

Epidemiology - Part 3

Feb. 18, 2025

Recap question:

Feb. 18, 2025

In the SI model, assume that there is one infected person on day 1, i.e., $I_1 = 1$ in a population of 100, and $\beta = 0.1$.

How many people are infected on day 3, i.e., what is I_3 ?

The SI model is defined by the equations

$$S_{t+1} = S_t - \beta \frac{S_t I_t}{N}$$

$$I_{t+1} = I_t + \beta \frac{S_t I_t}{N} = I_t + \beta I_t \left(1 - \frac{I_t}{N}\right)$$

Using the last one with $I_1 = 1$ gives

$$I_2 = I_1 + \beta I_1 \left(1 - \frac{I_1}{N}\right) = 1 + 0.1 \times 1 \times \left(1 - \frac{1}{100}\right) \approx 1.099$$

Plugging this value into the same equation gives

$$I_3 = I_2 + \beta I_2 \left(1 - \frac{I_2}{N}\right) = 1.099 + 0.1 \times 1.099 \times \left(1 - \frac{1.099}{100}\right) \approx 1.2077$$

Fractional values are okay: the model is an approximation which deals with average contacts between people

Epidemiology - Part 3

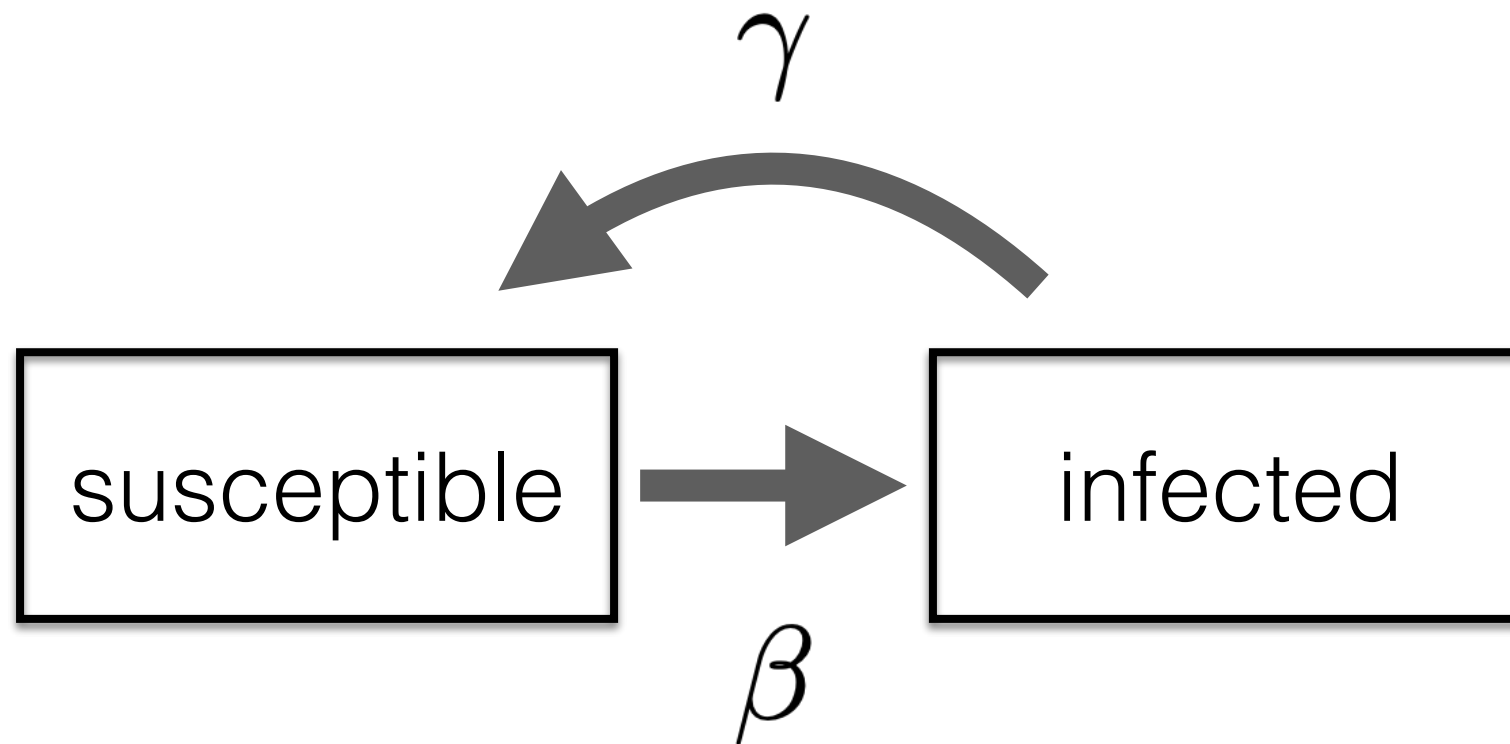
Feb. 18, 2025

By the end of this lecture, you will be able to:

1. Define the SIS and SIR models
2. Compute equilibrium values of the SIS model
3. Compute herd immunity thresholds for the SIR model

SIS model

In the SIS model, the infected individuals can return to the susceptible state after infection. This model is appropriate for diseases that commonly have repeated infections, for example, the common cold.



Basic reproduction number (R_0)

$$R_0 = \beta / \gamma$$

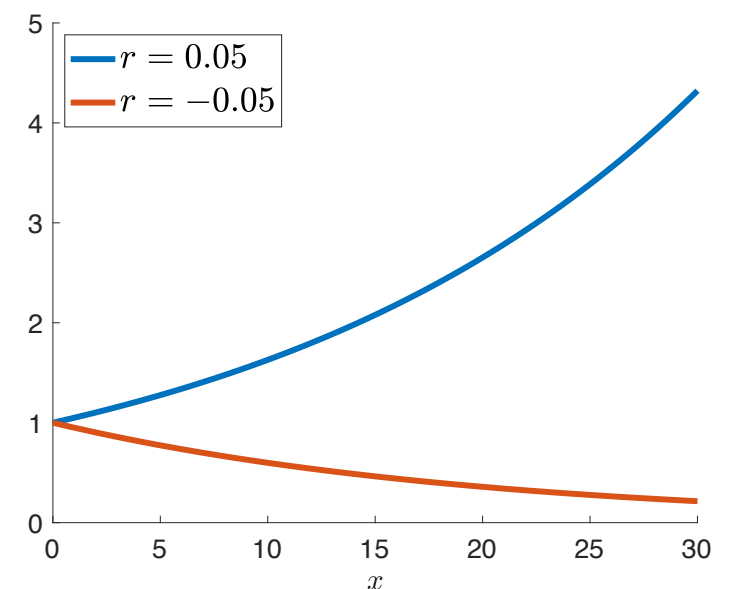
Rate of recovery (γ): the inverse of the duration of infection

The rate for the exponential growth now becomes proportional to $\beta - \gamma$

$$f(x) = a(1 + r)^x$$

$R_0 < 1$: the disease will die out

$R_0 > 1$: the disease will spread



Values of R_0 and herd immunity thresholds (HITs) of well-known infectious diseases prior to intervention

Disease	Transmission	R_0	HIT ^[a]
Measles	Aerosol	12–18 ^{[29][7]}	92–94%
Chickenpox (varicella)	Aerosol	10–12 ^[30]	90–92%
Mumps	Respiratory droplets	10–12 ^[31]	90–92%
Rubella	Respiratory droplets	6–7 ^[b]	83–86%
Polio	Fecal–oral route	5–7 ^[b]	80–86%
Pertussis	Respiratory droplets	5.5 ^[36]	82%
COVID-19 (Delta variant)	Respiratory droplets and aerosol	5.1 ^[37]	80%
Smallpox	Respiratory droplets	3.5–6.0 ^[38]	71–83%
COVID-19 (Alpha variant)	Respiratory droplets and aerosol	4–5 ^[39] ^[medical citation needed]	75–80%
HIV/AIDS	Body fluids	2–5 ^[40]	50–80%
COVID-19 (ancestral strain)	Respiratory droplets and aerosol ^[41]	2.9 (2.4–3.4) ^[42]	65% (58–71%)
SARS	Respiratory droplets	2–4 ^[43]	50–75%
Diphtheria	Saliva	2.6 (1.7–4.3) ^[44]	62% (41–77%)
Common cold	Respiratory droplets	2–3 ^[45] ^[medical citation needed]	50–67%
Influenza (1918 pandemic strain)	Respiratory droplets	2 ^[46]	50%
Ebola (2014 outbreak)	Body fluids	1.8 (1.4–1.8) ^[47]	44% (31–44%)
Influenza (2009 pandemic strain)	Respiratory droplets	1.6 (1.3–2.0) ^[2]	37% (25–51%)
Influenza (seasonal strains)	Respiratory droplets	1.3 (1.2–1.4) ^[48]	23% (17–29%)
Andes hantavirus	Respiratory droplets and body fluids	1.2 (0.8–1.6) ^[49]	16% (0–36%) ^[c]
Nipah virus	Body fluids	0.5 ^[50]	0% ^[c]
MERS	Respiratory droplets	0.5 (0.3–0.8) ^[51]	0% ^[c]

Values of R_0 and **herd immunity** thresholds (HITs) of well-known infectious diseases prior to intervention

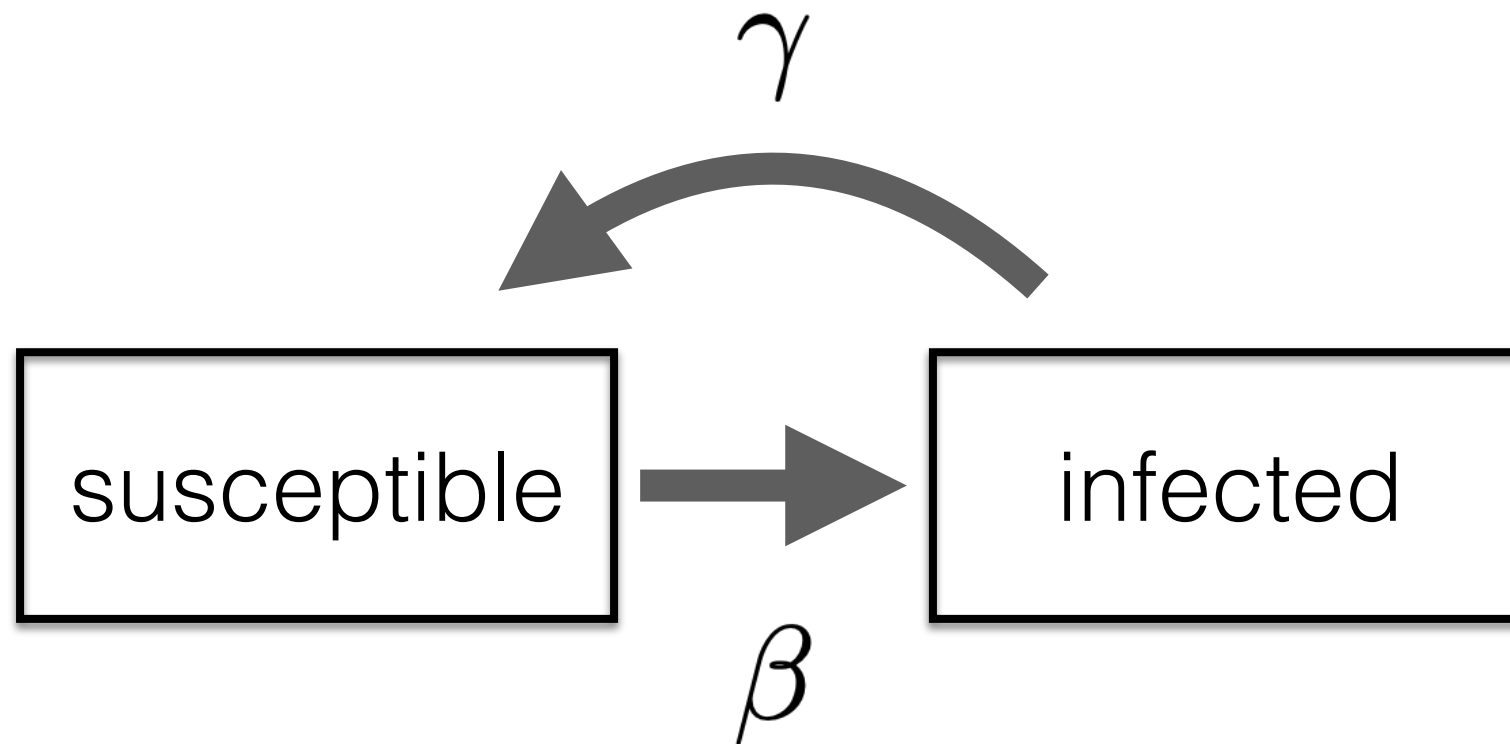
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Values of R_0 and **herd immunity** thresholds (HITs) for variants of SARS-CoV-2

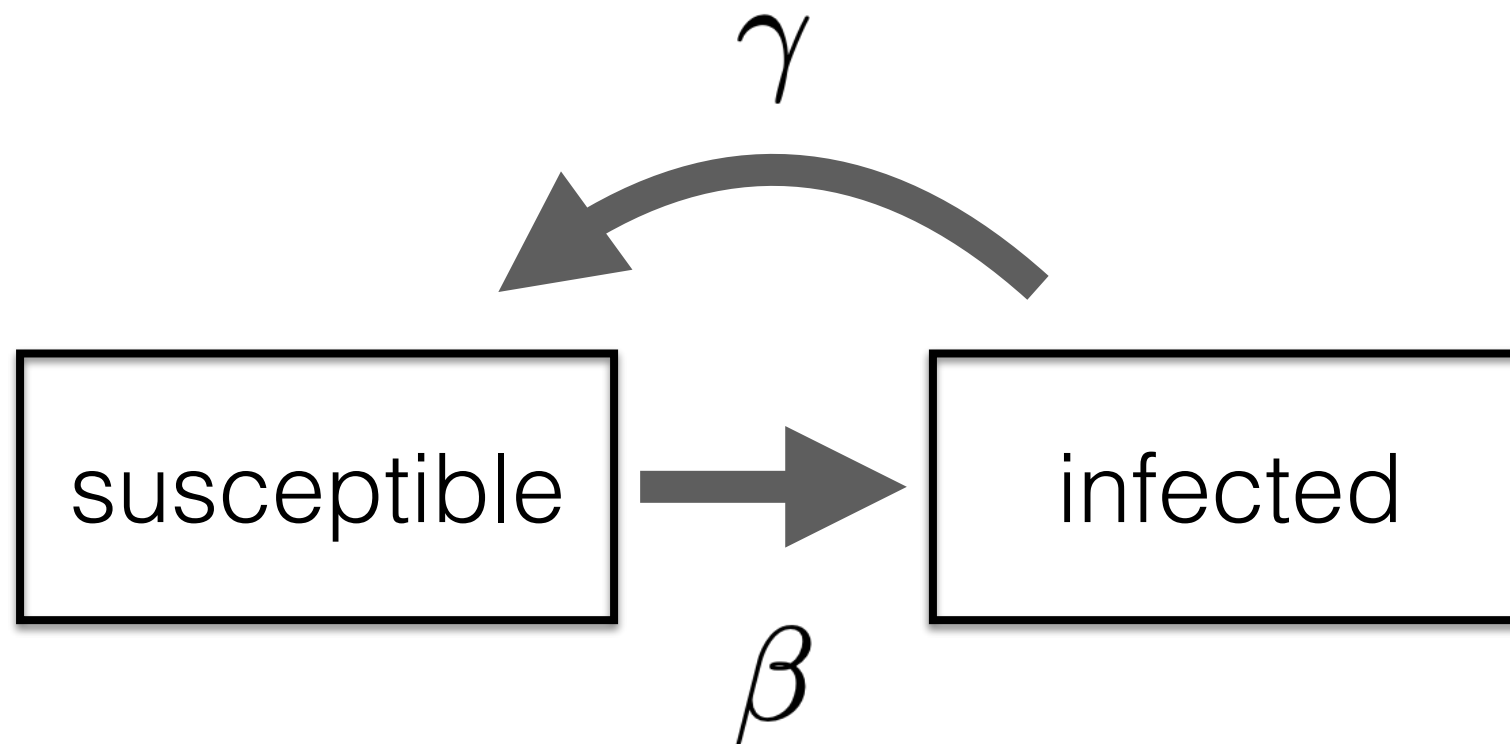
Disease	Transmission	R_0	HIT ^[e]
COVID-19 (Omicron variant)	Respiratory droplets and aerosol	9.5 ^[61]	89%
COVID-19 (Delta variant)	Respiratory droplets and aerosol	5.1 ^[62]	80%
COVID-19 (Alpha variant)	Respiratory droplets and aerosol	4–5 ^[63] ^[medical citation needed]	75–80%
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SIS model

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SIS model



Rate of transmission (β): the average number of infection-producing contacts per unit time

Rate of recovery (γ): one over the average duration of infection

Basic reproduction number (R_0): $R_0 = \beta/\gamma$

Basic reproduction number (R_0)

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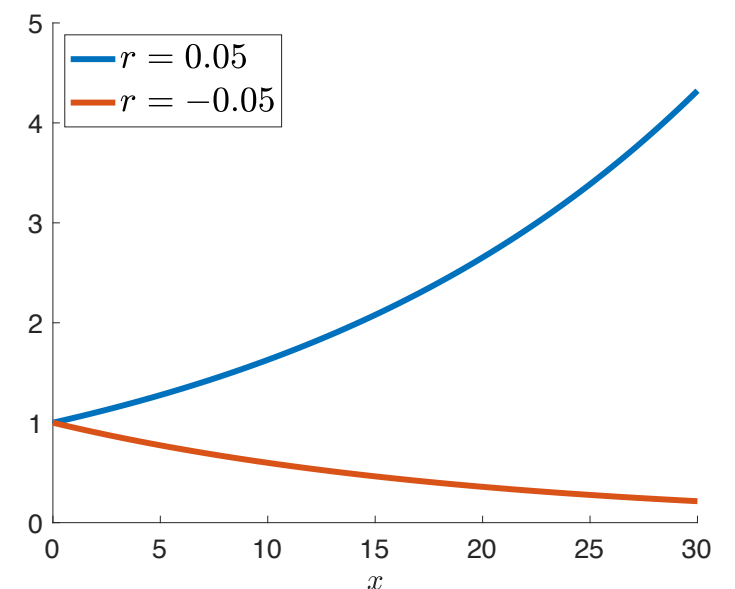
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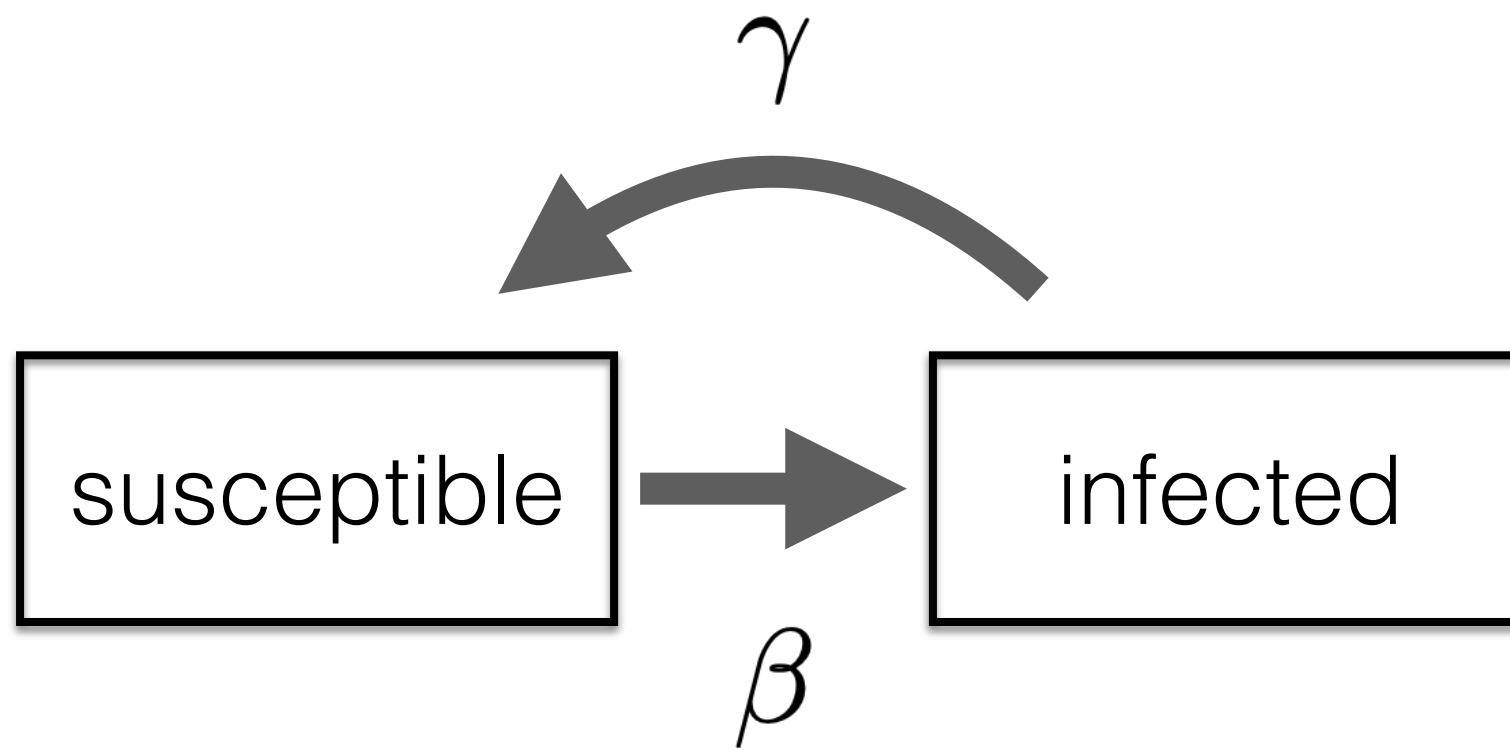
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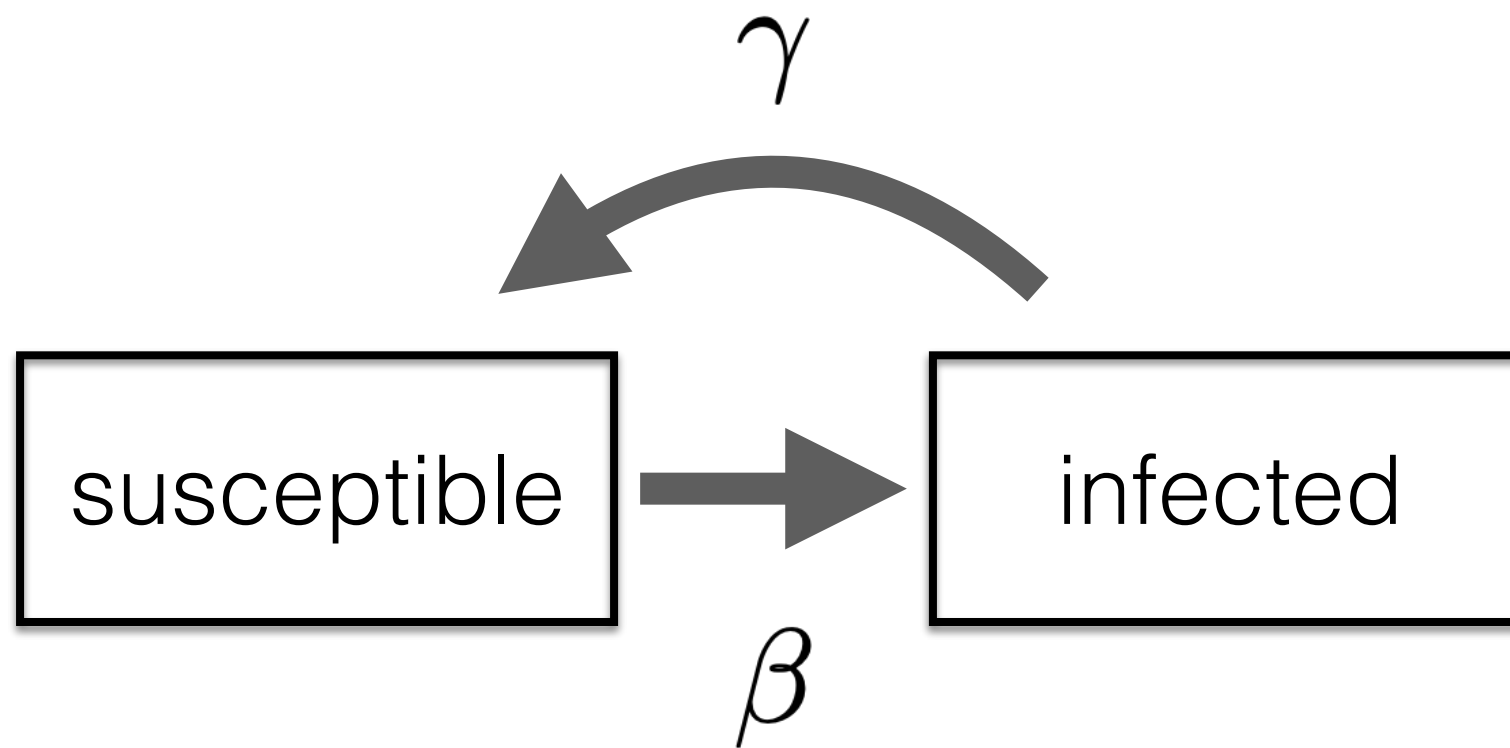
Susceptible
on day $t + 1$

Newly infected

$$S_{t+1} = S_t - \beta \frac{S_t I_t}{N} + \gamma I_t$$

Newly recovered

Susceptible
on day t



$$S_{t+1} = S_t - \beta \frac{S_t I_t}{N} + \gamma I_t$$

Newly infected

Newly recovered

$$I_{t+1} = I_t + \beta \frac{S_t I_t}{N} - \gamma I_t$$

$$= I_t + \beta I_t \left(1 - \frac{I_t}{N} \right) - \gamma I_t$$

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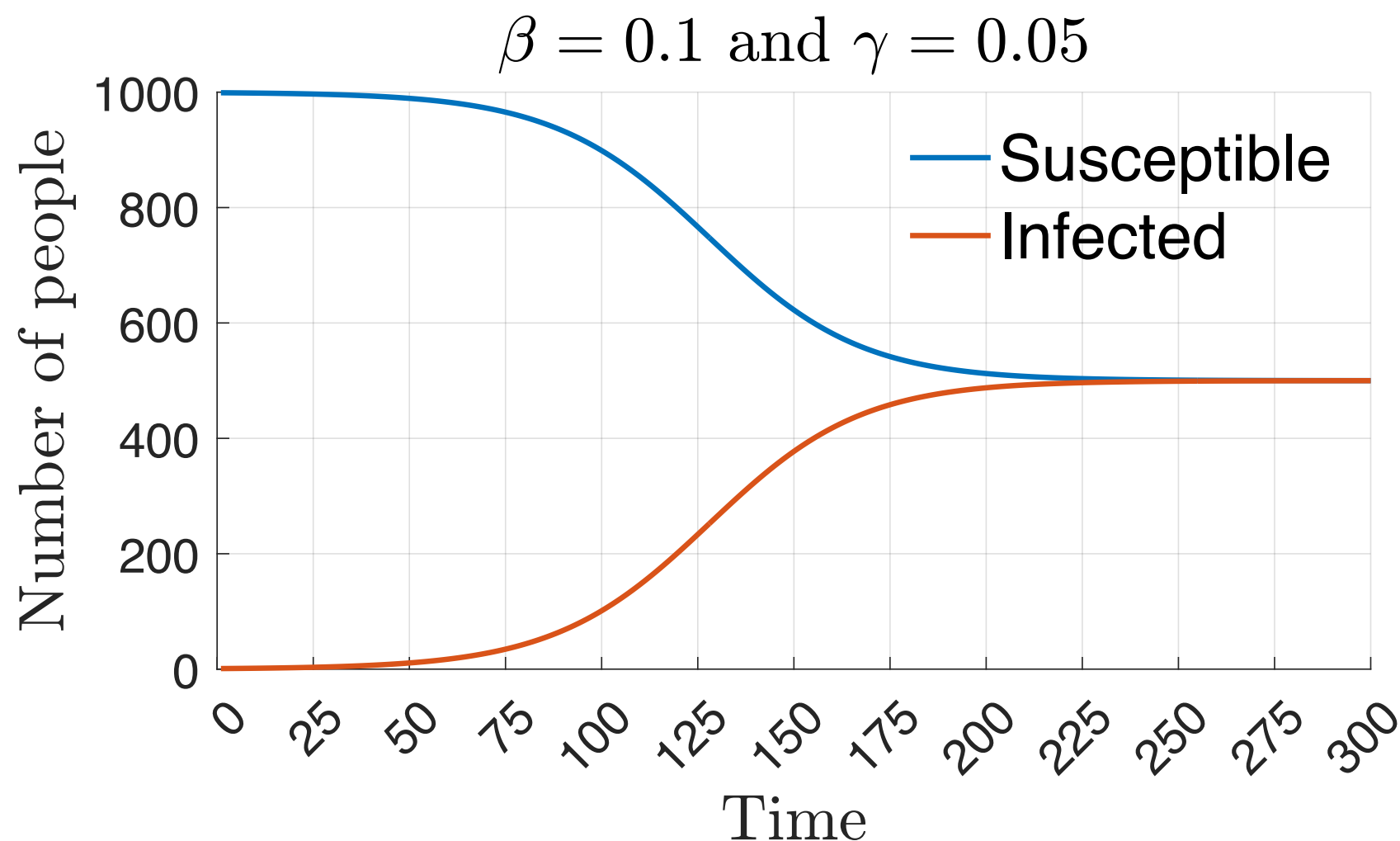
Newly recovered

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To simulate, start with a value for I_1 . Plug this in to get a value for I_2 . Plug this in to get a value for I_3 . Continue for as long as you'd like.

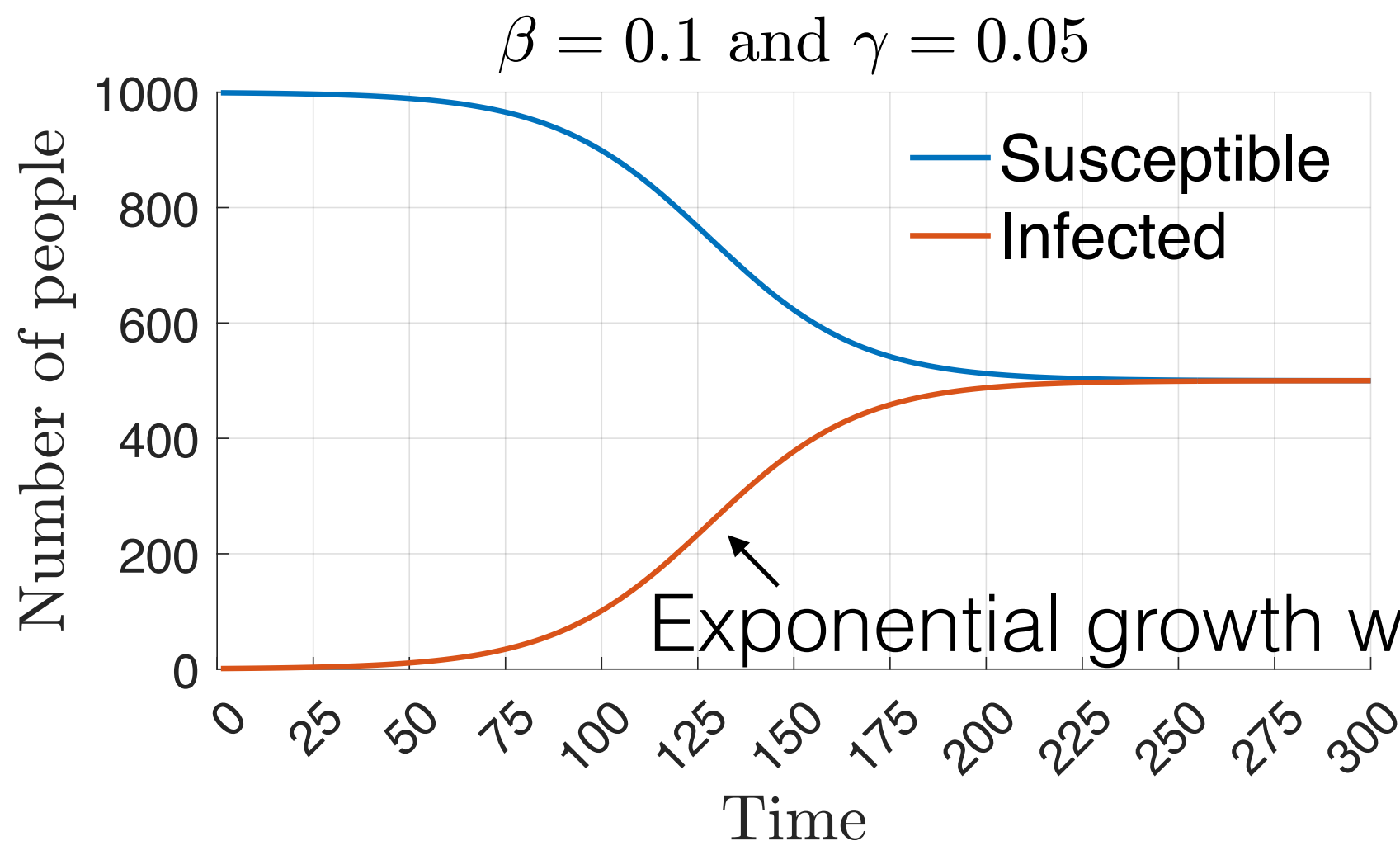
Example 1: In a closed environment with population size $N = 1,000$. Suppose that there is only one infection on day 1, where the transmission rate β is 0.1 per day, and the duration of infection is 20 days.



$$\gamma = \frac{1}{20}$$

$$R_0 = \beta / \gamma = 2 > 1$$

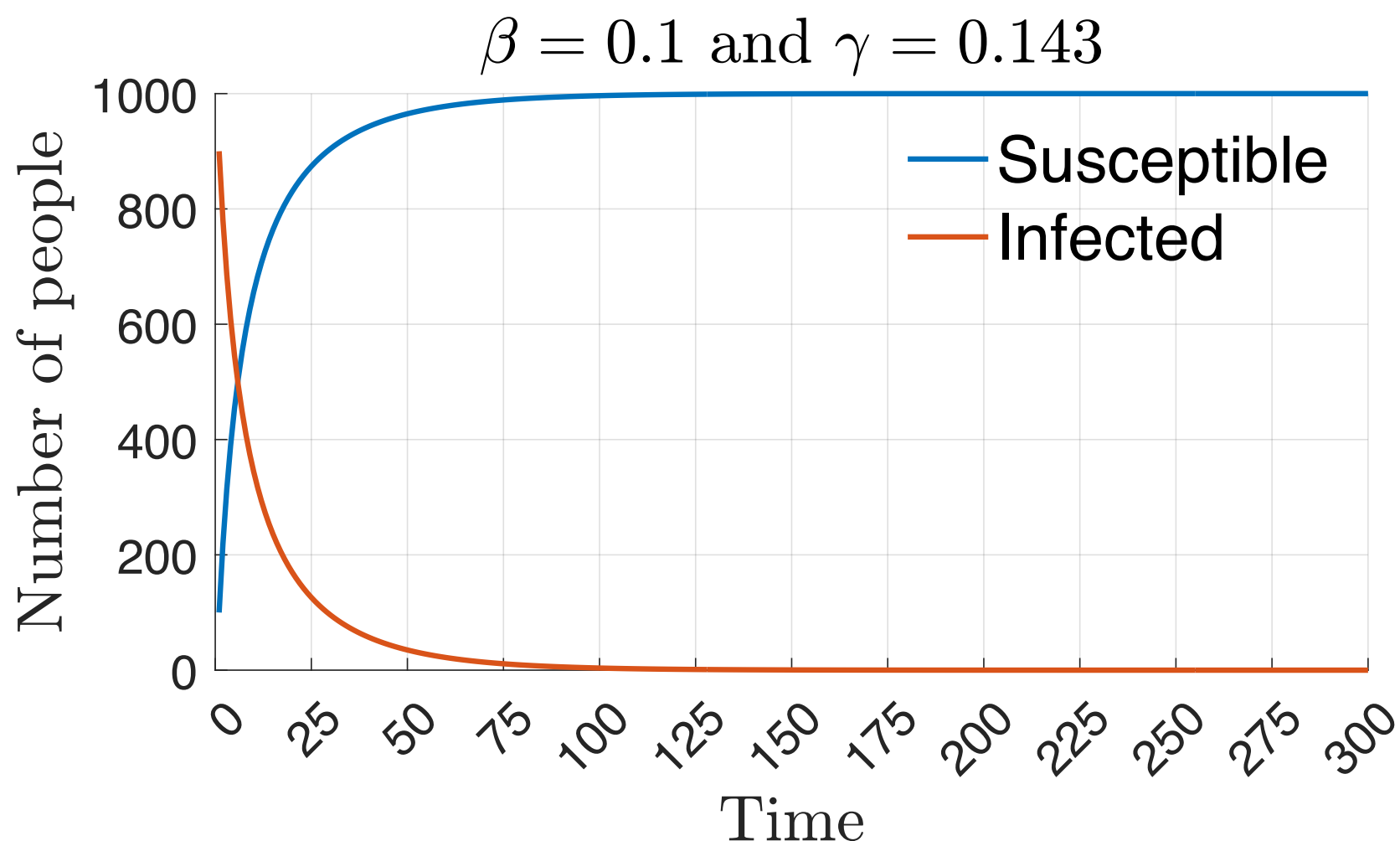
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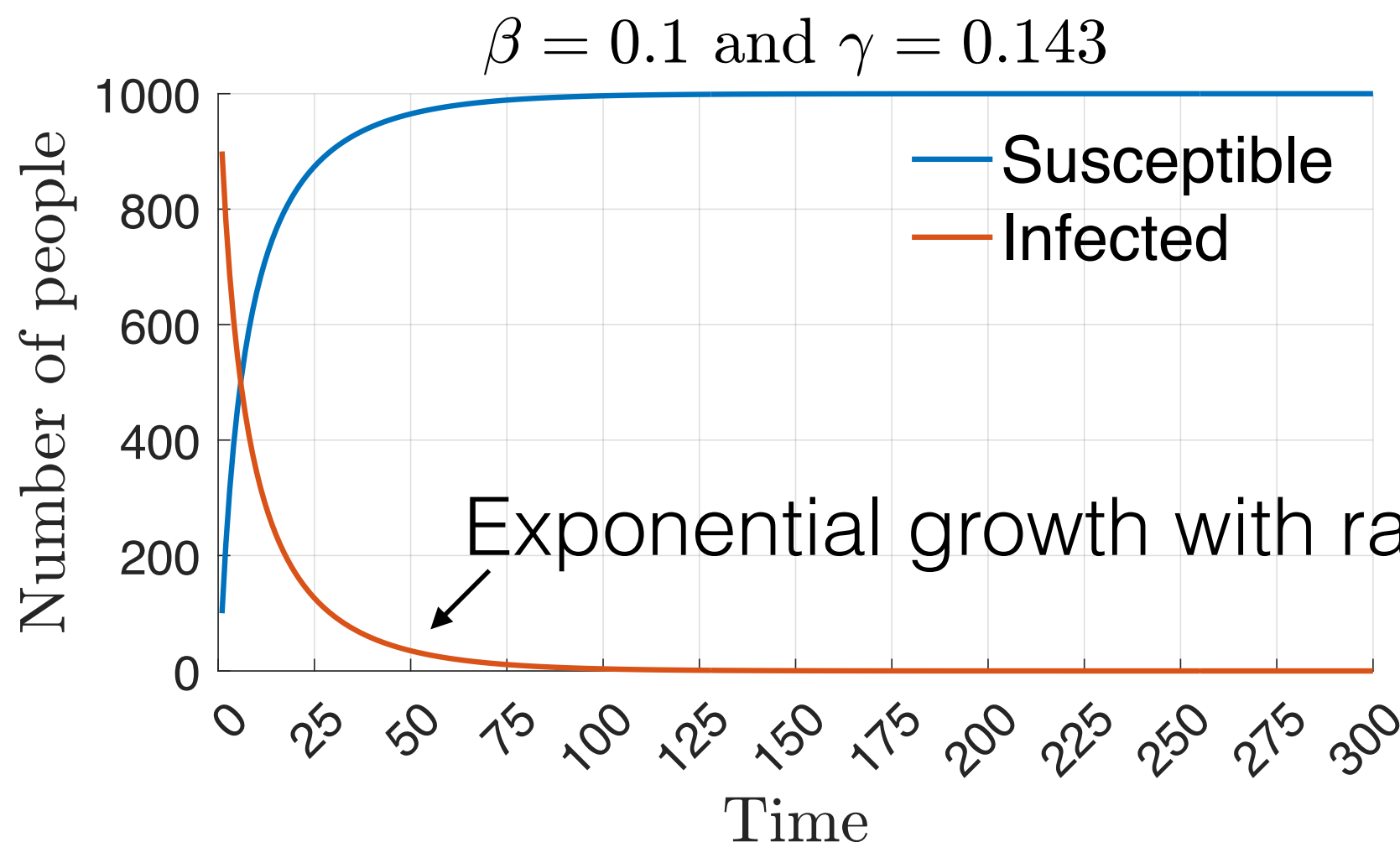
Example 2: In a closed environment with population size $N = 1,000$. Suppose that there are 900 infections on day 1, where the transmission rate β is 0.1 per day, and the duration of infection is 7 days.



$$\gamma = \frac{1}{7}$$

$$R_0 = \beta / \gamma = 0.7 < 1$$

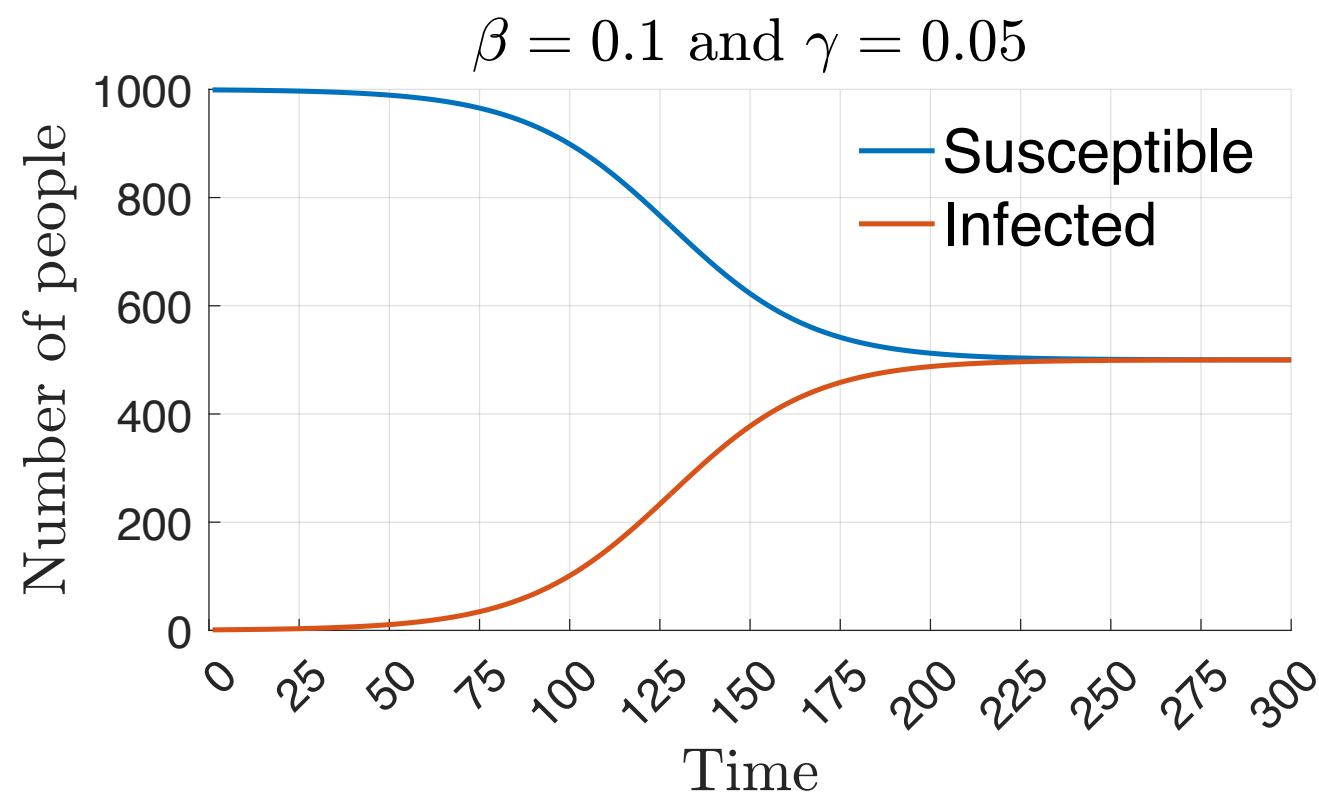
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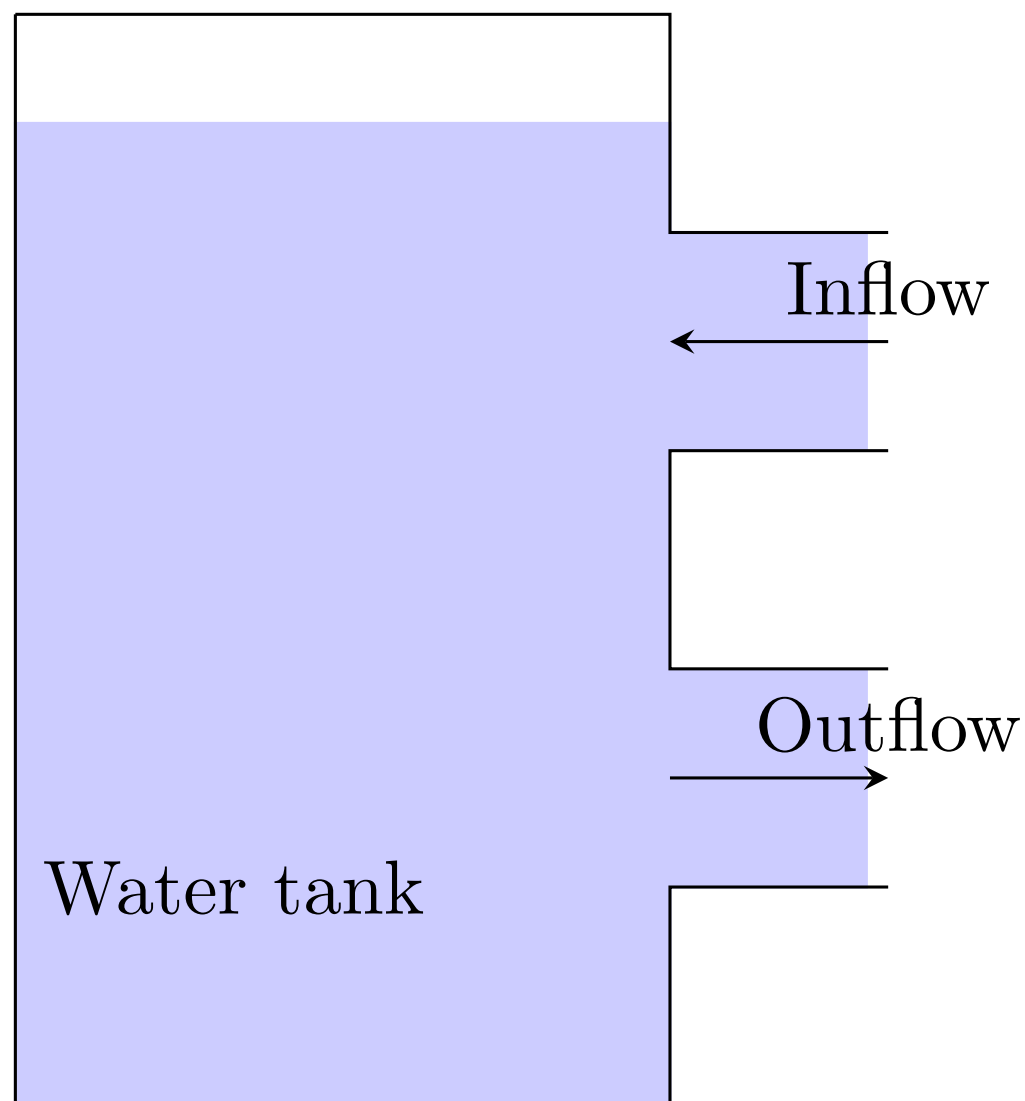
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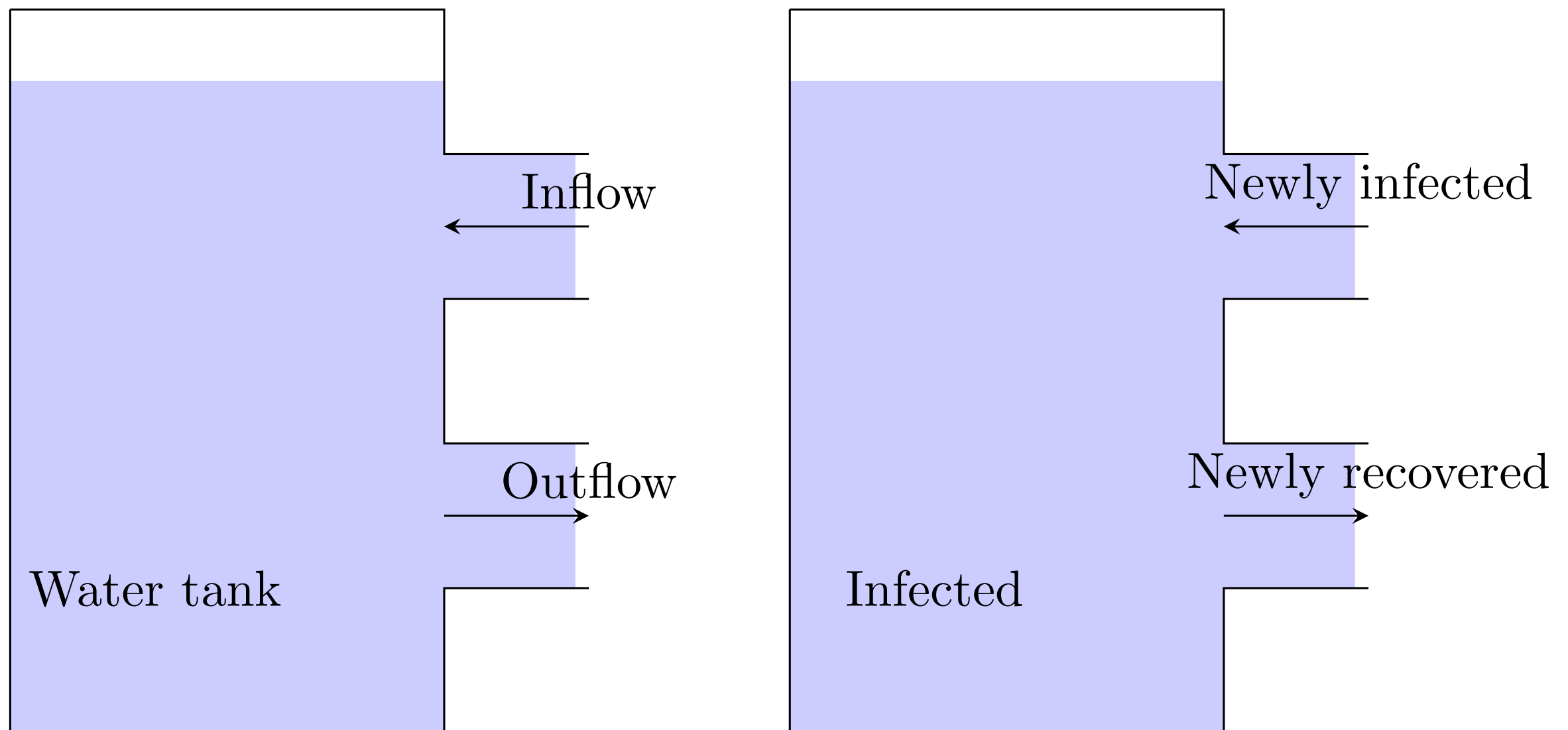
The system can find an equilibrium where the number of newly infected equals the number of newly recovered! The overall number of susceptible or infected then does not change over time.



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At equilibrium, $I_{t+1} = I_t$ so call both of these quantities I . The number of infected grows as

$$I_{t+1} = I_t + \beta I_t \left(1 - \frac{I_t}{N}\right) - \gamma I_t$$

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The only way for the product of these terms to be zero is if

$$I = 0 \quad \text{or} \quad \frac{\beta}{N} I + \gamma - \beta = 0$$

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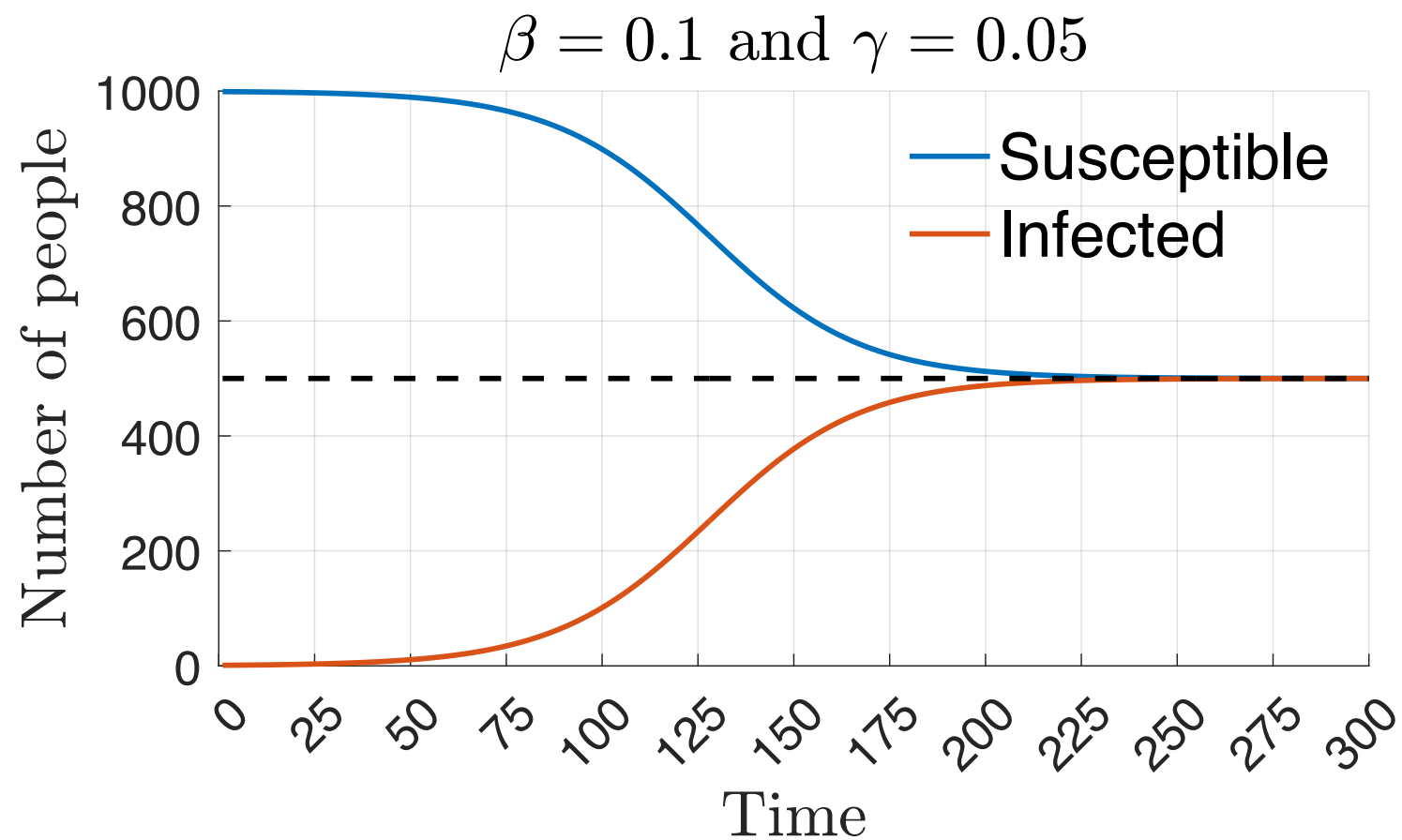
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The only way for the product of these terms to be zero is if $I = 0$ or $\frac{\beta}{N} I + \gamma - \beta = 0$ which simplifies to

$$I = N \left(1 - \frac{\gamma}{\beta} \right) \leftarrow \text{Equilibrium value}$$

$$I = N\left(1 - \frac{\gamma}{\beta}\right)$$

When $N = 1000$, $\gamma = 0.05$, $\beta = 0.1$, $N\left(1 - \frac{\gamma}{\beta}\right) = 500$.



SIR model

The SIR model consists of three compartments:

S: **Susceptible**

I: **Infected**

R: **Removed: recovered** (and immune) or **deceased**
individuals





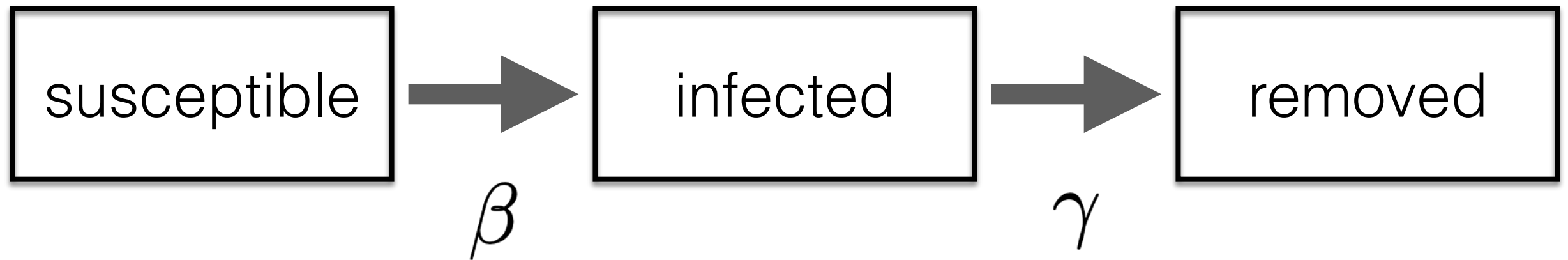
$$S_{t+1} = S_t - \beta \frac{S_t I_t}{N}$$

Newly infected

$$I_{t+1} = I_t + \beta \frac{S_t I_t}{N} - \gamma I_t$$

Newly removed

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



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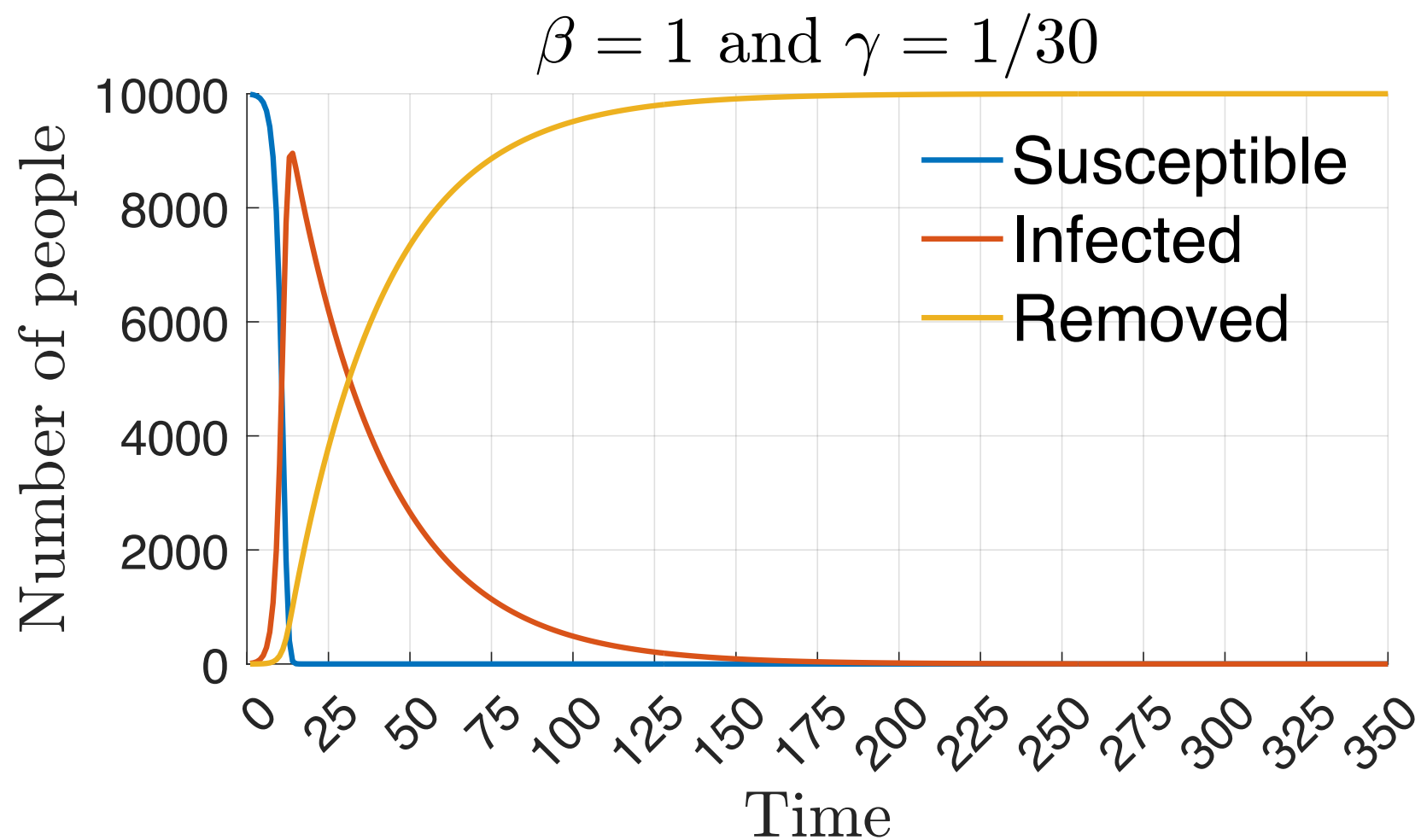
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Newly removed

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To simulate, start with values for S_1, I_1, R_1 , plug in to get values for S_2, I_2, R_2 . Plug these values in to get values for S_3, I_3, R_3 and continue.

Example 1: In a closed environment with population size $N = 10,000$. Suppose that there are 10 infections on day 1, and that $R_0 = 30$ and $\beta = 1$.

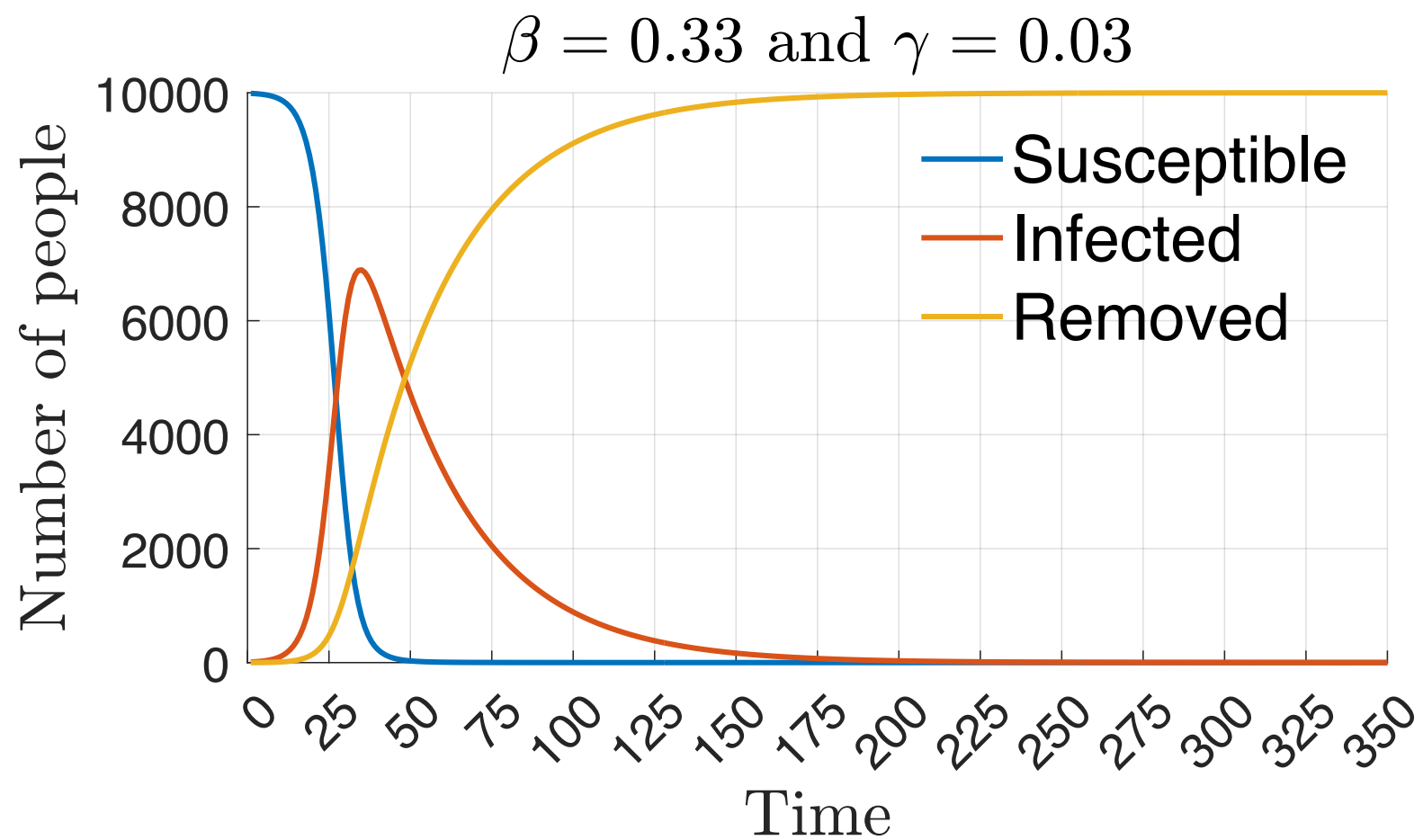


$$R_0 = \frac{\beta}{\gamma}$$

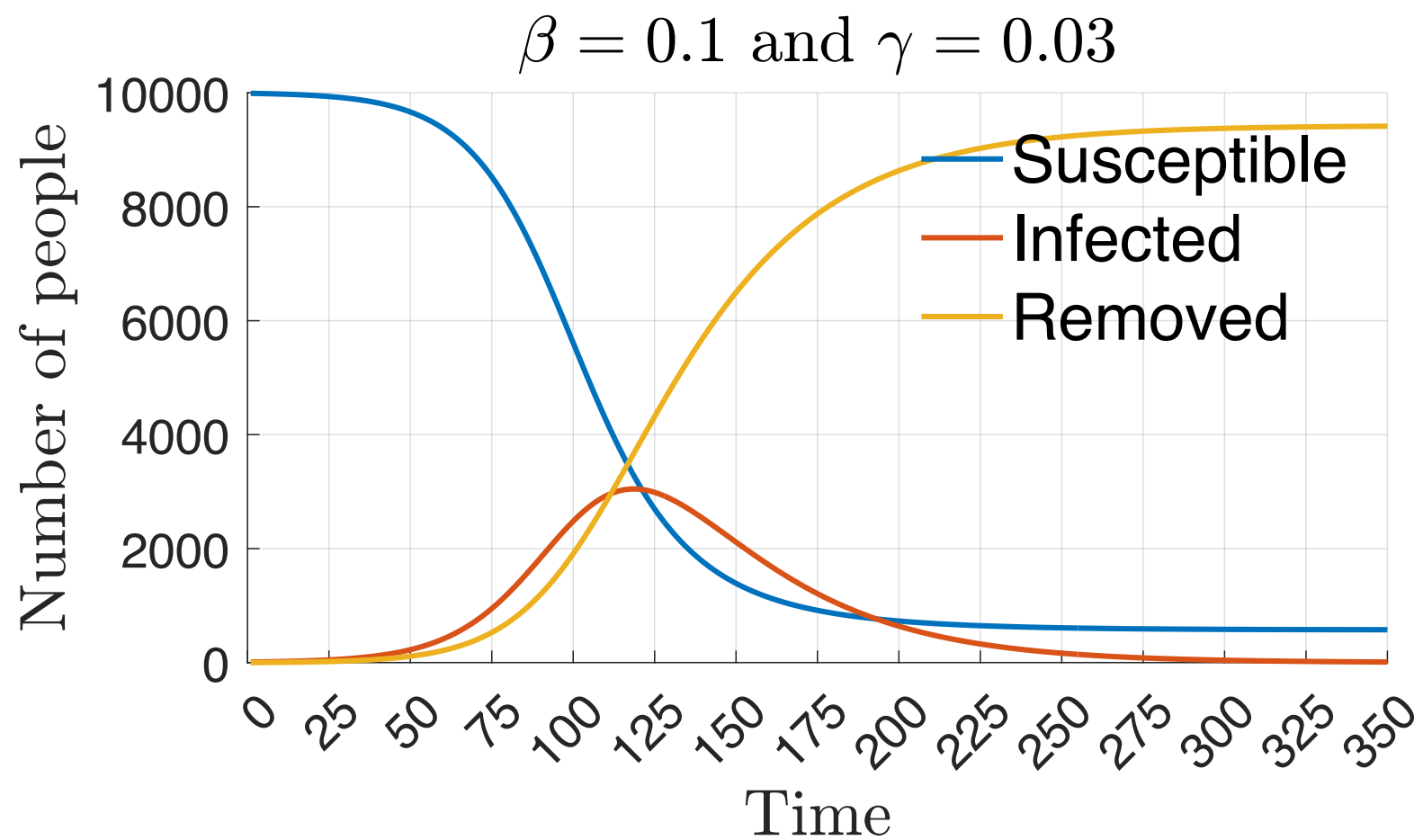
so $\gamma = \frac{\beta}{R_0}$

$$R_0 = 30$$

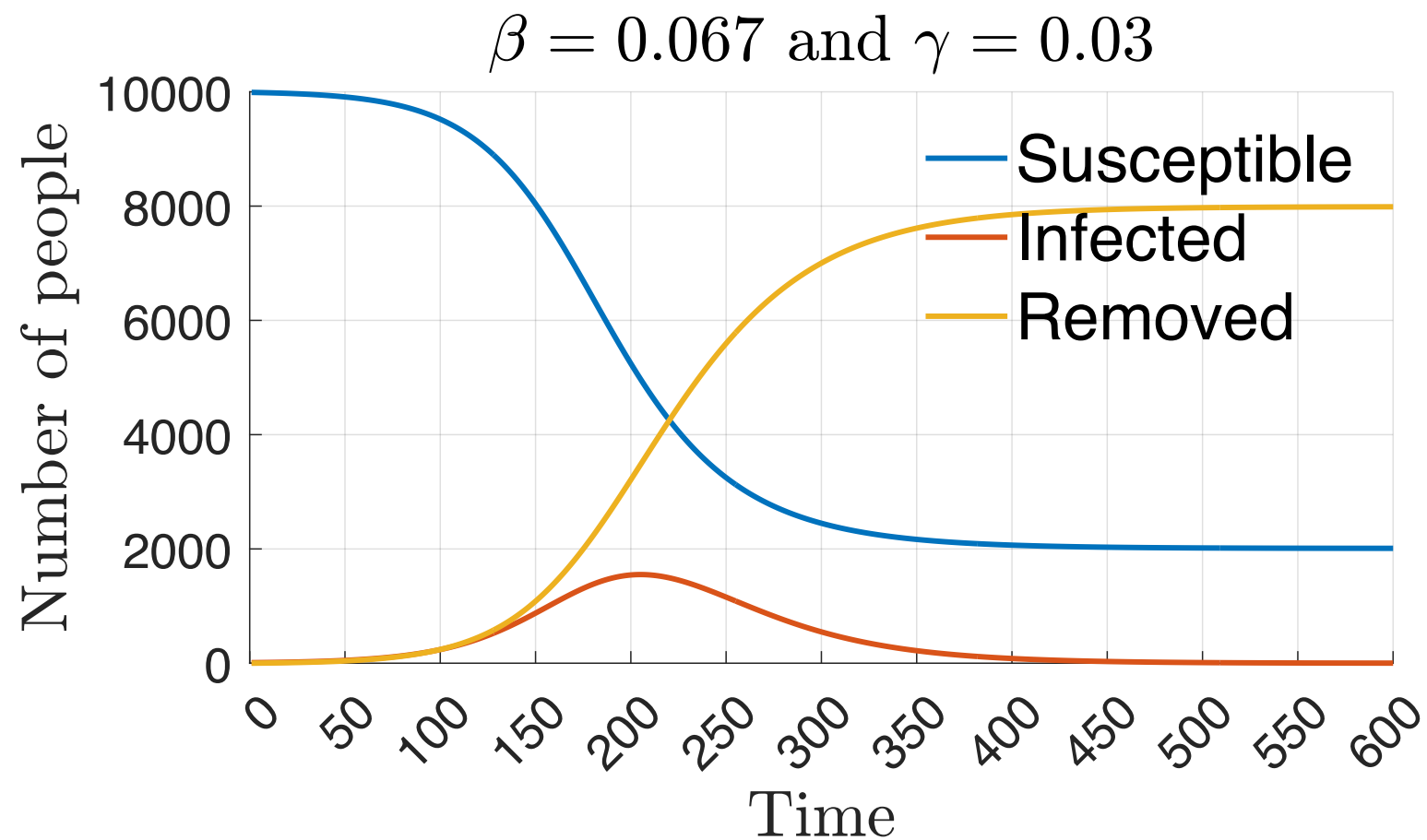
$$R_0 = 10$$



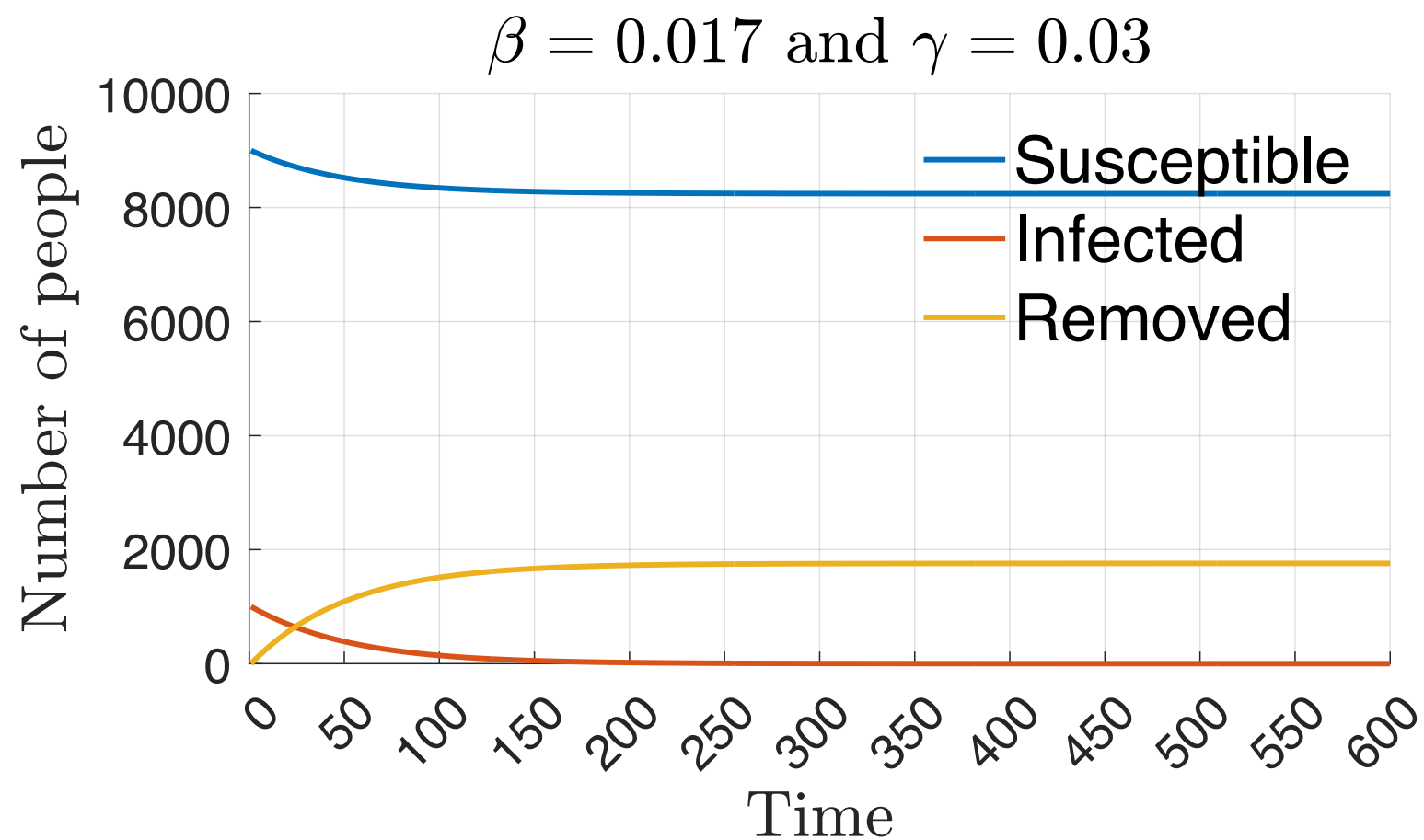
$$R_0 = 3$$



$$R_0 = 2$$



$$R_0 = 0.5$$



Disease dies
out when
 $R_0 < 1$

How well does this work in practice?

Look at data from the first 100 days (say) and find the β, γ that best describe the data. Then use those values to predict the future.

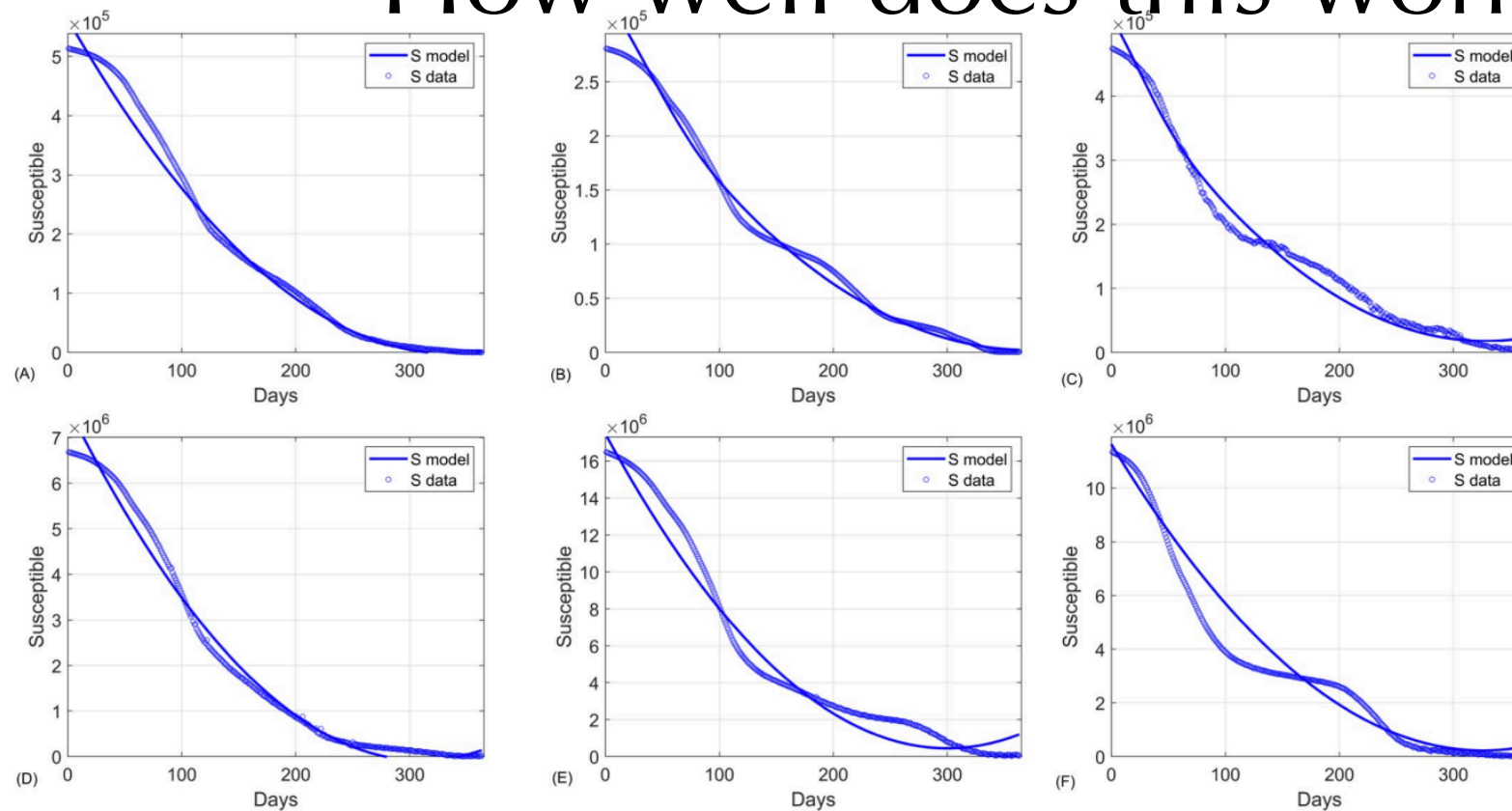


Fig 3. The extended SIR model fitted to the COVID-19 data of susceptible subpopulation in (A) Kansas City, (B) Saint Louis, (C) San Francisco, (D) Missouri, (E) Illinois, and (F) Arizona.

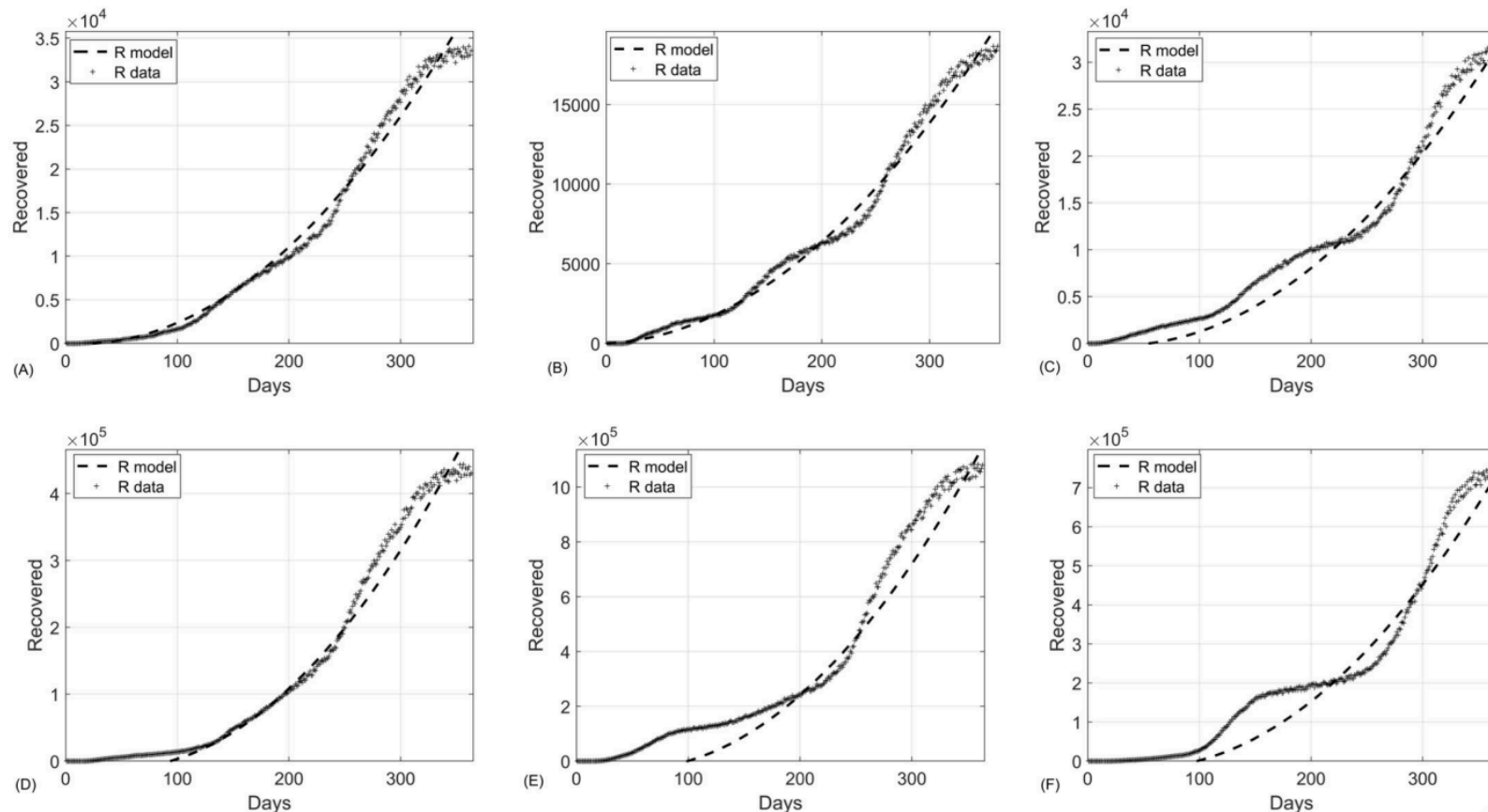


Fig 4. The extended SIR model fitted to the COVID-19 data of recovered subpopulation in (A) Kansas City, (B) Saint Louis, (C) San Francisco, (D) Missouri, (E) Illinois, and (F) Arizona.

From AlQadi H, Bani-Yaghoub M (2022) using a slightly different model.

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We now derive a condition for when this is true, which depends on the number of susceptible individuals and R_0 .

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so subtracting I_t from both sides gives

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This is positive when $\beta \frac{S_t I_t}{N} > \gamma I_t$.

Dividing both sides by βI_t and multiplying by N gives

$$S_t > N \frac{\gamma}{\beta} = \frac{N}{R_0}$$

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$$S_t > N \frac{\gamma}{\beta} = \frac{N}{R_0}$$

As long as there are sufficiently many susceptible people left in the population compared to R_0 , an epidemic will start. Vaccination reduces the number of susceptible, and other interventions (mask mandates, ...) reduce R_0 .

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so $I_{t+1} = I_t$ when $\beta \frac{S_t I_t}{N} = \gamma I_t$. Dividing by γI_t gives

$$\frac{\beta}{\gamma} \frac{S_t}{N} = R_0 \frac{S_t}{N} = 1$$

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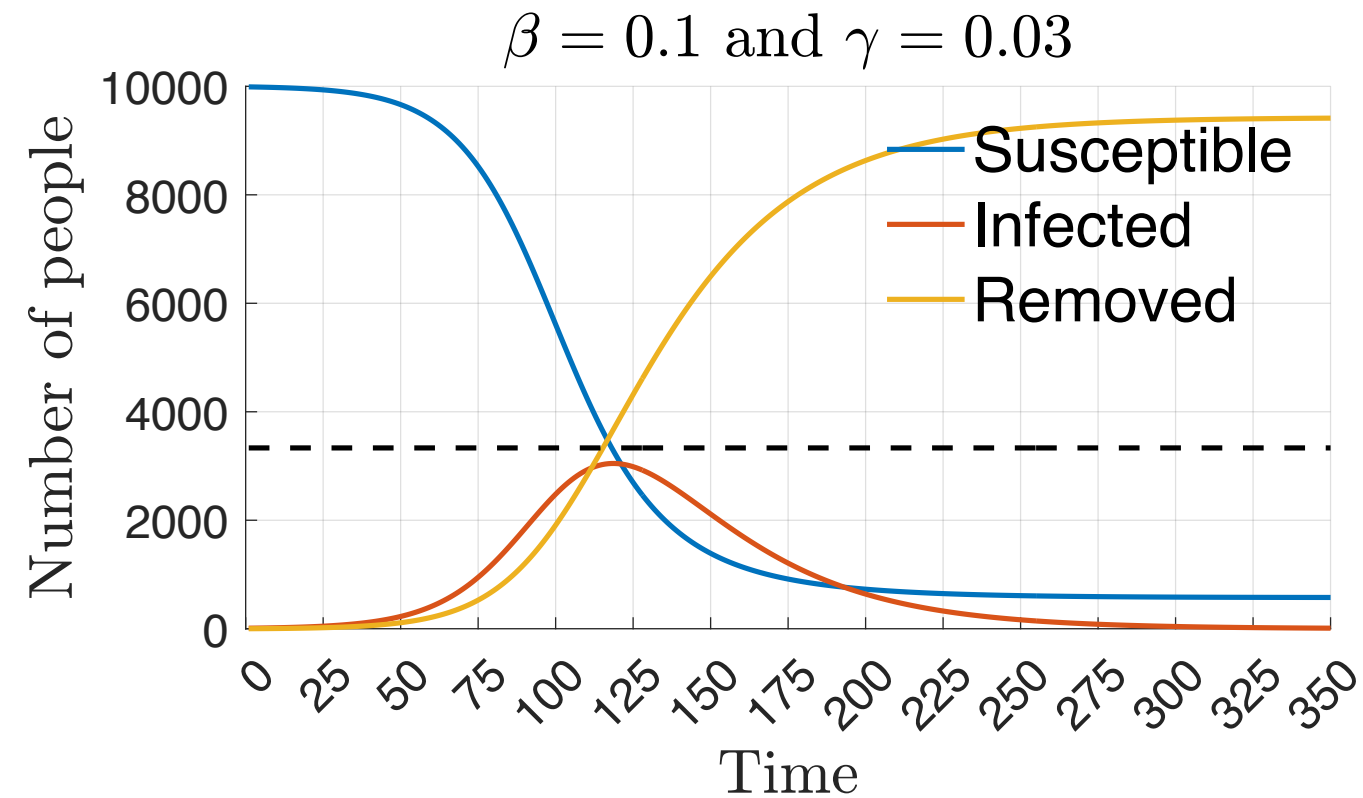
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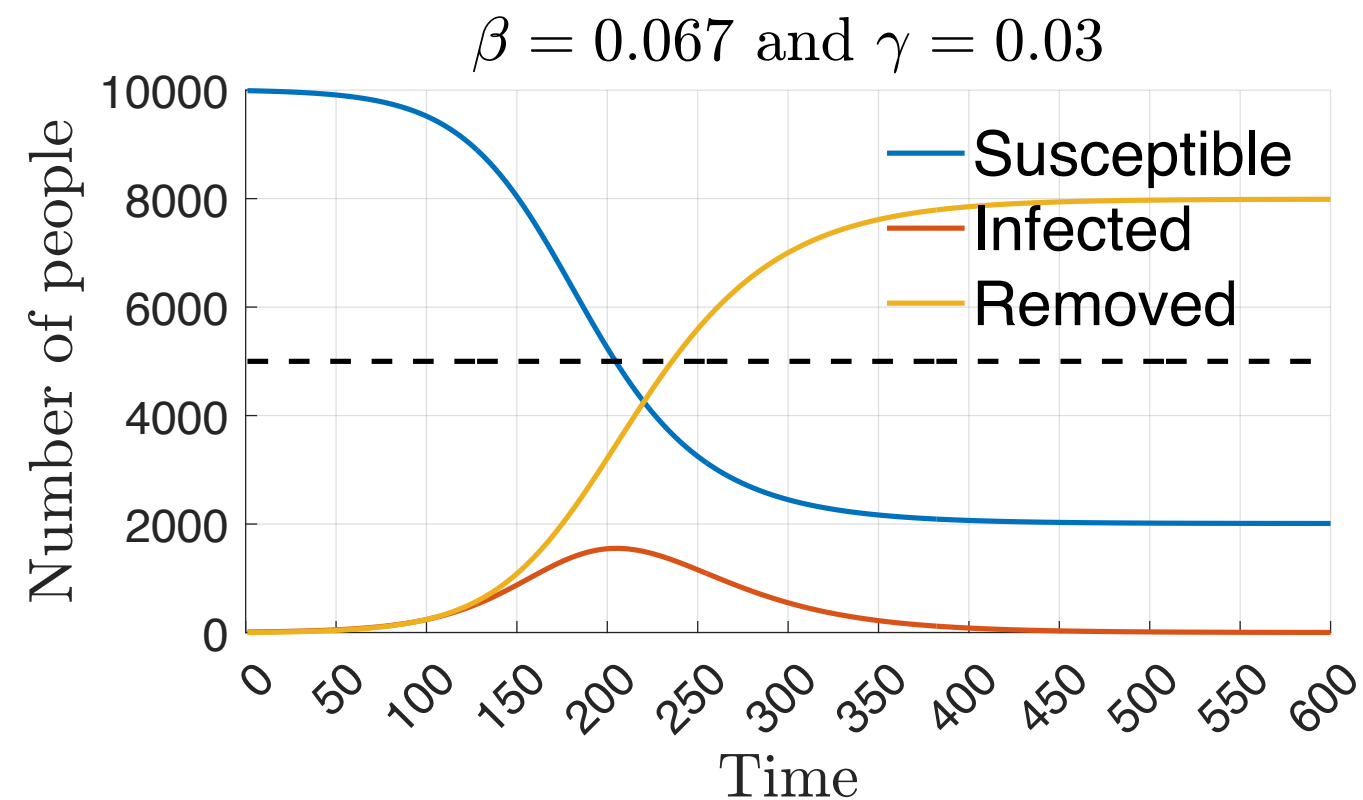
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$$\frac{\beta}{\gamma} \frac{S_t}{N} = R_0 \frac{S_t}{N} = 1 , \text{ i.e., } S_t = \frac{N}{R_0}$$

$$S_t = \frac{N}{R_0} \text{ indicated by dashed line}$$



$$R_0 = 3$$



$$R_0 = 2$$

p_c : the critical proportion of the population needed to be immune to stop the transmission of disease, which is also known as the **herd immunity threshold** (HIT).

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

which means that $1 - p_c = \frac{1}{R_0}$.

Rearranging the terms gives

$$p_c = 1 - \frac{1}{R_0}$$

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Measles	Aerosol	12–18 ^{[29][7]}	92–94%
Chickenpox (varicella)	Aerosol	10–12 ^[30]	90–92%
Mumps	Respiratory droplets	10–12 ^[31]	90–92%
Rubella	Respiratory droplets	6–7 ^[b]	83–86%
Polio	Fecal–oral route	5–7 ^[b]	80–86%
Pertussis	Respiratory droplets	5.5 ^[36]	82%
COVID-19 (Delta variant)	Respiratory droplets and aerosol	5.1 ^[37]	80%
Smallpox	Respiratory droplets	3.5–6.0 ^[38]	71–83%
COVID-19 (Alpha variant)	Respiratory droplets and aerosol	4–5 ^[39] ^[medical citation needed]	75–80%
HIV/AIDS	Body fluids	2–5 ^[40]	50–80%
COVID-19 (ancestral strain)	Respiratory droplets and aerosol ^[41]	2.9 (2.4–3.4) ^[42]	65% (58–71%)
SARS	Respiratory droplets	2–4 ^[43]	50–75%
Diphtheria	Saliva	2.6 (1.7–4.3) ^[44]	62% (41–77%)
Common cold	Respiratory droplets	2–3 ^[45] ^[medical citation needed]	50–67%
Influenza (1918 pandemic strain)	Respiratory droplets	2 ^[46]	50%
Ebola (2014 outbreak)	Body fluids	1.8 (1.4–1.8) ^[47]	44% (31–44%)
Influenza (2009 pandemic strain)	Respiratory droplets	1.6 (1.3–2.0) ^[2]	37% (25–51%)
Influenza (seasonal strains)	Respiratory droplets	1.3 (1.2–1.4) ^[48]	23% (17–29%)
Andes hantavirus	Respiratory droplets and body fluids	1.2 (0.8–1.6) ^[49]	16% (0–36%) ^[c]
Nipah virus	Body fluids	0.5 ^[50]	0% ^[c]
MERS	Respiratory droplets	0.5 (0.3–0.8) ^[51]	0% ^[c]

When the proportion of the population that is immune is larger than the herd immunity threshold

$$p > p_c = 1 - \frac{1}{R_0}$$

the number of infections would gradually decrease

$$I_{t+1} = I_t + \beta \frac{S_t I_t}{N} - \gamma I_t$$
$$< I_t$$

If herd immunity has been established and maintained in a population for a sufficient time, the disease is inevitably eliminated – no more endemic transmissions occur. If elimination is achieved worldwide and the number of cases is permanently reduced to zero, then a disease can be declared eradicated.

To date, rinderpest and smallpox have been eradicated using herd immunity and vaccination. Eradication efforts that rely on herd immunity are currently underway for polio.

SIRD model

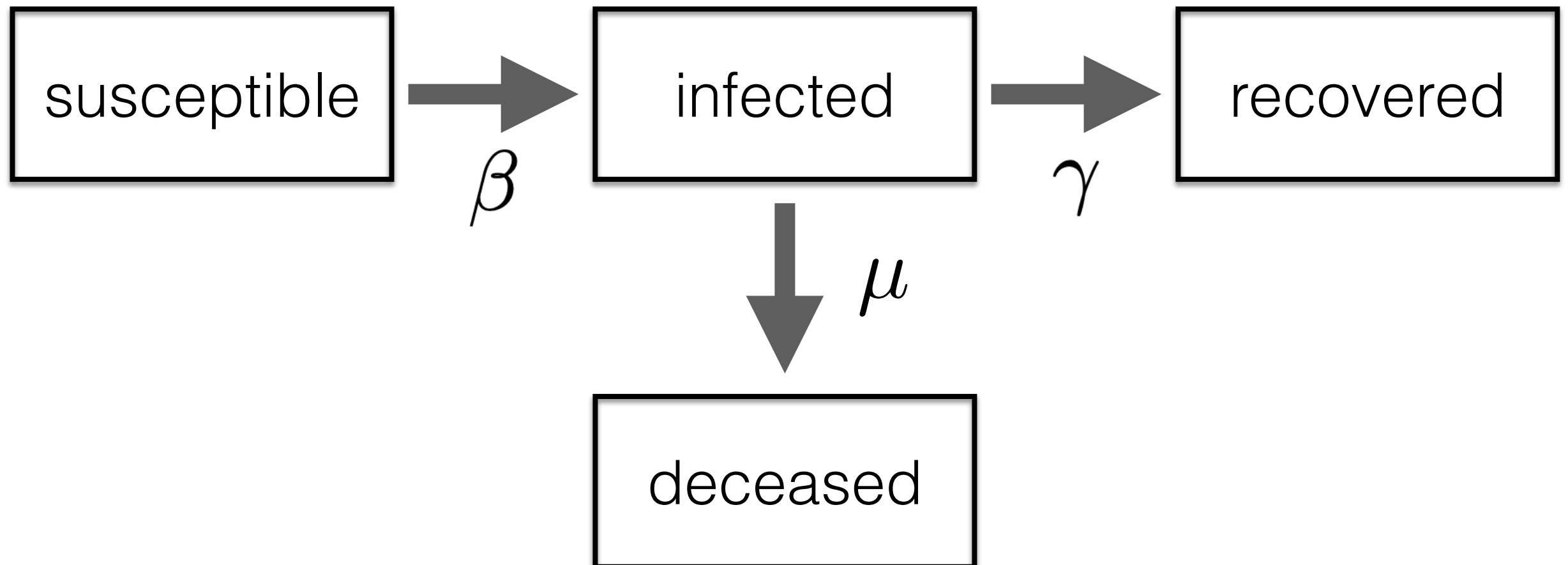
The SIRD model separates recovered and deceased into their own compartments:

S: **Susceptible**

I: **Infected**

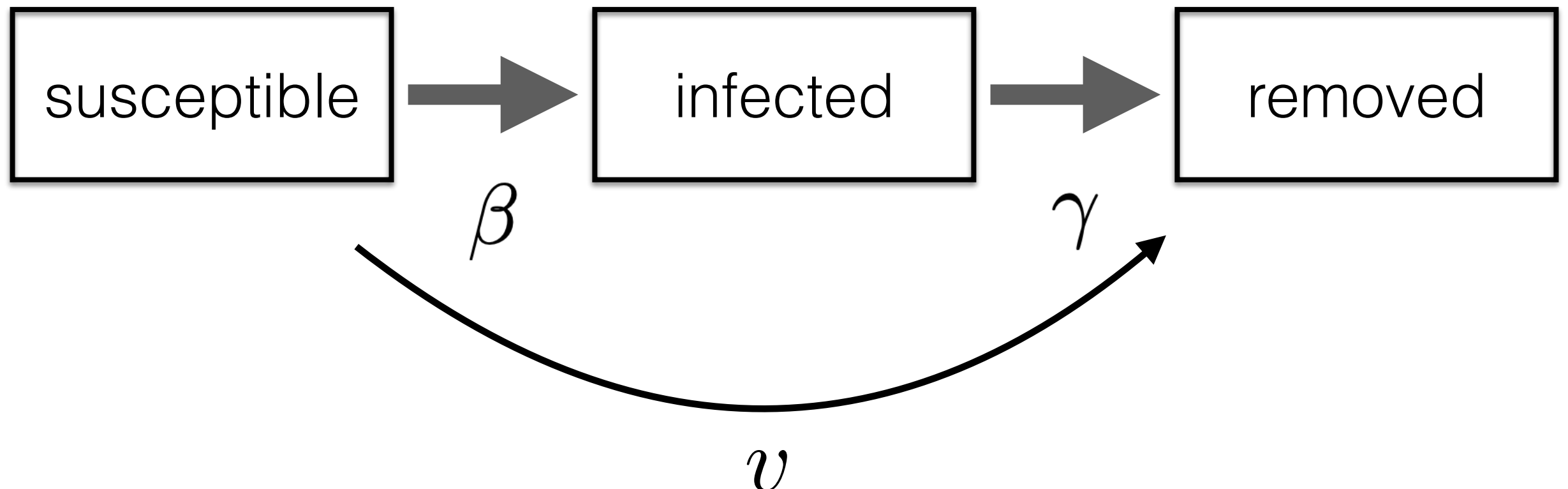
R: **Recovered**

D: **Deceased**



SIR model with vaccination

The vaccination rate (v) moves susceptible people into the removed group.



SIR model for misinformation

The SIR model can also be used to model the spread of epidemics which are not biological in nature. One example is the spread of misinformation and conspiracy theories on social media.

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People who believe the conspiracy theory tend to spread it to others so we could expect the SIR model to be a good model.

SIR model for misinformation

Example: 5G and COVID-19 on Twitter (from Kauk 2021).

Table 2. Frequency table of the ten most used hashtags indicating that 5G is harmful or connected to SARS-CoV-2.

Hashtag	Frequency
#5gcoronavirus	2171
#5gkills	1311
#stop5g	842
#5gcorona	466
#wuhan5g	228
#5gvirus	213
#5gdeadlyweapon	207
#no5g	85
#saynoto5g	43
#5gcononavirus	45
#(Total)	5611

SIR model for misinformation

Example: 5G and COVID-19 on Twitter (from Kauk 2021).

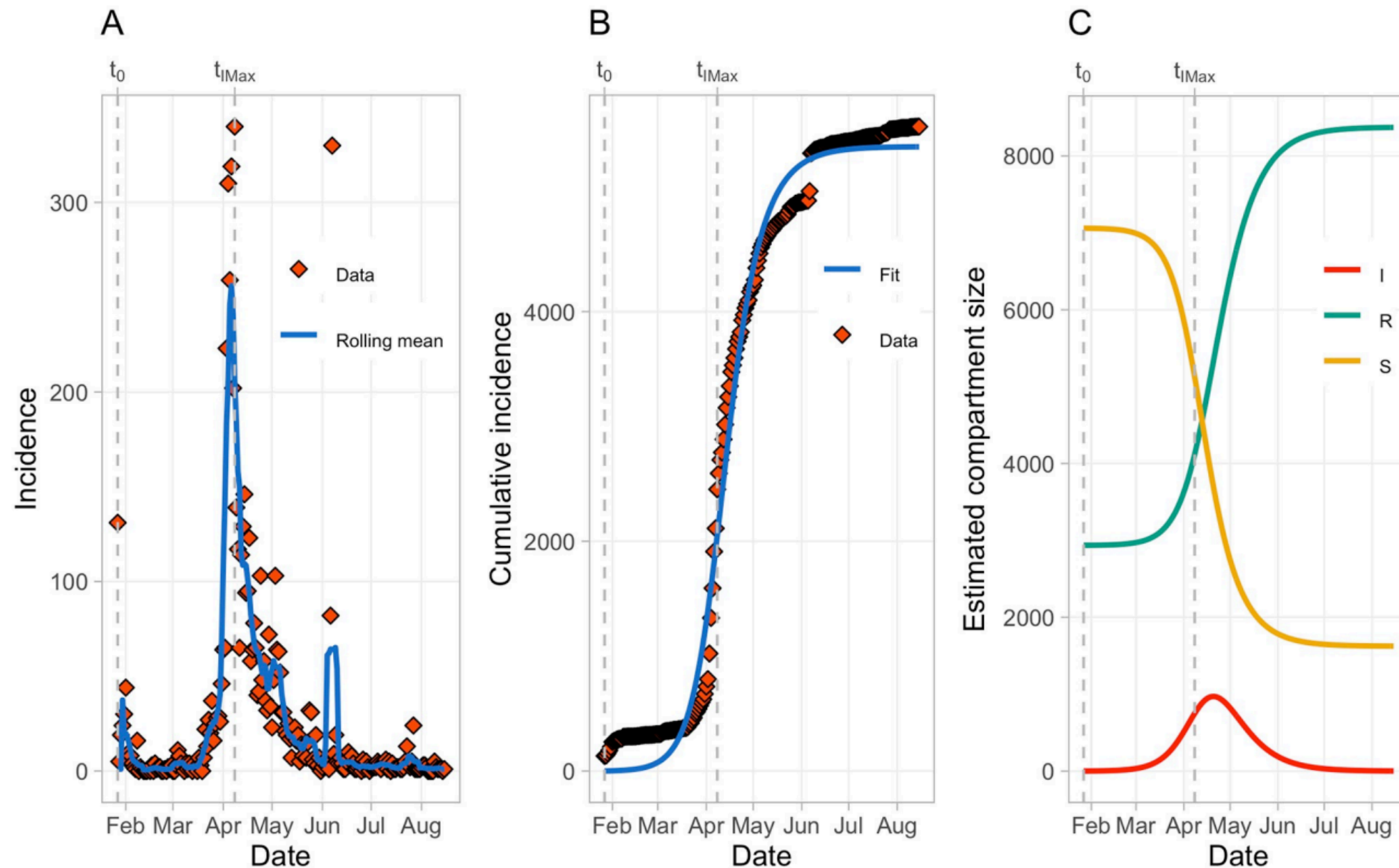


Fig 1. Acceptable correspondence of observed and predicted hashtag incidence. (A) Hashtag incidence over time. Please note that “Rolling mean” refers to the simple moving average with the rolling window $k = 7$. (B) Best basic SIR model fit. (C) Model predictions of the compartment sizes over time.

References

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