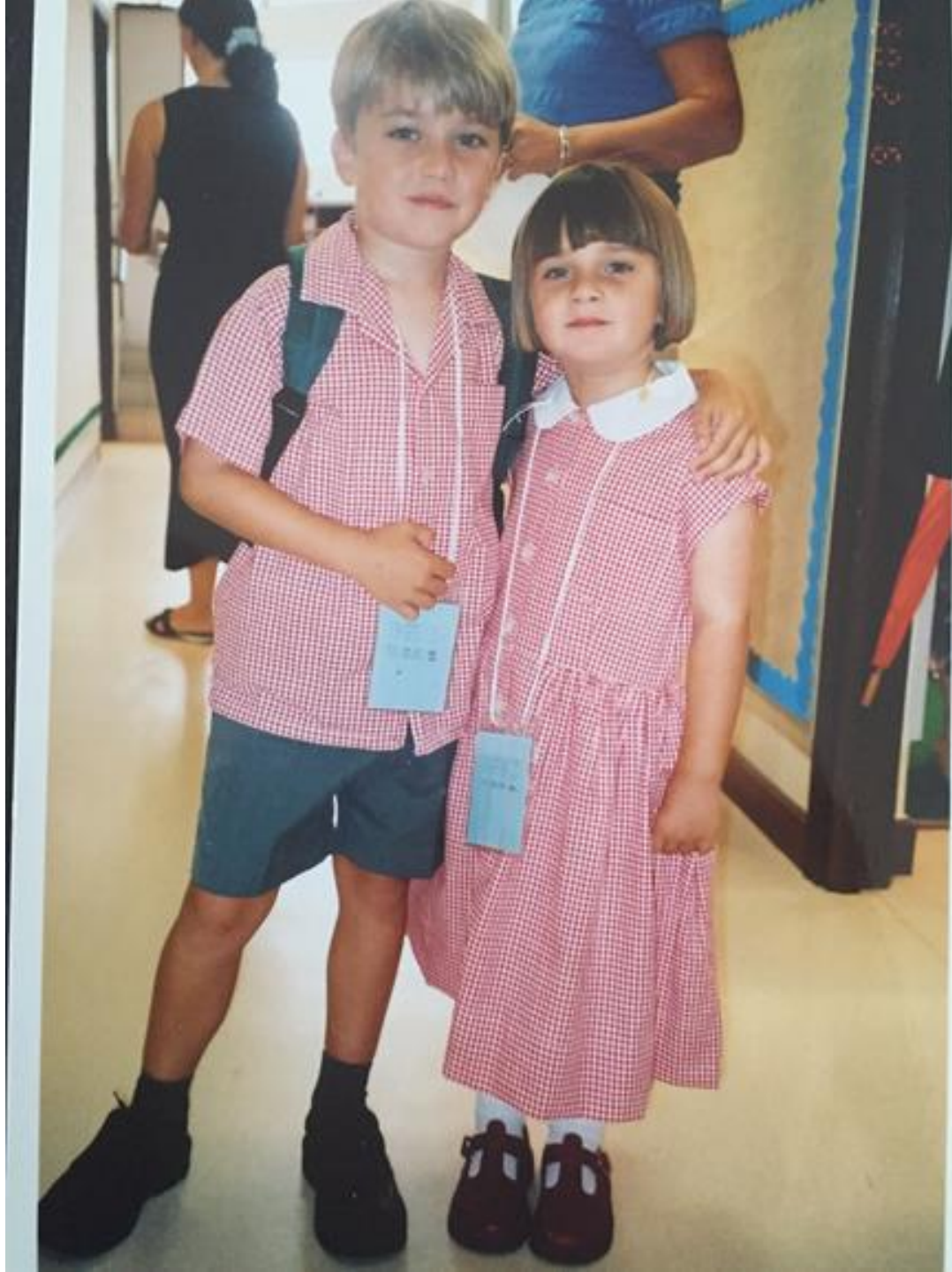


# Early Epidemiological Model Parameters for COVID-19

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*“It’s time for facts, not fear”*

-Tedros Adhanom, Feb 15<sup>th</sup> 2020

*“It’s time for facts, not fear”*

*“It’s impossible to predict which direction this epidemic will take”*

-Tedros Adhanom, Feb 15<sup>th</sup> 2020

# Background

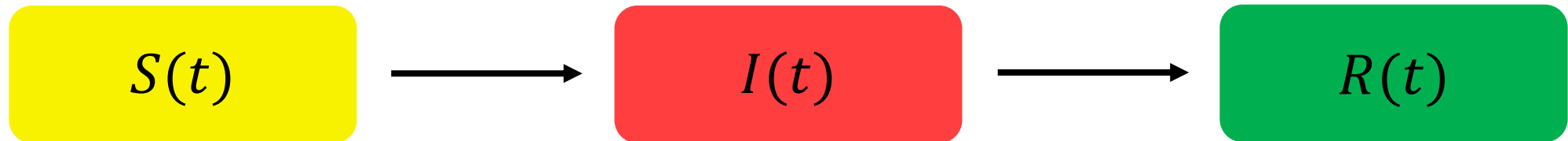
- Coronaviruses: A family of zoonotic viruses that cause illness ranging from the common cold to more severe diseases such as MERS-CoV and SARS-CoV
- 2019 novel coronavirus (2019-nCoV or COVID-19) has 70% similarity in genetic sequence to SARS-CoV
- First identified in Wuhan when a cluster of cases were linked to the Huanan Seafood Wholesale Market

# SIR Model

$S(t)$  = {number of susceptible individuals at time  $t$ }

$I(t)$  = {number of infected individuals at time  $t$ }

$R(t)$  = {number of removed individuals at time  $t$ }

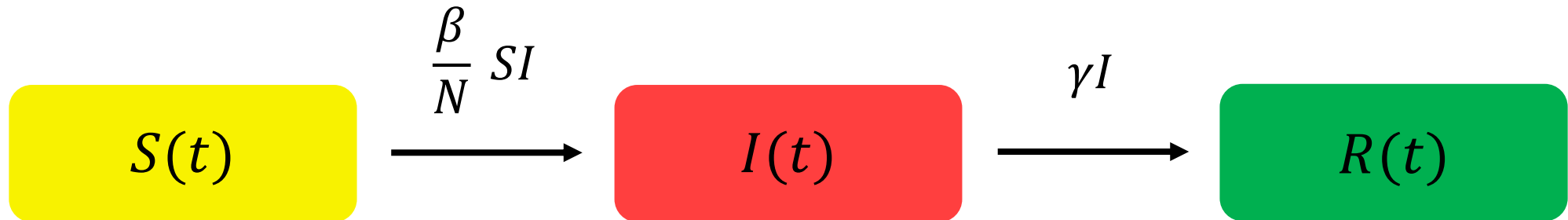


# SIR Model

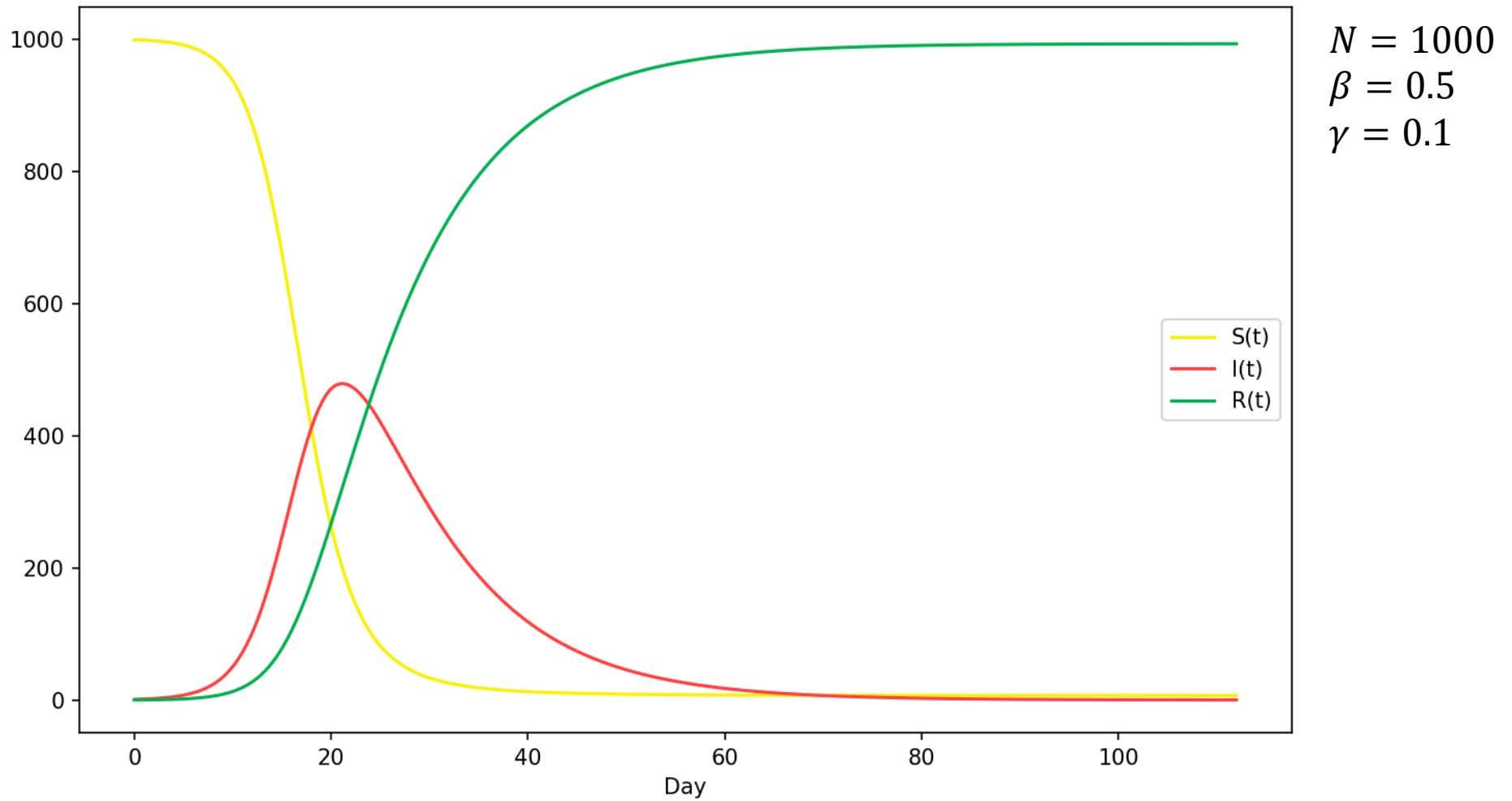
$$\frac{dS}{dt} = -\frac{\beta}{N} S(t)I(t)$$

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

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



# SIR Model





# Assumptions

- For all  $t$ ,  $S(t) + I(t) + R(t) = N$
- Homogeneous mixing of the population ( $\beta$  is constant)
- Constant rate of removal ( $\gamma$  is constant)
- No incubation period

# Methodology

- Use new cases, deaths and recoveries data from the NHC to find the distribution of the infected population  $I(t)$  in mainland China from January 24 to February 11

## 卫生应急办公室

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### 截至2月16日24时新型冠状病毒肺炎疫情最新情况

发布时间: 2020-02-17 来源: 卫生应急办公室



2月16日0—24时, 31个省(自治区、直辖市)和新疆生产建设兵团报告新增确诊病例2048例, 新增死亡病例105例(湖北100例, 河南3例, 广东2例), 新增疑似病例1563例。

当日新增治愈出院病例1425例, 解除医学观察的密切接触者28179人, 重症病例减少628例。

截至2月16日24时, 据31个省(自治区、直辖市)和新疆生产建设兵团报告, 现有确诊病例57934例(其中重症病例10644例), 累计治愈出院病例10844例, 累计死亡病例1770例, 累计报告确诊病例70548例, 现有疑似病例7264例。累计追踪到密切接触者546016人, 尚在医学观察的密切接触者150539人。

湖北新增确诊病例1933例(武汉1690例), 新增治愈出院病例1016例(武汉543例), 新增死亡病例100例(武汉76例), 现有确诊病例49847例(武汉36385例), 其中重症病例9797例(武汉8056例)。累计治愈出院病例6639例(武汉3458例), 累计死亡病例1696例(武汉1309例), 累计确诊病例58182例(武汉41152例)。新增疑似病例909例(武汉338例), 现有疑似病例4826例(武汉1971例)。

累计收到港澳台地区通报确诊病例87例: 香港特别行政区57例(出院2例, 死亡1例), 澳门特别行政区10例(出院5例), 台湾地区20例(出院2例, 死亡1例)。

(注: 媒体引用时, 请标注“信息来自国家卫生健康委员会官方网站”。)

分享到

# Methodology

- Assume exponential growth in the first few days to fill in missing data since the first confirmed cases in early January

For small  $t$ ,  $S(t) \sim N$ , so

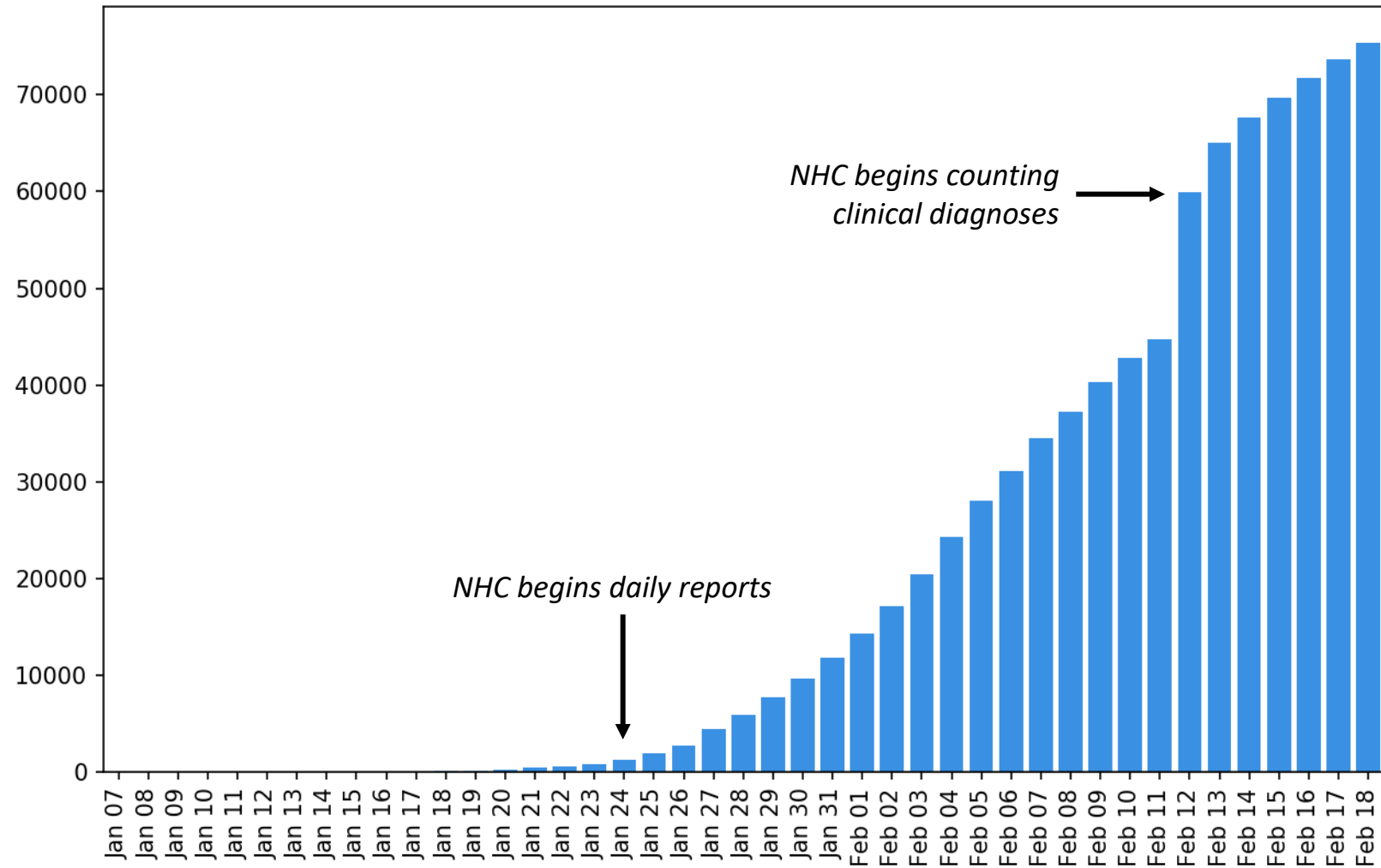
$$\begin{aligned}\frac{dI}{dt} &= \frac{\beta}{N} S(t) I(t) - \gamma I(t) \\ &\sim \beta I(t) - \gamma I(t) \\ &= I(t)(\beta - \gamma)\end{aligned}$$

$I(t) = Ce^{(\beta - \gamma)t}$  is a solution

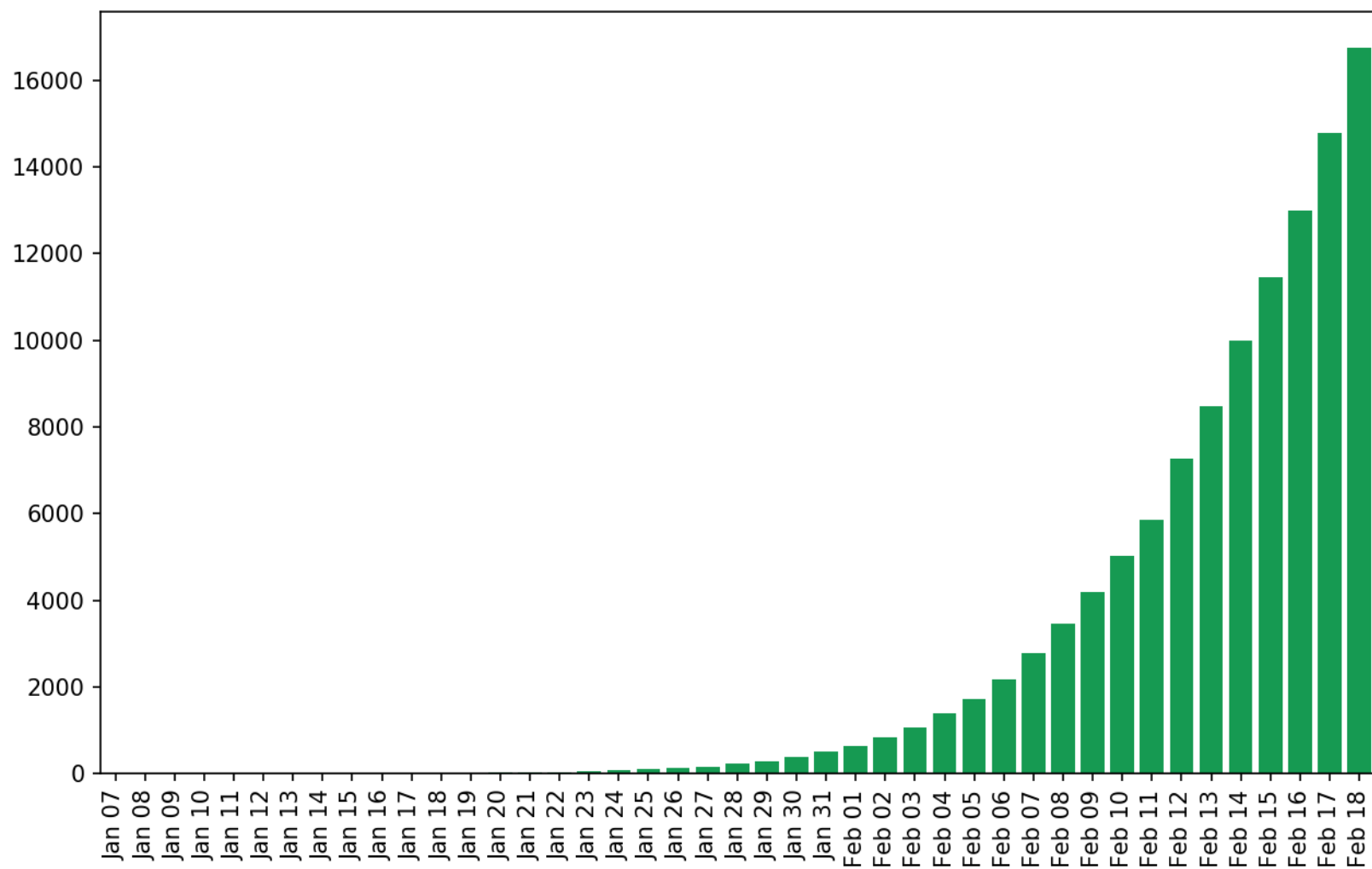
# Methodology

- Define an objective function that returns the sum of squared differences between the infected population data and the model prediction
- Minimize this objective function using a numerical optimization method
- Extract optimal beta and gamma
- Analysis and simulation

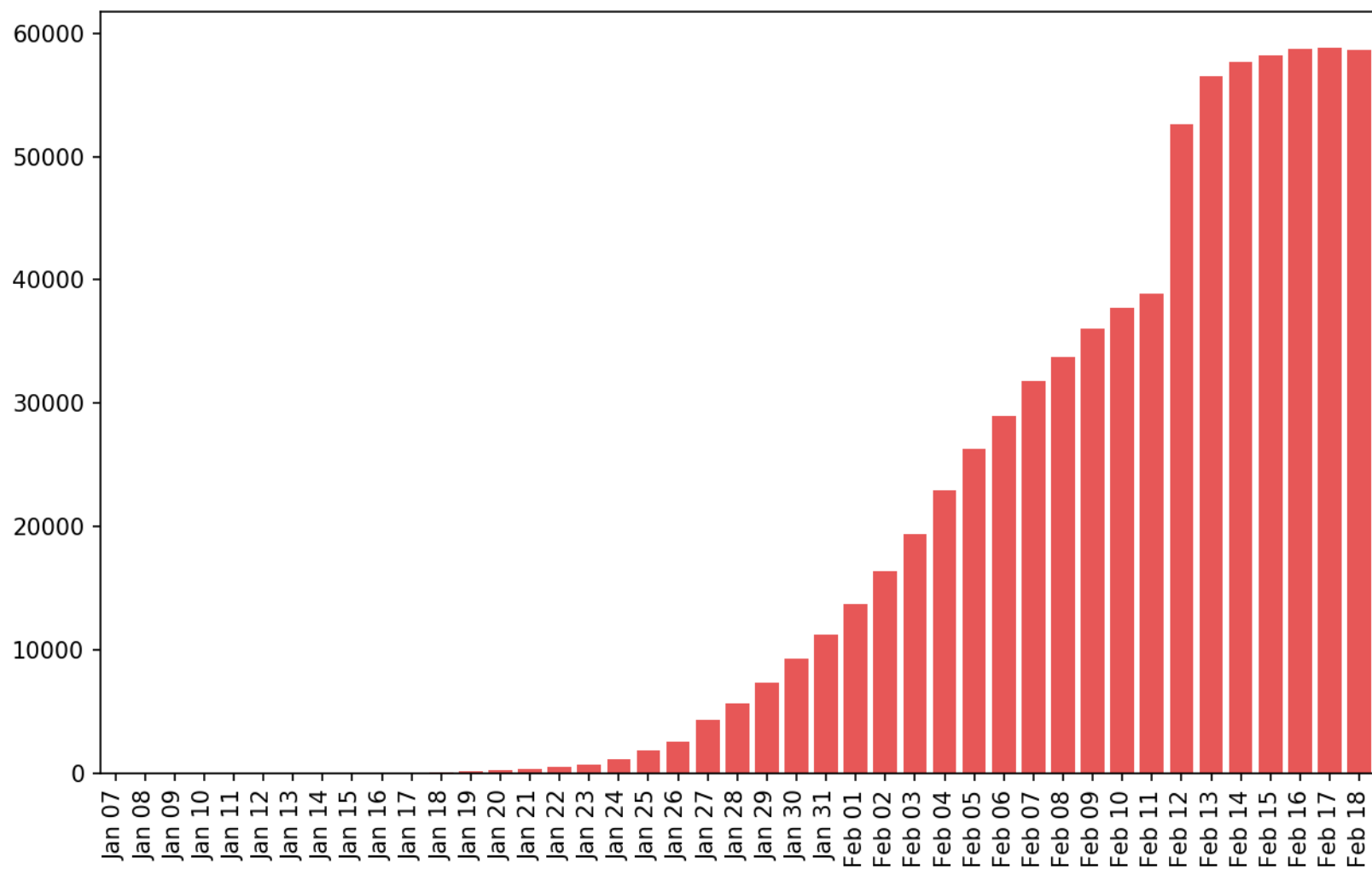
# Cumulative Cases



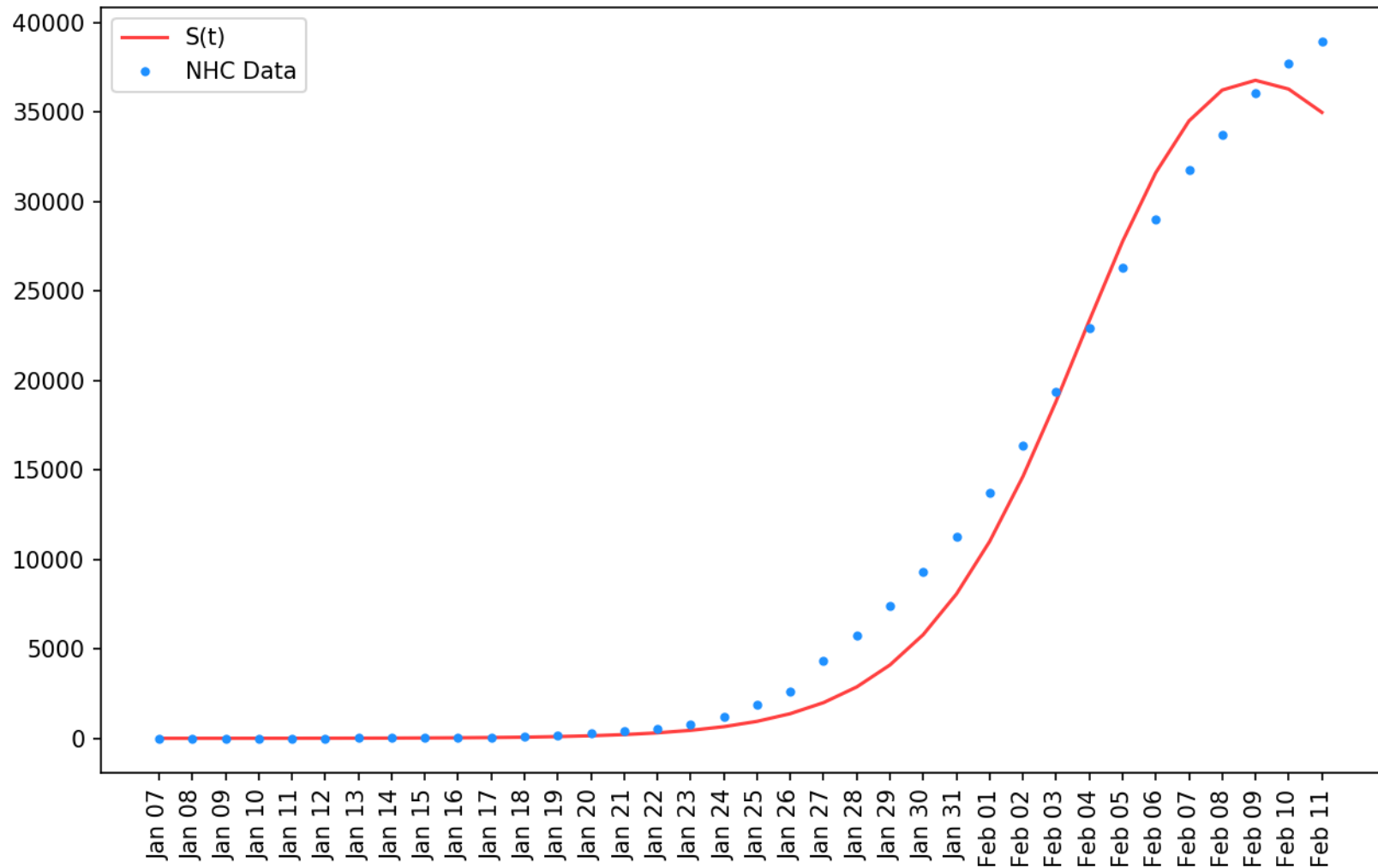
# Distribution of $R(t)$



# Distribution of $I(t)$



# Fitted Model



$\beta = 0.528$   
 $\gamma = 0.146$



# Basic Reproduction Number $R_0$

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

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

# Basic Reproduction Number $R_0$

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

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

At  $t = 0$ ,

$$\frac{dI}{dt} = \left( \frac{\beta}{N\gamma} S(0) - 1 \right) \gamma I(0) = \left( \frac{R_0 S(0)}{N} - 1 \right) \gamma I(0)$$

# Basic Reproduction Number $R_0$

$$\frac{dI}{dt}(0) = \left( \frac{R_0 S(0)}{N} - 1 \right) \gamma I(0)$$

Therefore  $R_0 > \frac{N}{S(0)} \sim 1 \implies \frac{dI}{dt}(0) > 0$ ,

whereas  $R_0 < \frac{N}{S(0)} \sim 1 \implies \frac{dI}{dt}(0) < 0$

# Estimating Epidemic Length

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

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

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

We want to express  $\frac{dS}{dt}$  in terms of only  $S$  and  $t$

# Estimating Epidemic Length

$$\frac{dI}{dS} = \frac{dI/dt}{dS/dt} = \frac{\frac{\beta}{N}S(t)I(t) - \gamma I(t)}{-\frac{\beta}{N}S(t)I(t)} = \frac{\beta S(t) - N\gamma}{-\beta S(t)} = \frac{N\gamma}{\beta S(t)} - 1$$

# Estimating Epidemic Length

$$\frac{dI}{dS} = \frac{dI/dt}{dS/dt} = \frac{\frac{\beta}{N}S(t)I(t) - \gamma I(t)}{-\frac{\beta}{N}S(t)I(t)} = \frac{\beta S(t) - N\gamma}{-\beta S(t)} = \frac{N\gamma}{\beta S(t)} - 1$$

$$\int \frac{dI}{dS} dS = \int \left( \frac{N\gamma}{\beta S(t)} - 1 \right) dS$$

$$\Rightarrow I(t) = \frac{N\gamma}{\beta} \ln S(t) - S(t) + c$$

# Estimating Epidemic Length

$$\frac{dI}{dS} = \frac{dI/dt}{dS/dt} = \frac{\frac{\beta}{N}S(t)I(t) - \gamma I(t)}{-\frac{\beta}{N}S(t)I(t)} = \frac{\beta S(t) - N\gamma}{-\beta S(t)} = \frac{N\gamma}{\beta S(t)} - 1$$

$$\int \frac{dI}{dS} dS = \int \left( \frac{N\gamma}{\beta S(t)} - 1 \right) dS$$

$$\Rightarrow I(t) = \frac{N\gamma}{\beta} \ln S(t) - S(t) + c$$

$$c = I(0) - \frac{N\gamma}{\beta} \ln S(0) + S(0) = N \left( 1 - \frac{\ln(N-1)}{R_0} \right)$$

# Estimating Epidemic Length

$$\begin{aligned}\frac{dS}{dt} &= -\frac{\beta}{N}S(t)I(t) \\ &= -\frac{\beta}{N}S(t)\left(\frac{N\gamma}{\beta}\ln S(t) - S(t) + c\right) \\ &= -\gamma S(t)\ln S(t) + \frac{\beta}{N}S^2(t) - \frac{\beta}{N}S(t)c\end{aligned}$$



# Estimating Epidemic Length

Call the length of the epidemic  $T$ . Then

$$T = \int_{S(0)}^{S(T)} \frac{1}{-\gamma S(t) \ln S(t) + \frac{\beta}{N} S^2(t) - \frac{\beta}{N} S(t)c} dS$$

# Estimating Epidemic Length

Call the length of the epidemic  $T$ . Then

$$T = \int_{S(0)}^{S(T)} \frac{1}{-\gamma S(t) \ln S(t) + \frac{\beta}{N} S^2(t) - \frac{\beta}{N} S(t)c} dS$$

We get  $S(T)$  by finding where

$$I(t) = \frac{N\gamma}{\beta} \ln S(t) - S(t) + c$$

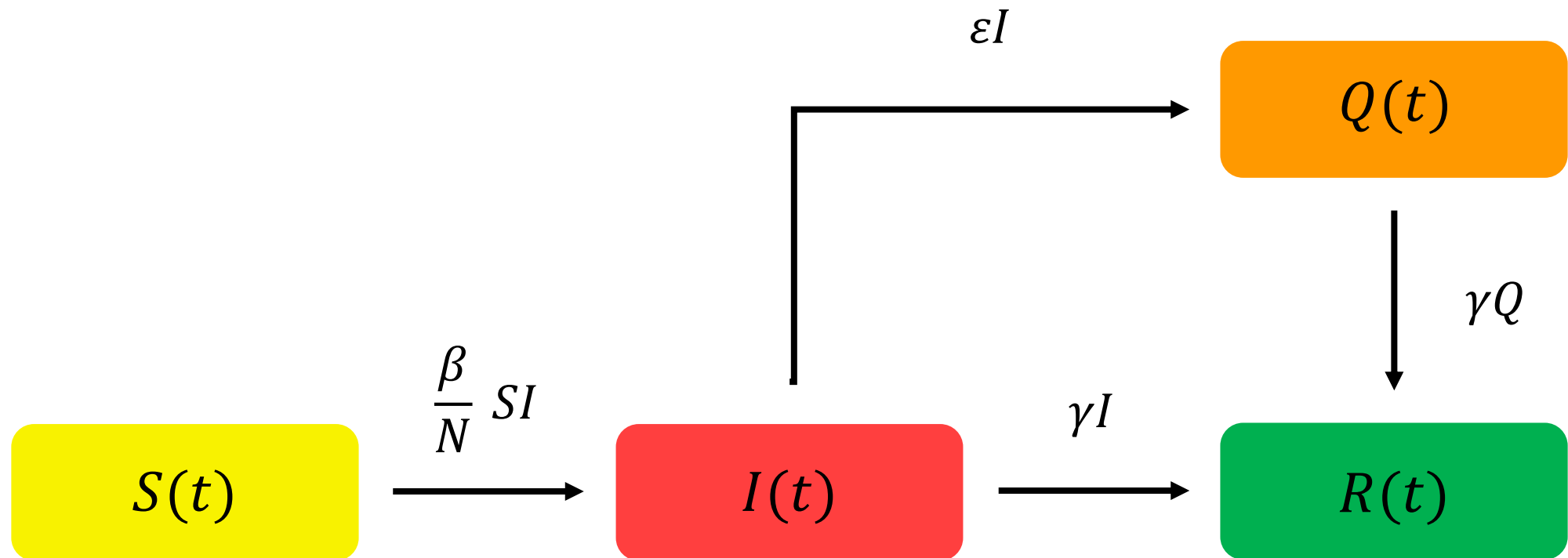
is equal to zero

# Epidemiological Parameters

	<b>COVID-19</b>	<b>SARS-CoV<sup>1</sup></b>
$\beta$	0.528	0.2586
$\gamma$	0.146	0.0821
$1/\gamma$	~7 days	~12 days
$R_0$	3.614	3.1511
$T$	~110 days	~120 days

<sup>1</sup>Mkhatshwa, Thembinkosi, and Anna Mummert. "Modeling Super-Spreading Events for Infectious Diseases: Case Study SARS." 15 Oct. 2010.

# Simulation at Williams



# SIQR Model

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

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

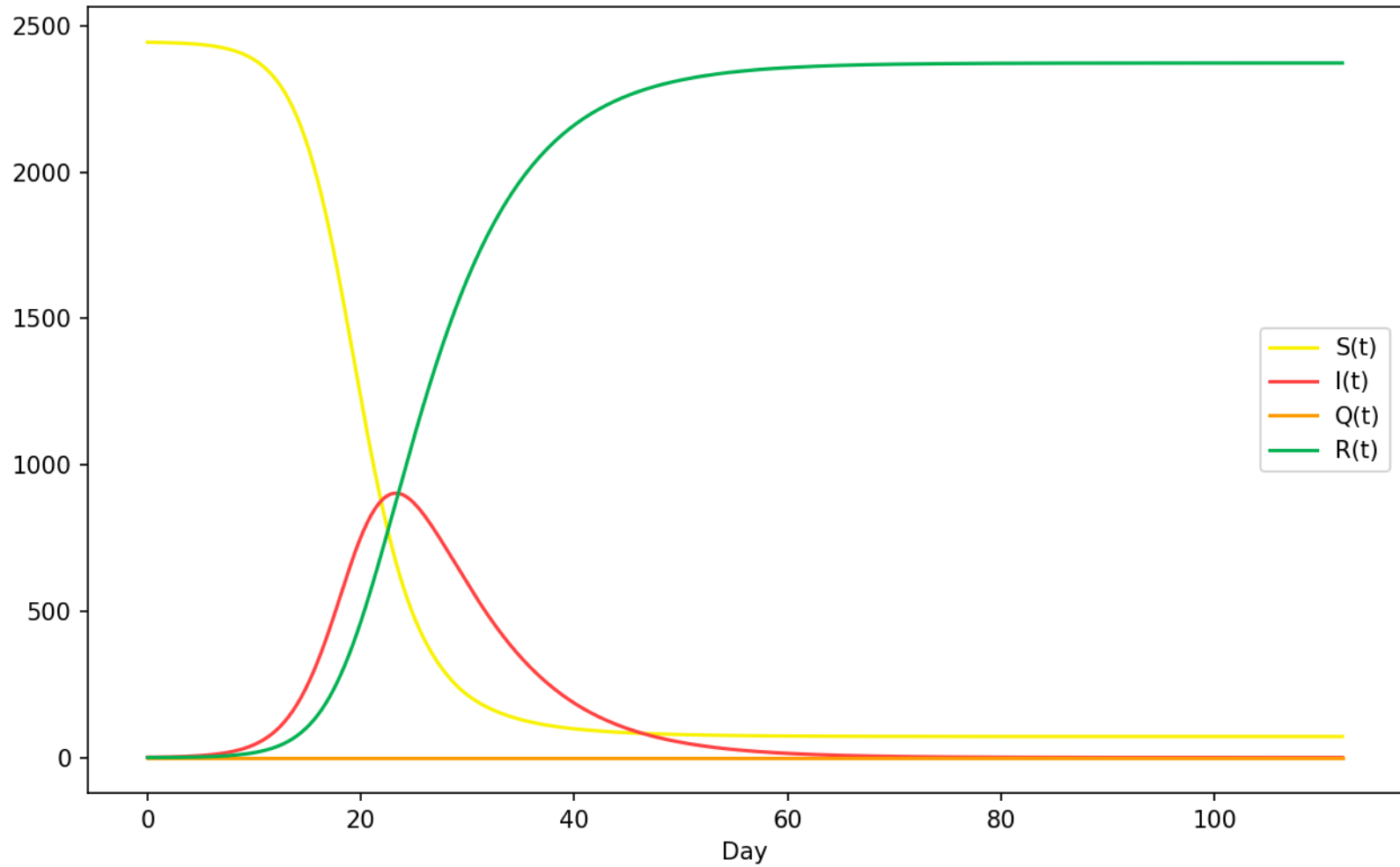
$$\frac{dQ}{dt} = \varepsilon I(t) - \gamma Q(t)$$

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

# Assumptions

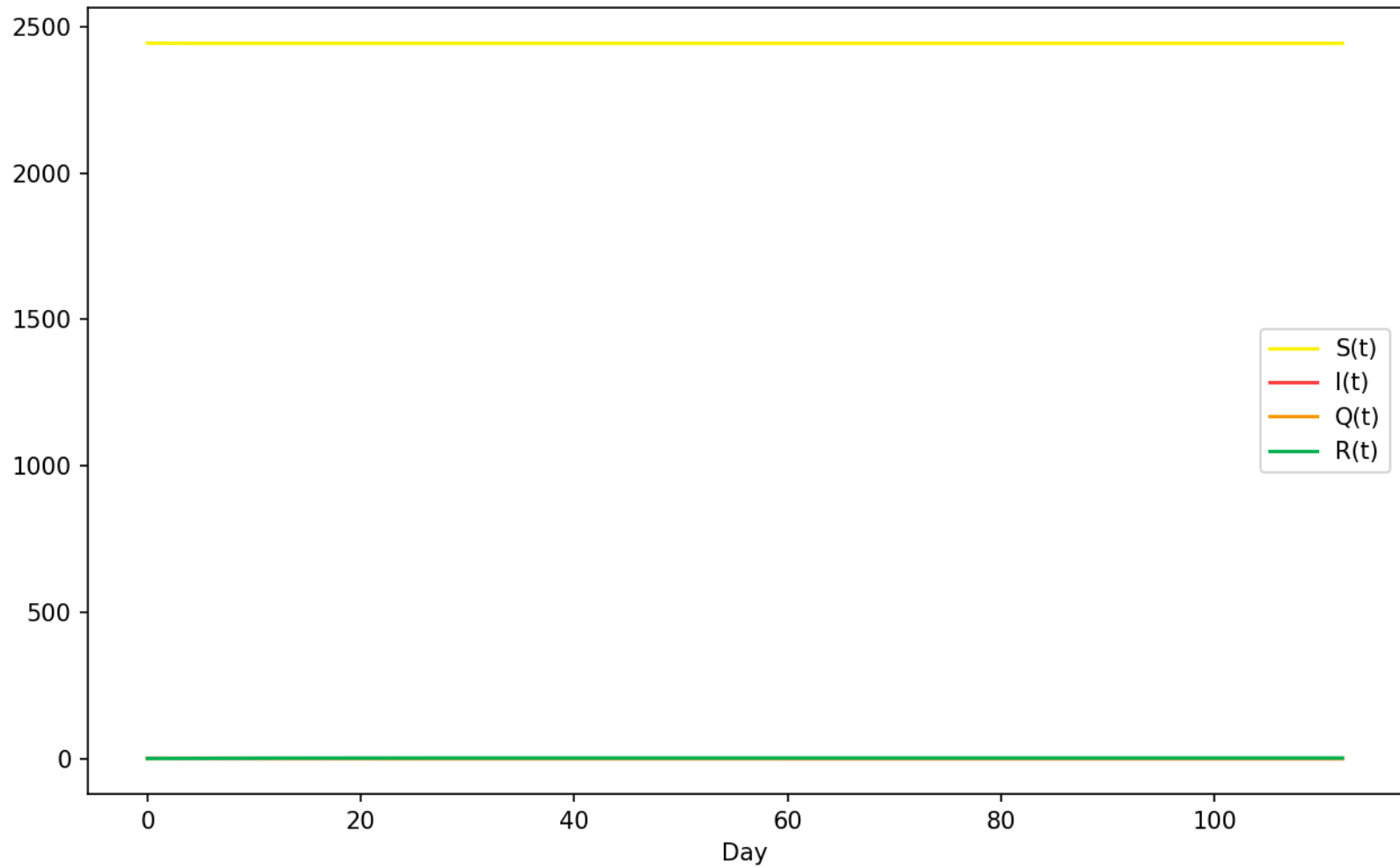
- For all  $t$ ,  $S(t) + I(t) + Q(t) + R(t) = N = 2444$
- Homogeneous mixing of the population ( $\beta$  is constant)
- Constant rate of removal ( $\gamma$  is constant)
- No incubation period

# Simulation with $\varepsilon = 0$



$N = 2444$   
 $\beta = 0.528$   
 $\gamma = 0.146$

# Simulation with $\varepsilon = 1$



$N = 2444$   
 $\beta = 0.528$   
 $\gamma = 0.146$



## Critical Value for $\varepsilon$

$$\frac{dI}{dt} = \frac{\beta}{N} S(t) I(t) - \gamma I(t) - \varepsilon I(t) = \left( \frac{\beta}{N\gamma} S(t) - 1 - \frac{\varepsilon}{\gamma} \right) \gamma I(t)$$

$$\frac{dI}{dt}(0) = \left( \frac{\beta}{N\gamma} S(0) - 1 - \frac{\varepsilon}{\gamma} \right) \gamma I(0)$$

## Critical Value for $\varepsilon$

$$\frac{dI}{dt} = \frac{\beta}{N} S(t) I(t) - \gamma I(t) - \varepsilon I(t) = \left( \frac{\beta}{N\gamma} S(t) - 1 - \frac{\varepsilon}{\gamma} \right) \gamma I(t)$$

$$\frac{dI}{dt}(0) = \left( \frac{\beta}{N\gamma} S(0) - 1 - \frac{\varepsilon}{\gamma} \right) \gamma I(0)$$

An epidemic will occur if  $\frac{dI}{dt}(0) > 0$ , i.e.

$$\frac{\beta}{N\gamma} S(0) - 1 - \frac{\varepsilon}{\gamma} > 0 \implies \varepsilon < \frac{\beta}{N} S(0) - \gamma \sim \beta - \gamma$$

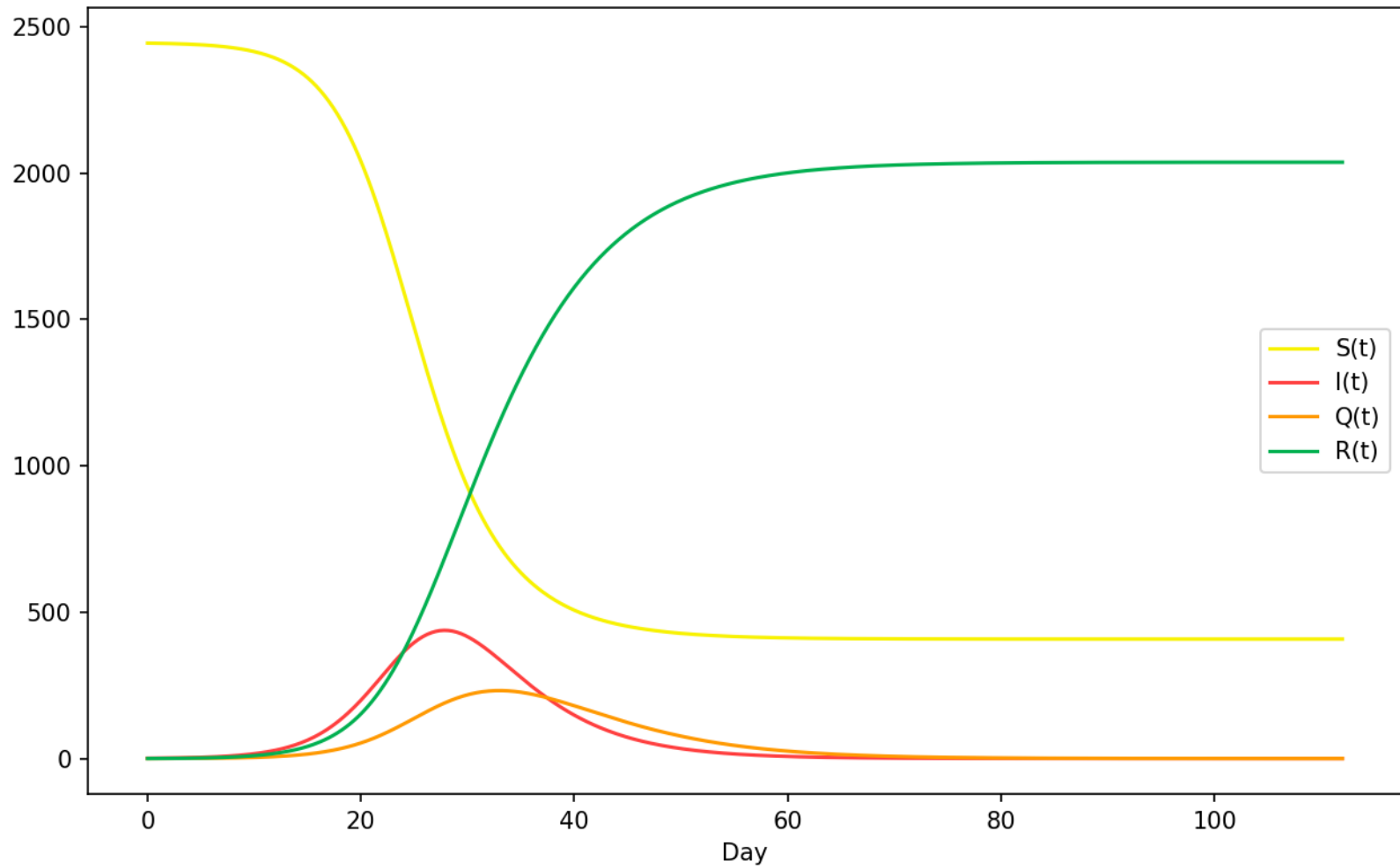
# Critical Value for $\varepsilon$

Define  $\varepsilon_{CV} = \beta - \gamma$

Therefore  $\varepsilon < \varepsilon_{CV} \implies \frac{dI}{dt}(0) > 0$ ,

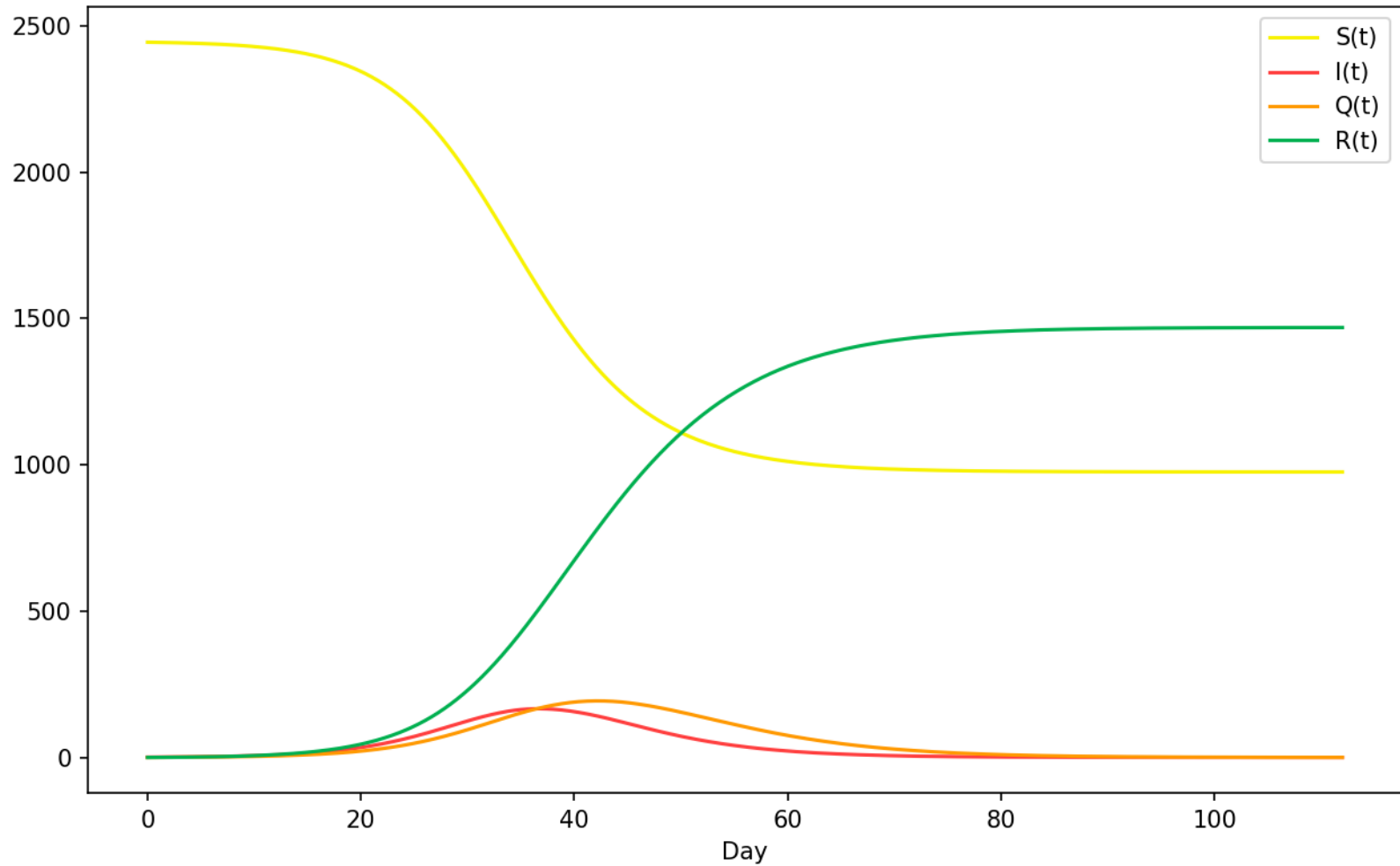
whereas  $\varepsilon > \varepsilon_{CV} \implies \frac{dI}{dt}(0) < 0$

# Simulation with $\varepsilon = 0.1 < \varepsilon_{CV}$



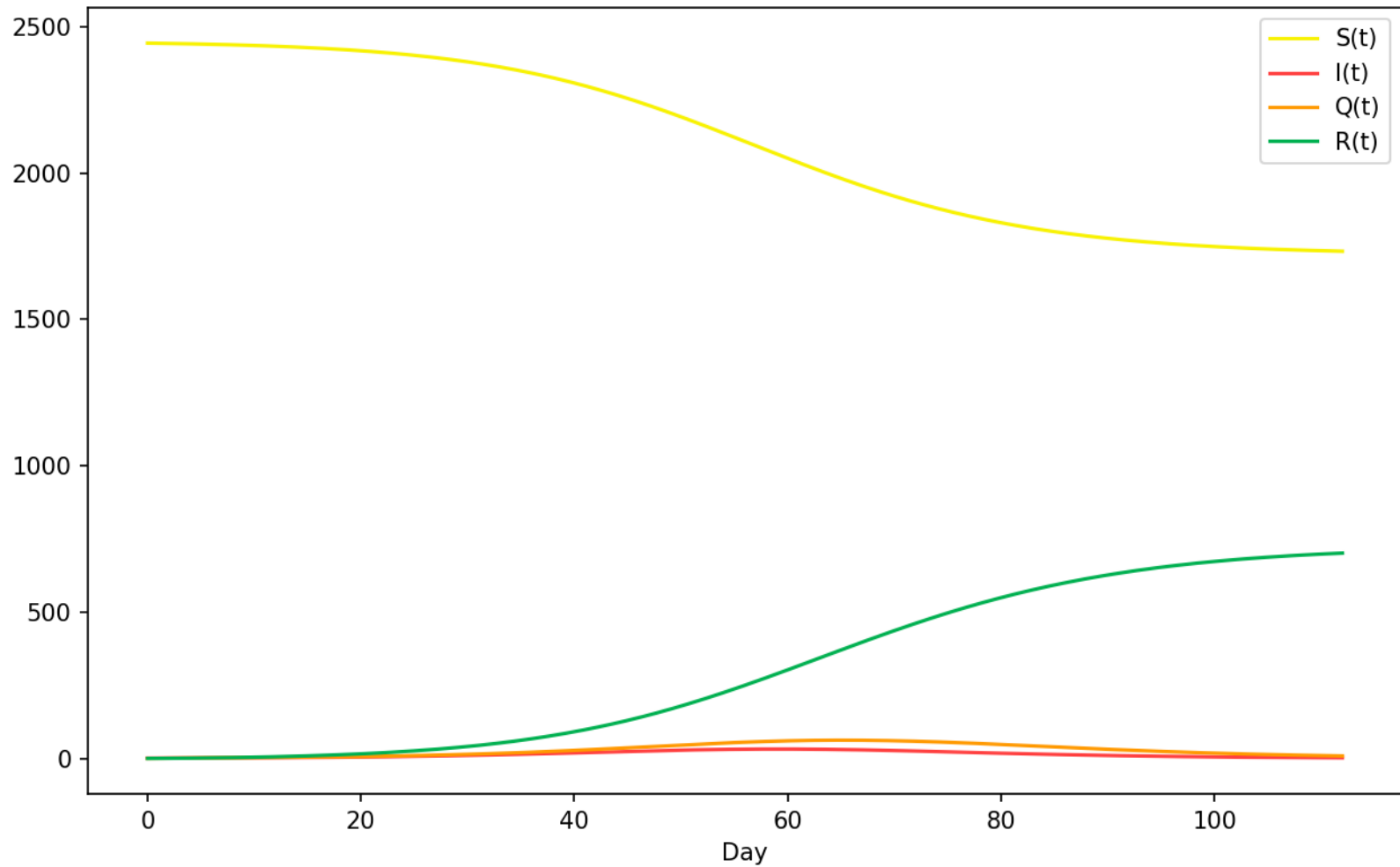
$N = 2444$   
 $\beta = 0.528$   
 $\gamma = 0.146$   
 $\varepsilon_{CV} = 0.382$

# Simulation with $\varepsilon = 0.2 < \varepsilon_{CV}$



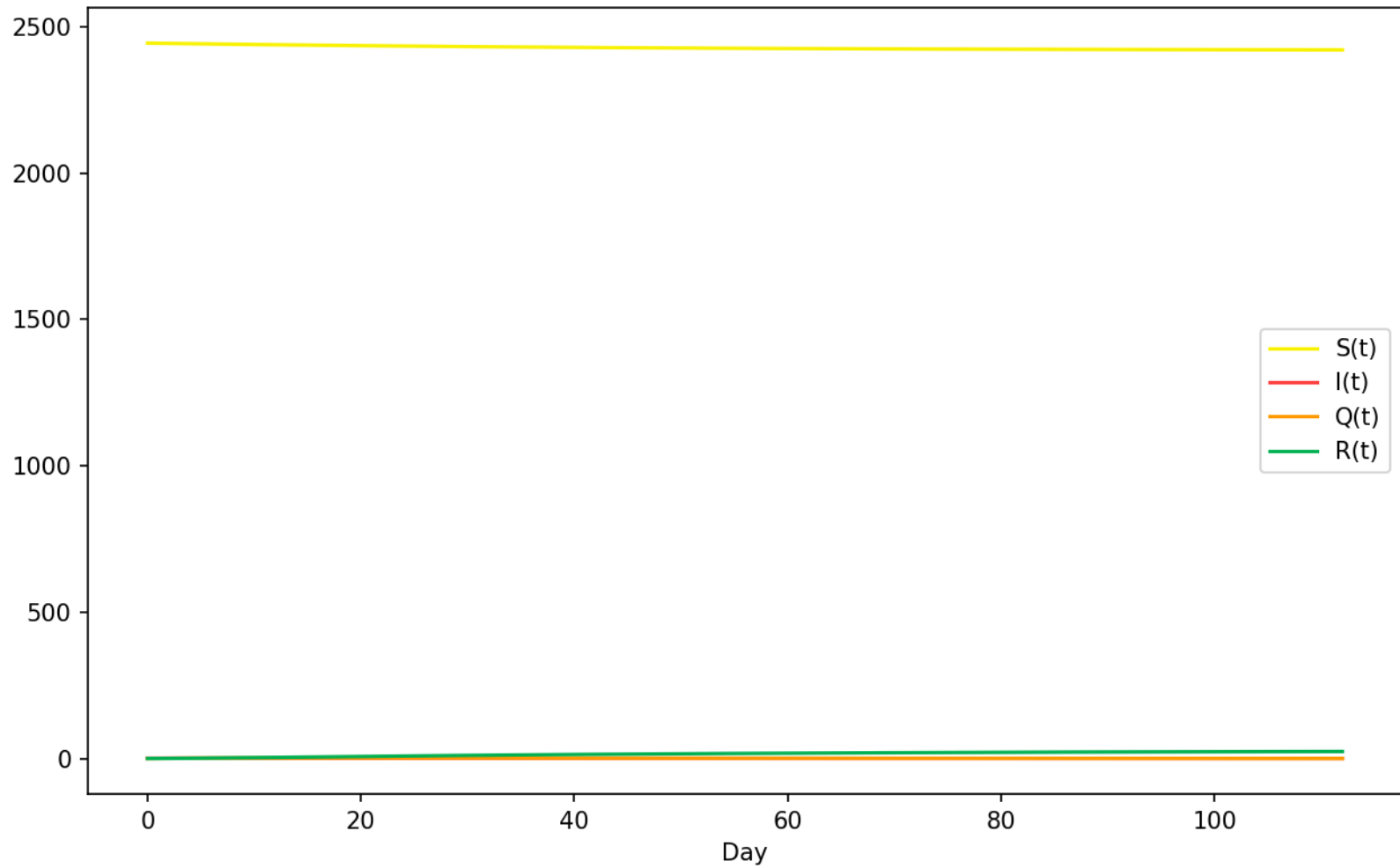
$N = 2444$   
 $\beta = 0.528$   
 $\gamma = 0.146$   
 $\varepsilon_{CV} = 0.382$

# Simulation with $\varepsilon = 0.3 < \varepsilon_{CV}$



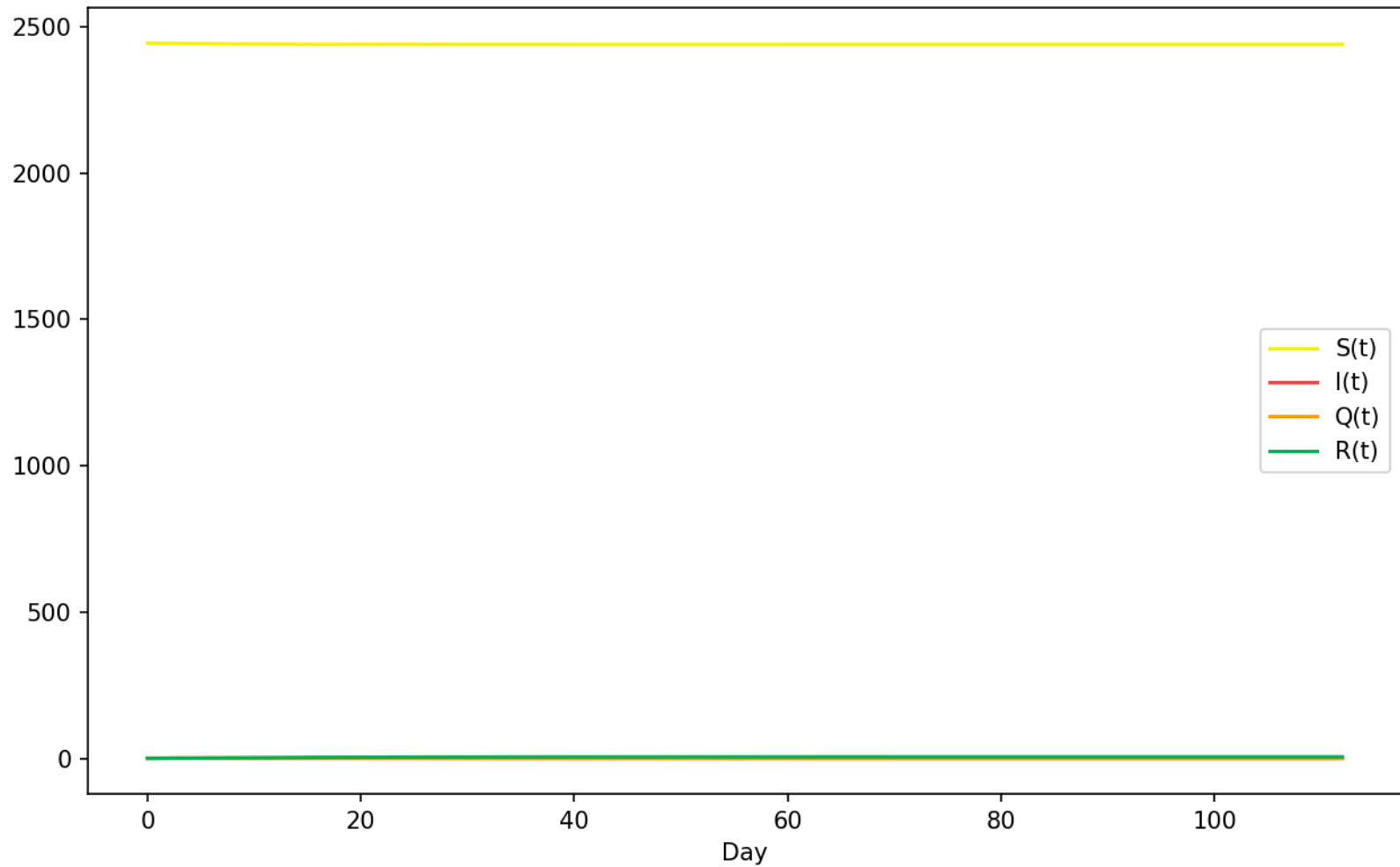
$N = 2444$   
 $\beta = 0.528$   
 $\gamma = 0.146$   
 $\varepsilon_{CV} = 0.382$

# Simulation with $\varepsilon = 0.4 > \varepsilon_{CV}$



$N = 2444$   
 $\beta = 0.528$   
 $\gamma = 0.146$   
 $\varepsilon_{CV} = 0.382$

# Simulation with $\varepsilon = 0.5 > \varepsilon_{CV}$



$N = 2444$   
 $\beta = 0.528$   
 $\gamma = 0.146$   
 $\varepsilon_{CV} = 0.382$



# Limitations and Extensions

- Inaccuracy of  $\beta$  and  $\gamma$
- Population segmentations with different mixing rates