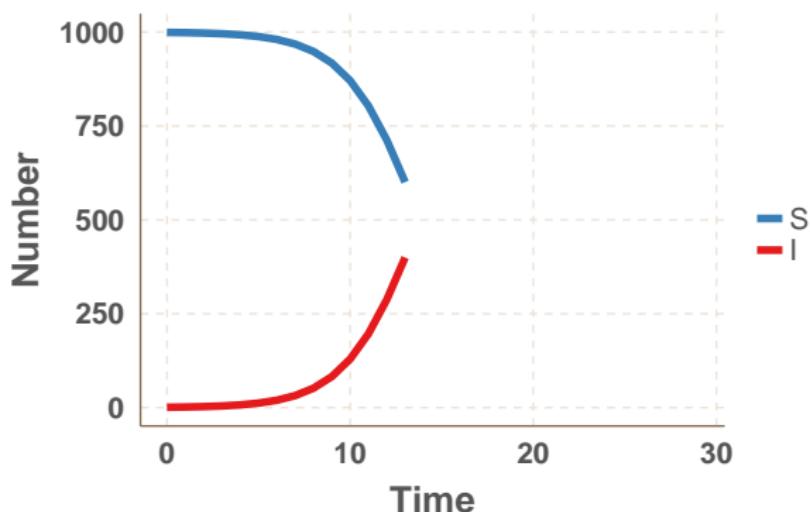
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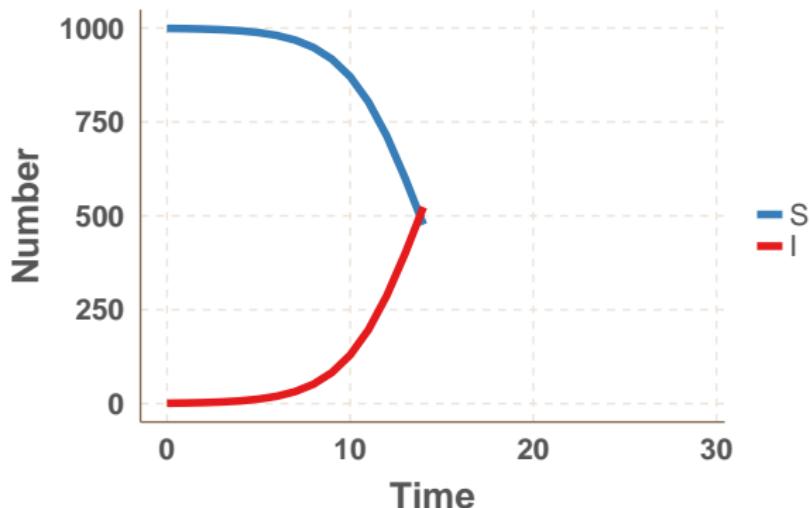
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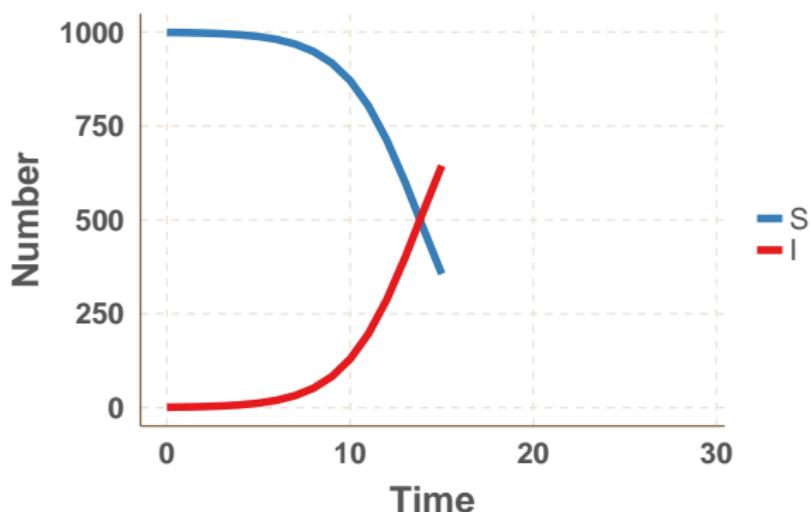
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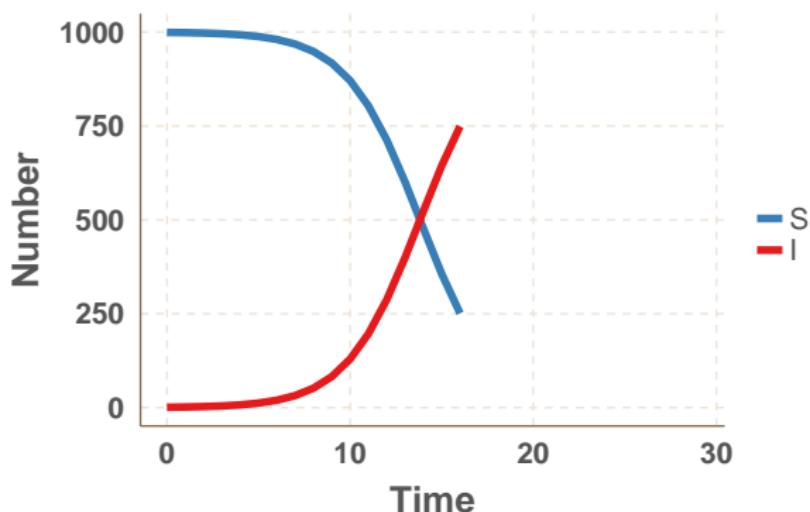
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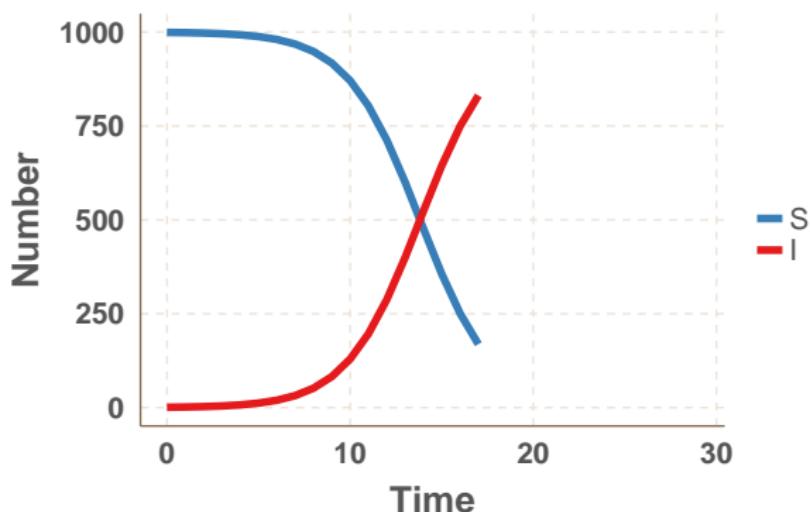
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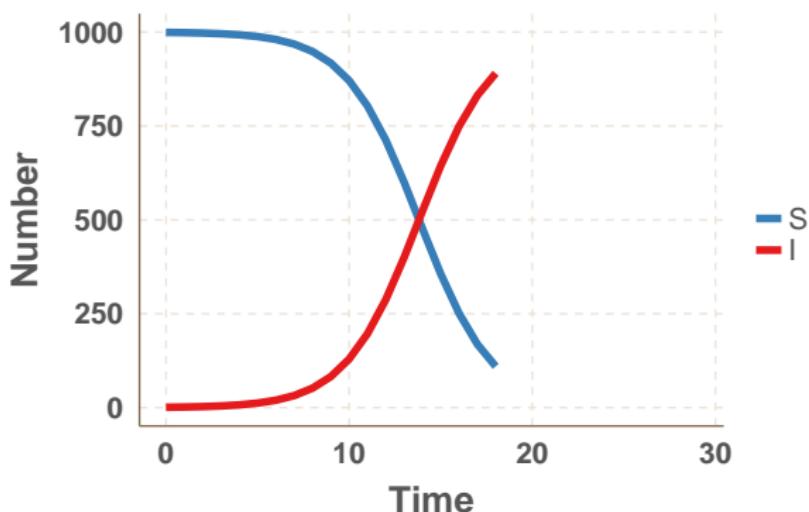
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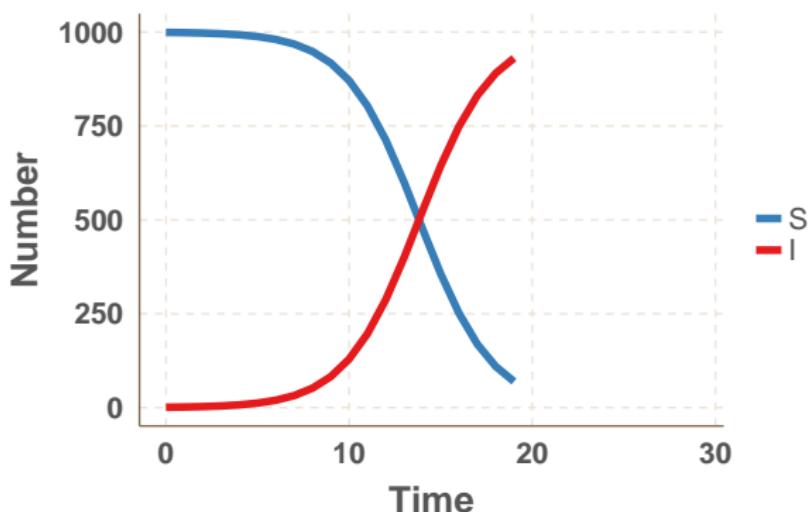
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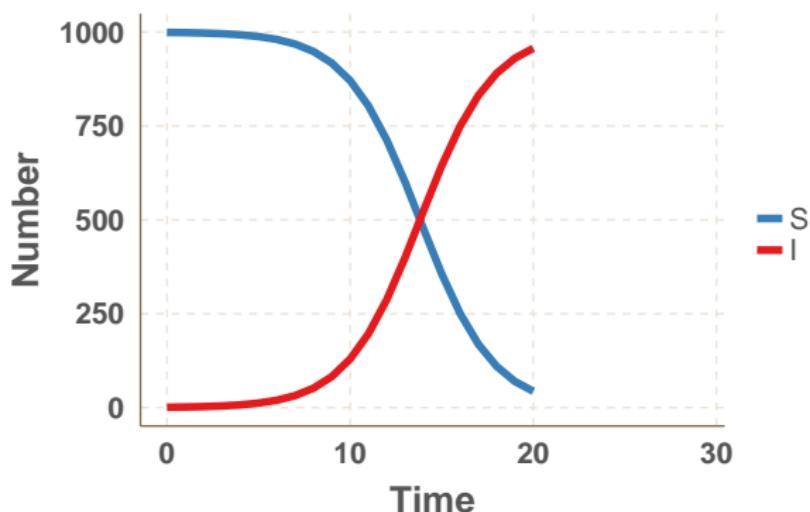
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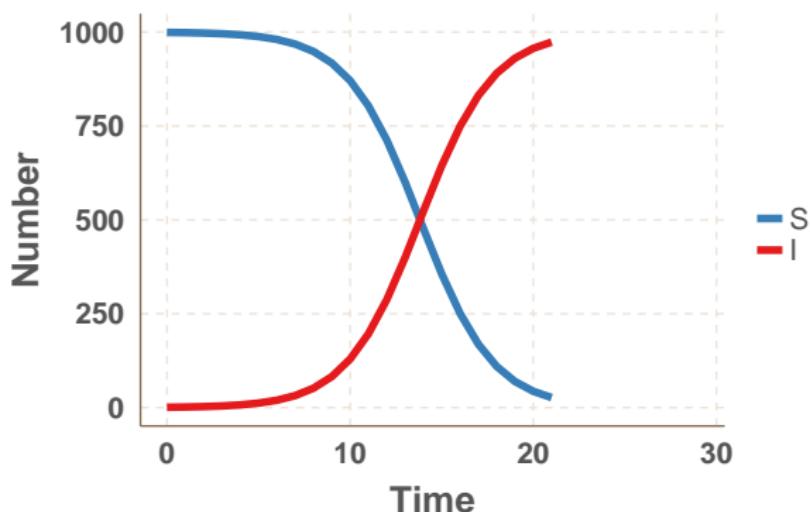
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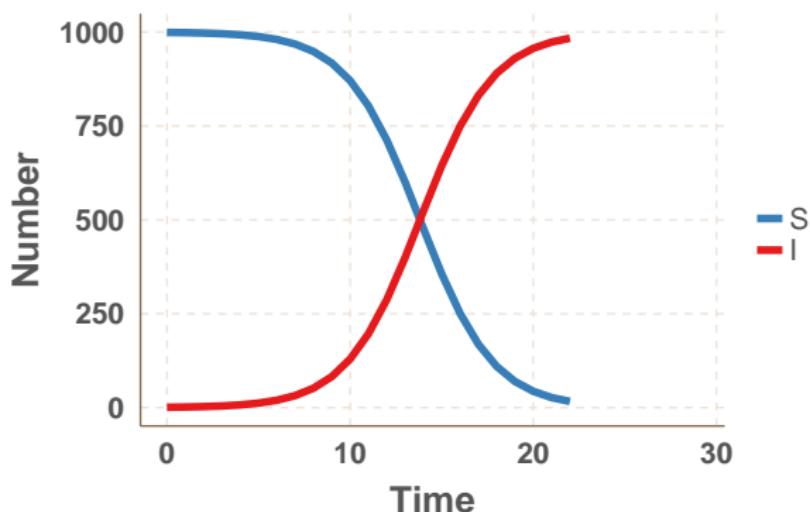
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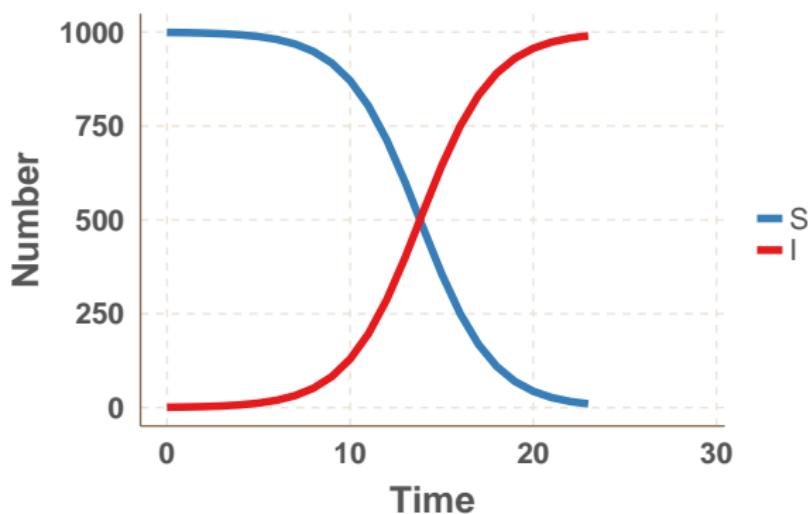
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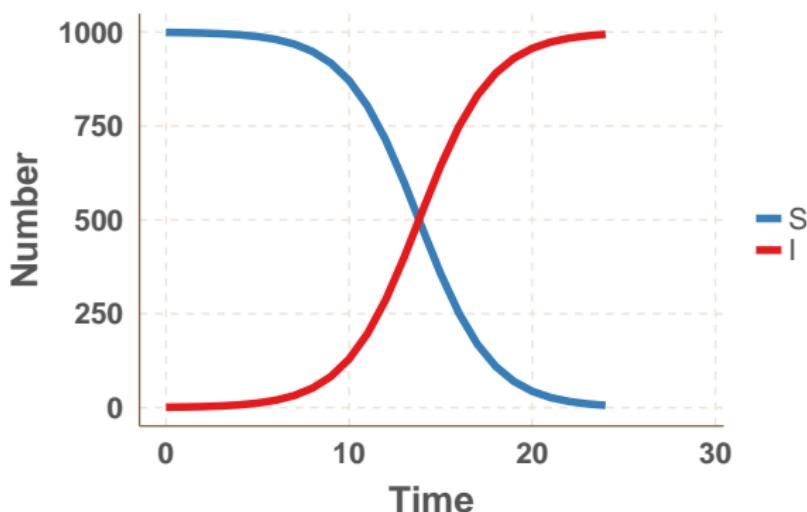
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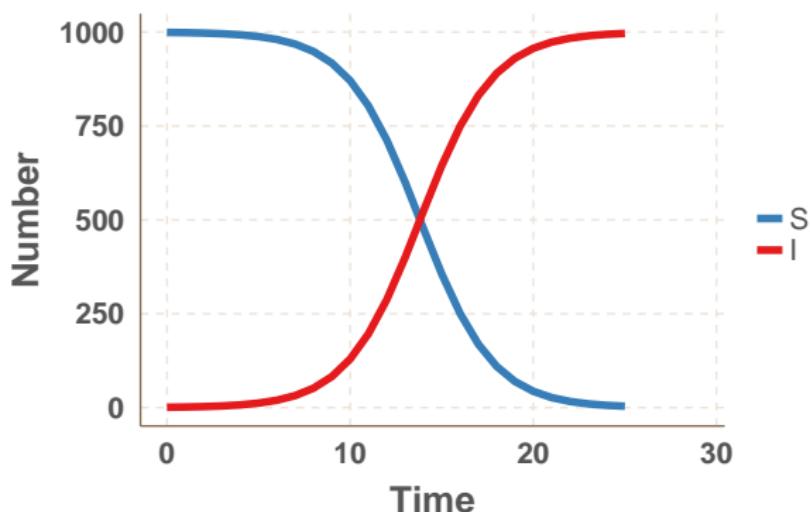
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## Simulating the SI model using differential equations

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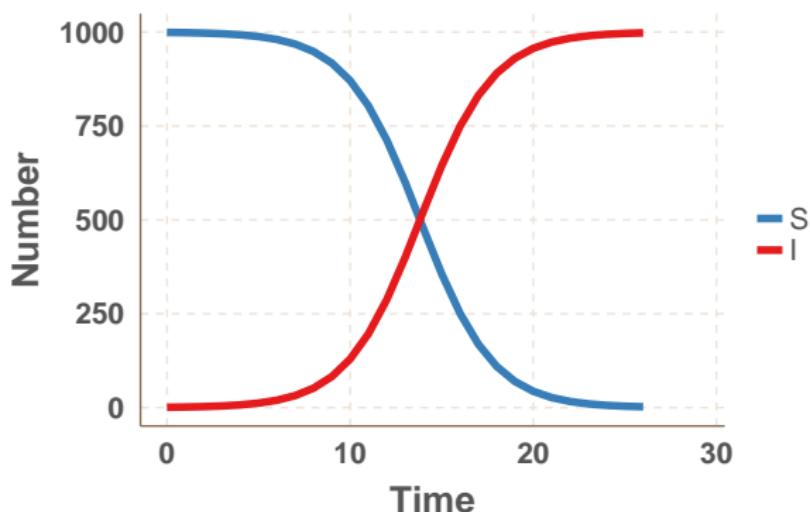
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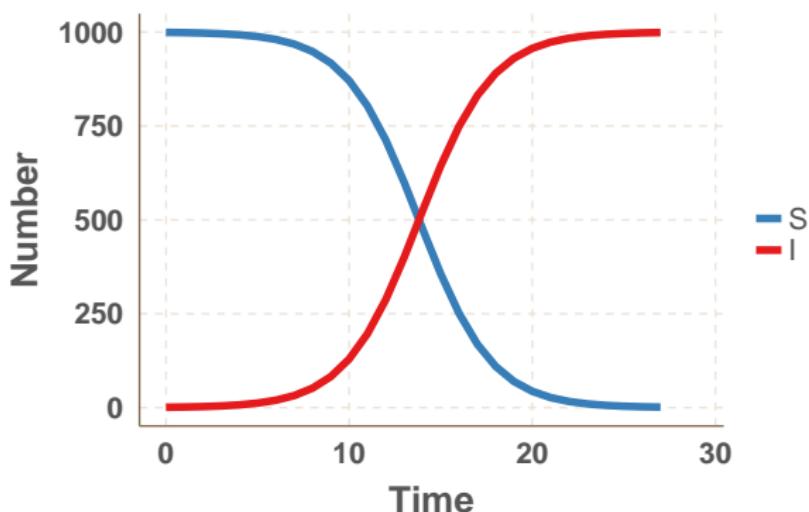
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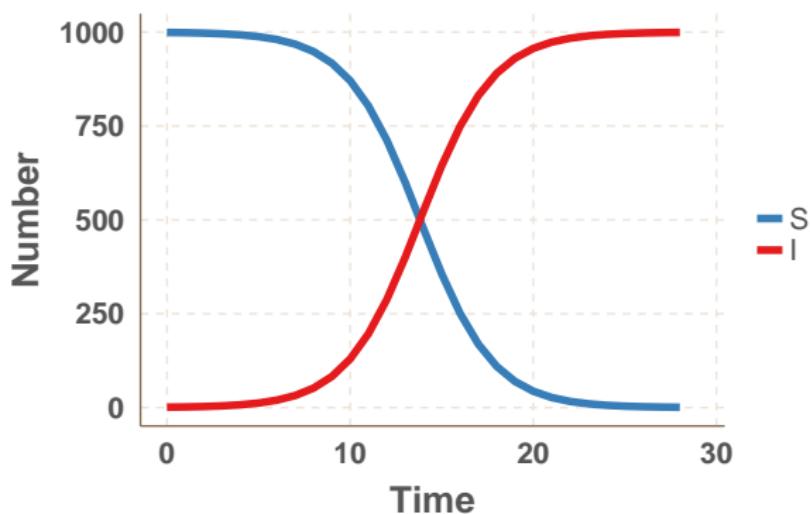
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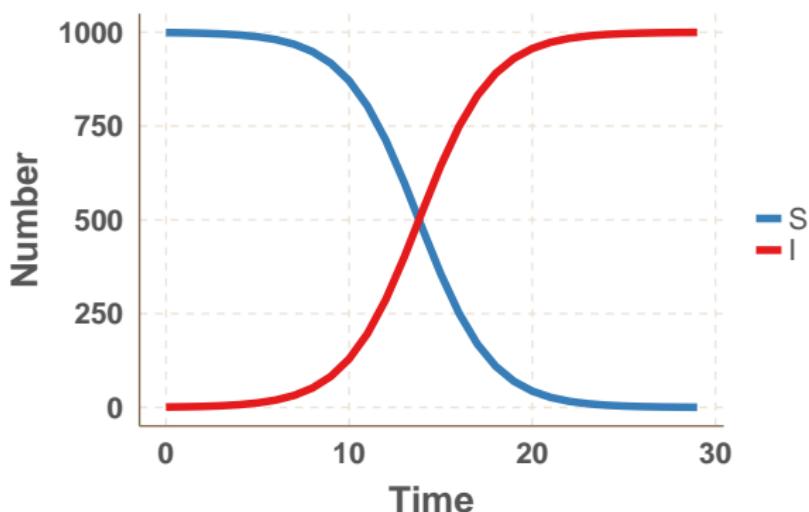
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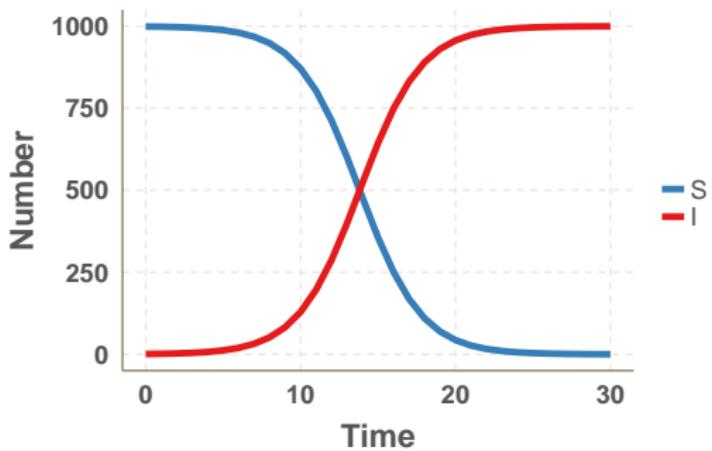
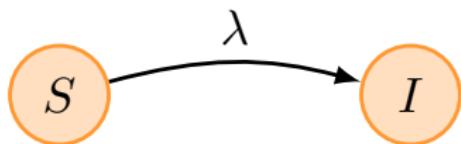
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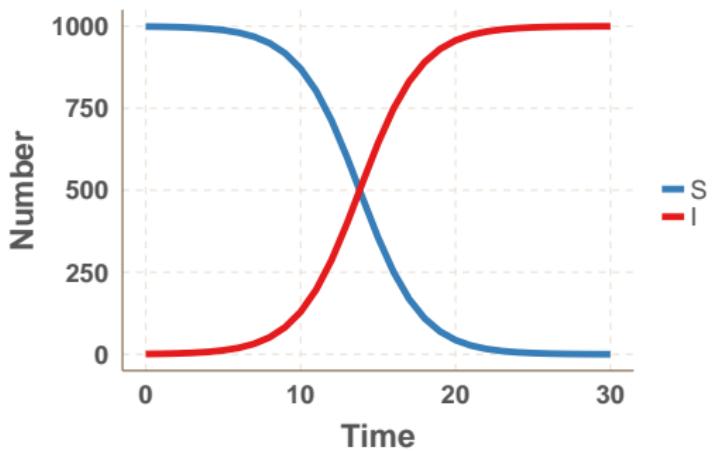
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## Properties of the SI model

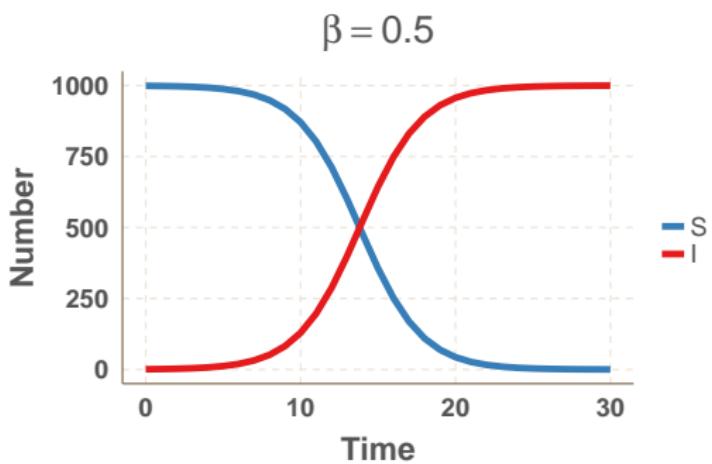


## Properties of the SI model



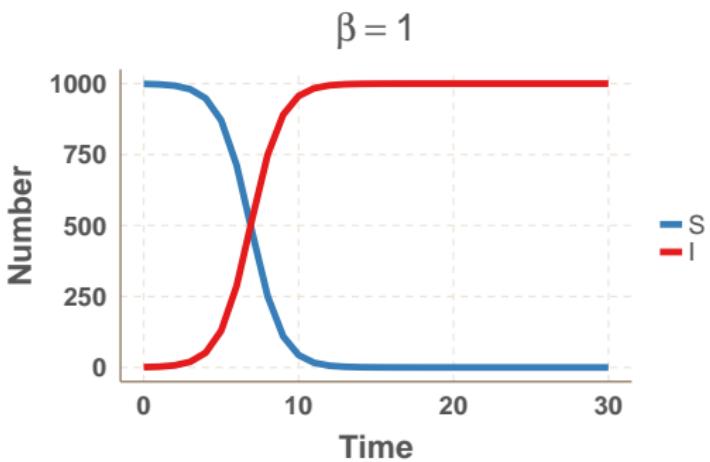
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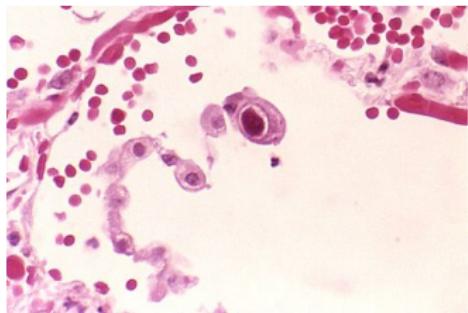
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For which infection is this a good model?

- Cytomegalovirus (CMV)

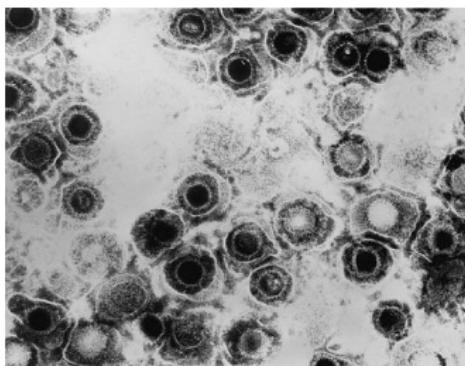
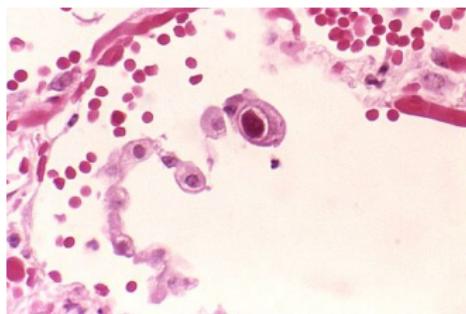


## Applications of the SI model

- Everyone in the population eventually gets infected
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For which infection is this a good model?

- Cytomegalovirus (CMV)
- Herpes simplex virus



## Extending the SI model

- The SI model assumes that people who get infected **stay** infectious **forever**

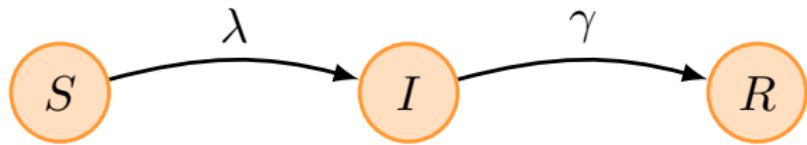
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- This is not the case for most infections (e.g., influenza, measles, etc.)

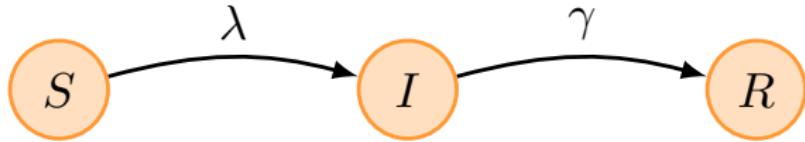
## Extending the SI model

- The SI model assumes that people who get infected stay infectious forever
- This is not the case for most infections (e.g., influenza, measles, etc.)
- Recovery from infection usually implies (some) immunity

## The SIR model

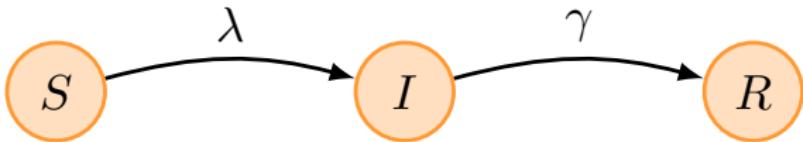


## The SIR model



- $R$ : Number of **recovered** (immune) people

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- $R$ : Number of **recovered** (immune) people
- $\gamma$ : recovery rate, or the probability of recovery per day (or per week, or per year). This is the inverse of the duration of infection  $D$ :  $\gamma = 1/D$

## Writing the SIR model as differential equations

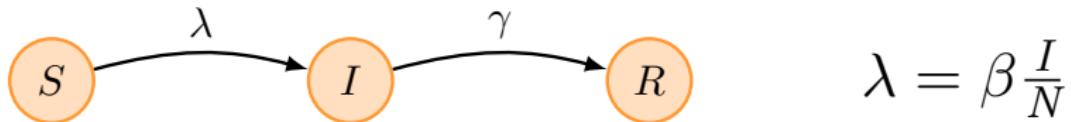


## Writing the SIR model as differential equations



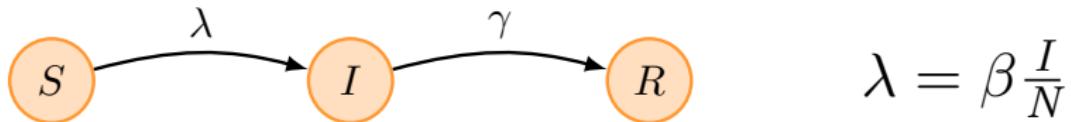
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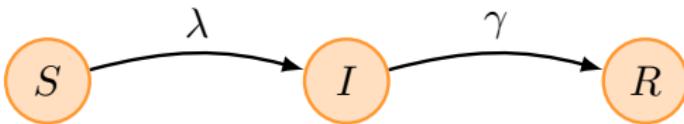
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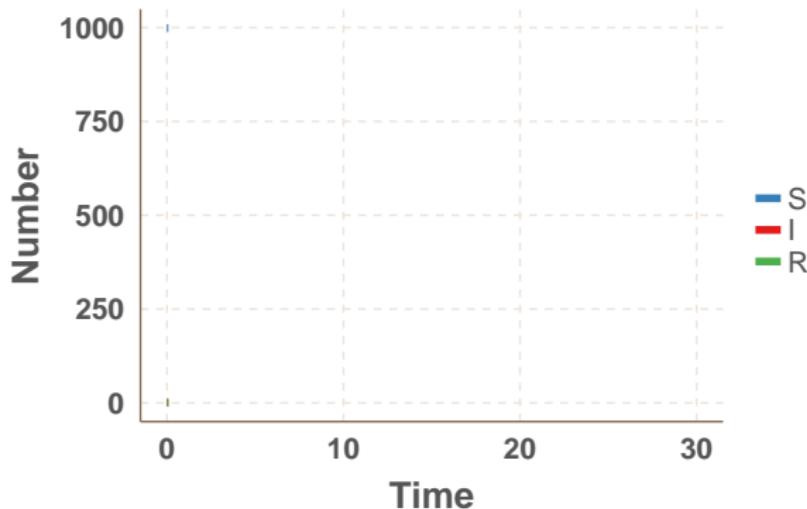
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## Simulating the SIR model using differential equations

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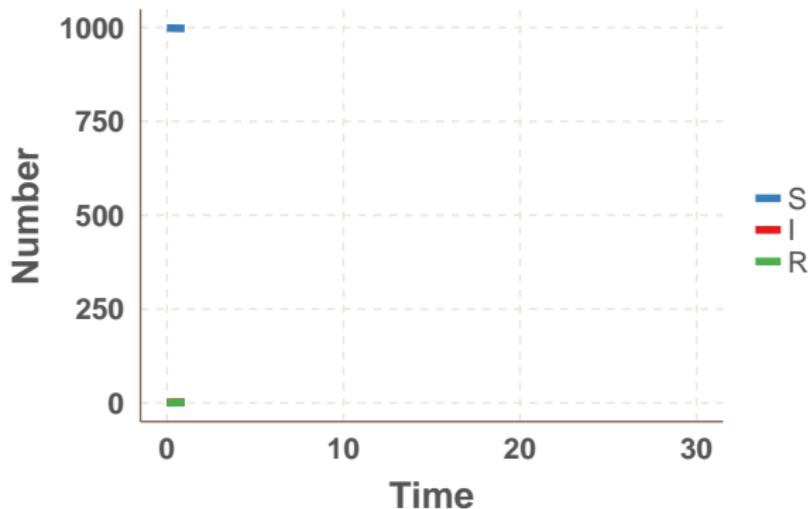


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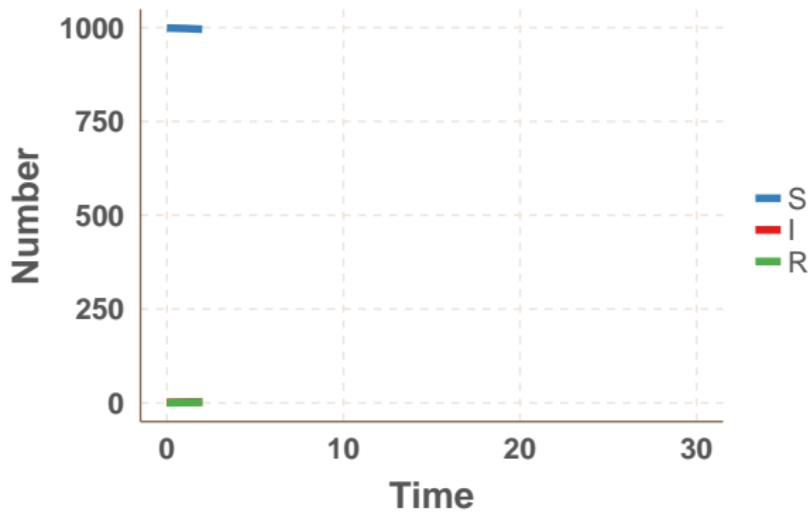


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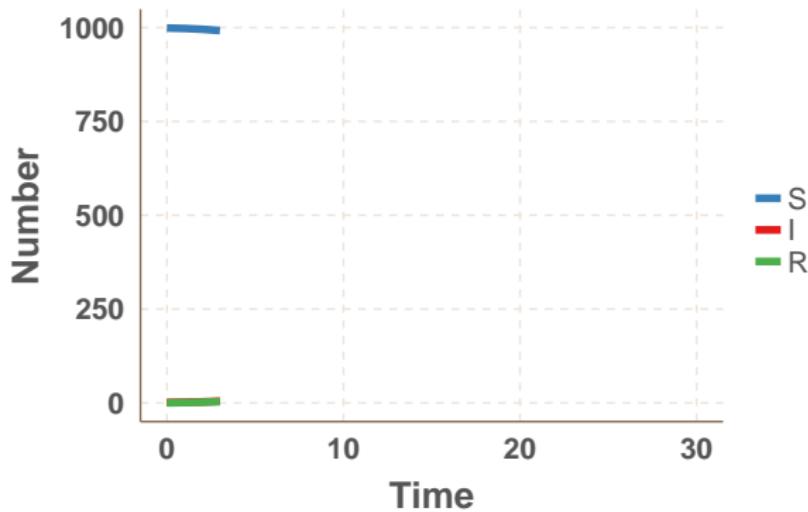


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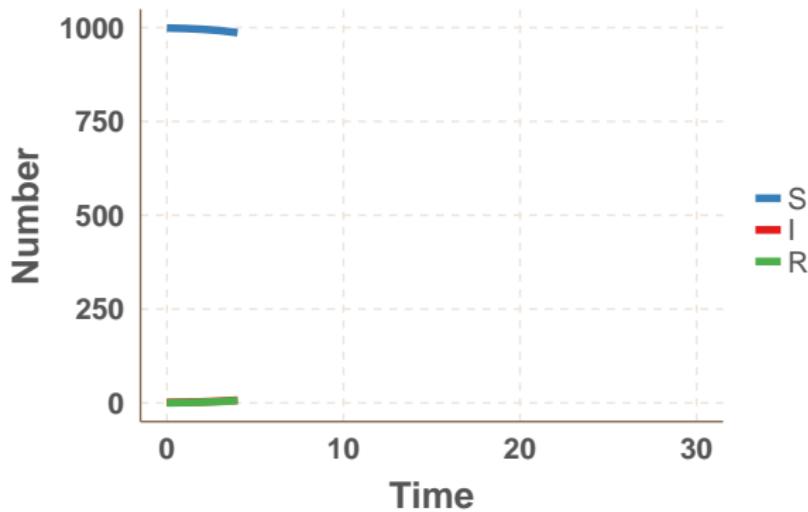


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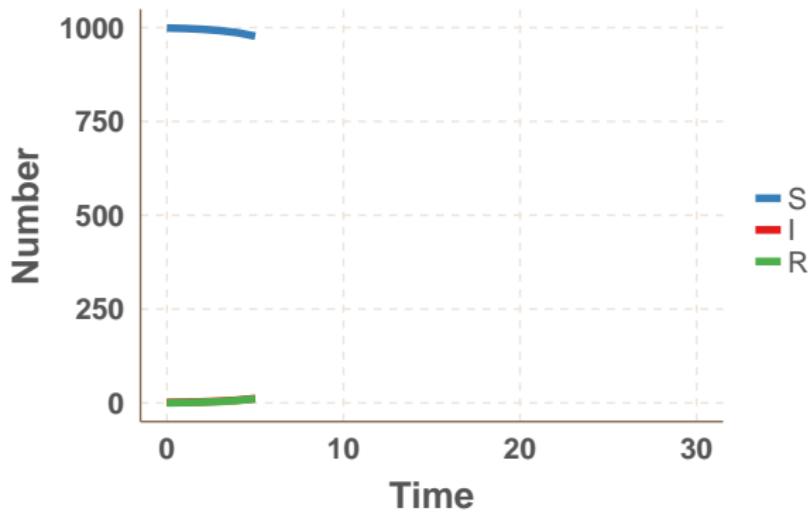


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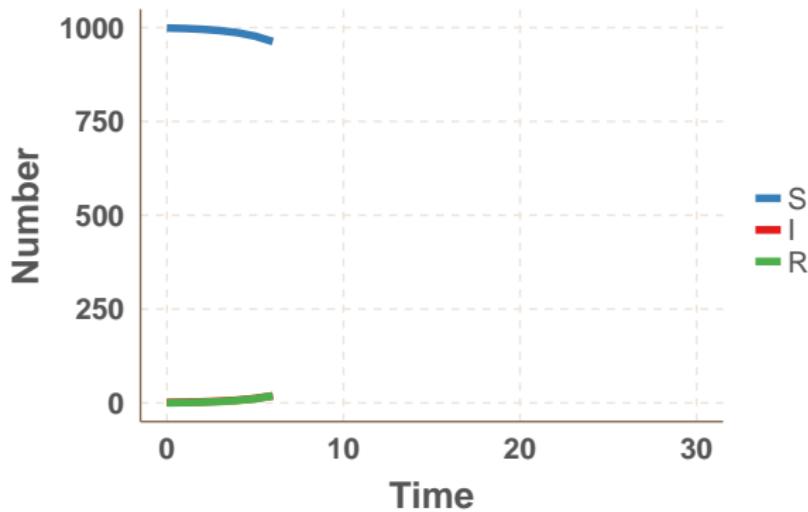


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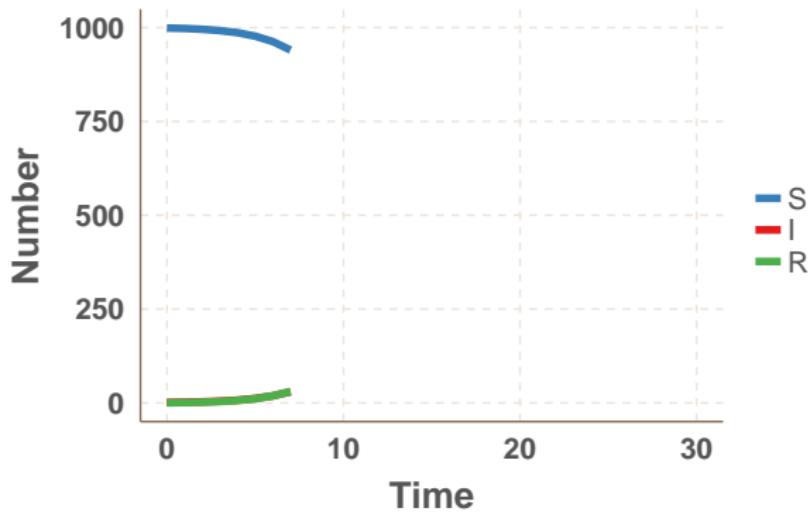


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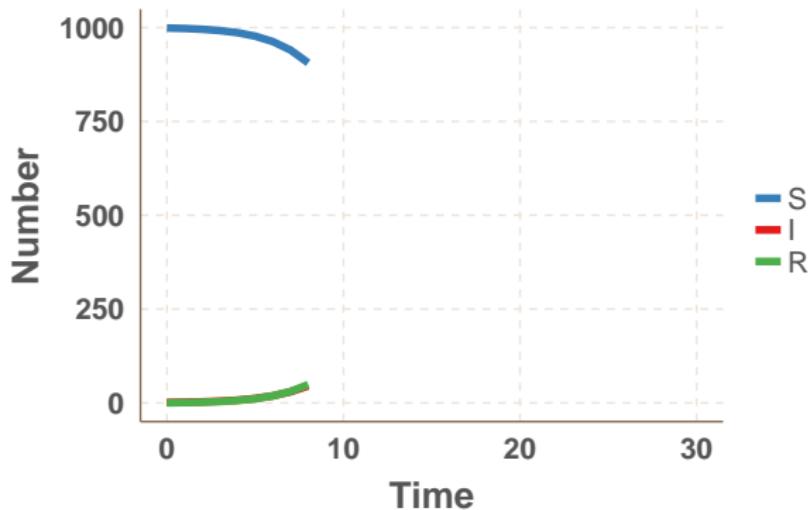


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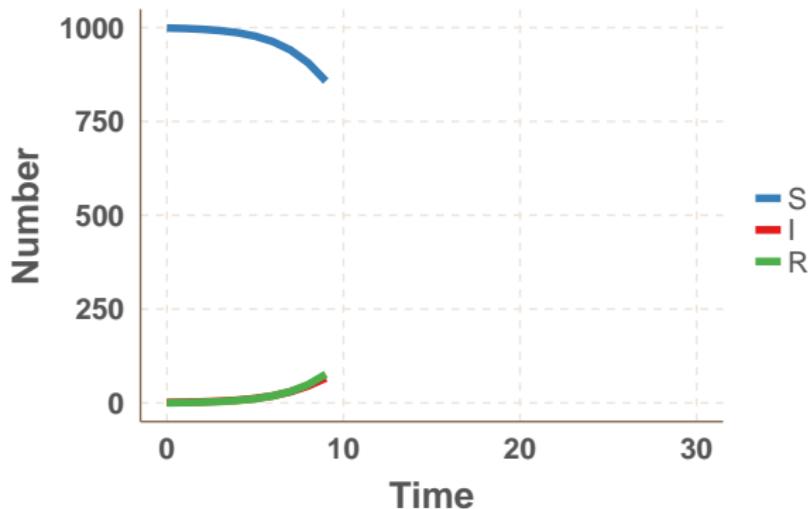


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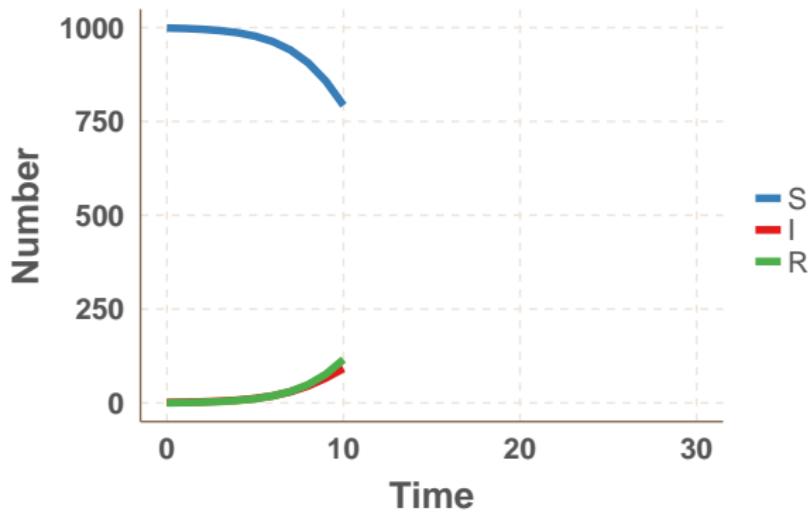


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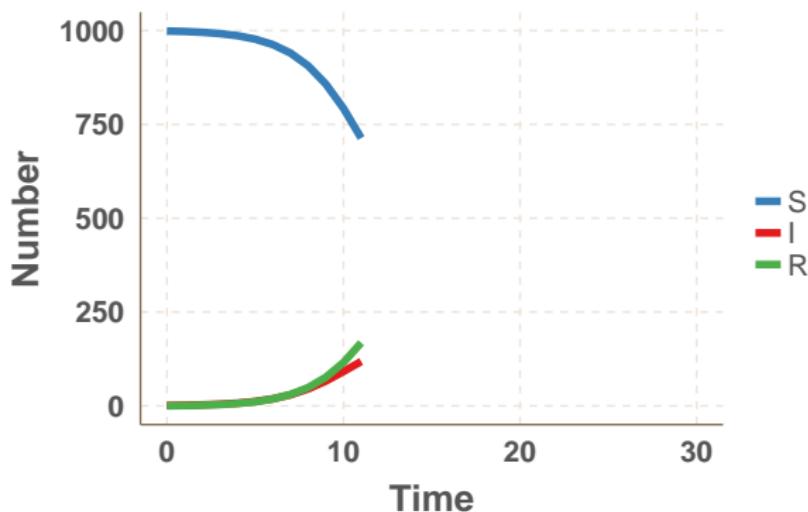


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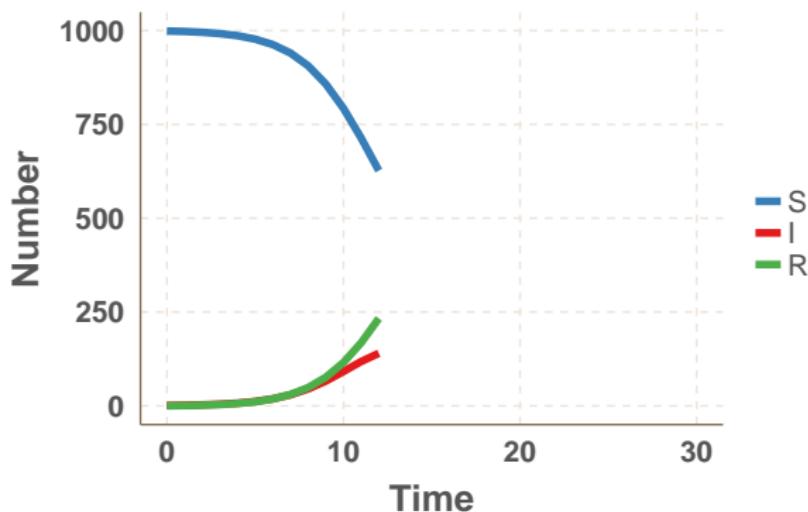


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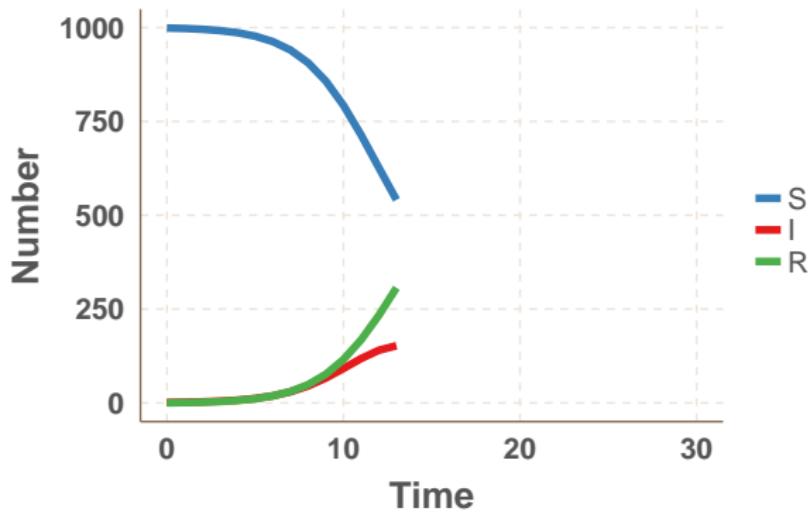


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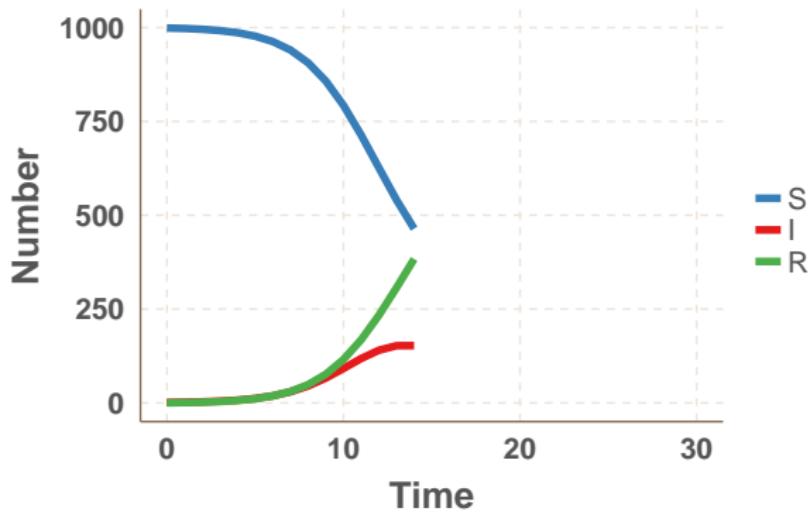


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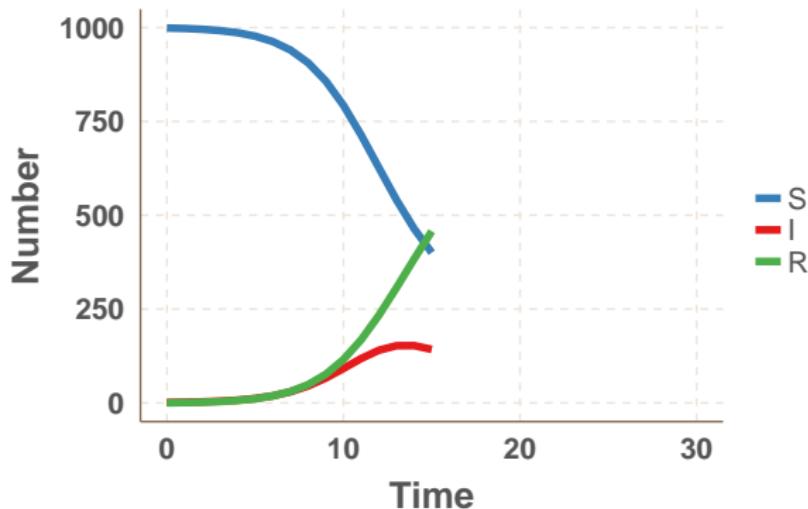


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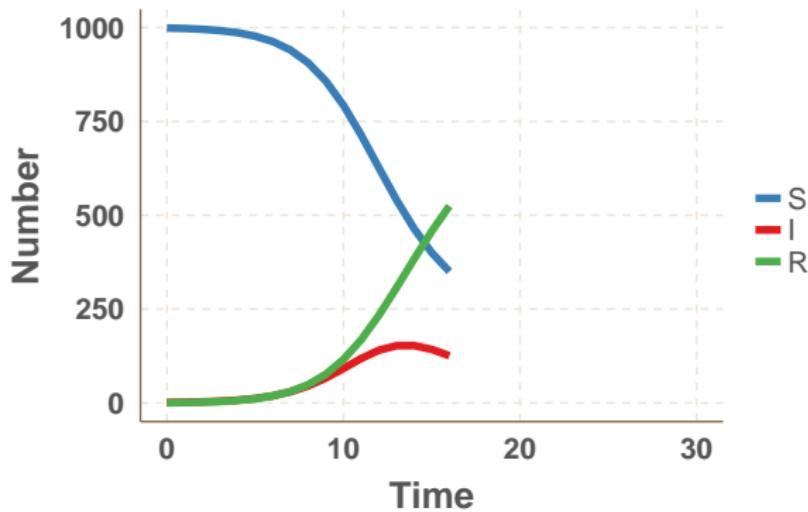


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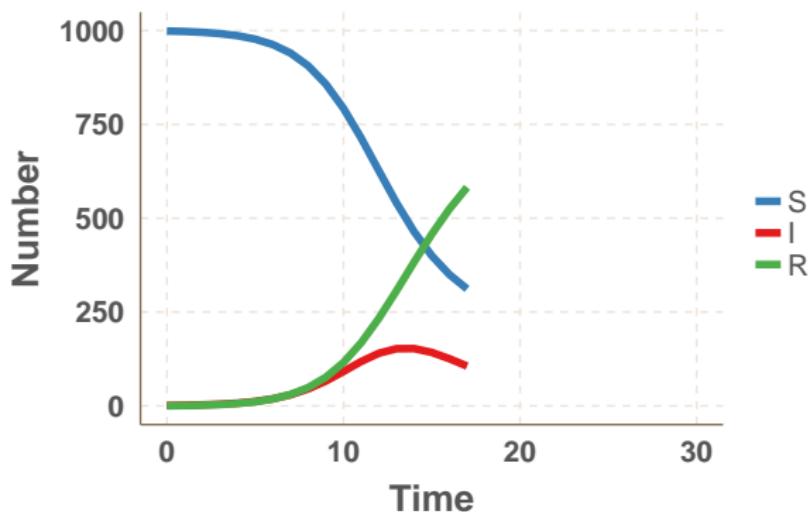


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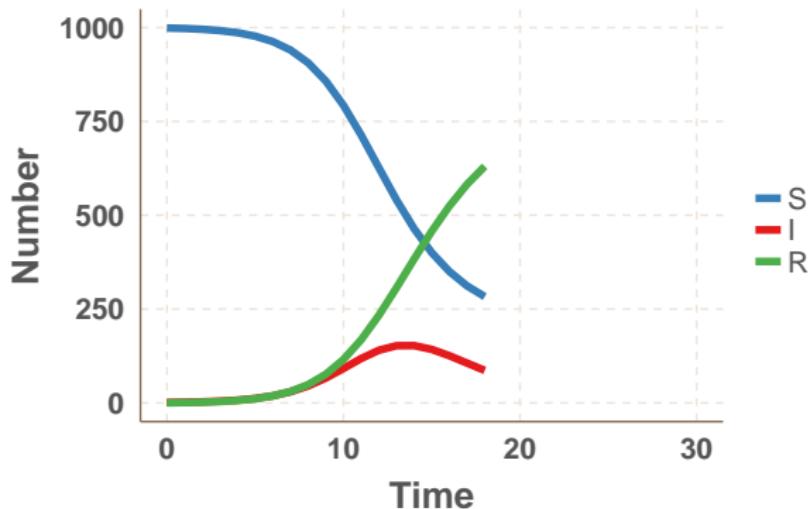


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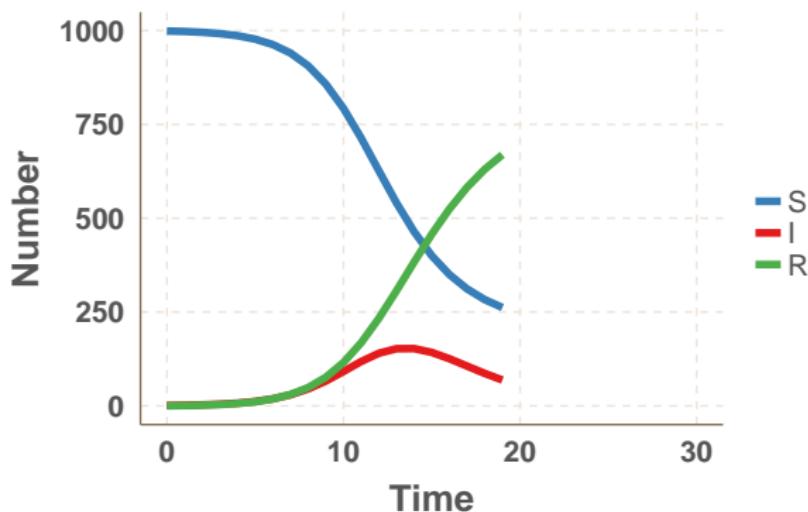


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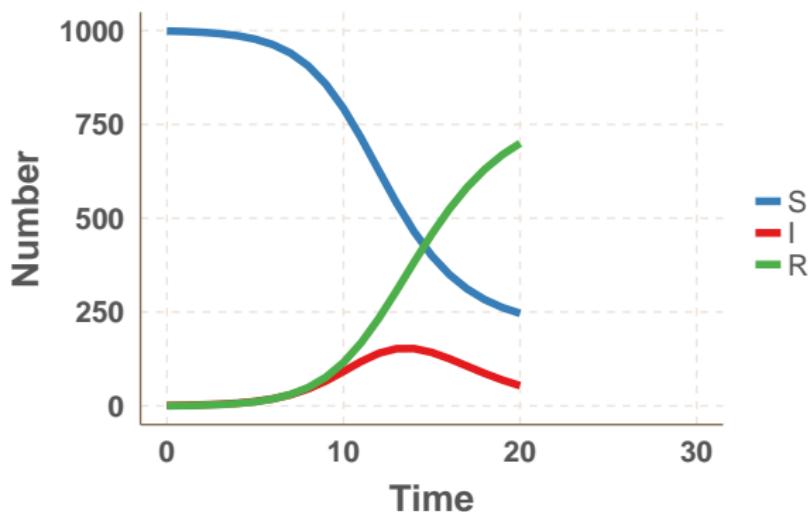


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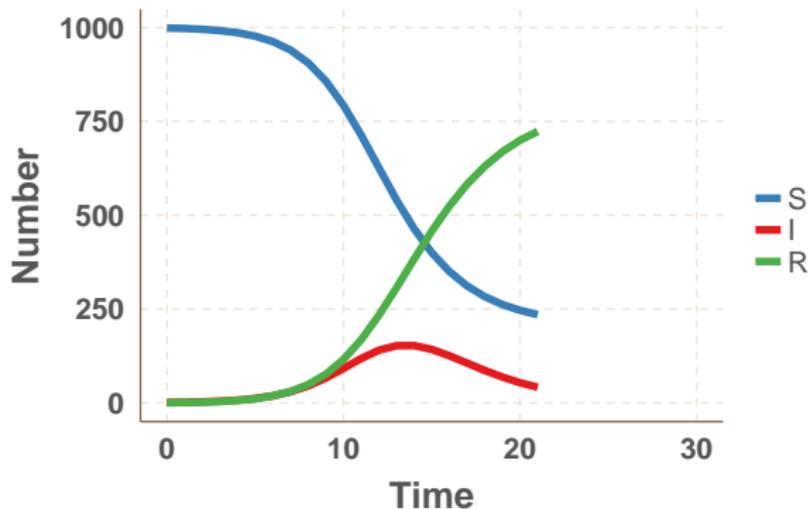


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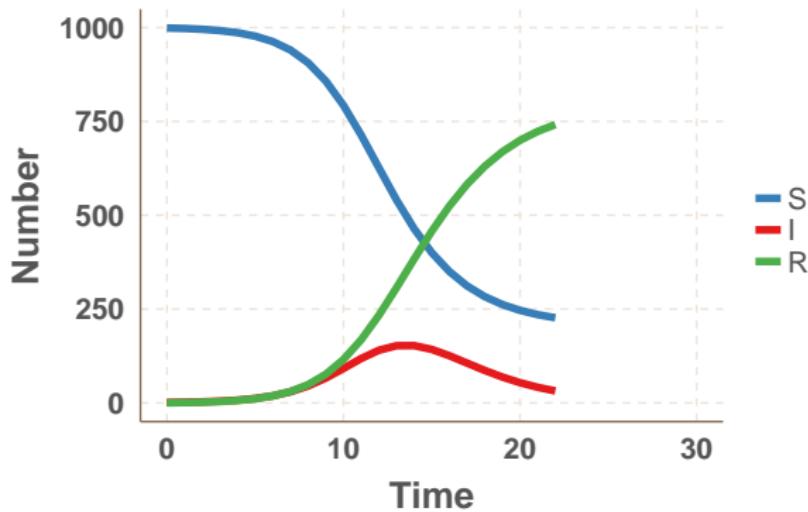


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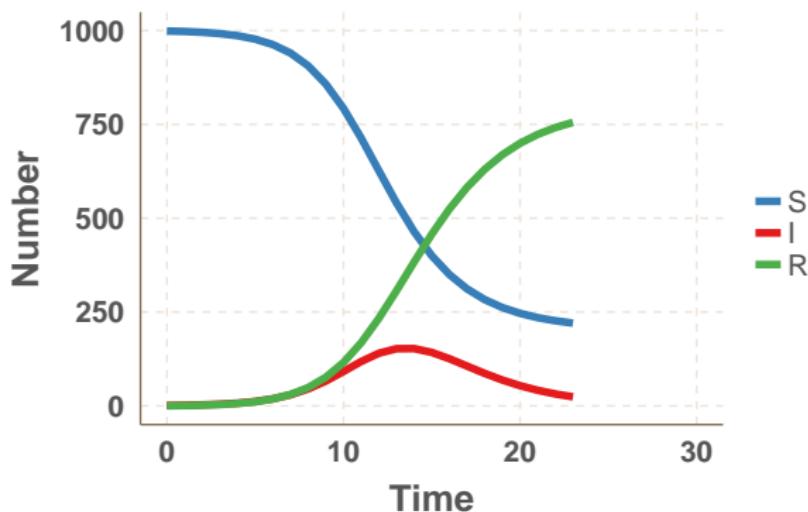


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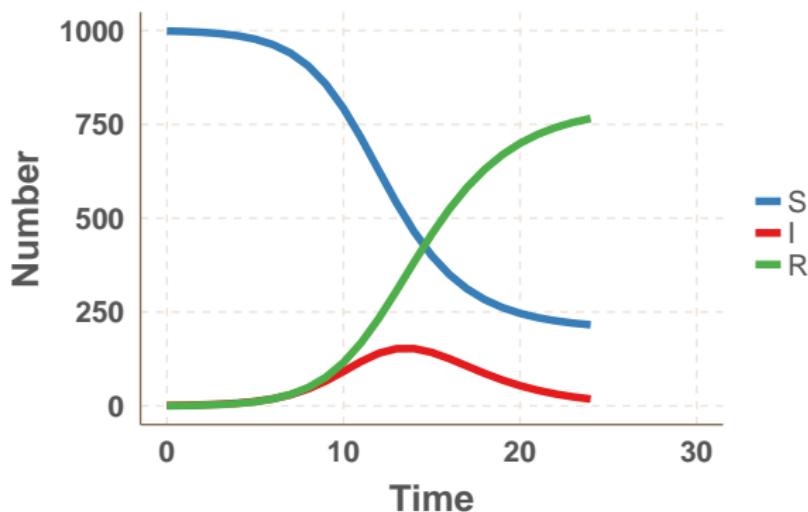


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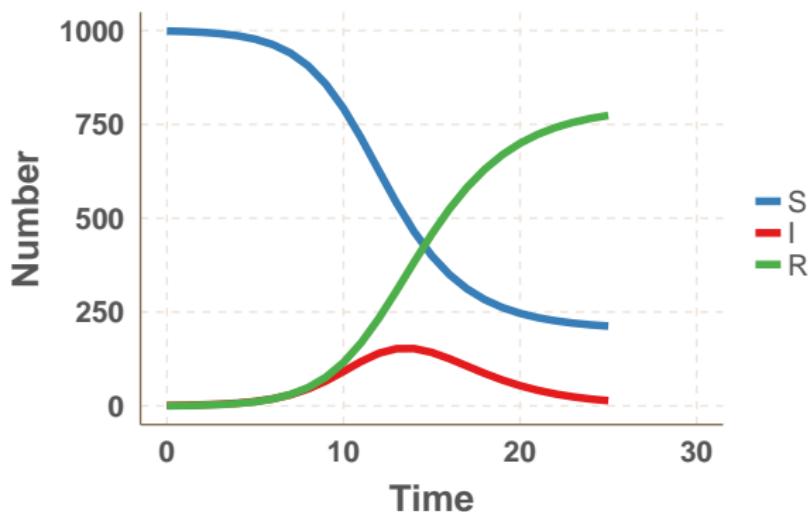


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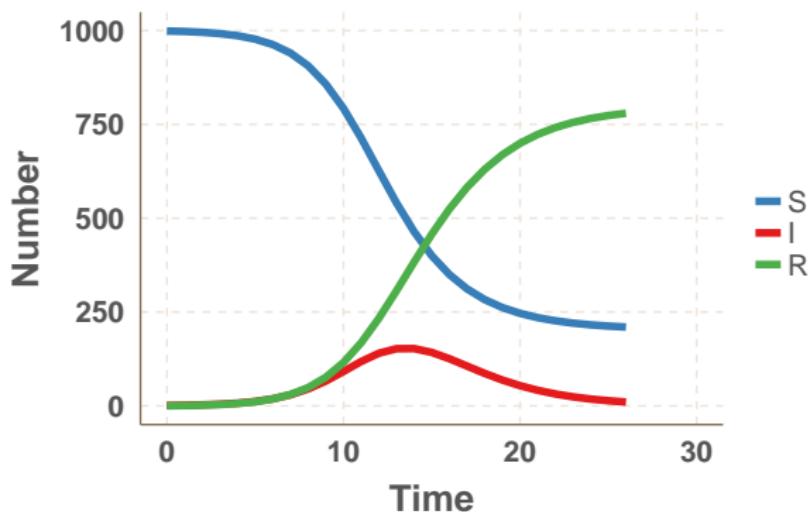


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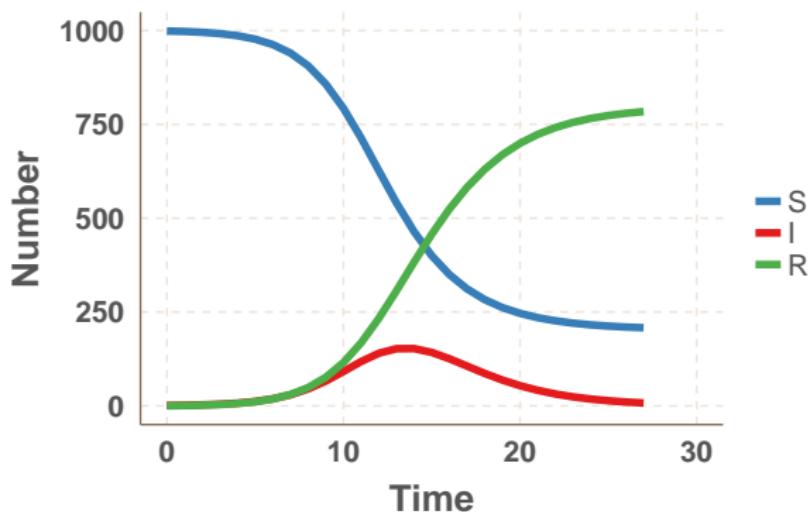


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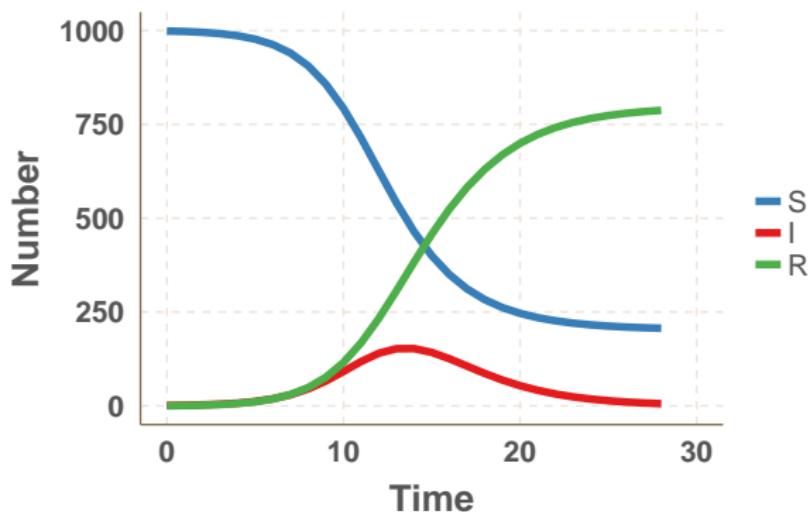


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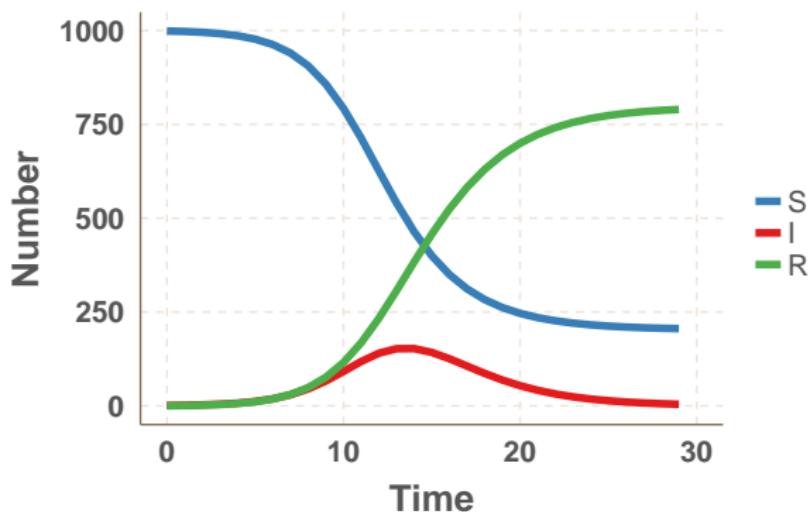


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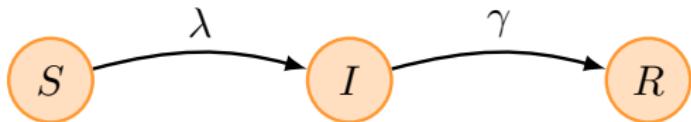
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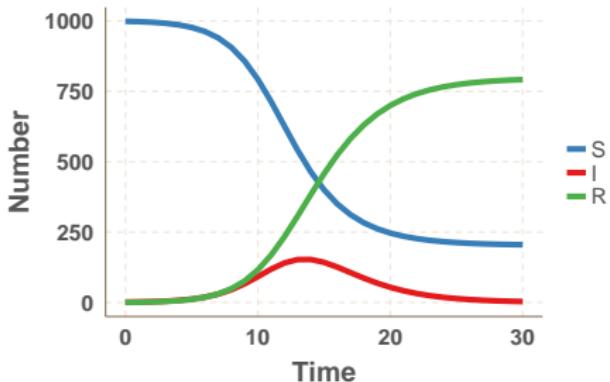
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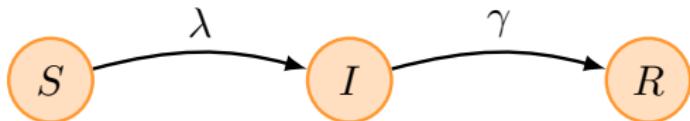
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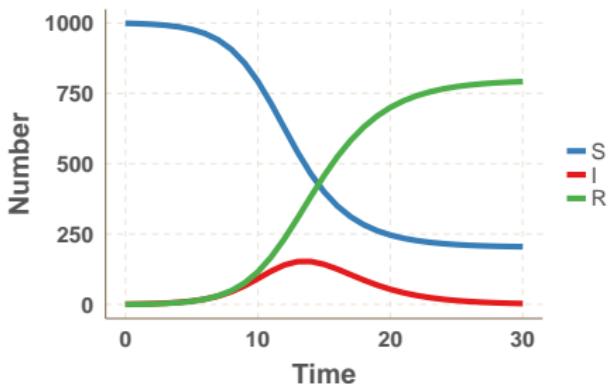
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## Properties of the SIR model

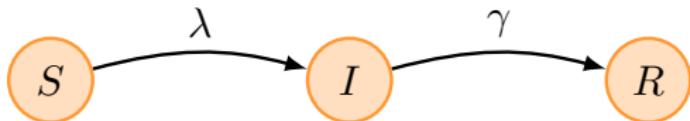


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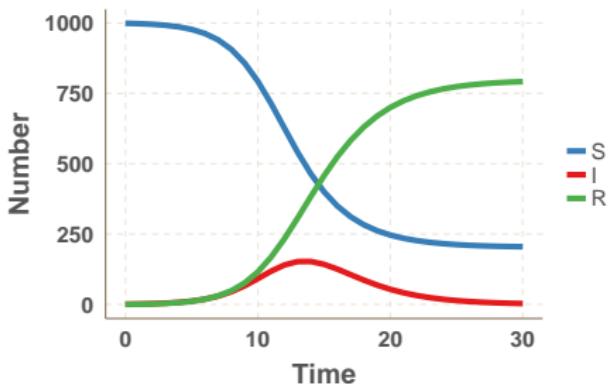


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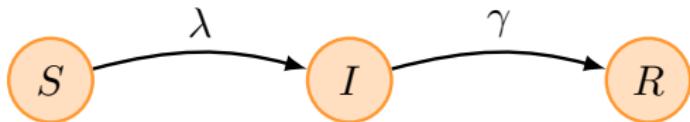


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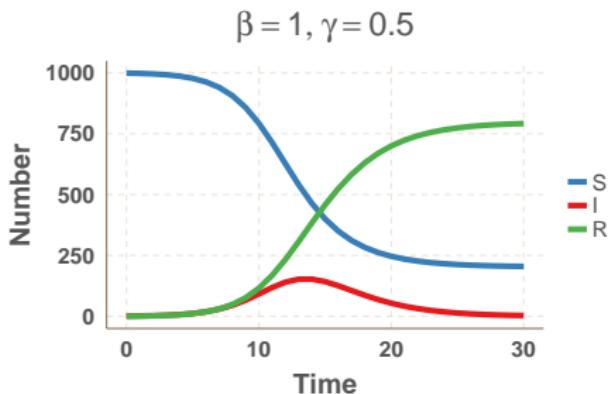


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## Properties of the SIR model

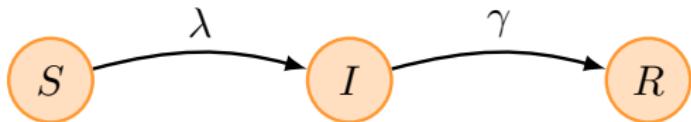


$$\lambda = \beta \frac{I}{N}$$

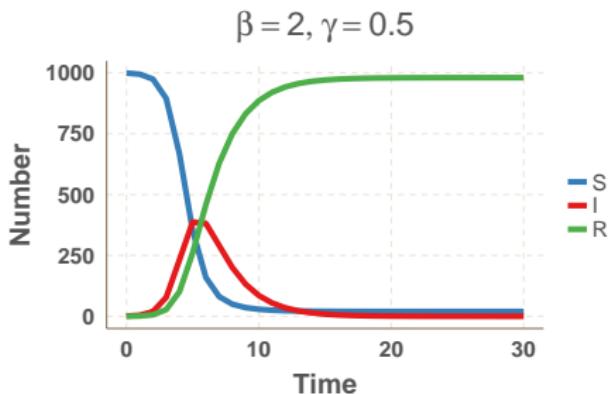


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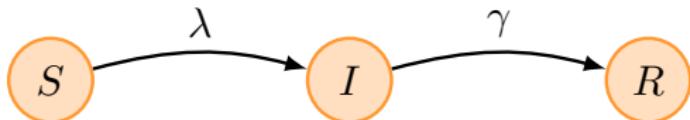


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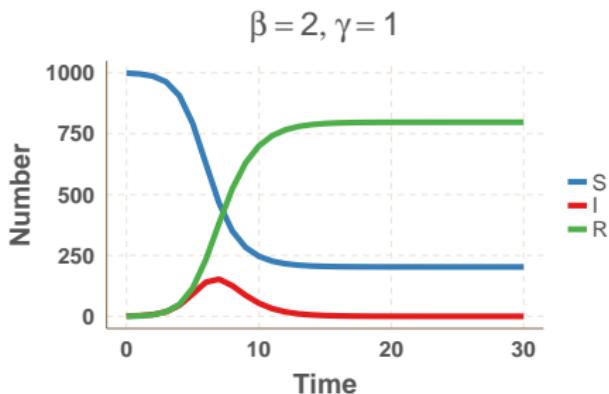


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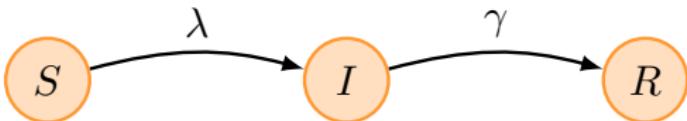


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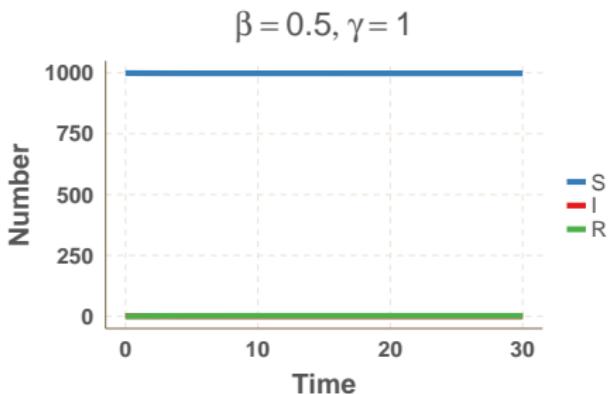


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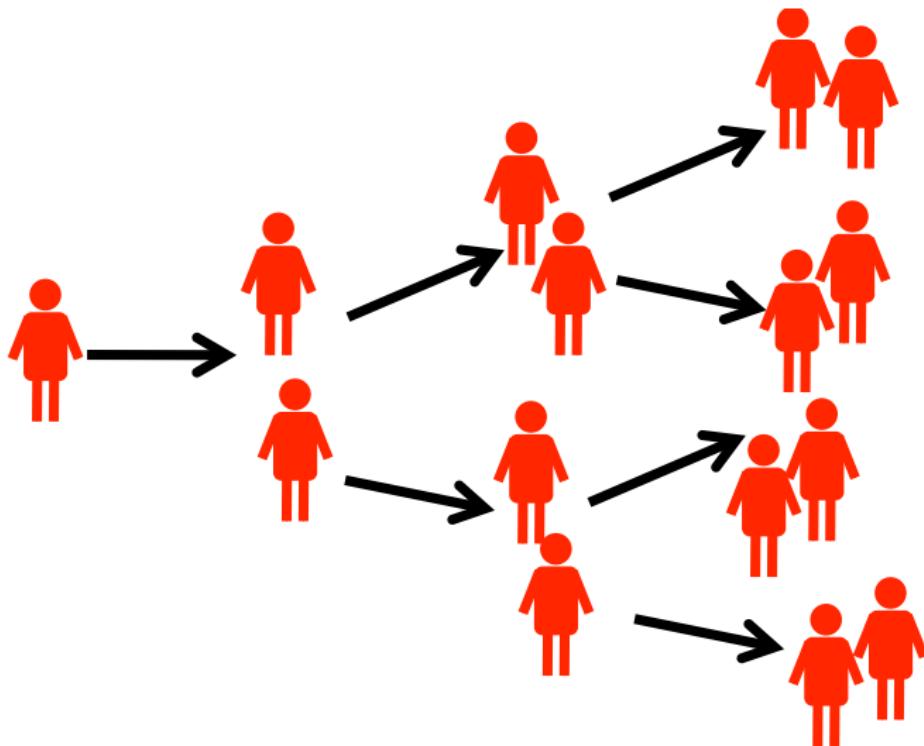
- Not everyone in the population eventually gets infected.
- The time and height of the peak, and the total number of people infected depends on  $\beta$  and  $\gamma$
- Sometimes almost nobody gets infected

# 4. The basic and net reproduction numbers

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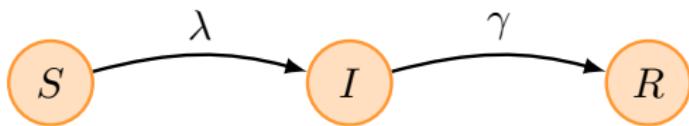
## Definition

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



## The basic reproduction number in the SIR model

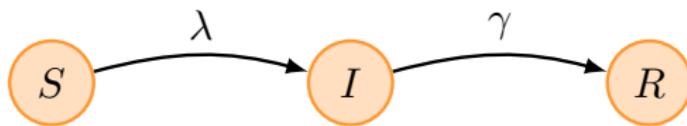
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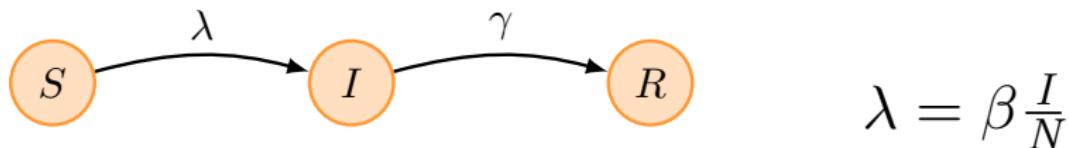


$$\lambda = \beta \frac{I}{N}$$

- single infectious case:  $I = 1$

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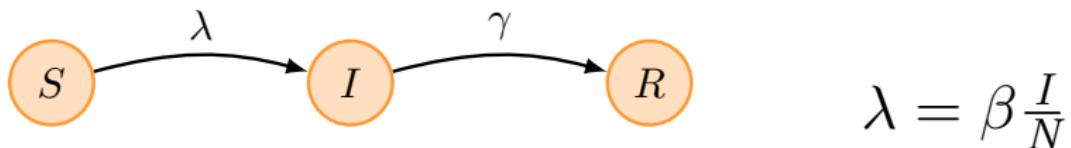
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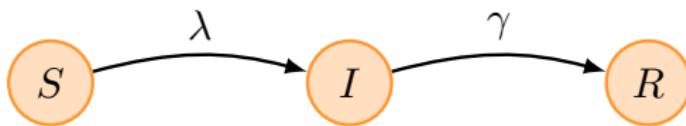
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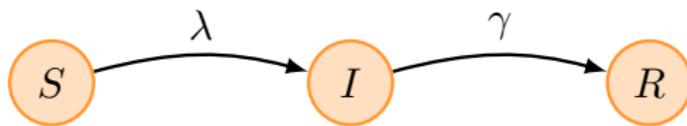


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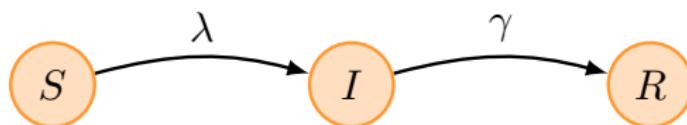


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$$R_0 = \beta D = \frac{\beta}{\gamma}$$

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How does the number of infected change?

$$dI/dt = \beta \frac{I}{N} S - \gamma I$$

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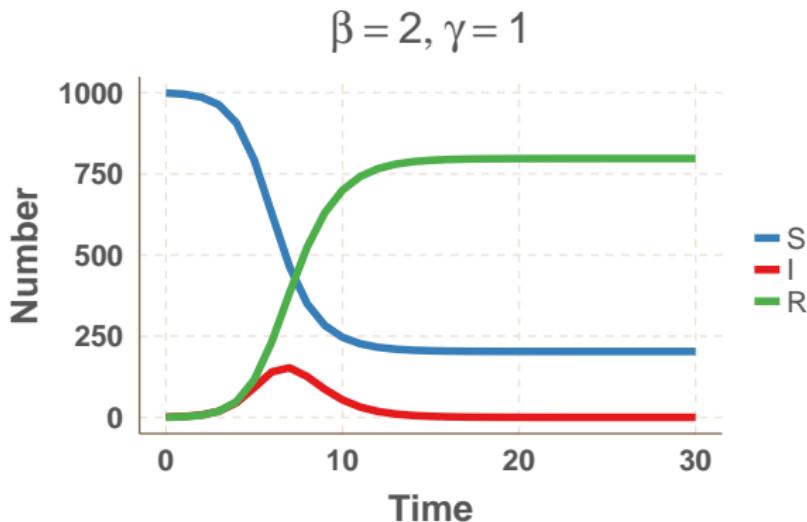
- **increase** if  $R_0 > 1$
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The value of  $R_0$  reveals if a newly introduced disease will spread or die out.

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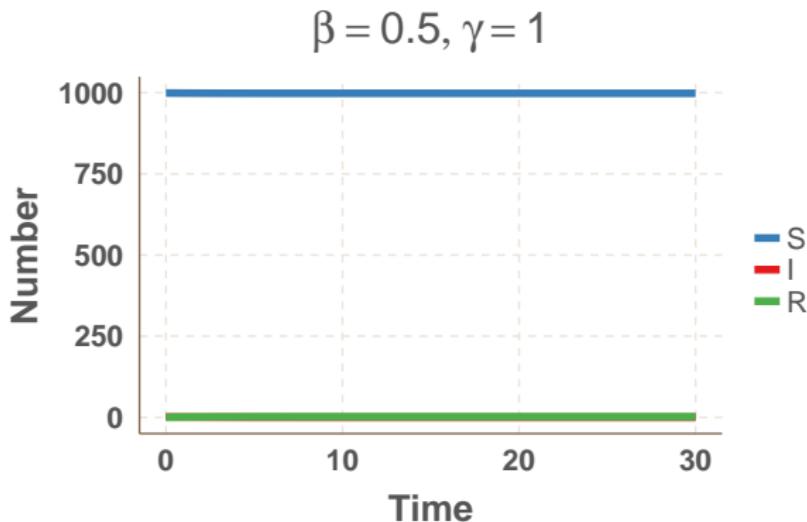


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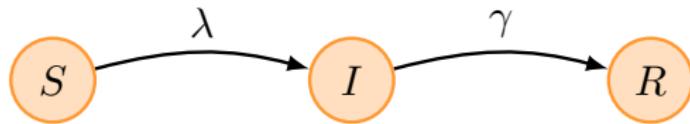
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$$R_0 = 0.5$$

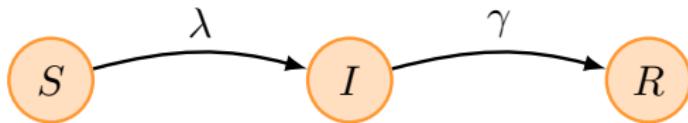
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The average number of **secondary infectious cases** resulting from **each infectious case** in a given population.



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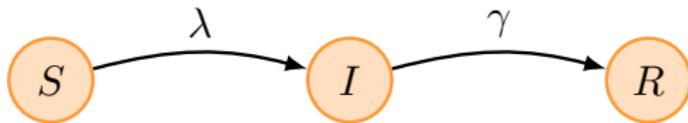
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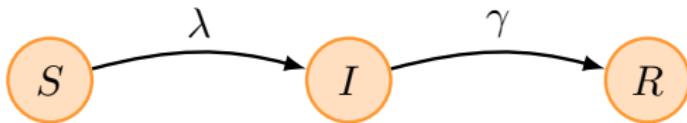
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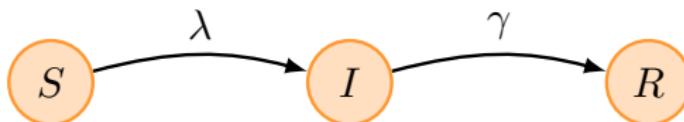
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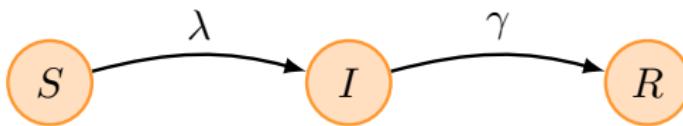


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$$R_n = \frac{\beta}{\gamma} \frac{S}{N} = R_0 \frac{S}{N}$$

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$$R_n = \frac{\beta}{\gamma} \frac{S}{N} = R_0 \frac{S}{N}$$

The net reproduction number is the basic reproduction number multiplied with the **proportion** of the population that is currently **susceptible**.

## Properties of $R_n$ in the SIR model

$$R_n = \frac{\beta}{\gamma} \frac{S}{N}$$

How does the number of infectious change over time?

$$dI/dt = \beta \frac{I}{N} S - \gamma I$$

We can rewrite this as

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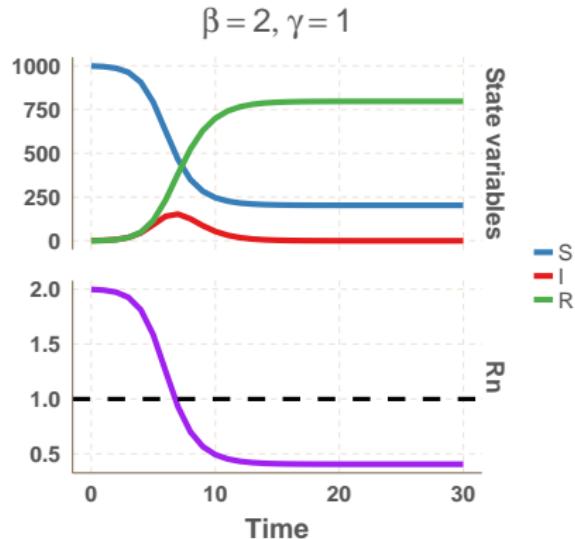
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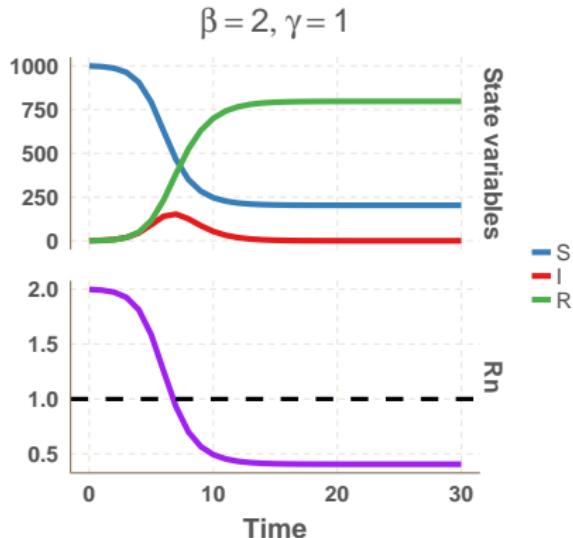
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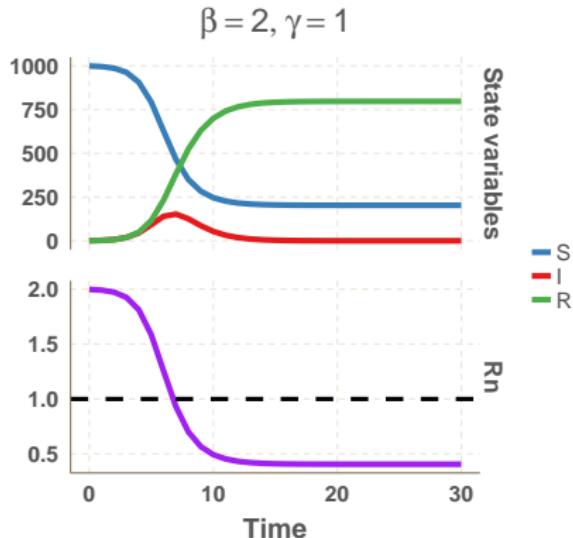


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- This is called the herd immunity threshold.
- Important: You do not have to vaccinate everyone (herd immunity)

## Examples: The herd immunity threshold

Infectious disease	Herd immunity threshold (%)
Malaria	99
Measles	90-95
Whooping cough	90-95
Chickenpox	85-90
Mumps	85-90
Rubella	82-87
Polio	82-87
Diphtheria	82-87
Smallpox	70-80
Influenza	40-60

## Applications of the SIR model

- Not everyone in the population eventually gets infected
- If  $R_0 > 1$ , the infection spreads and then dies out

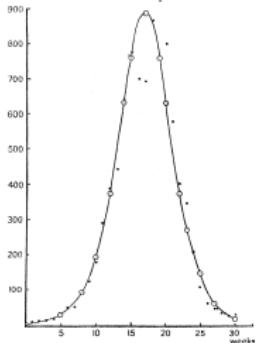
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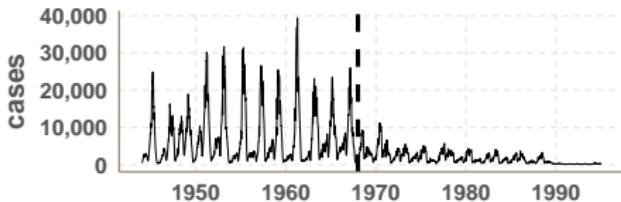
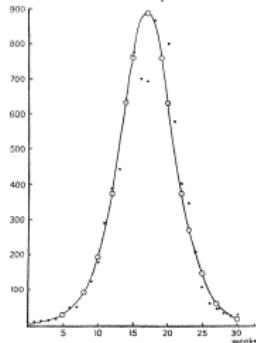


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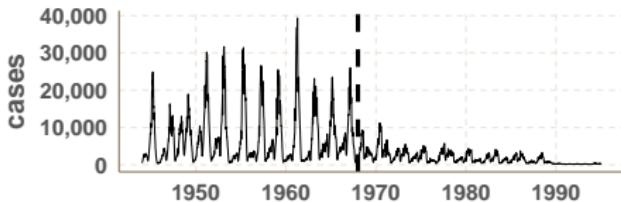
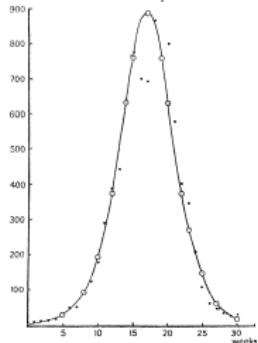


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- Influenza?



# 5. Modelling endemic diseases

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  - births (“childhood diseases”)

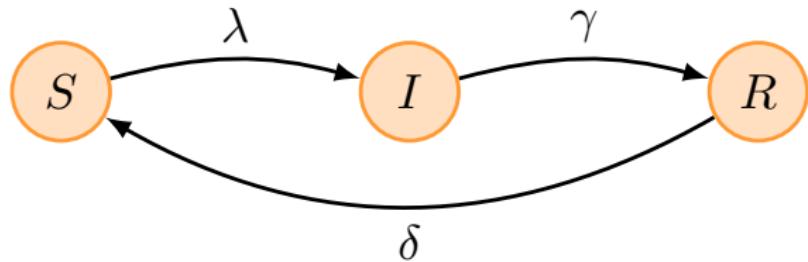
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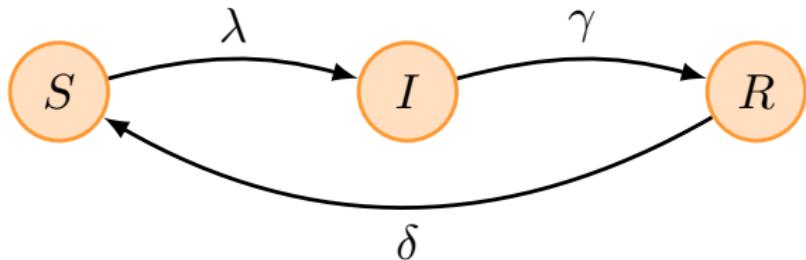
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  - loss of immunity (examples: Cholera, many others)
  - immigration (not usually a significant factor)

## The SIRS model

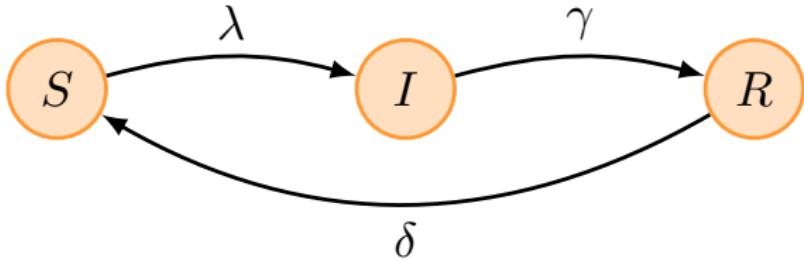


## The SIRS model



- $\delta$ : rate of immunity loss, or the probability of losing immunity per day (or per week, or per year). This is the inverse of the duration of immunity  $M$ :

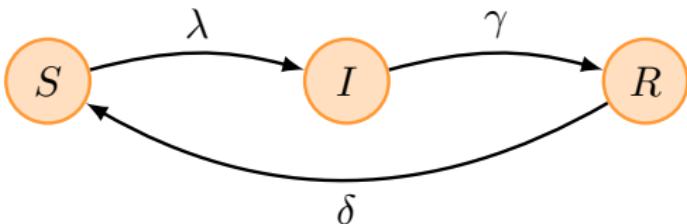
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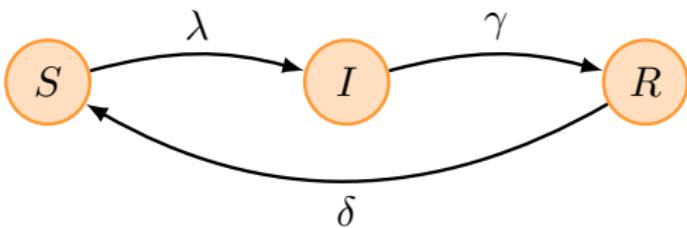
$$\delta = \frac{1}{M}$$

## Writing the SIRS model as differential equations



- $S$ : Number of people susceptible
- $I$ : Number of people infectious
- $R$ : Number of people recovered
- How does the number of people susceptible, infectious and recovered change over time?

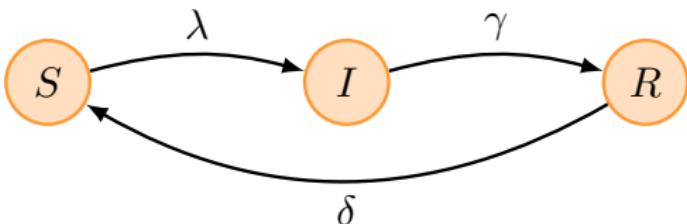
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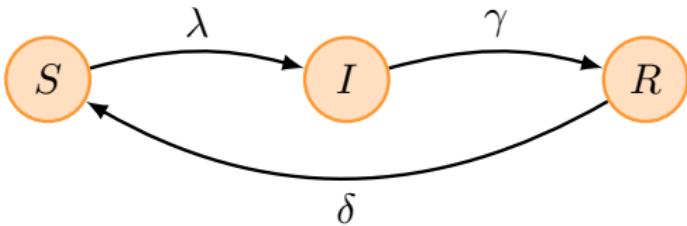


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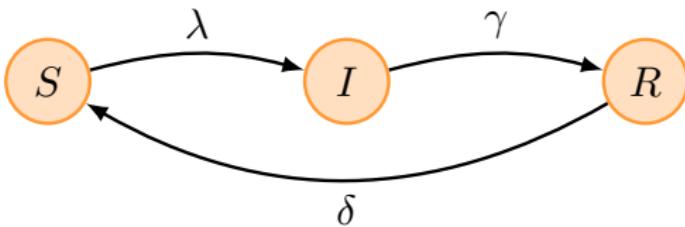
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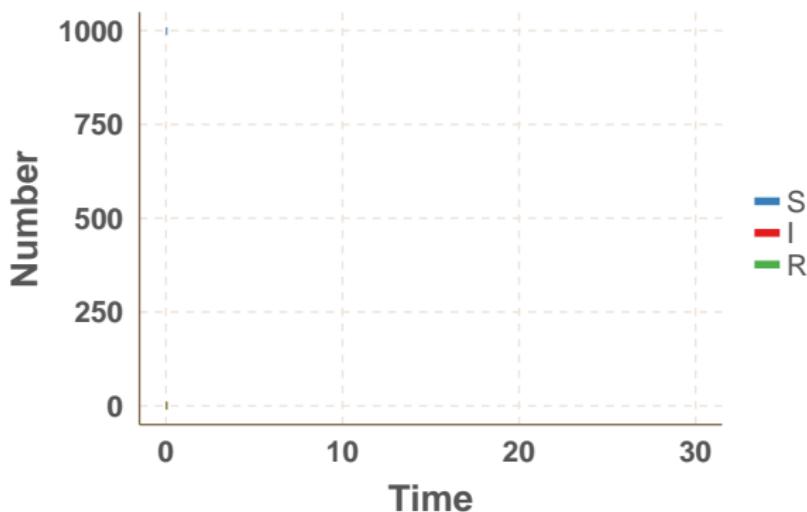
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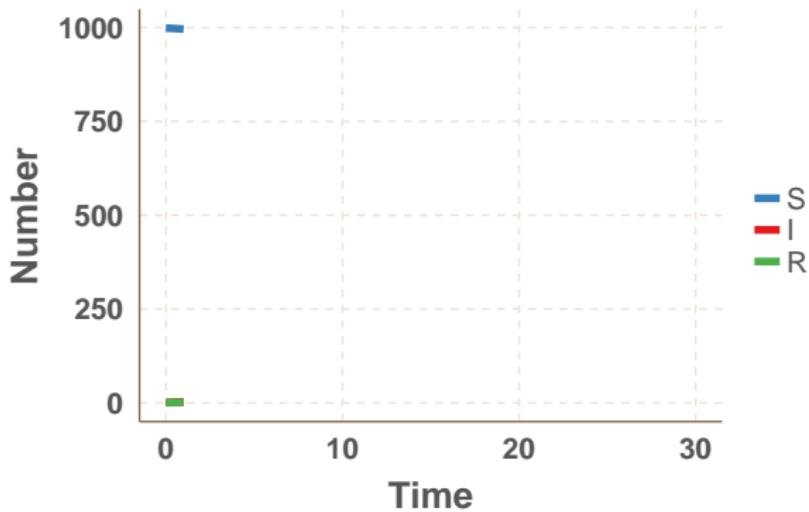


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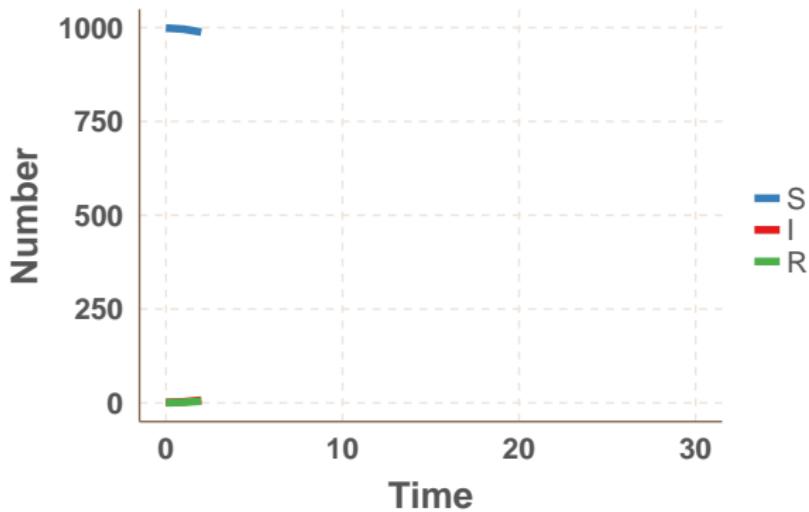


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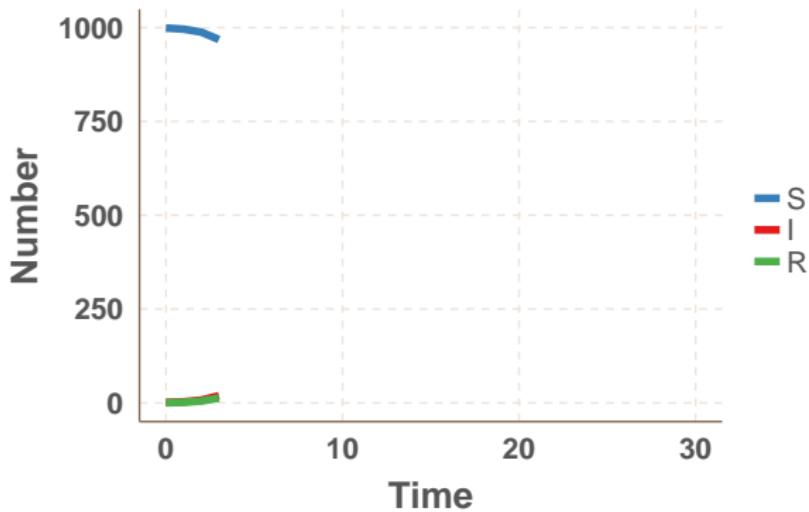


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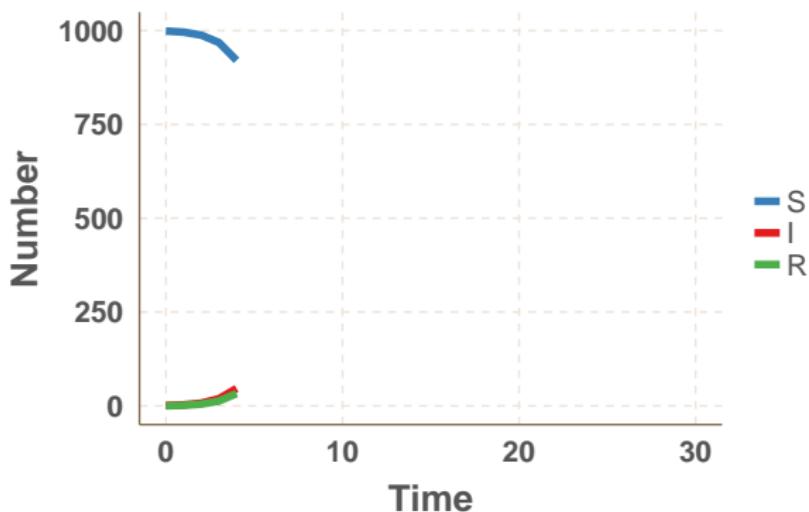


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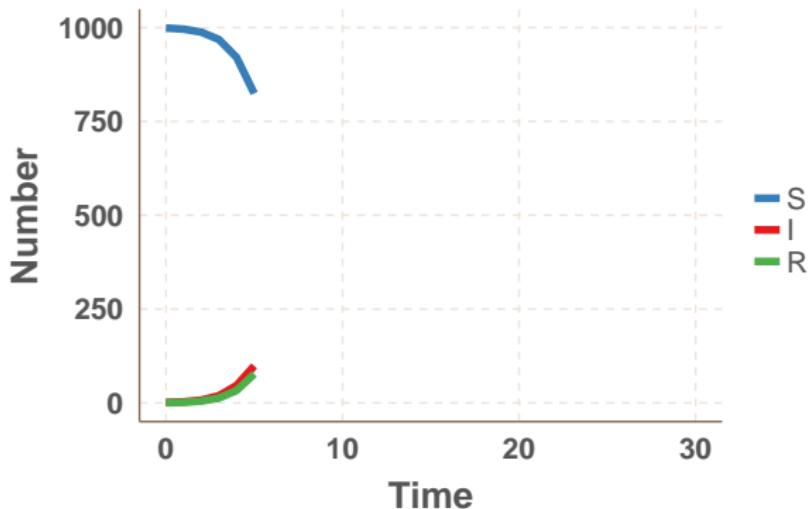


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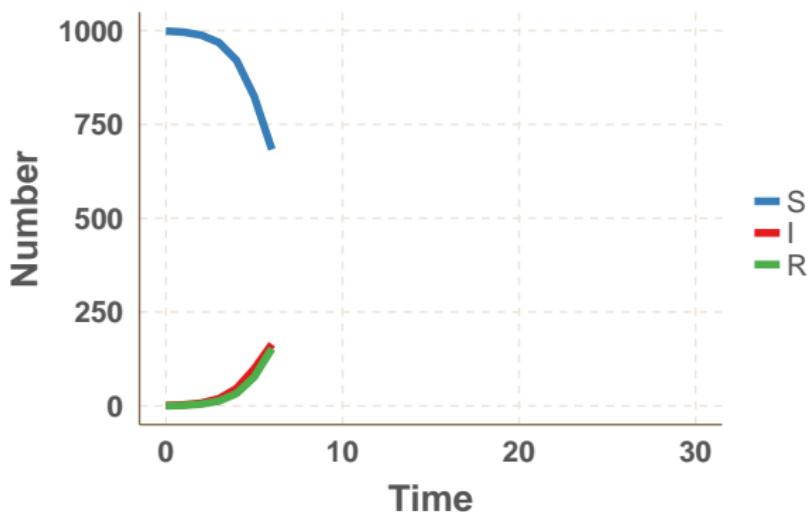


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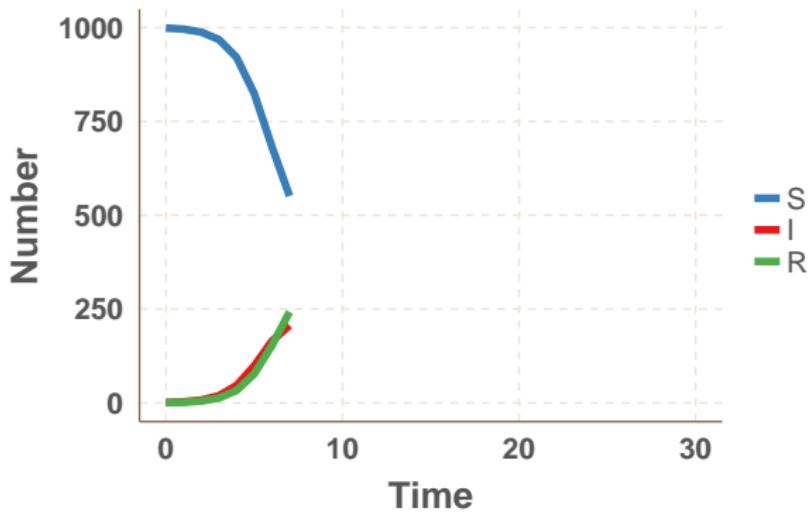


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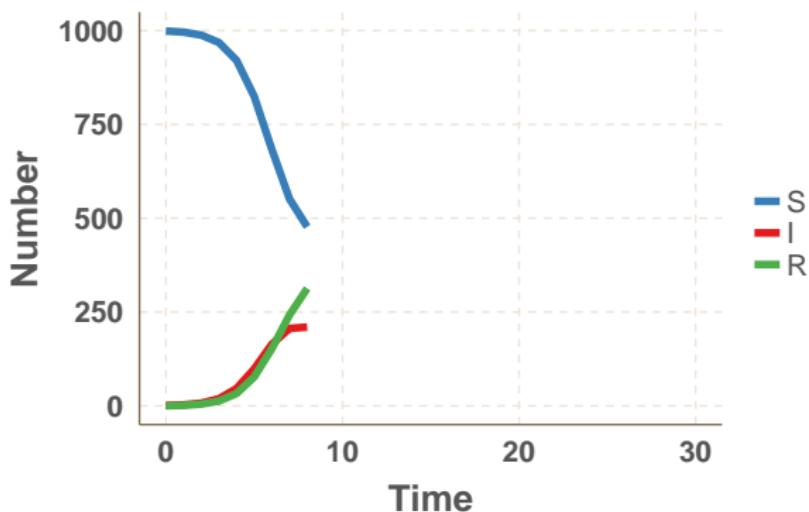


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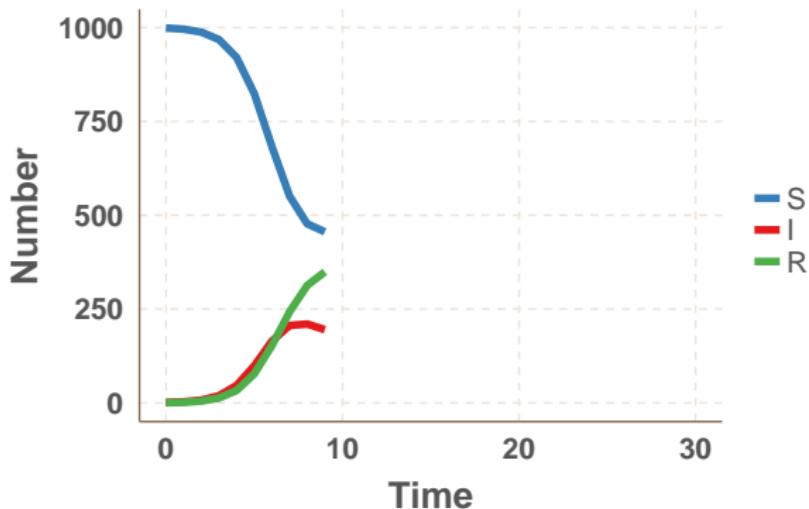


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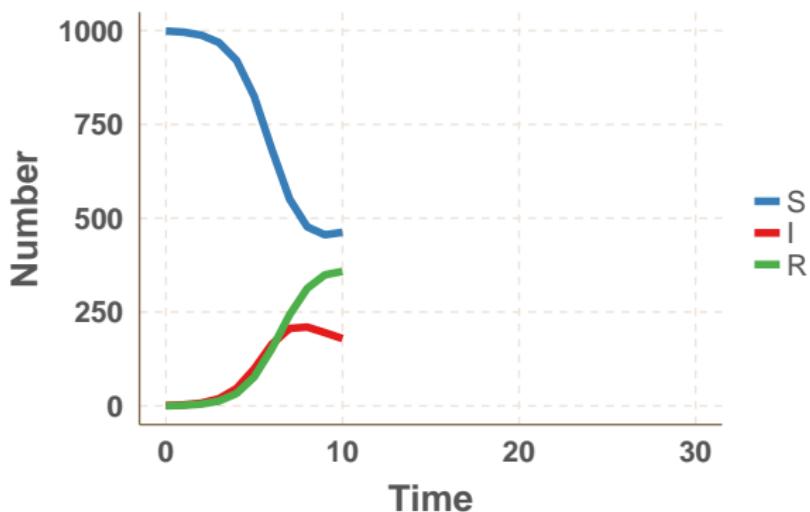


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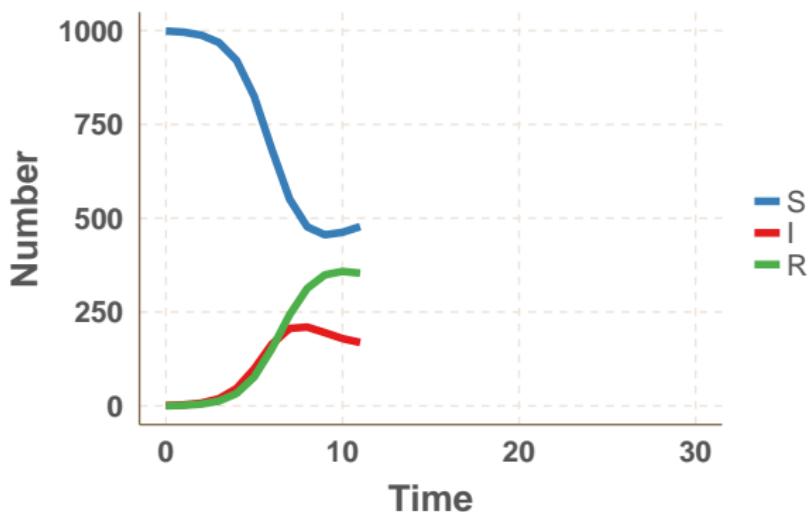


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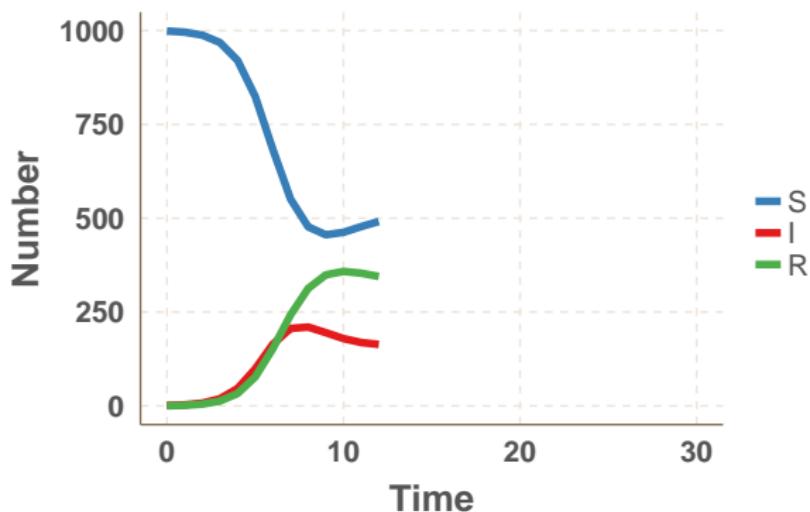


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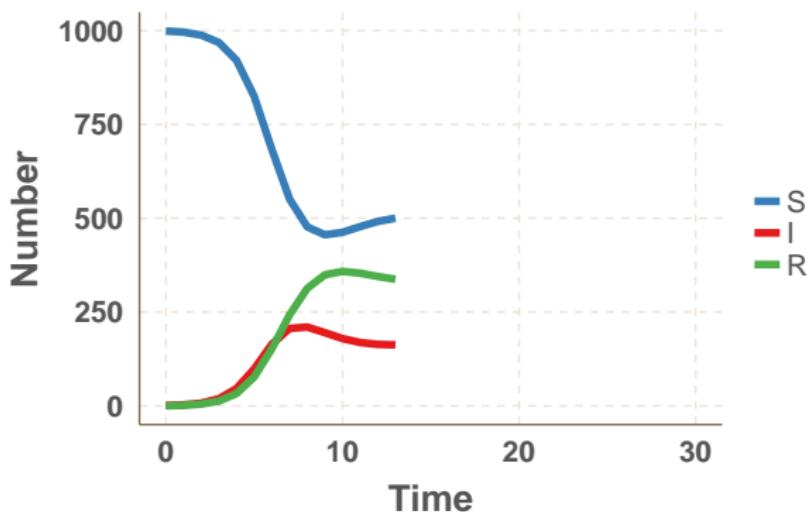


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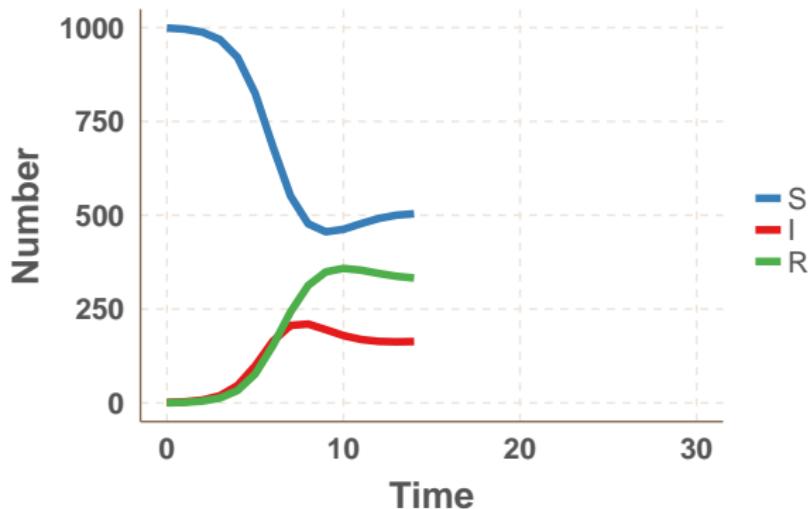


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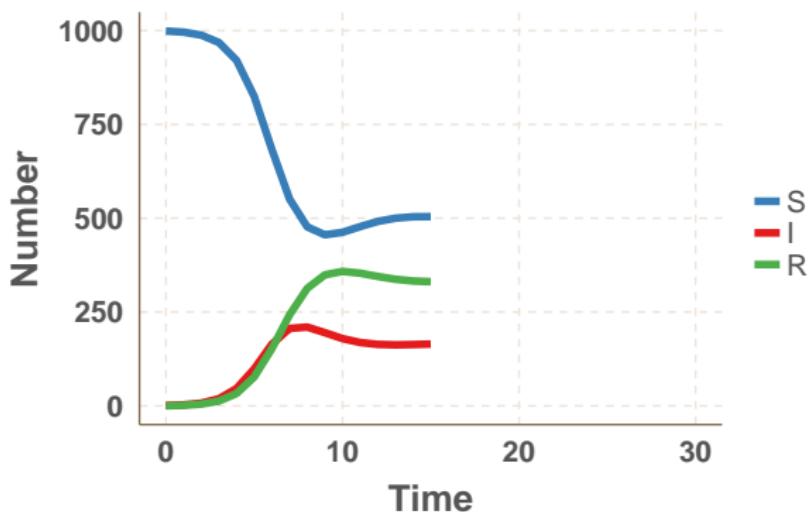


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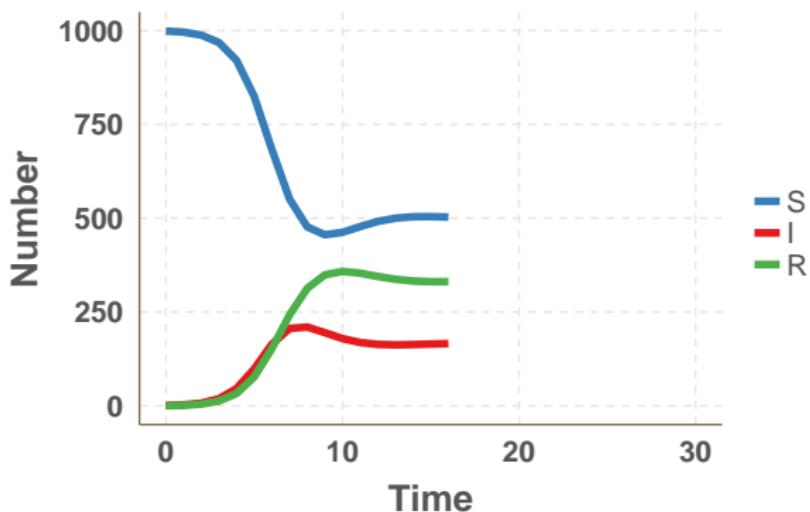


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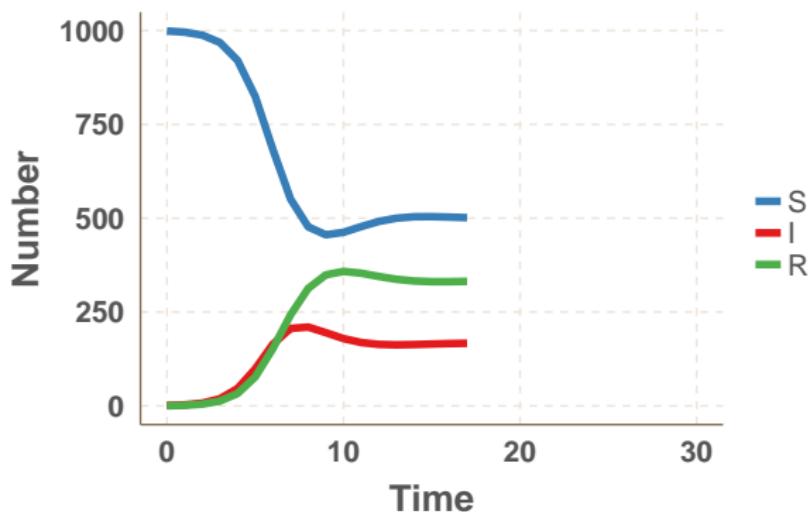


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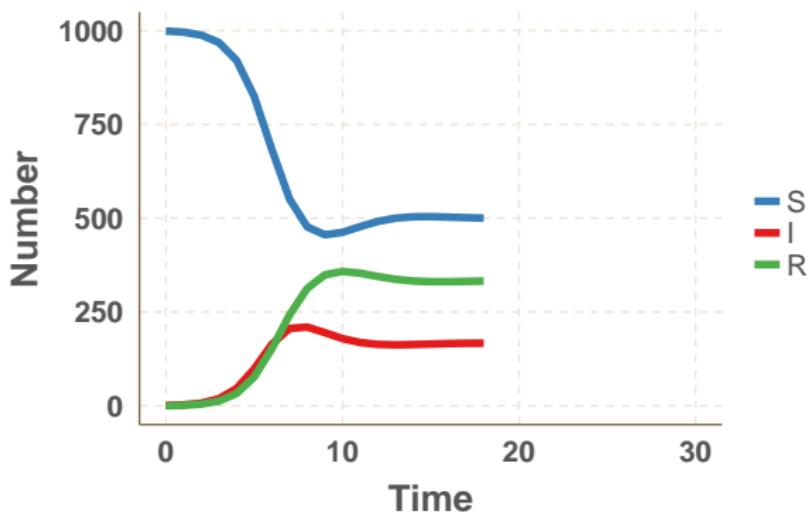


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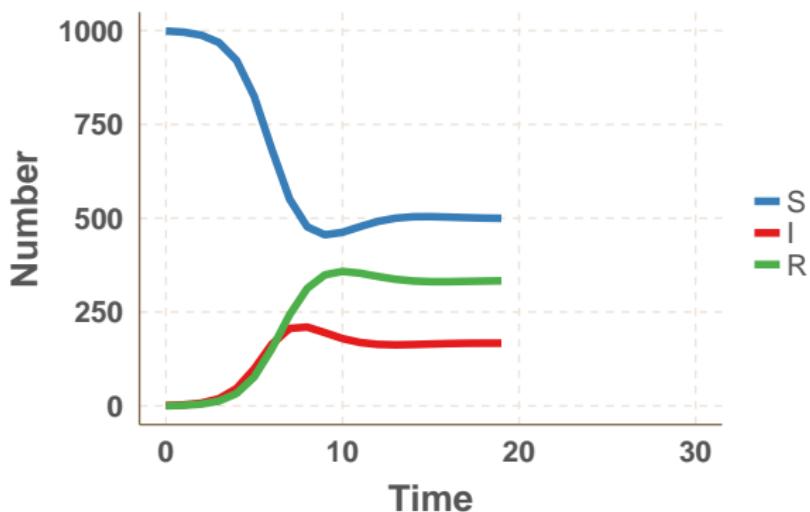


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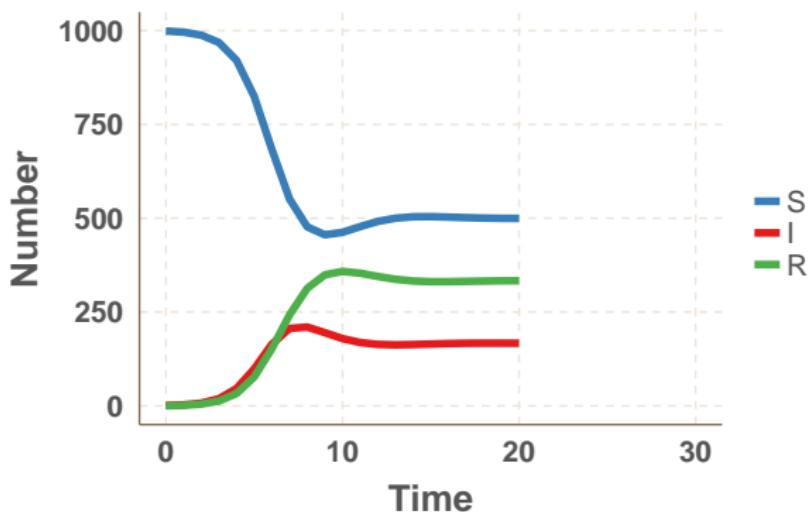


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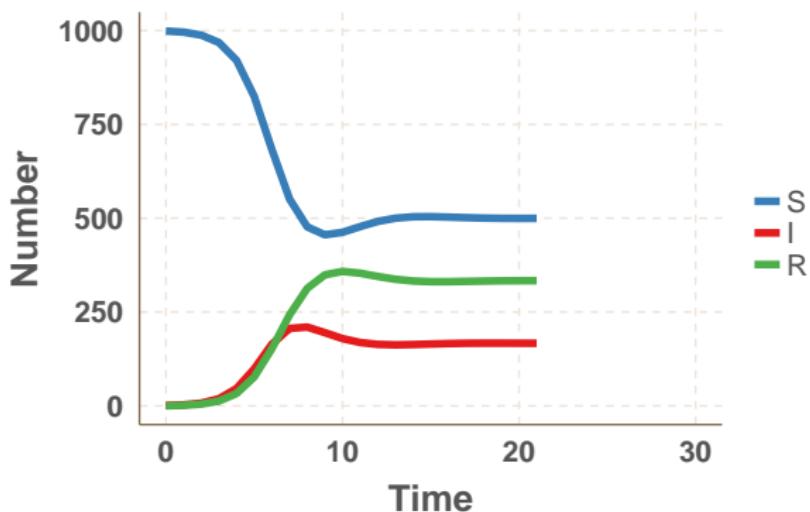


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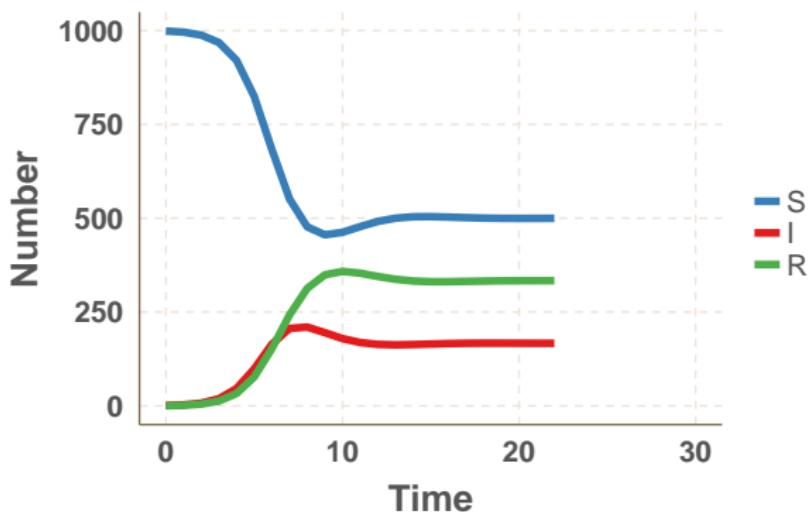


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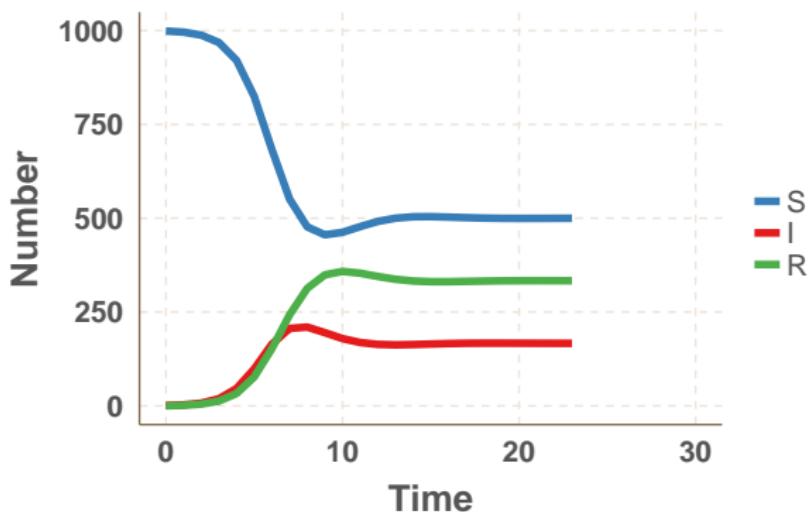


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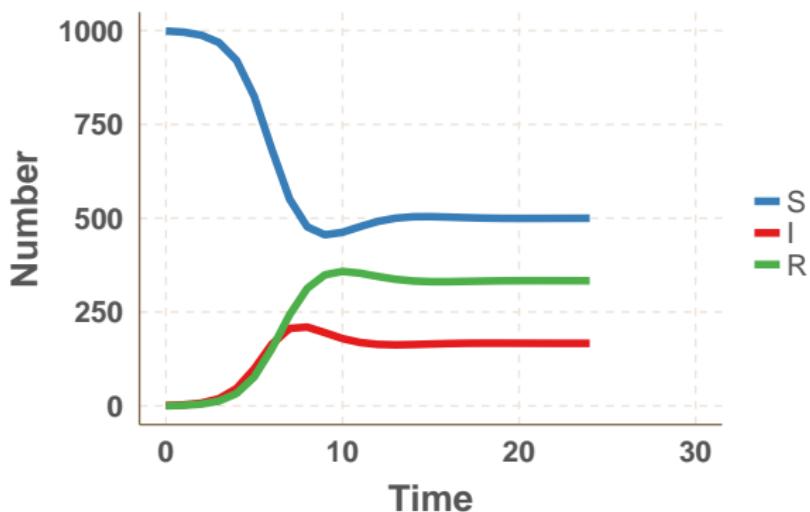


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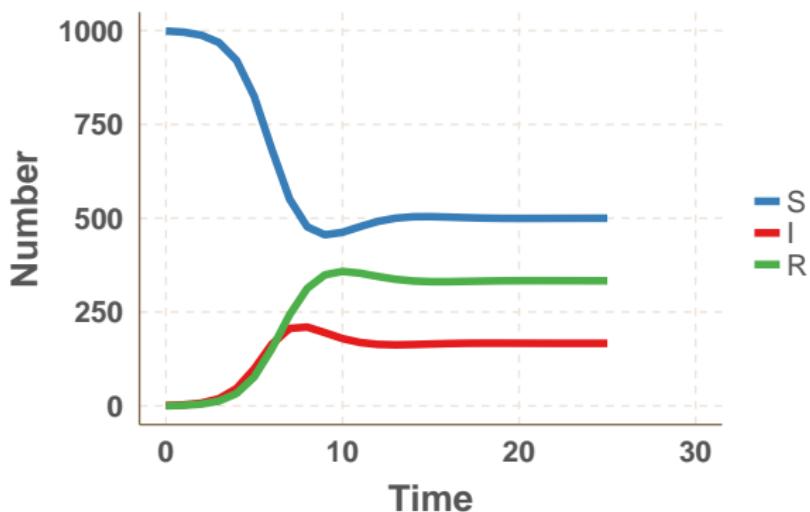


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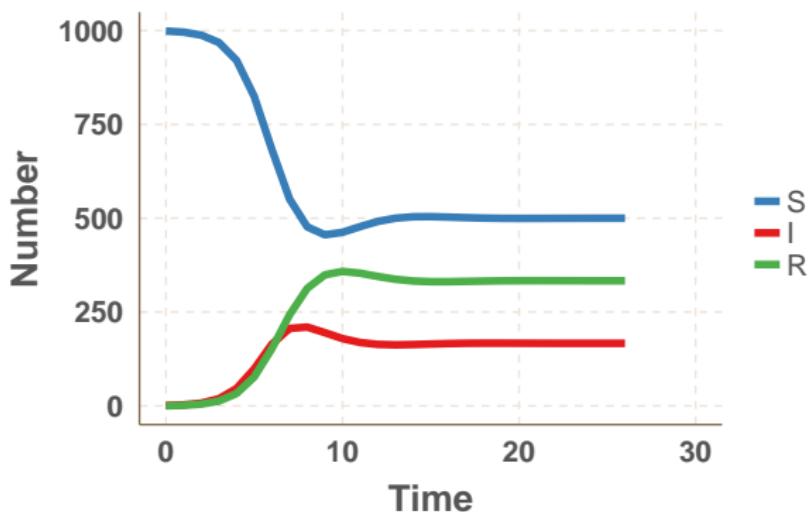


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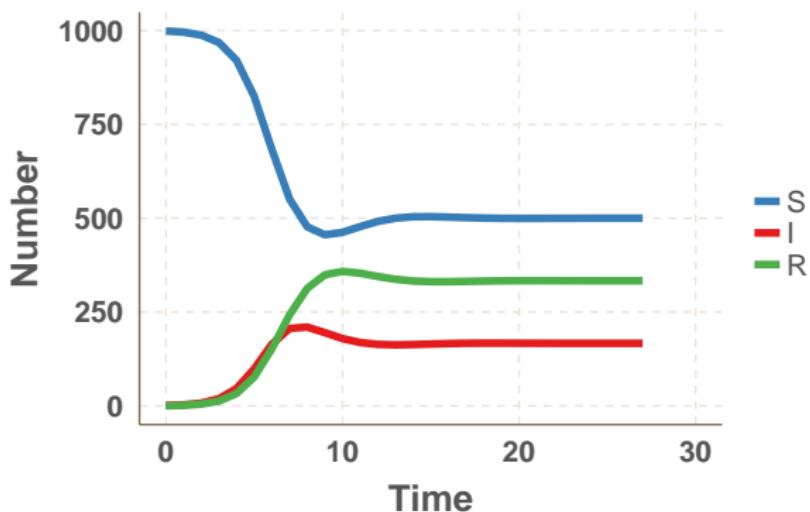


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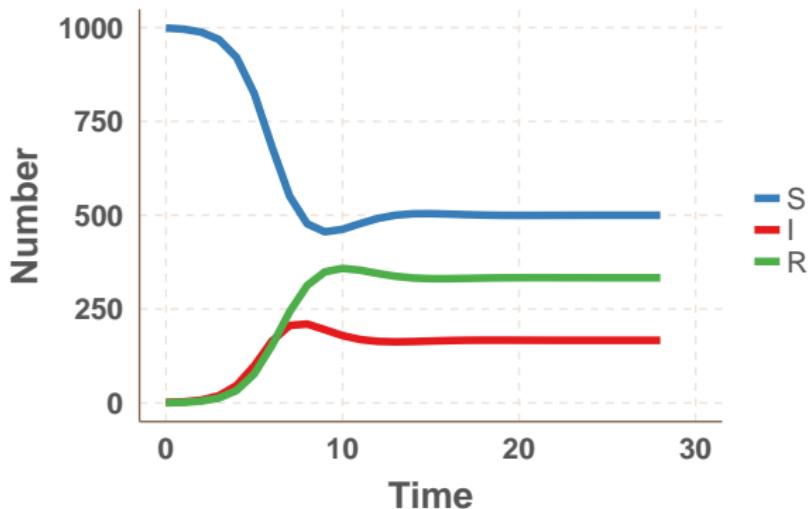


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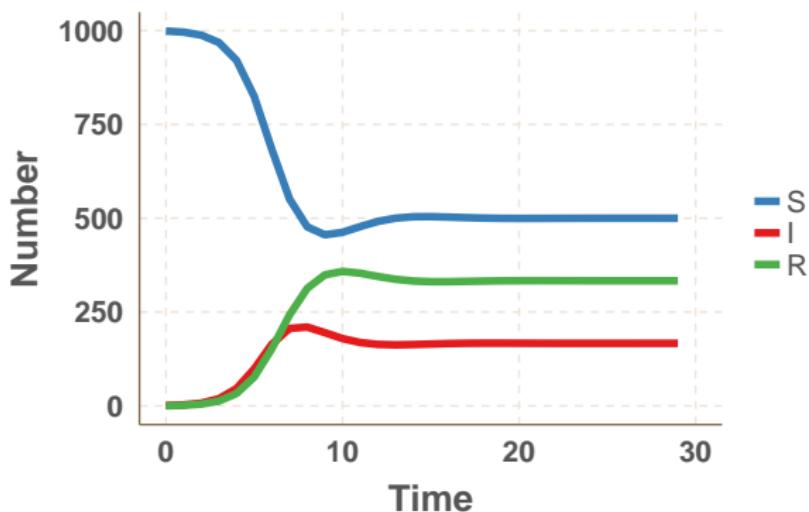


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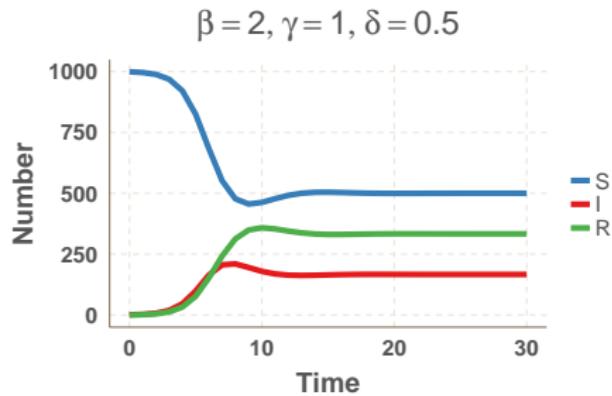
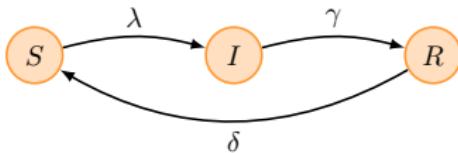
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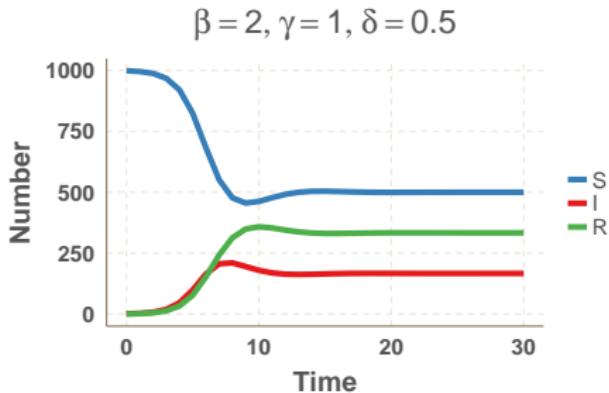
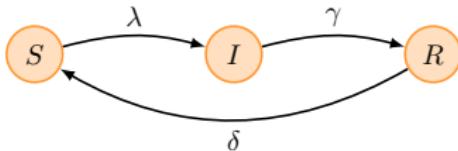
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## Properties of the SIRS model

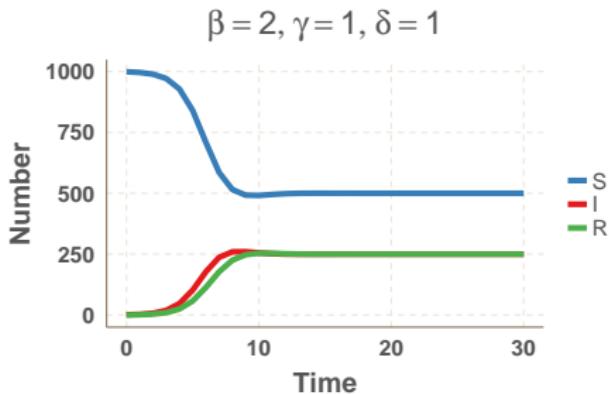
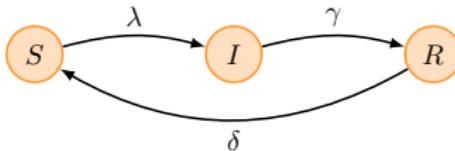


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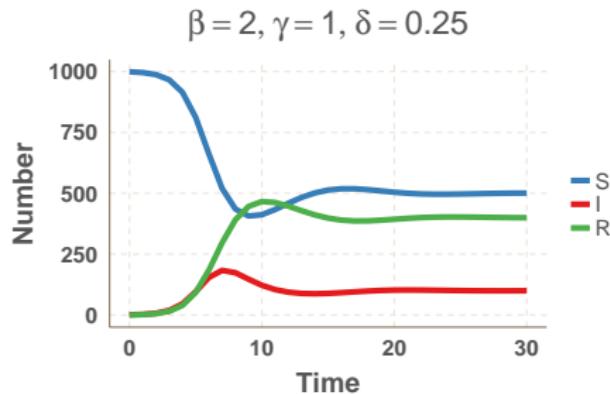
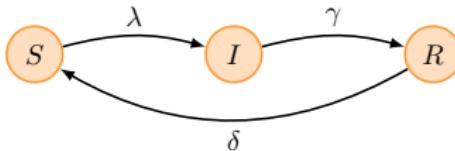
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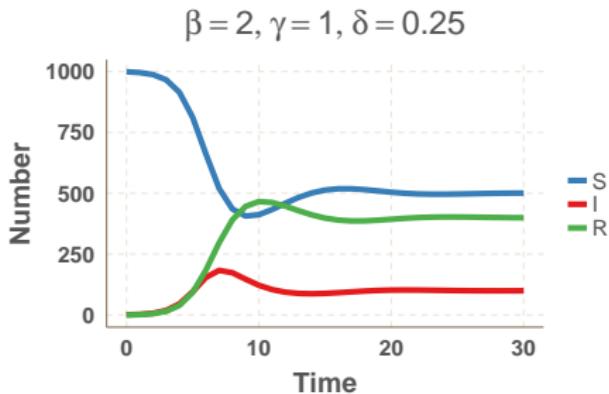
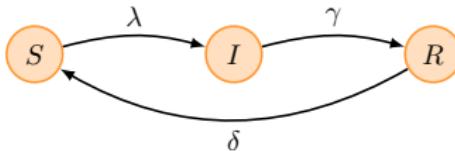
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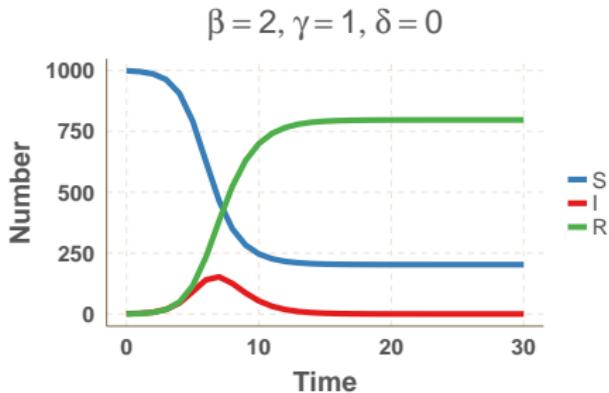
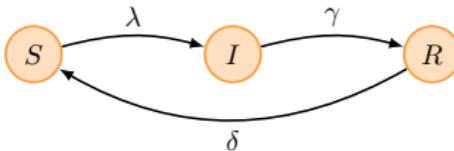
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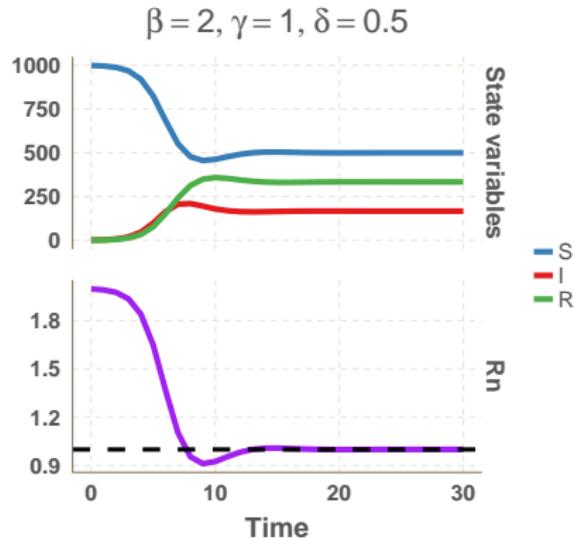
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- The infection becomes **endemic** (does not die out)
- The **number of people infectious** at any time depends on  $\beta$ ,  $\gamma$  and  $\delta$
- If  $\delta = 0$ , this is the SIR model, and the disease dies out

## $R_n$ and endemic diseases

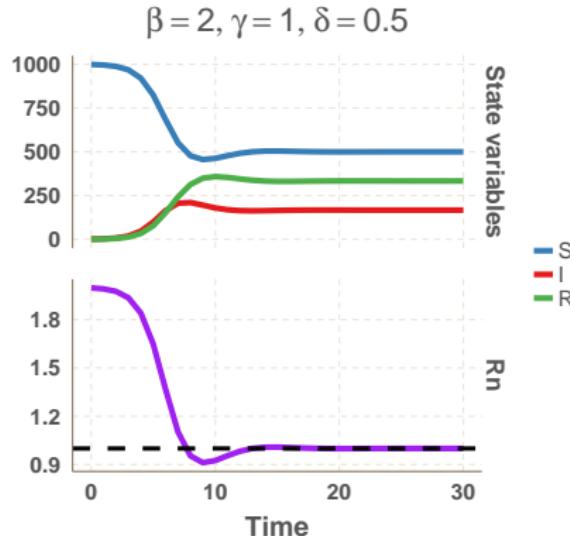
The value of  $R_n$  determines if, at any time, a disease will increase or decrease.



$$R_0 = 2$$

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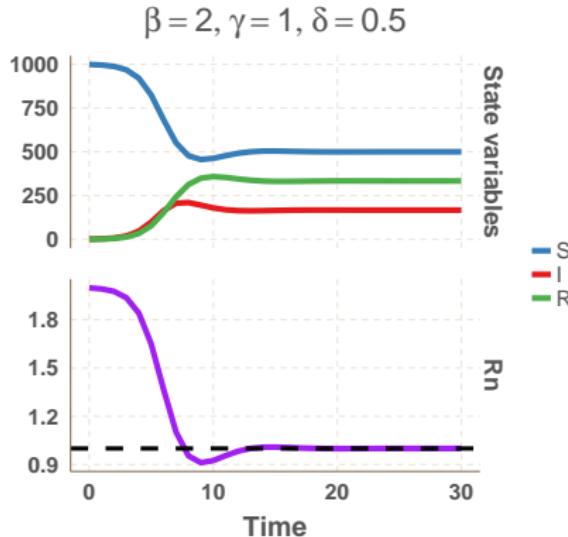


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$$R_0 = 2$$

- At the beginning,  $R_n = R_0$
- At endemic level,  $R_n = 1$

## Applications of the SIRS model

- Immunity is lost (after a while)
- The infection reaches an endemic level

For which infection is this a good model?

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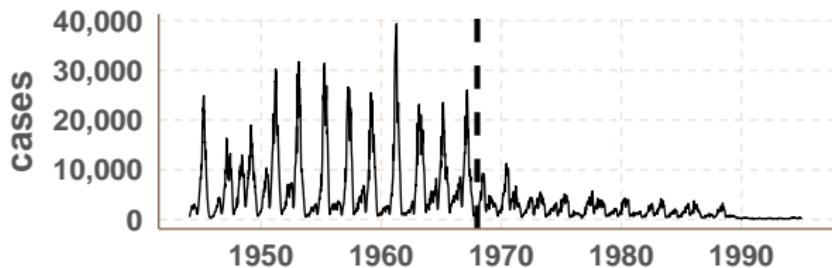
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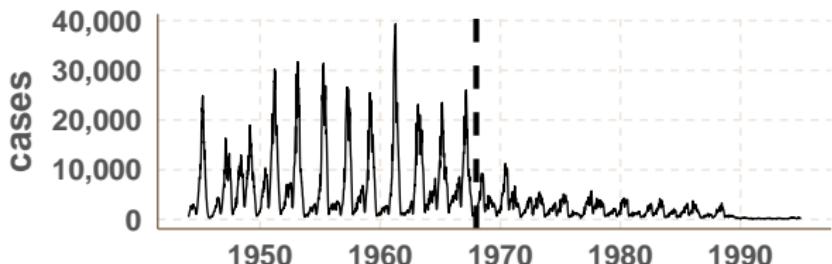
- Cholera?
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What about measles?

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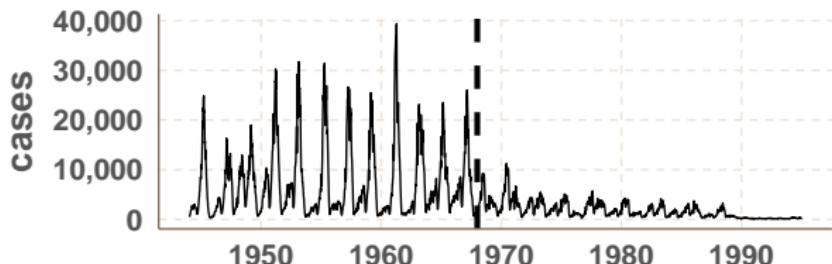


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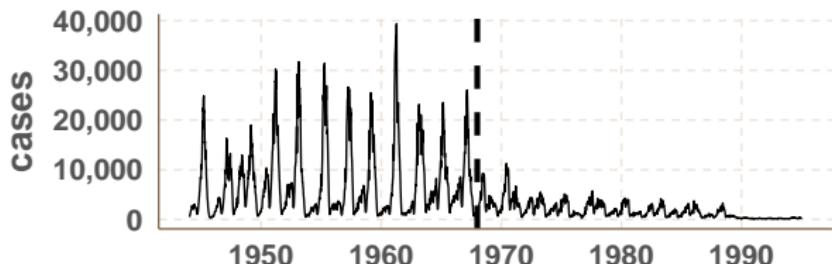
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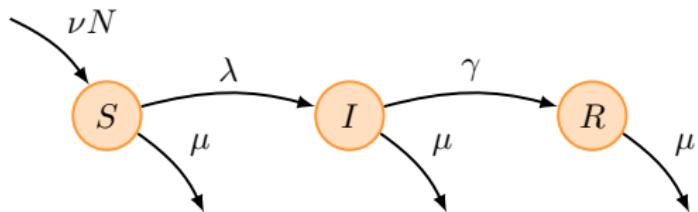
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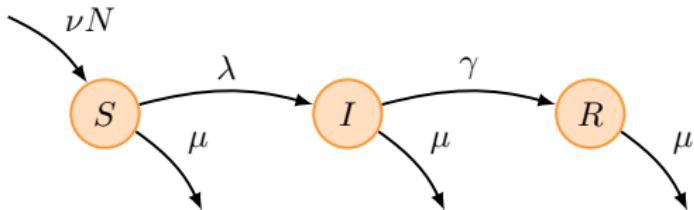


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- New susceptibles through births ("**childhood**" disease)

## The SIR model with births (and deaths)

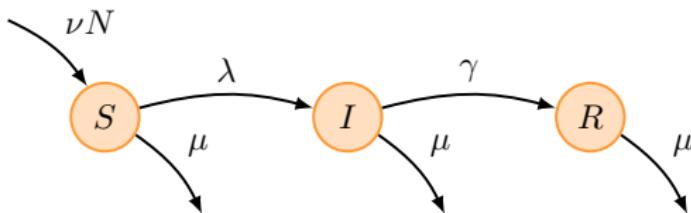


## The SIR model with births (and deaths)



- $\nu$  is the per-capita birth rate

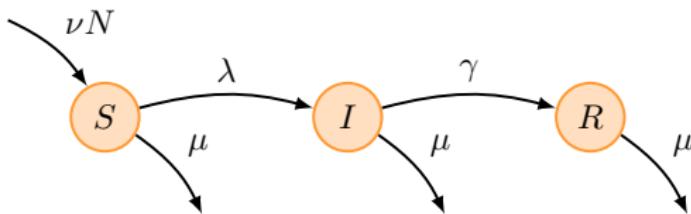
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- $\nu$  is the per-capita birth rate
- $\mu$  is the per-capita death rate. It is the inverse of the life expectancy  $L$

$$\mu = \frac{1}{L}$$

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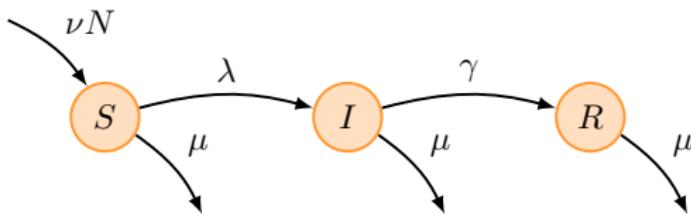


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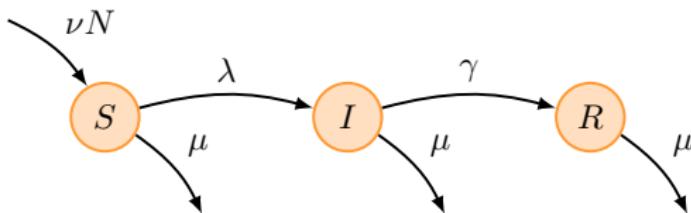


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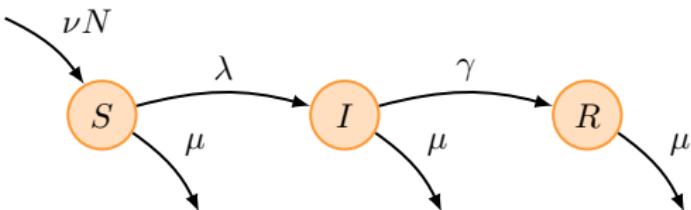


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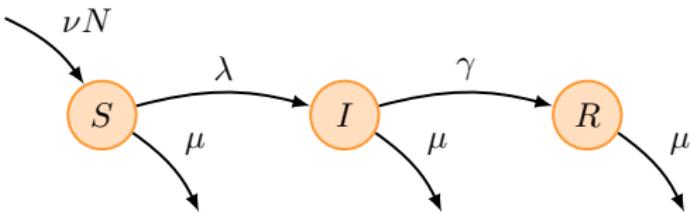
- If  $\mu = \nu$ : population size  $N$  stays constant
- If  $\nu > \mu$ : population grows
- If  $\mu < \nu$ : population shrinks

## The SIR model with births/deaths as differential equations



- *S*: Number of people susceptible
- *I*: Number of people infectious
- *R*: Number of people recovered
- How does the number of people susceptible, infectious and recovered change over time?

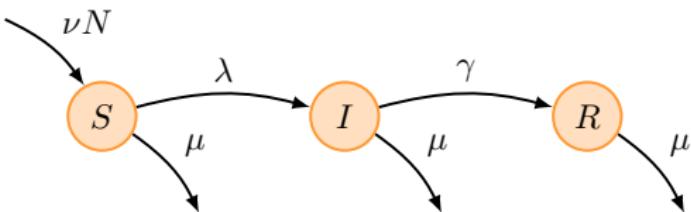
## The SIR model with births/deaths as differential equations



- $S$ : Number of people susceptible
- $I$ : Number of people infectious
- $R$ : Number of people recovered
- How does the number of people susceptible, infectious and recovered change over time?

$$dS/dt = -\lambda S + \nu N$$

## The SIR model with births/deaths as differential equations

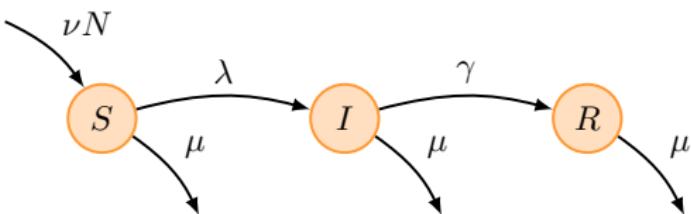


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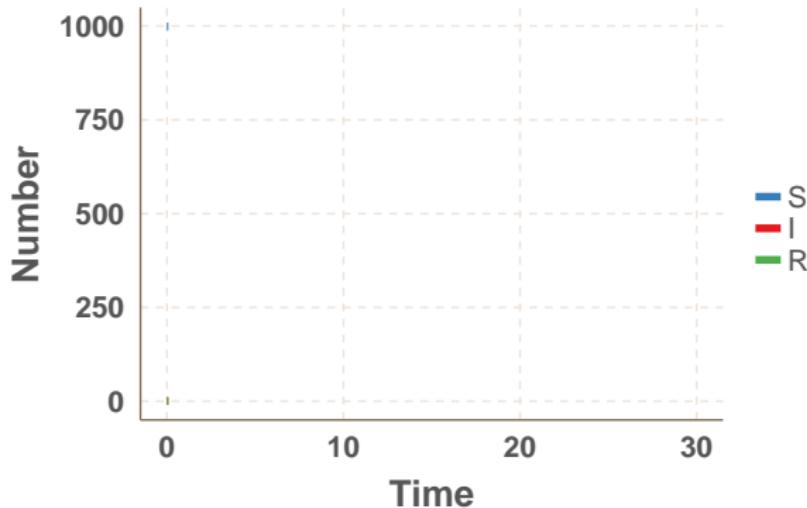
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## Simulating the SIR model with births/deaths using differential equations

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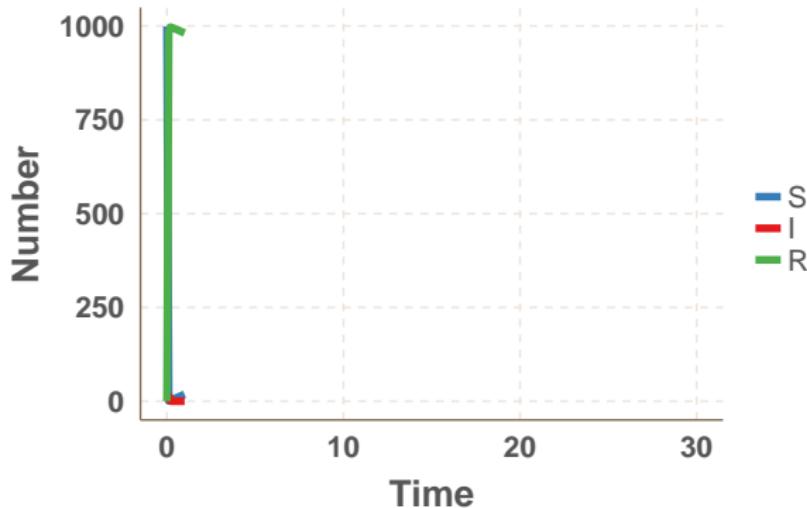


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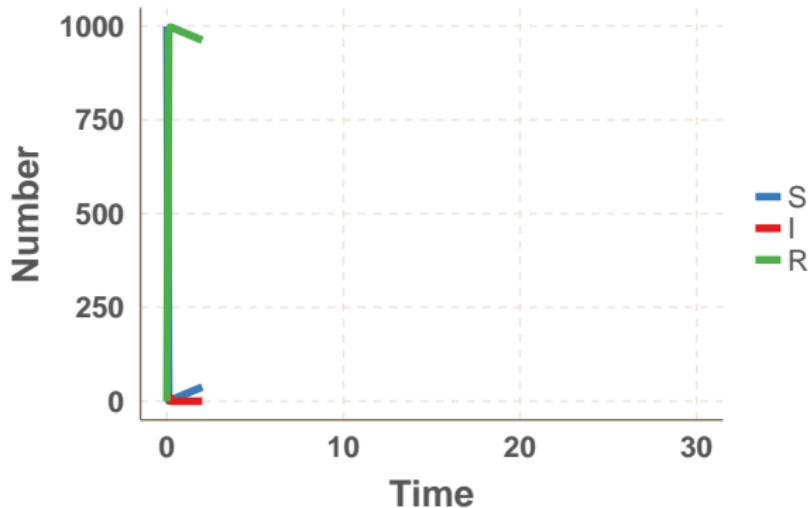


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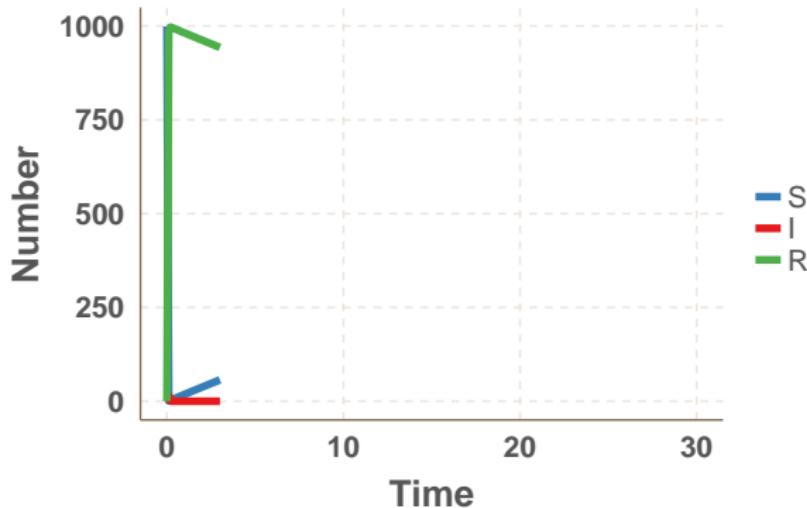


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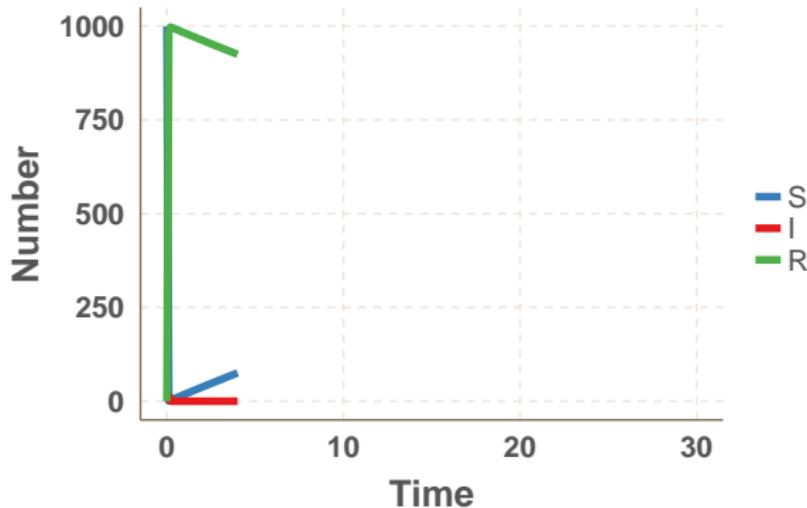


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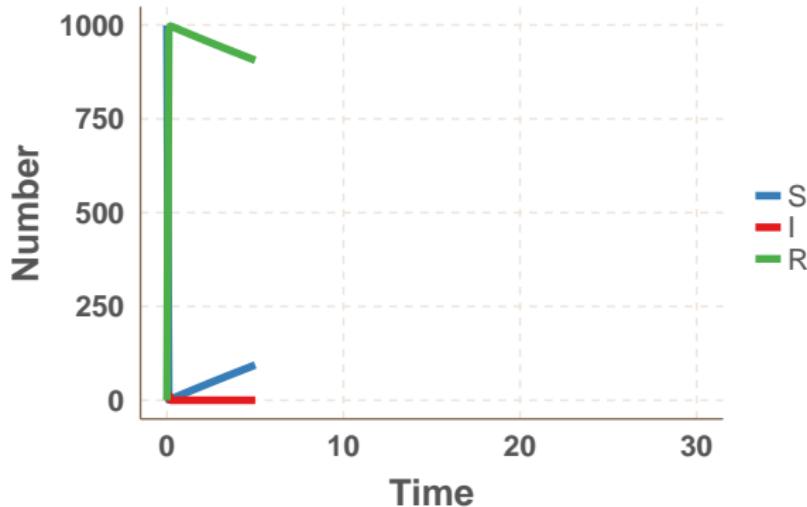


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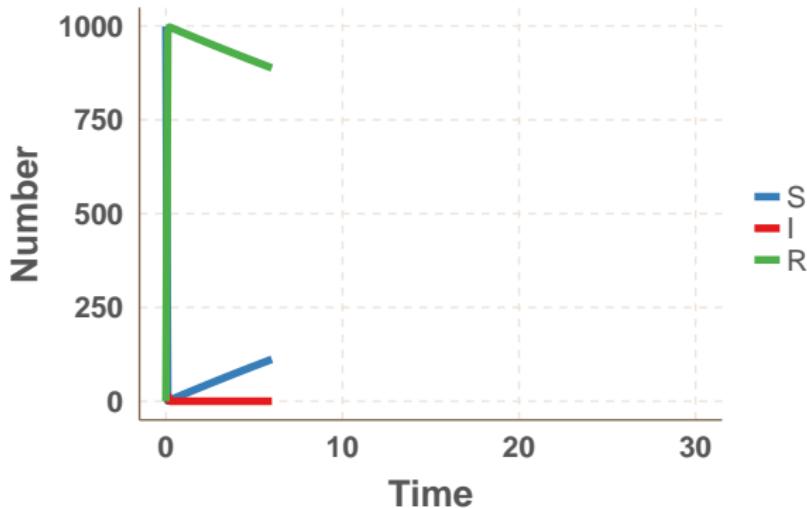


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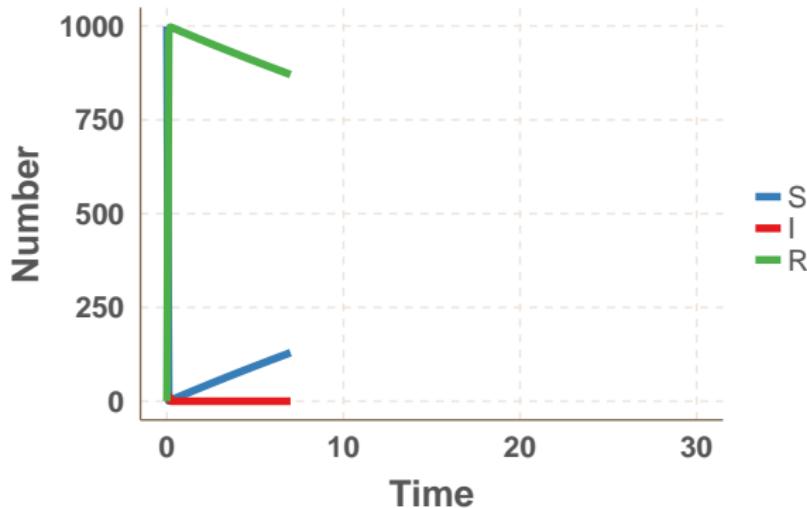


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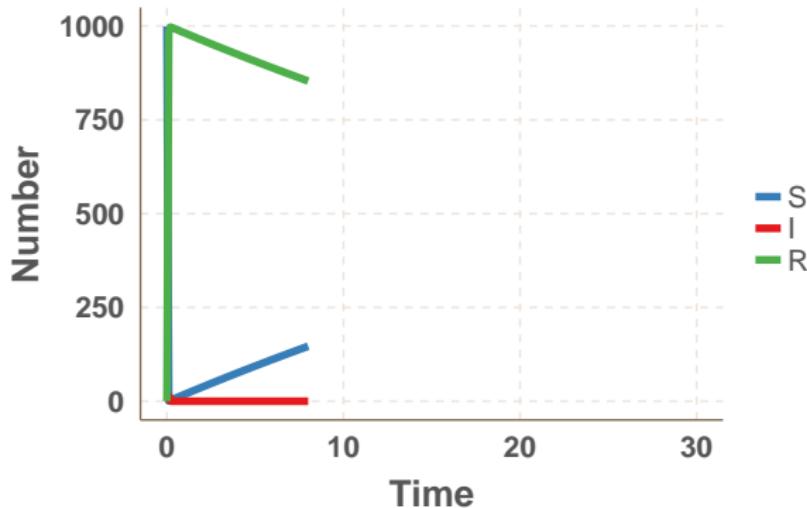


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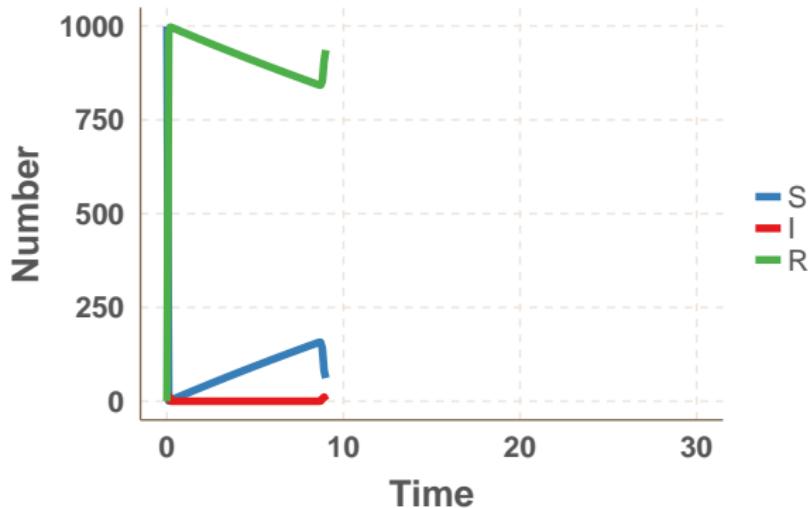


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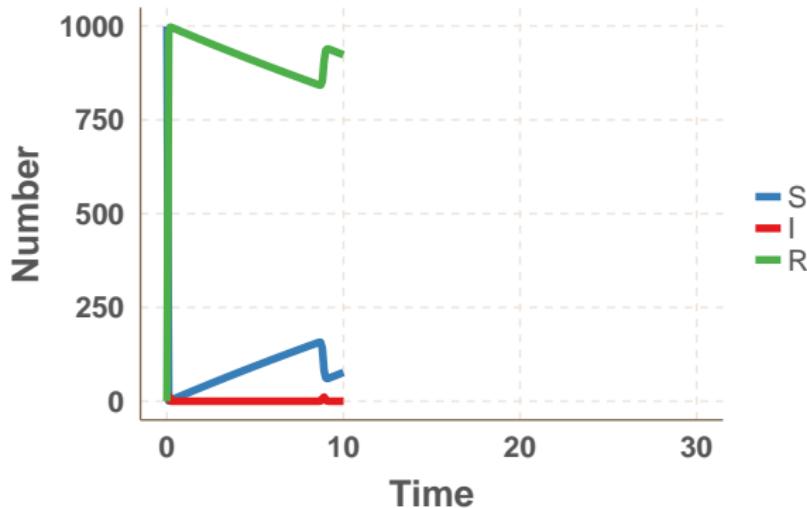


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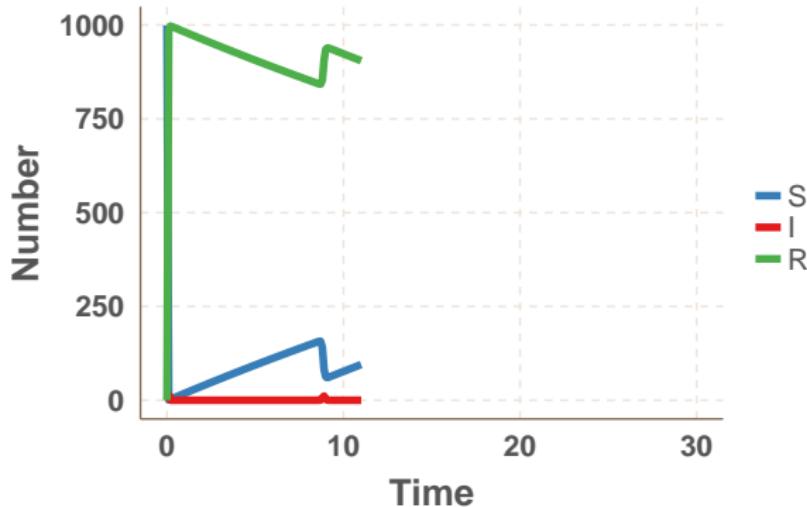


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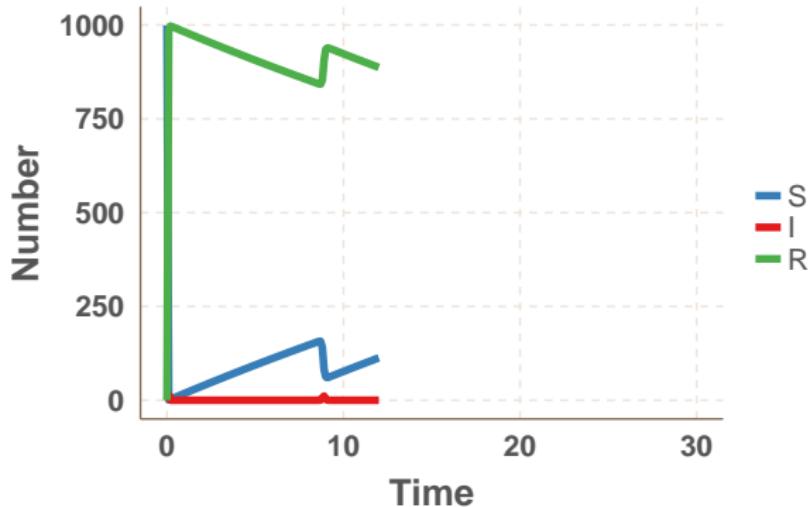


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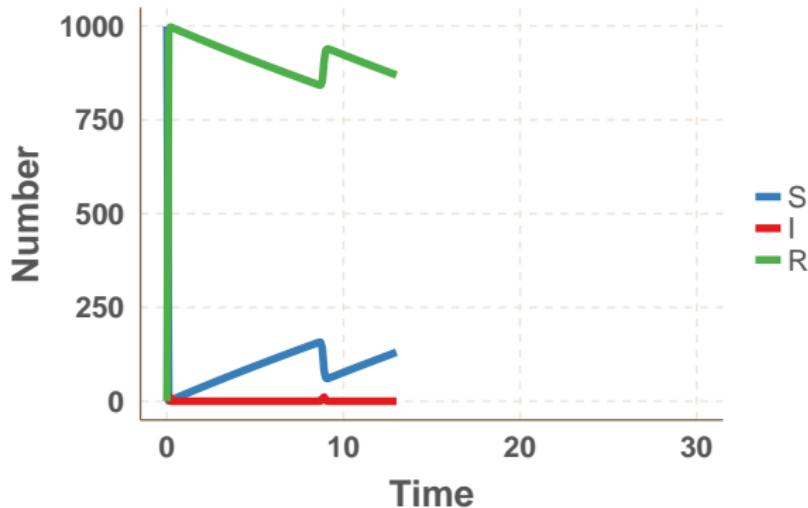


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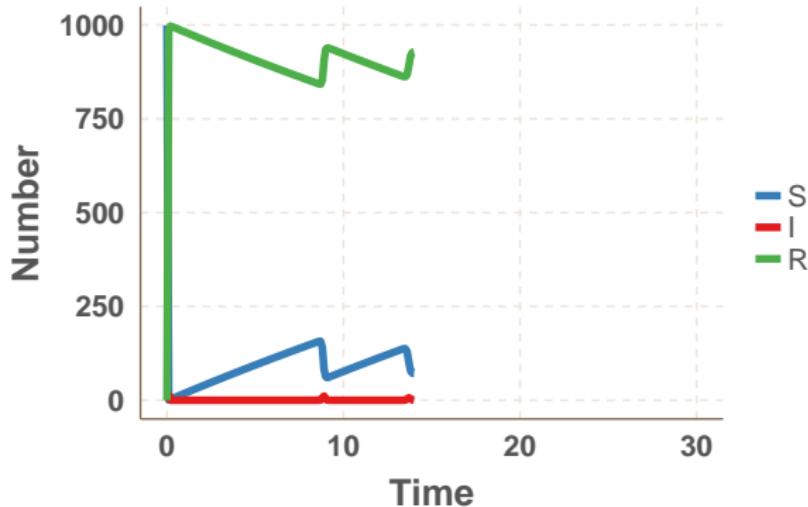


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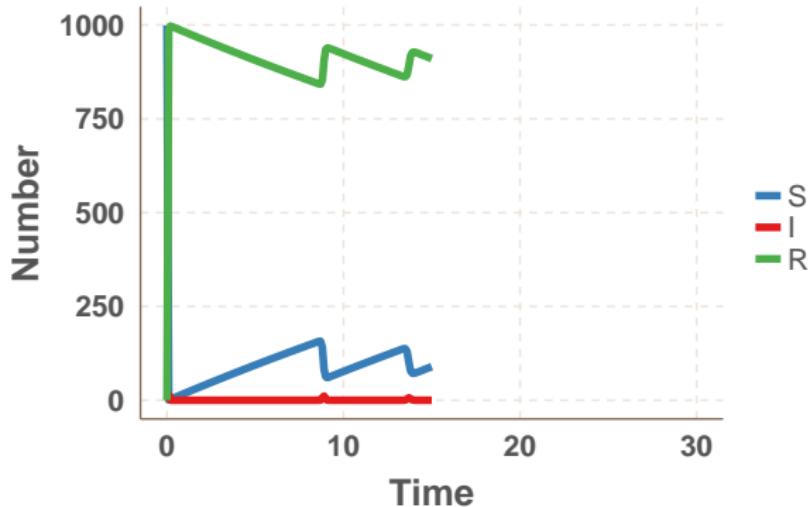


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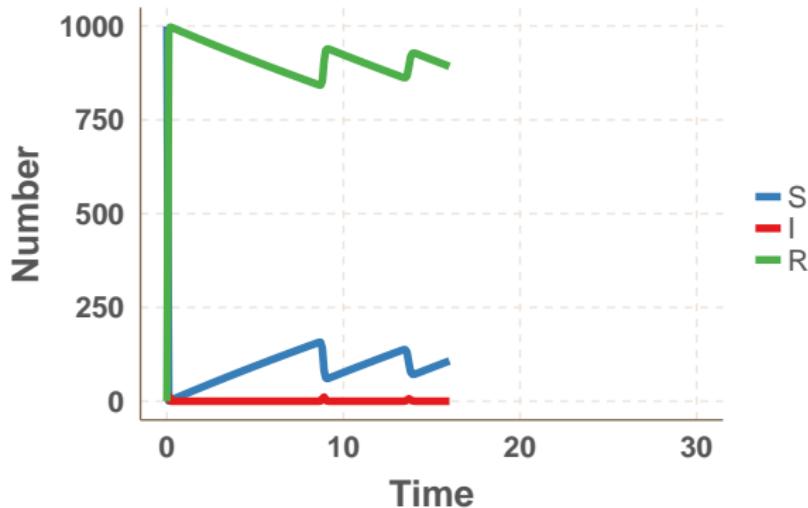


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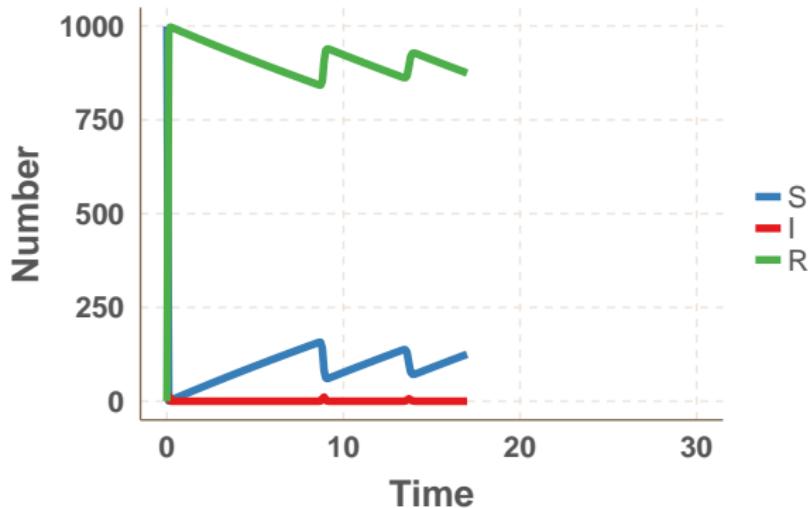


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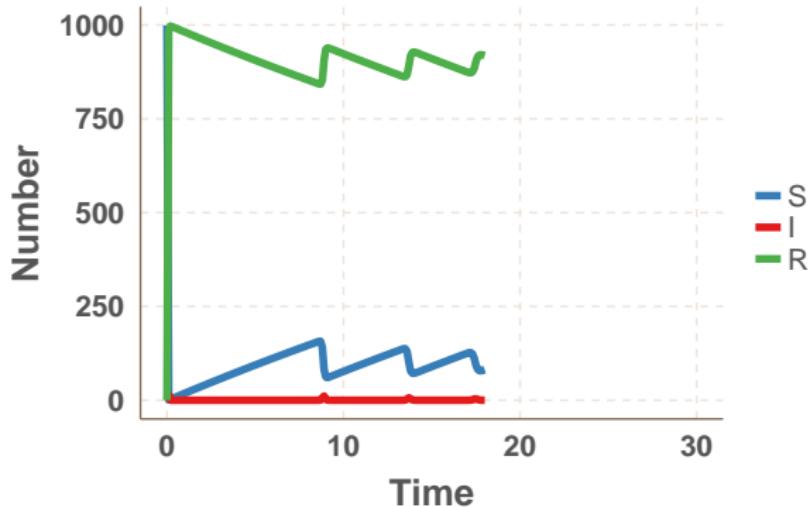


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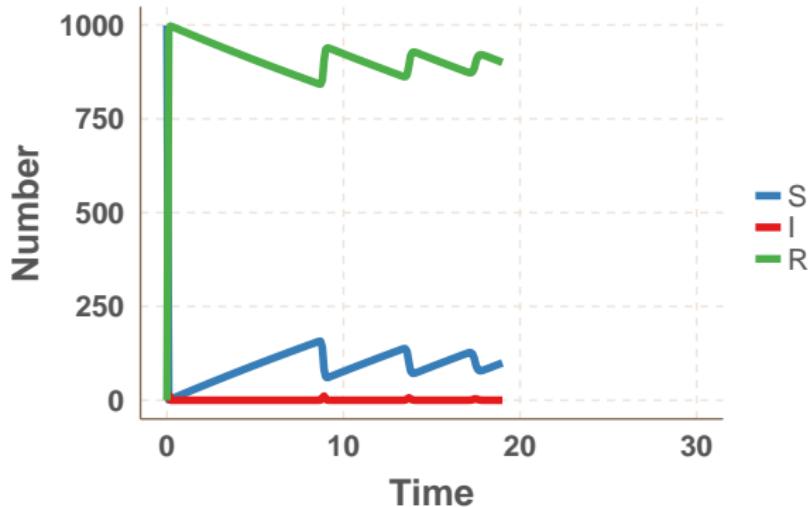


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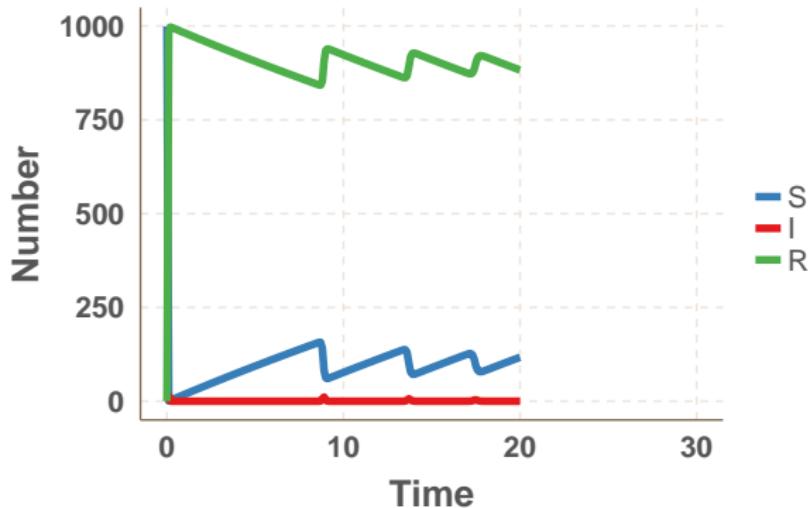


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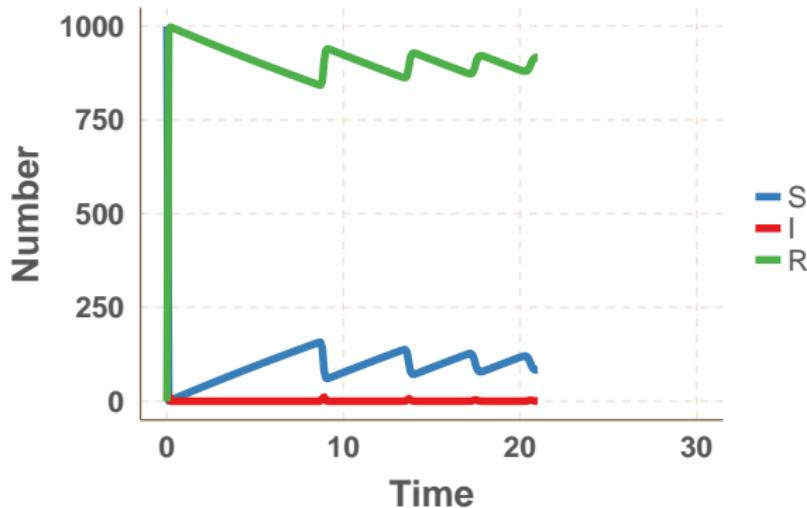


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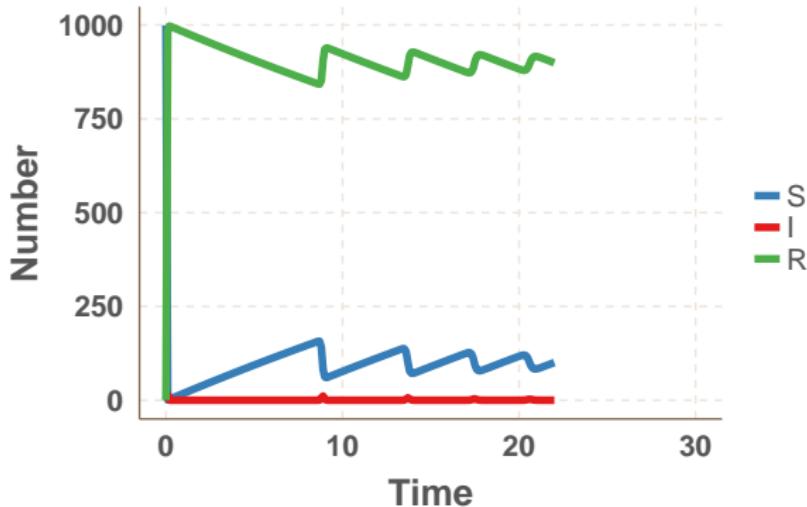


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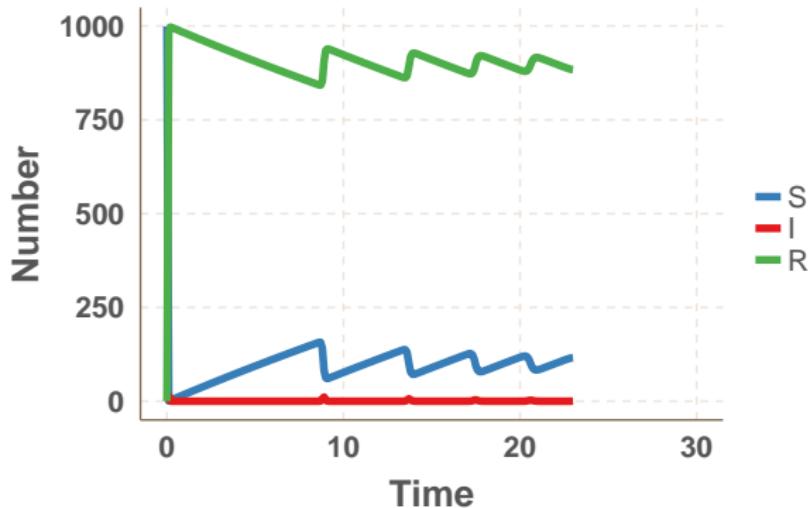


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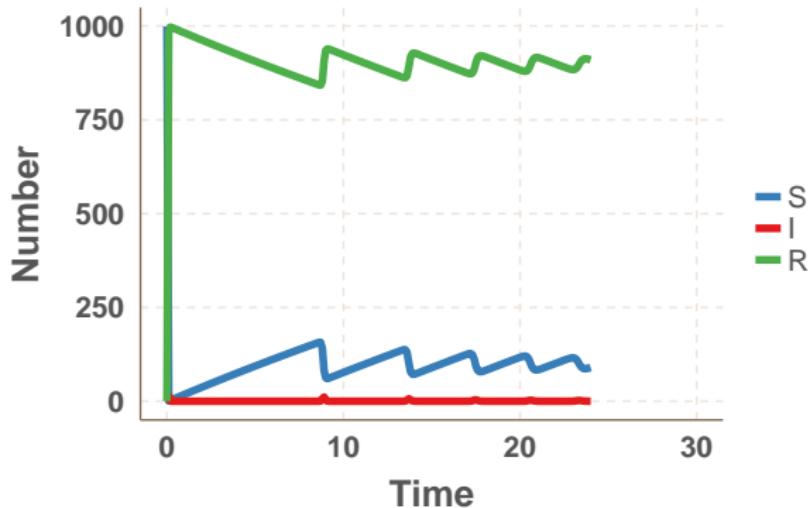


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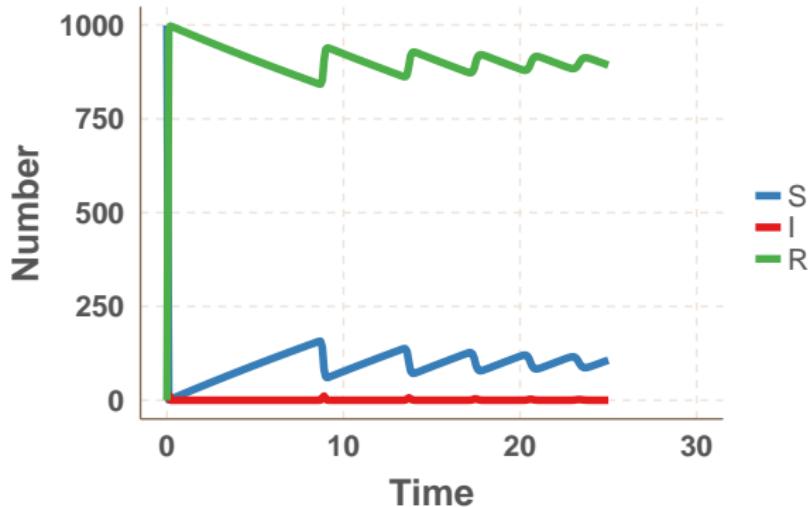


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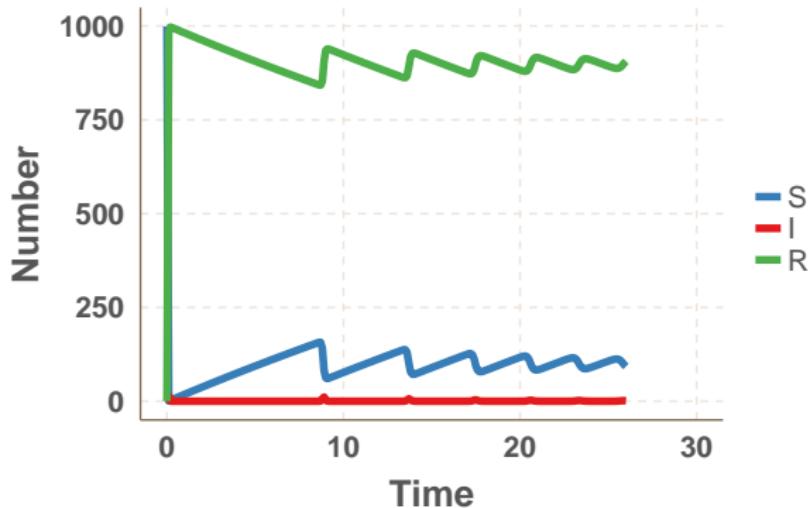


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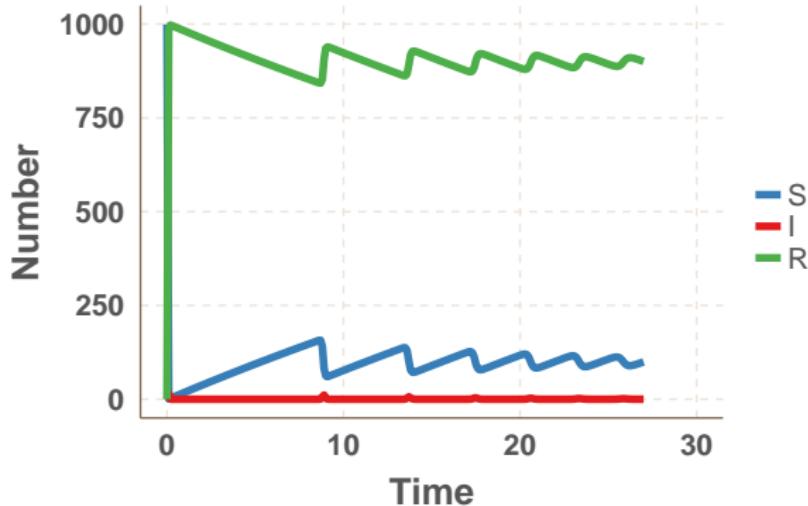


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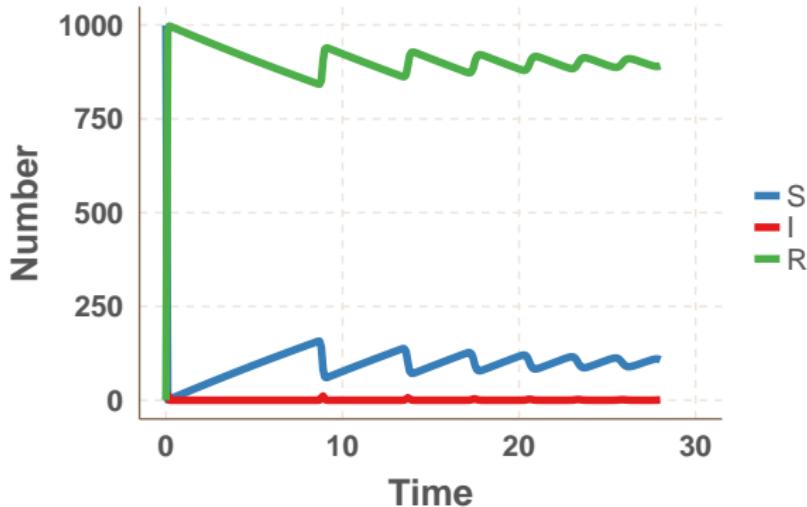


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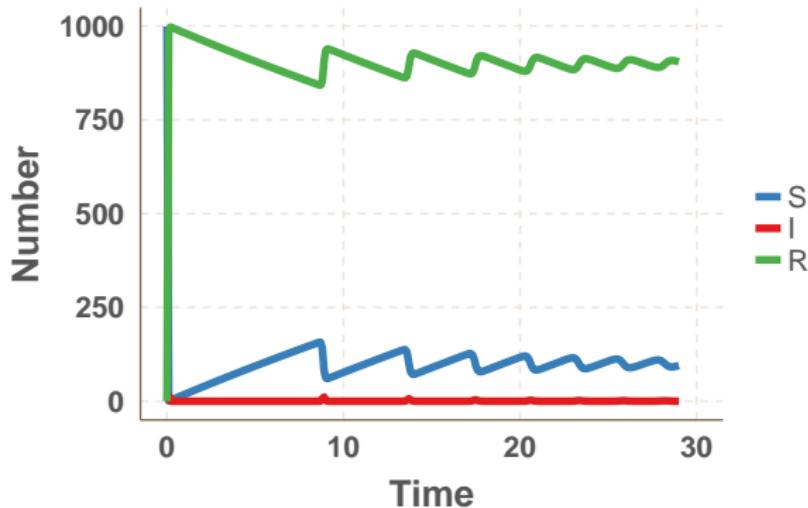


## Simulating the SIR model with births/deaths using differential equations

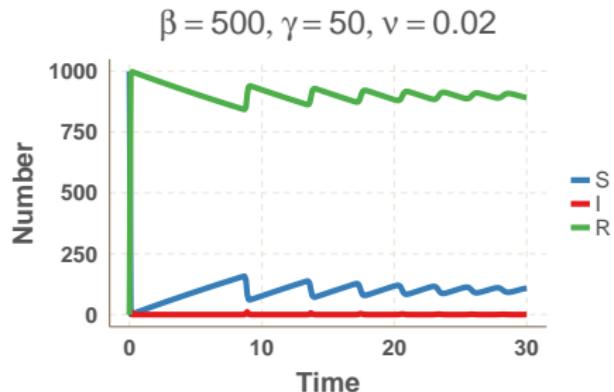
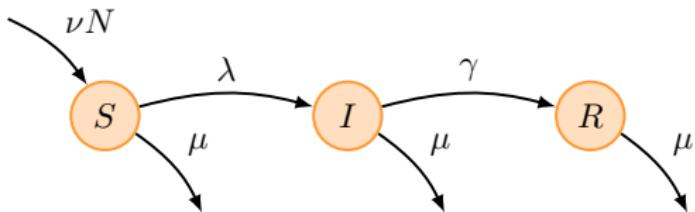
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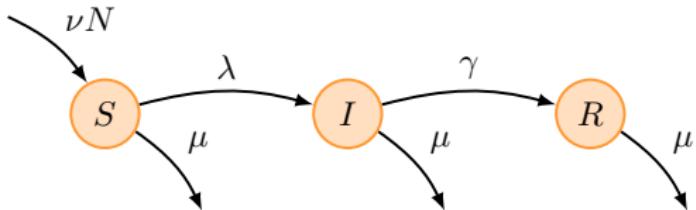
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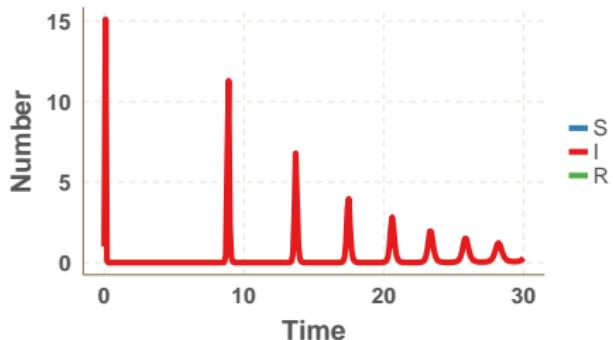
## Properties of the SIR model with births/deaths



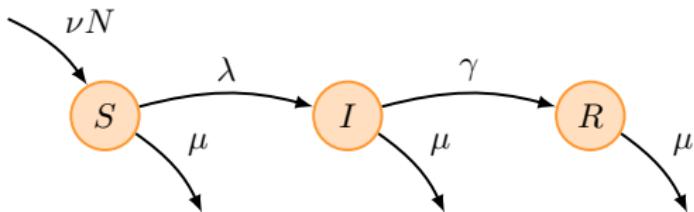
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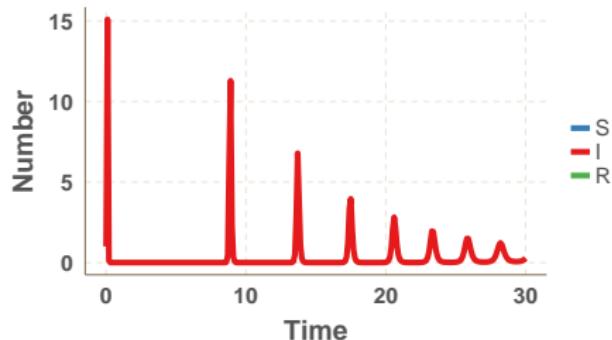
$$\beta = 500, \gamma = 50, \nu = 0.02$$



## Properties of the SIR model with births/deaths

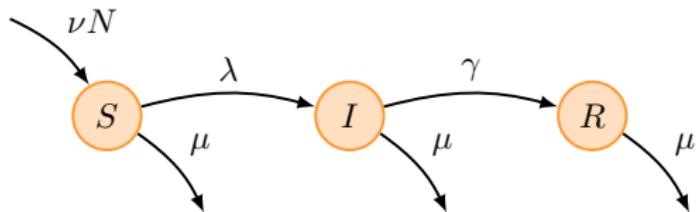


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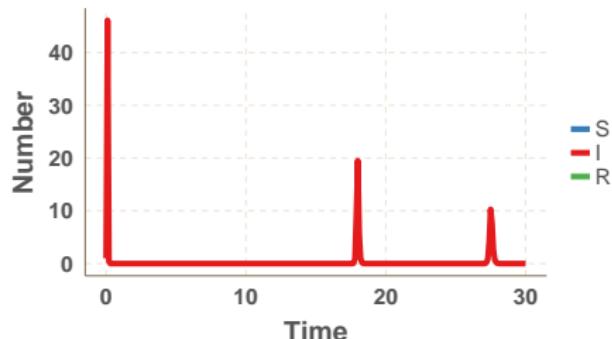


- The infection appears in **cycles**

## Properties of the SIR model with births/deaths

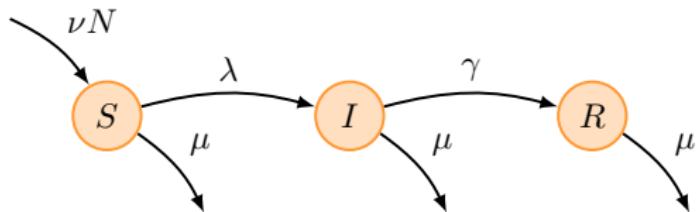


$$\beta = 250, \gamma = 50, \nu = 0.02$$

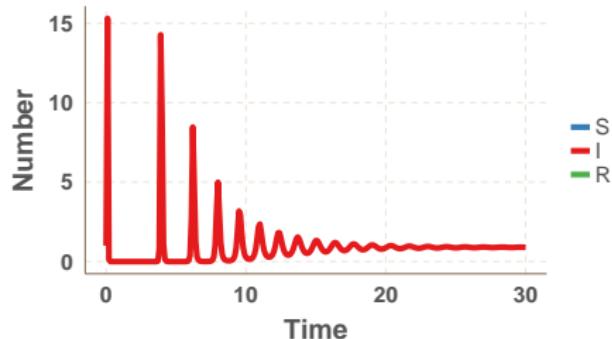


- The infection appears in **cycles**

## Properties of the SIR model with births/deaths

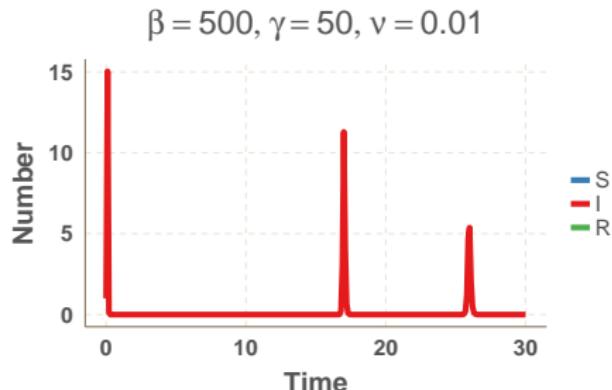
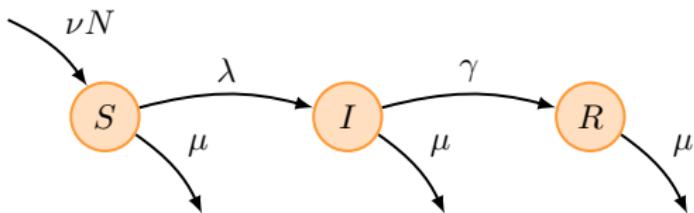


$$\beta = 500, \gamma = 50, \nu = 0.05$$



- The infection appears in **cycles**

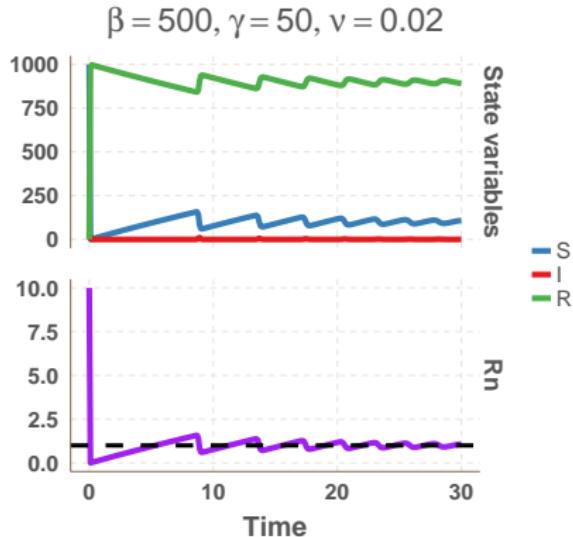
## Properties of the SIR model with births/deaths



- The infection appears in **cycles**
- The **height** and **frequency** of cycles depends on  $\beta$ ,  $\gamma$  and  $\nu$

## $R_n$ and cycles

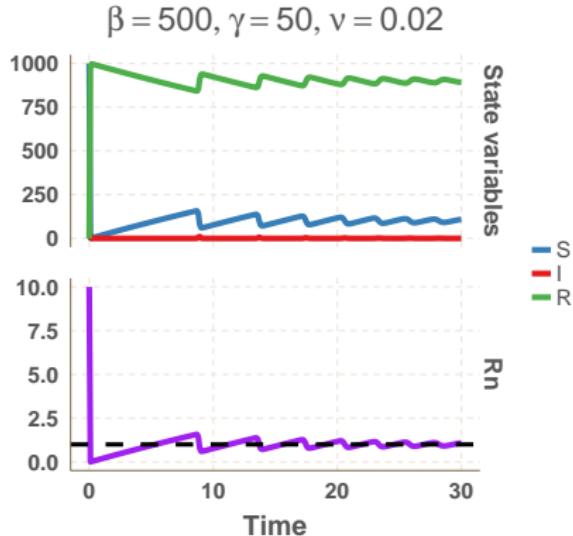
The value of  $R_n$  determines if, at any time, a disease will increase or decrease.



$$R_0 = 10$$

## $R_n$ and cycles

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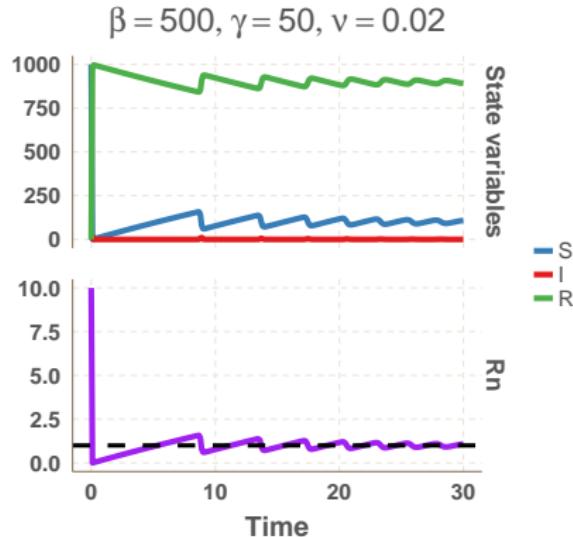


$$R_0 = 10$$

- At the beginning,  $R_n = R_0$

## $R_n$ and cycles

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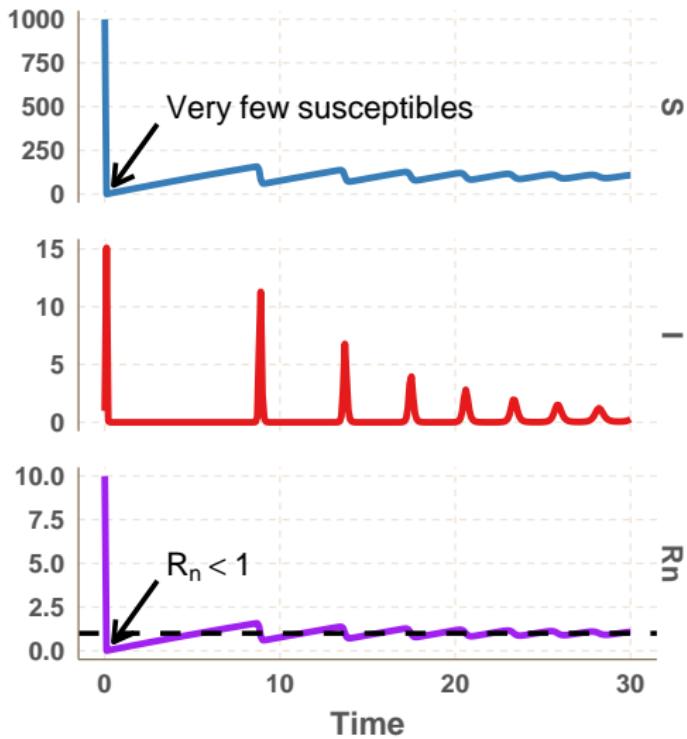


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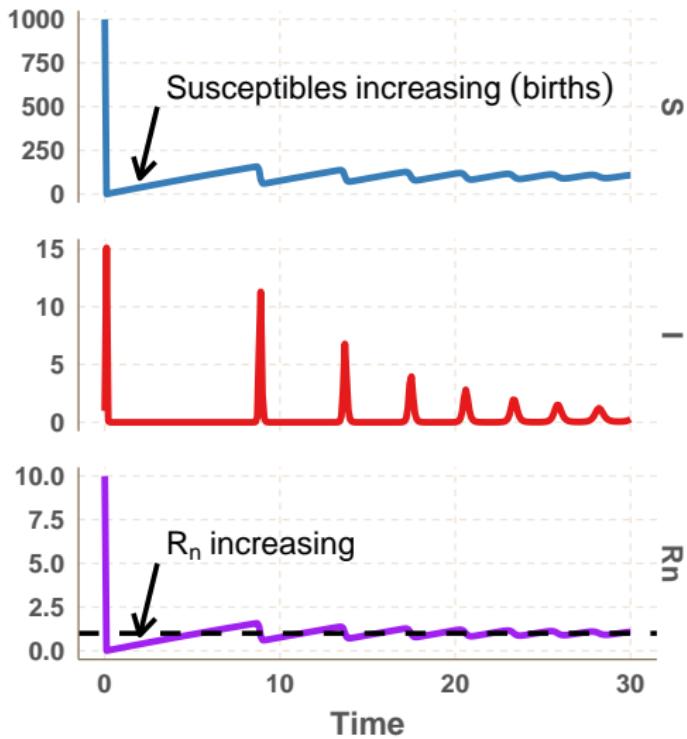
- At the beginning,  $R_n = R_0$
- At endemic level,  $R_n$  oscillates around 1

## A closer look at cycles

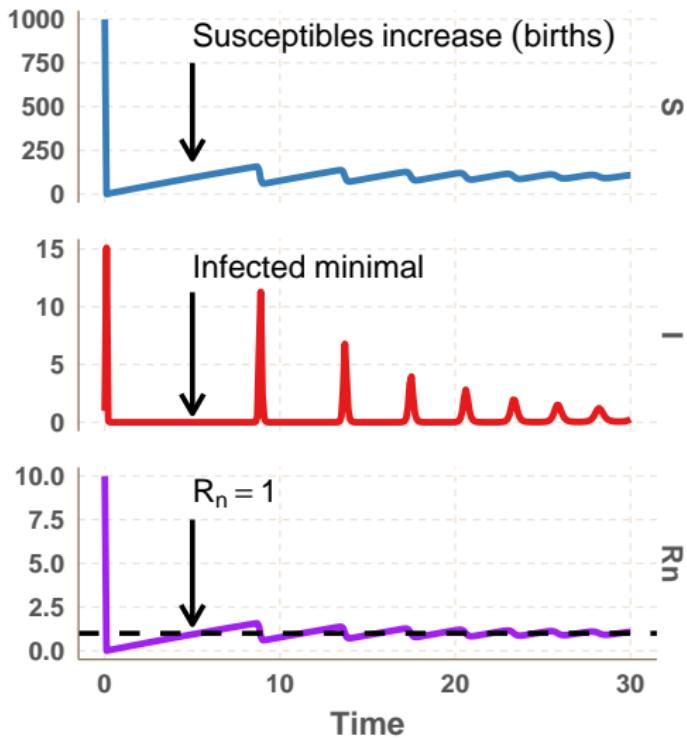
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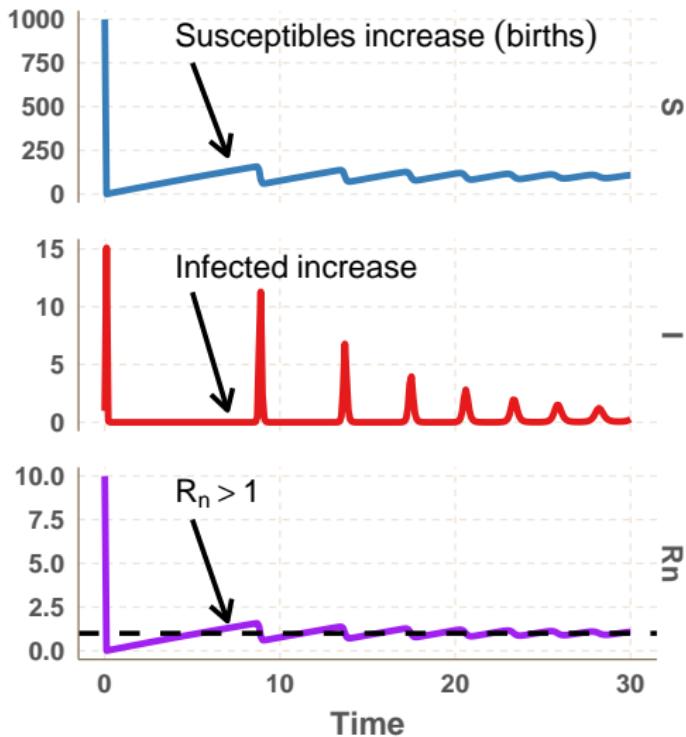
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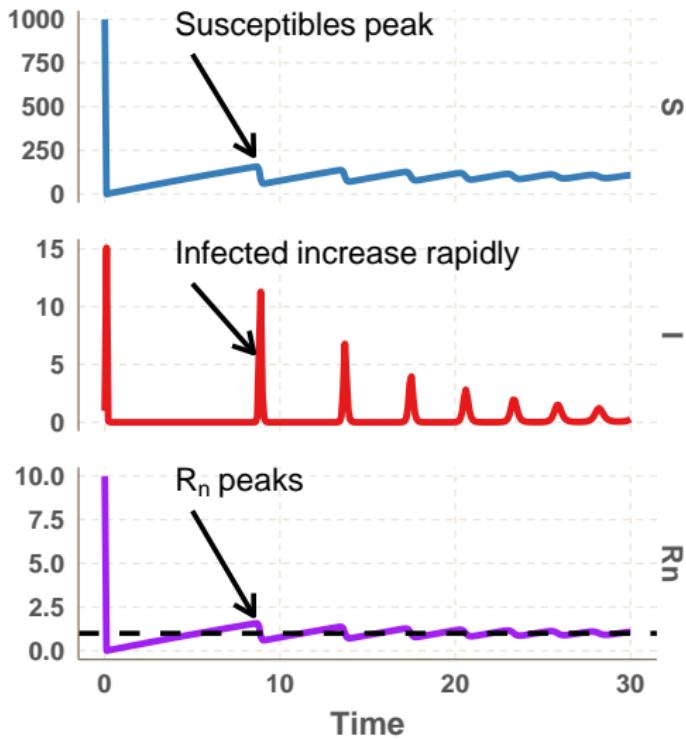
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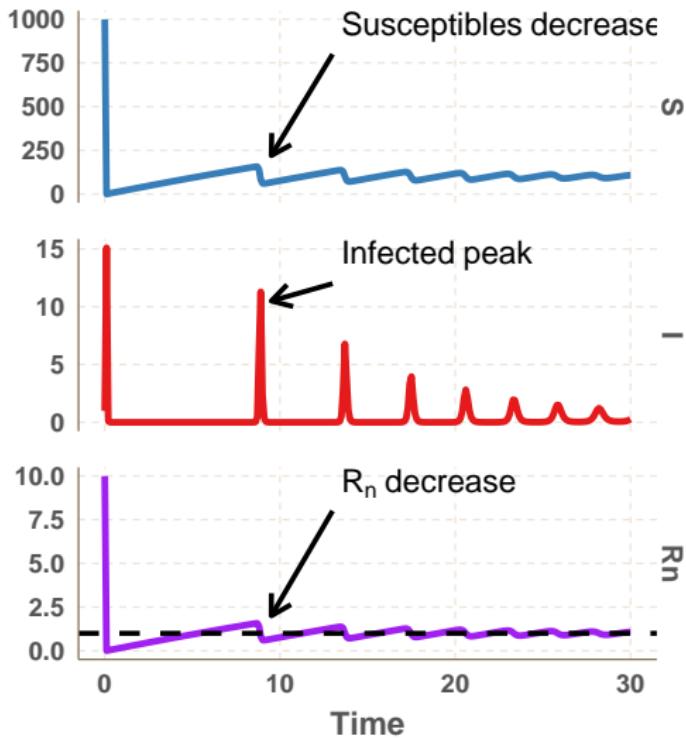
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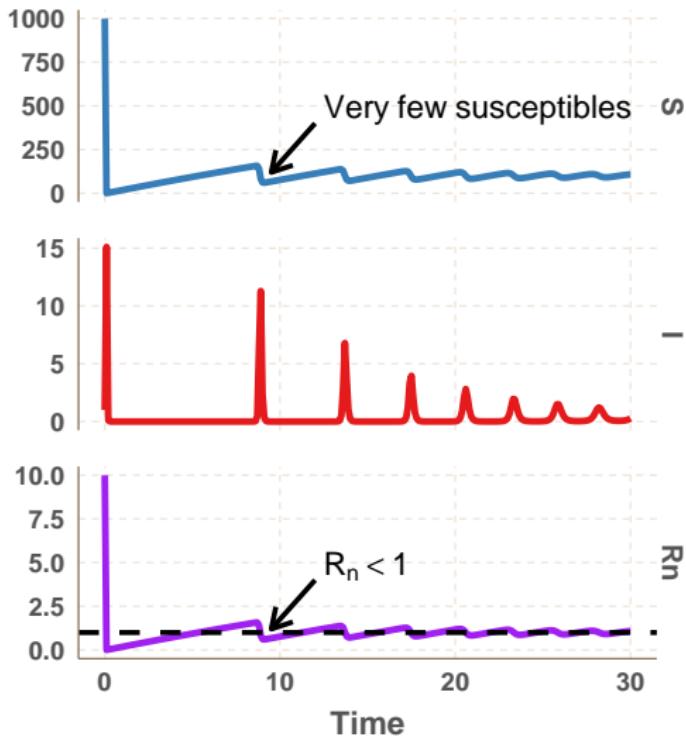
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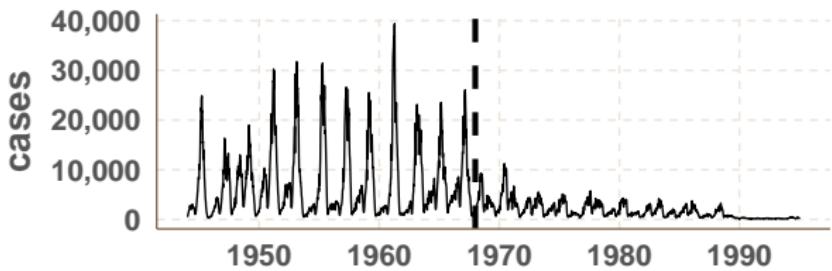


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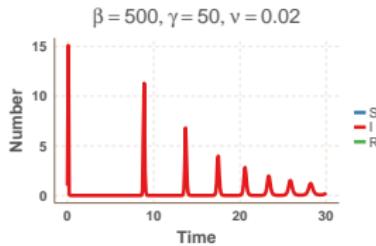
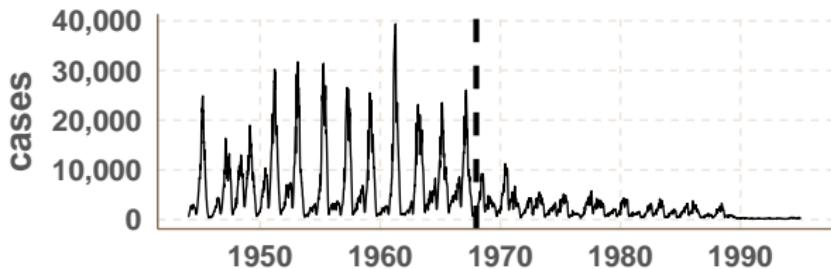


The cycle begins again

## What about measles?

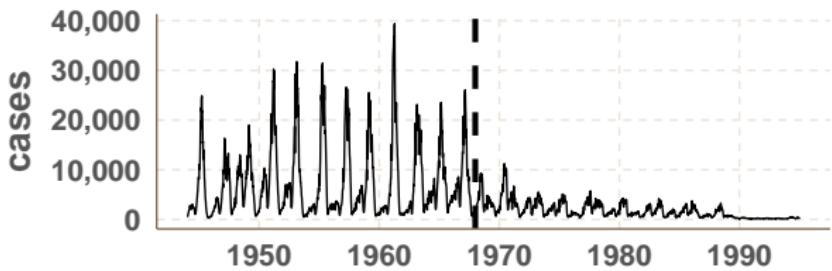


## What about measles?

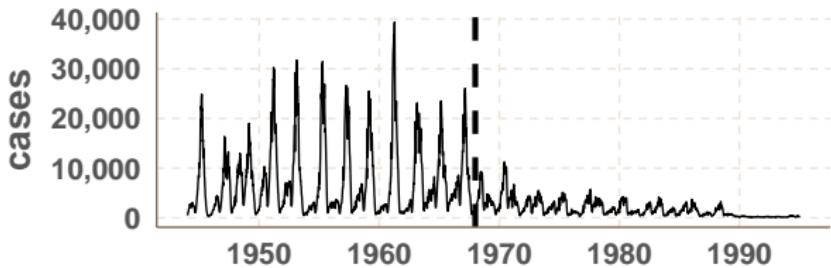


- In the SIR model with births/deaths, the endemic cycles **decline** over time

## What about measles?

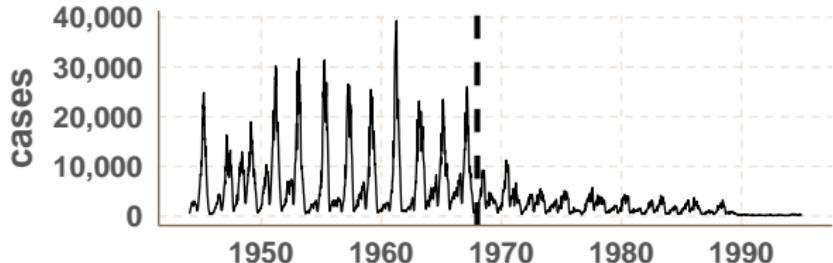


## What about measles?



- stable cycles occur if contact rate  $\beta$  changes periodically
- so-called **seasonal forcing** by the school year  
(transmission is low in the **summer vacation**)

## What about measles?



- stable cycles occur if contact rate  $\beta$  changes periodically
- so-called **seasonal forcing** by the school year  
(transmission is **low** in the **summer vacation**)
- it can be shown that the **interepidemic period**  $T$  (the time between peaks of infection) is given by

$$T \approx 2\pi \sqrt{\frac{D}{b(R_0 - 1)}}$$

## Interepidemic periods – theory vs data

Infection	Location	Inter-epidemic period	
		Calculated	Observed
<b>Measles</b>	England and Wales 1948-68	2	2
	Aberdeen, Scotland 1883-1902	2	2
	Baltimore, USA 1900-27	2	2
	Paris, France 1880-1910	2	2
	Yaounde Cameroon, 1968-75	1-2	1
	Ilesha, Nigeria, 1958-61	1-2	1
<b>Rubella</b>	Manchester, UK 1916-83	4-5	3.5
	Glasgow, Scotland, 1929-64	4-5	3.5
<b>Mumps</b>	England and Wales 1948-82	3	3
	Baltimore, USA 1928-73	3-4	2-4
<b>Polio</b>	England and Wales, 1948-65	4-5	3-5
<b>Smallpox</b>	India, 1868-1948	4-5	5
<b>Chickenpox</b>	New York City, USA, 1928-72	3-4	2-4
	Glasgow, Scotland, 1929-64	3-4	2-4
<b>Scarlet fever</b>	England and Wales, 1897-1978	4-5	3-6
<b>Diphtheria</b>	England and Wales, 1897-1979	4-5	4-6
<b>Pertussis</b>	England and Wales, 1970-82	3-4	3-4

# 6. Extending simple models

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- More complex models need more (good) data

## Extending simple models

Compartmental models can be easily extended

- Maternal immunity
- Carrier/latent states
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Simple vs. complex models

- More complex models need more (good) data
- Without good data, simple models are recommended

## Why model?

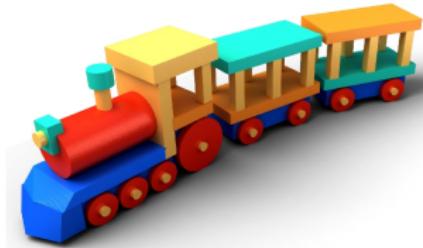
1. understand transmission dynamics
2. assess control strategies
3. predict future course

## Why model?

1. understand transmission dynamics
2. assess control strategies
3. predict future course

- Modelling can be used to make powerful predictions, many of which have been confirmed by field data
- We have seen how to build simple models to describe the spread of an infection in a population
- Models are frequently used to investigate the impact of interventions such as vaccination.

# Models must be challenged



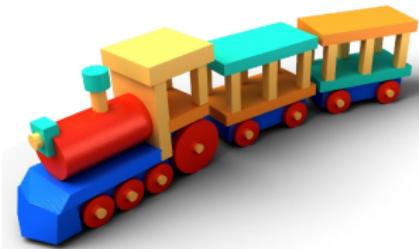
Simple



Complicated



# Models must be challenged



Simple

Complicated

- What is wrong with the model?
- What are the assumptions; are they reasonable?
- How would you improve the model?
- Are the right data available?

## 7. Summary

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## Summary I

- A mathematical model of an infectious disease is a **mathematical** description (through rules and equations) of the **dynamical process** of infectious disease transmission in a population.
- Compartmental models divide the population into **compartments**. They describe the model with **state variables** and **parameters**
- Two basic compartmental models are the **SI model** and the **SIR model**
- We can **simulate** these models using differential equations
- The value of  $R_0$  reveals if a newly introduced disease will **spread** or **die out**.
- The value of  $R_n$  determines if, at any time, a disease will **increase** or **decrease**.
- The proportion of the population one needs to **vaccinate** to prevent outbreaks is  $1 - \frac{1}{R_0}$  (herd immunity threshold)

## Summary II

- **Endemic** diseases are ones that are established in a population, and do not die out
- The simple SI or SIR models do **not** describe endemic diseases, because there is no source of **new susceptibles**
- The SIRS model describes diseases that can be endemic through **loss of immunity** (e.g., influenza)
- The SIR model can describe endemic diseases if we include **births**
- The SIR model with births produces **cycles**
- Sustained cycles only occur when there is **seasonal forcing** (e.g., school year)