

# Controlling the spread of infectious disease

홍유빈

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# Research article

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RESEARCH ARTICLE

## Modeling the Transmission of Middle East Respiratory Syndrome Corona Virus in the Republic of Korea

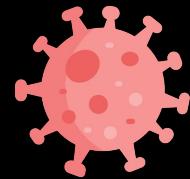
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Backgrounds



Transmission model in the article



Computer modelling

- Parameter estimation in MERS & COVID-19

# MERS-CoV

Middle East Respiratory Syndrome Coronavirus

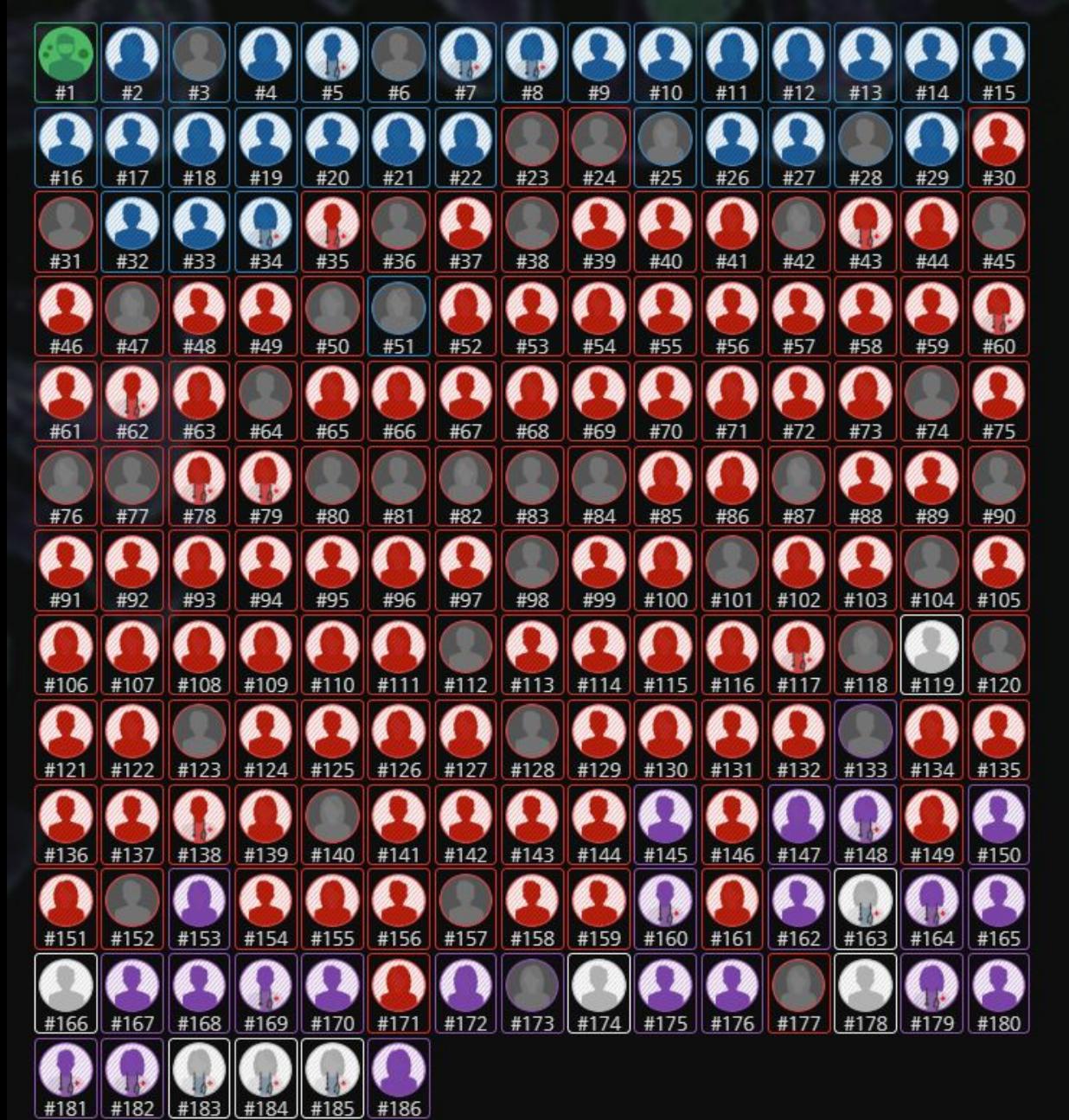
Table 1. Number of MERS-CoV cases by country and year (as of 7 July 2015)

	2012	2013	2014	2015	Total
Algeria	0	0	2	0	2
Austria	0	0	1	0	1
China	0	0	0	1	1
Egypt	0	0	1	0	1
France	0	2	0	0	2
Germany	1	1	0	1	3
Greece	0	0	1	0	1
Iran	0	0	5	1	6
Italy	0	1	0	0	1
Jordan	2	0	10	0	12
Kuwait	0	2	1	0	3
Lebanon	0	0	1	0	1
Malaysia	0	0	1	0	1
Netherlands	0	0	2	0	2
Oman	0	1	1	4	6
Philippines	0	0	0	2	2
Qatar	0	7	2	4	13
Republic of Korea	0	0	0	185	185
Saudi Arabia	5	136	679	217	1037
Thailand	0	0	0	1	1
Tunisia	0	3	0	0	3
Turkey	0	0	1	0	1
United Arab Emirates	0	12	57	7	76
United Kingdom	1	3	0	0	4
United States of America	0	0	2	0	2
Yemen	0	0	1	0	1
<b>Total</b>	<b>9</b>	<b>168</b>	<b>768</b>	<b>423</b>	<b>1368</b>

Saudi Arabia is the first and largest MERS outbreak country

Republic of Korea is the second largest outbreak country

MERS is usually occurred in Middle East



**186**  
Total case



39  
death case

Fatality 20.9%



May 4 : returned to Korea from Bahrain

May 11: symptoms onset until this day and  
**visit 3 hospitals, close contact**

May 17 : hospitalized in **multi-bedroom**  
without specific disease name

**OUT OF CONTROL**

May 18 : patient's doctor suspected MERS  
and report it to the government  
but the government **rejected it at first**

## First MERS case

- 68,-years-old, Male
- flying back from Bahrain
- confirmed in May 20, 2015

May 19 : process MERS examination

May 20 : confirmed MERS and isolated

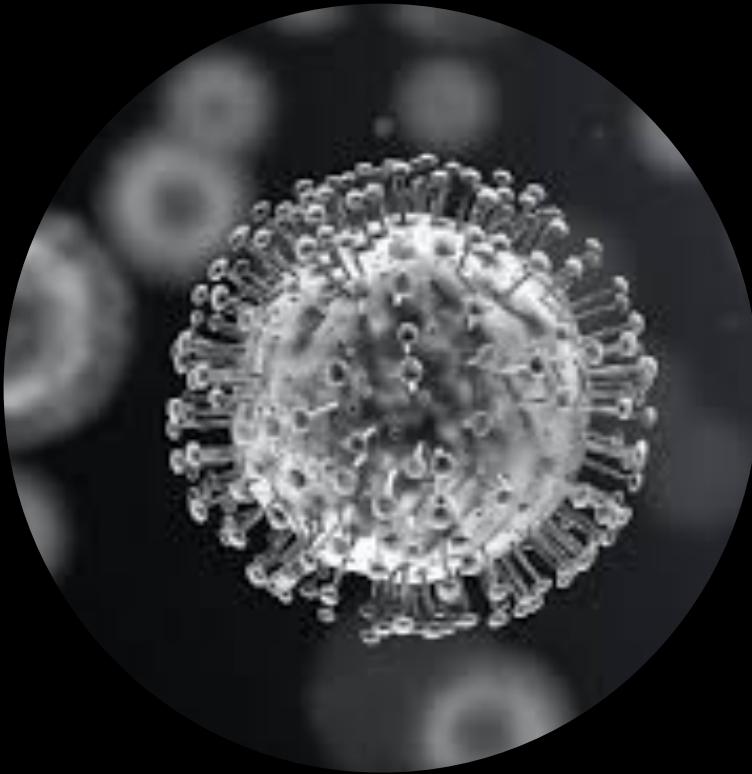
# Transmission Model

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- It shows how the diseases will be progressed and transmitted
- If modelling with parameters that affect the spread of disease, it can predict how the epidemics spread
- We recognize what parameters should be reduced or raised to **prevent epidemics** by transmission model

# Coronavirus

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- SARS, MERS, COVID-19
- RNA virus → high rate of variation
- cause respiratory and digestive infections → usually slight cold symptoms(fever, cough)
- a tendency to attack the lungs directly in severe cases
- danger to chronic patients

# MERS & COVID19 transmission

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MERS	COVID-19
<ul style="list-style-type: none"><li>- droplet infection</li><li>- human to human transmission is possible</li><li>- asymptomatic infection</li></ul>	
<ul style="list-style-type: none"><li>- start at Saudi Arabia, 2012</li><li>- reservoir host : bat, camel</li><li>- 186 cases, 36 deaths in Republic of Korea, 2015(fatality <b>20.9%</b>)</li></ul>	<ul style="list-style-type: none"><li>- start at China, 2020</li><li>- reservoir host : bat</li><li>- 11,947 cases, 276 deaths in Republic of Korea (fatality <b>2.3%</b>, until June 12, 2020)</li></ul>

# Physical(social) distancing

코로나바이러스감염증-19 중앙재난안전대책본부 정례브리핑

## 여전히 엄중한 상황, 강화된 '사회적 거리두기' 2주 더 연장합니다



- ✓ '사회적 거리두기' 실행에 따른 효과
- ✓ 강력한 '사회적 거리두기' 2주 연장이 불가피한 이유

2020.4.4. 기준

보건복지부 질병관리본부

중증비상 대응체계 충동비상 대응체계

## 강도 높은 사회적 거리두기 국민 행동 지침

- 불필요한 외출, 모임, 외식, 행사, 여행 등 모두 연기 또는 취소
- 발열 또는 호흡기 증상 (기침, 인후통 등) 시 출근하지 않고 집에서 휴식
- 생필품 구매, 의료기관 방문, 출퇴근 제외한 외출 자제
- 악수 등 신체 접촉 피하고, 2m 건강거리 두기
- 손씻기, 기침예절 등 개인위생수칙 준수
- 매일 주변 환경을 소독하고 환기 시키기

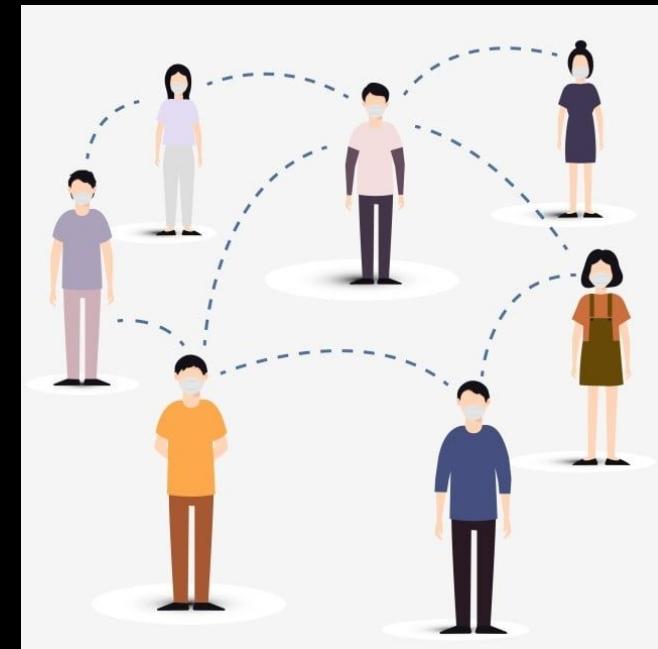
행정안전부 질병관리본부 KCDC

# Overview

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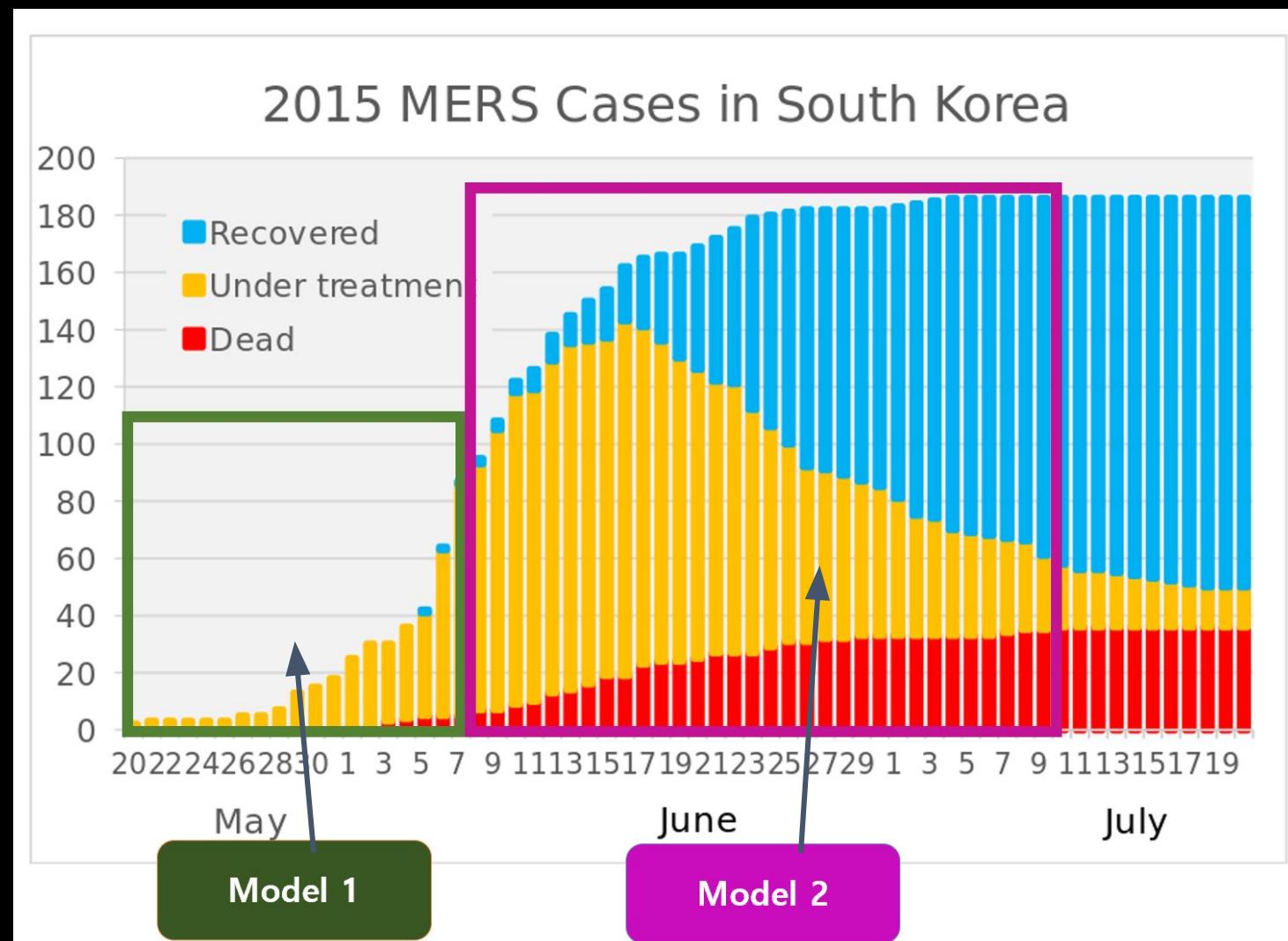
Model 1



Model 2

# Model Data

- Based on the detailed data of patients by WHO
- duration : 5/20 ~ 7/10
- Model 1 : Before Control (5/20 ~ 6/8)
- Model 2 : After Control (6/9 ~ 7/10)



# Overview

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⋮



We will see how much “**Control**” is important!



⋮



Model 1

Model 2

# Propagation Mechanism – SIR Model

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S : the number of susceptible individuals

I : the total number of infected patients

R : the number of removed cases [ 회복된 사람 수 + 사망자 수 ]



# Propagation Mechanism – SEIR Model

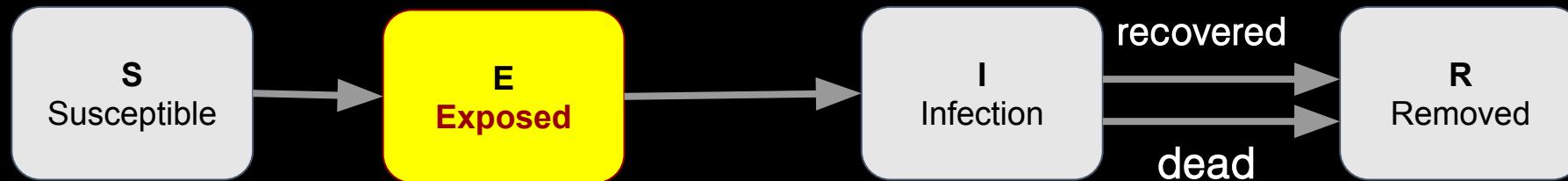
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S : the number of susceptible individuals

E : the number of exposed(잠복기) individuals

I : the total number of infected patients

R : the number of removed cases[ 회복된 사람 수 + 사망자 수 ]



# Propagation Mechanism – SEAHIR Model

S : the number of susceptible individuals

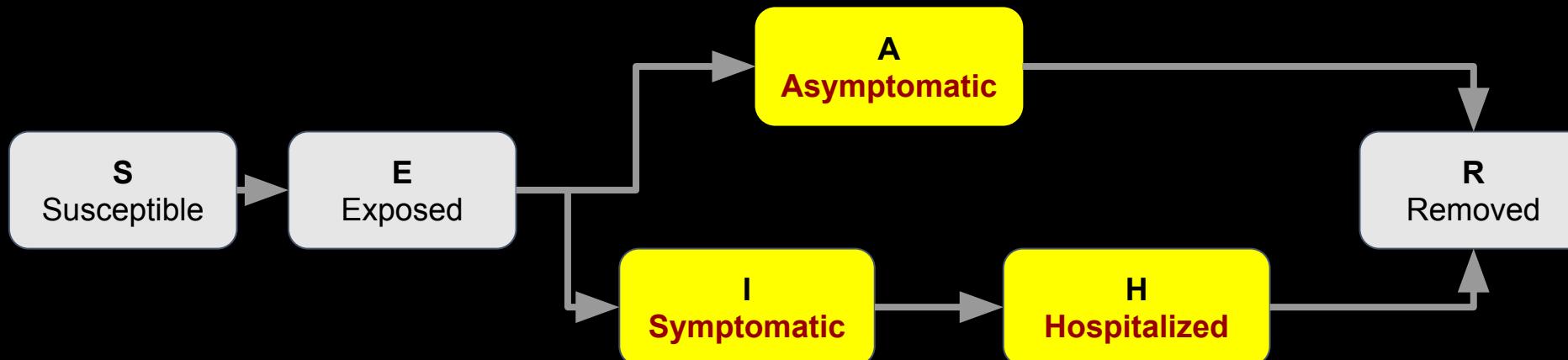
E : the number of exposed individuals

A : the number of asymptomatic infected cases

I : the total number of mild and severe infected patients

H : the number of hospitalized cases

R : the number of removed cases [ 회복된 사람 수 + 사망자 수 ]



# Meaning of arrows?

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Arrows represent the transitions from one compartment to another

$$\frac{\text{rate} \cdot \text{probability} \cdot \text{population}}{\longrightarrow}$$

Rate : the transmission coefficient

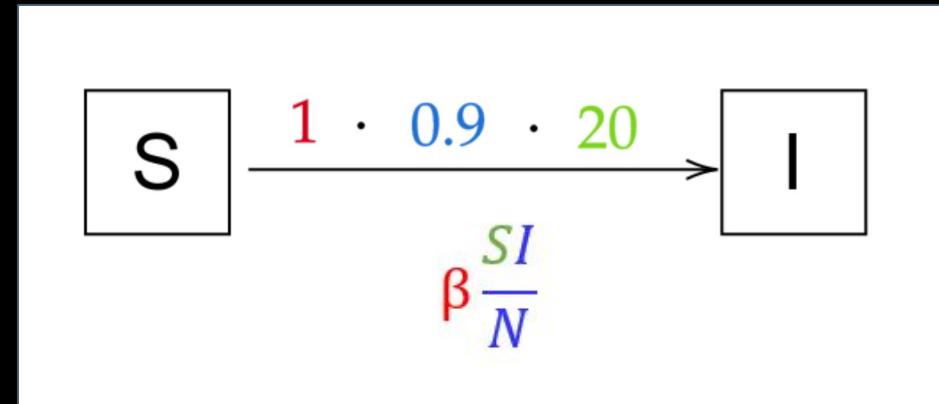
Probability : the probability of the transition taking place for an individual

Population : the group of individuals

# Meaning of arrows? – Example

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Transitions from one compartment to another are represented by arrows!



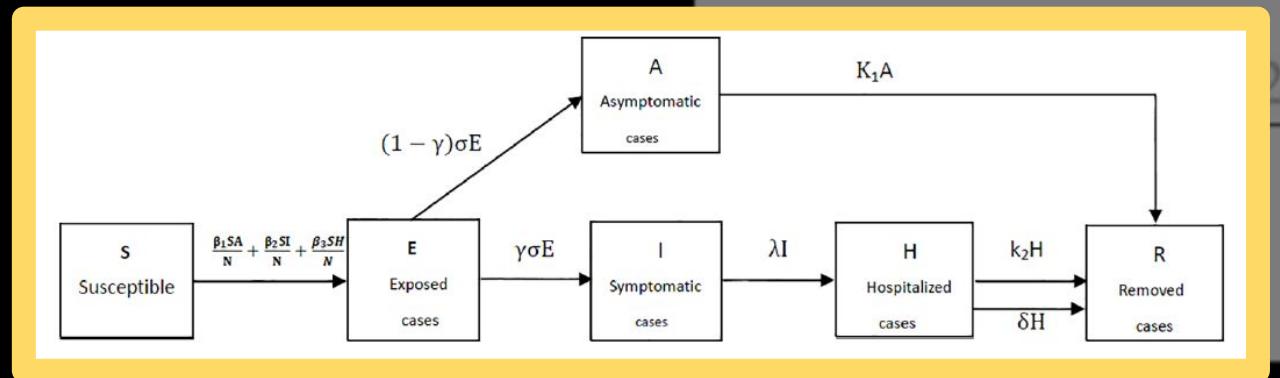
**Rate** : the transmission coefficient(Beta) [1]

**Probability** : I/N [90%]

**Population** : the number of S [20]

# Meaning of arrows? – Example

Transitions from one compartment to another are represented by arrows!



Rate : the transmission coefficient(

Probability : I/N [90%]

Population : the number of S [20]

$$\left\{ \begin{array}{l} \frac{dS}{dt} = -\beta_1 \frac{SA}{N} - \beta_2 \frac{SI}{N} - \beta_3 \frac{SH}{N}, \\ \frac{dE}{dt} = \beta_1 \frac{SA}{N} + \beta_2 \frac{SI}{N} + \beta_3 \frac{SH}{N} - \sigma E, \\ \frac{dA}{dt} = (1 - \gamma)\sigma E - k_1 A, \\ \frac{dI}{dt} = \gamma\sigma E - \lambda I, \\ \frac{dH}{dt} = \lambda I - k_2 H - \delta H, \\ \frac{dR}{dt} = k_1 A + k_2 H + \delta H, \end{array} \right.$$

# Model 1 – Assumptions

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1. The whole population is initially susceptible except the first confirmed case
2. There is no zoonotic infections in Korea, only considering the epidemic spread in the human beings
3. There is no effective control measures before June 8, 2015

# SEAHIR Model – Model 1 (Before control)

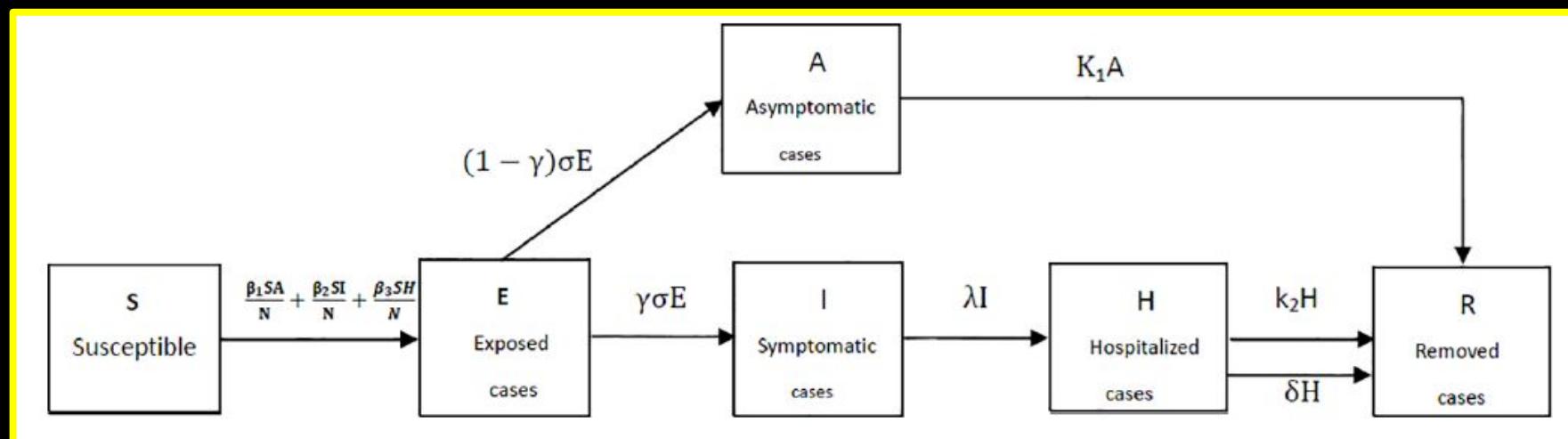
Table 2. Parameters value in system [Eq\(1\)](#).

Parameter	Range	Mean and 95%CI	Source
$\frac{1}{\sigma}$	(3~8)	5.2	[16]
$\frac{1}{\lambda}$	(3~7)	5	[16]
$\frac{1}{k_1}$	(3~7)	5	[16]
$\frac{1}{k_2}$	(5~10)	7	[16]
$\frac{1}{\tau}$	(0~42)	15.16	Calculated
$\beta_1$	-	0.8756(0.853 ~ 0.9324)	Estimated
$\beta_2$	-	0.7833(0.5925 ~ 0.8592)	Estimated
$\beta_3$	-	0.4568(0.3839 ~ 0.6751)	Estimated
$v$	-	0.0348(0.0285 ~ 0.353)	Estimated
$N$	49520000	-	[26]
$S_0$	49519960	-	[26]
$E_0$	16 ~ 32	-	[27]
$A_0$	16 ~ 36	-	[27]
$I_0$	1	-	[27]
$H_0$	0	-	[27]
$R_0$	0	-	[27]

# SEAHIR Model – Model 1 (Before control)

## Estimated parameters

- $\beta_1$  : Transmission coefficient of the asymptomatic infected cases
- $\beta_2$  : Transmission coefficient of the symptomatic infected cases to the susceptible
- $\beta_3$  : Transmission coefficient of the hospitalized cases
- $\gamma$  : clinical outbreak rate in all the infected cases



# SEAHIR Model – Model 1(Before control)

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## Parameters(times)

- $1/\sigma$  : the mean time of incubation period(잠복기 기간)  
<3~8 days>
- $1/\lambda$  : the mean time from data of symptoms onset to data of hospitalization (입원 중 증상이 나타나는 기간) <3~7 days>
- $1/k_1$  : mean infectious period of asymptomatic infected person for survivors (무증상 감염자의 감염기간) <3~7 days>
- $1/k_2$  : mean duration for hospitalized cases for survivors (입원한 사람 중 회복된 사람의 기간) <5~10 days>
- $1/\delta$  : mean duration from hospitalization to death (입원 중 사망까지의 기간) <0~42days>

# SEAHIR Model – Model 1 (Before control)

## ODE Equations

$$\begin{cases} \frac{dS}{dt} = -\beta_1 \frac{SA}{N} - \beta_2 \frac{SI}{N} - \beta_3 \frac{SH}{N}, \\ \frac{dE}{dt} = \beta_1 \frac{SA}{N} + \beta_2 \frac{SI}{N} + \beta_3 \frac{SH}{N} - \sigma E, \\ \frac{dA}{dt} = (1 - \gamma) \sigma E - k_1 A, \\ \frac{dI}{dt} = \gamma \sigma E - \lambda I, \\ \frac{dH}{dt} = \lambda I - k_2 H - \delta H, \\ \frac{dR}{dt} = k_1 A + k_2 H + \delta H, \end{cases}$$

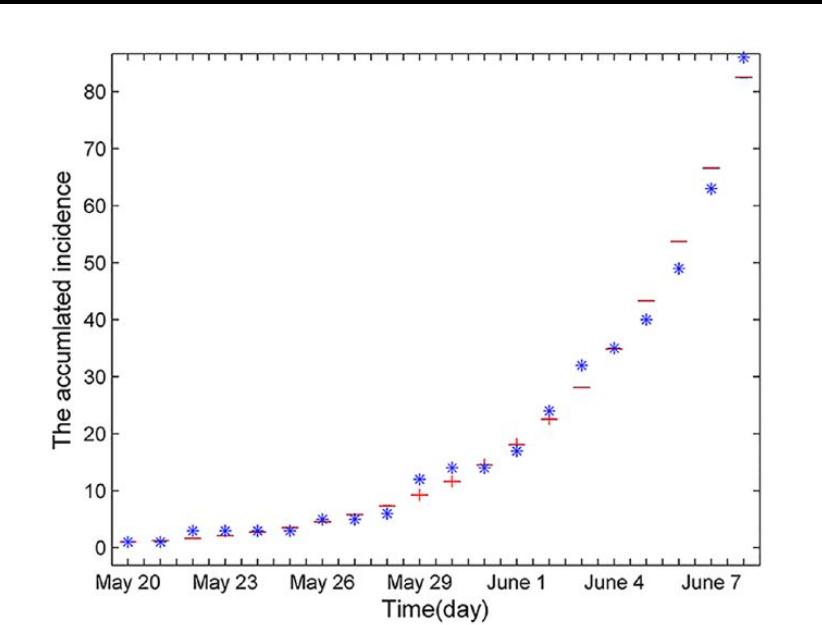
## Parameter estimation

Using Least– square method  
> estimate parameter values

The sum of squared errors  
between actual data and  
solution of equation is  
minimum.

$$f = \sum_{t=1}^n [I_{total}(t) - \overline{I_{total}}(t)]^2$$

## Fitting curve



$$\beta_1 = 0.8756, \beta_2 = 0.7833, \beta_3 = 0.4568 \text{ and } \gamma = 0.0348.$$

# Model 2 – Main Control Measures

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1. Early and complete identification and investigation of all contacts;
2. Robust quarantine/isolation and monitoring of all contacts and suspected cases;
3. Full implementation of infection prevention and control measures;
4. Prevention of travel, especially international, of infected persons and contacts
5. Washing your hands regularly with soap and water and maintaining good personal hygiene;
6. Avoiding close contact with people who are sick;
7. Covering your mouth and nose with a tissue or your sleeve when coughing or sneezing.

## **Model 2 - Main Control Measures**

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1. Early and complete identification and investigation of all contacts;
2. Robust quarantine/isolation and monitoring of all contacts and suspected cases:

**① Improving of self-protecting ability of susceptible.**

**② Isolating or monitoring all the close contacts**

personal hygiene;

6. Avoiding close contact with people who are sick;
7. Covering your mouth and nose with a tissue or your sleeve when coughing or sneezing.

## Model 2 - Main Control Measures

---

1. Early and complete identification and investigation of all contacts;
2. Robust quarantine/isolation and monitoring of all contacts and suspected cases:

**What parameters should be added?**

personal hygiene;

6. Avoiding close contact with people who are sick;
7. Covering your mouth and nose with a tissue or your sleeve when coughing or sneezing.

# What parameter should be added?

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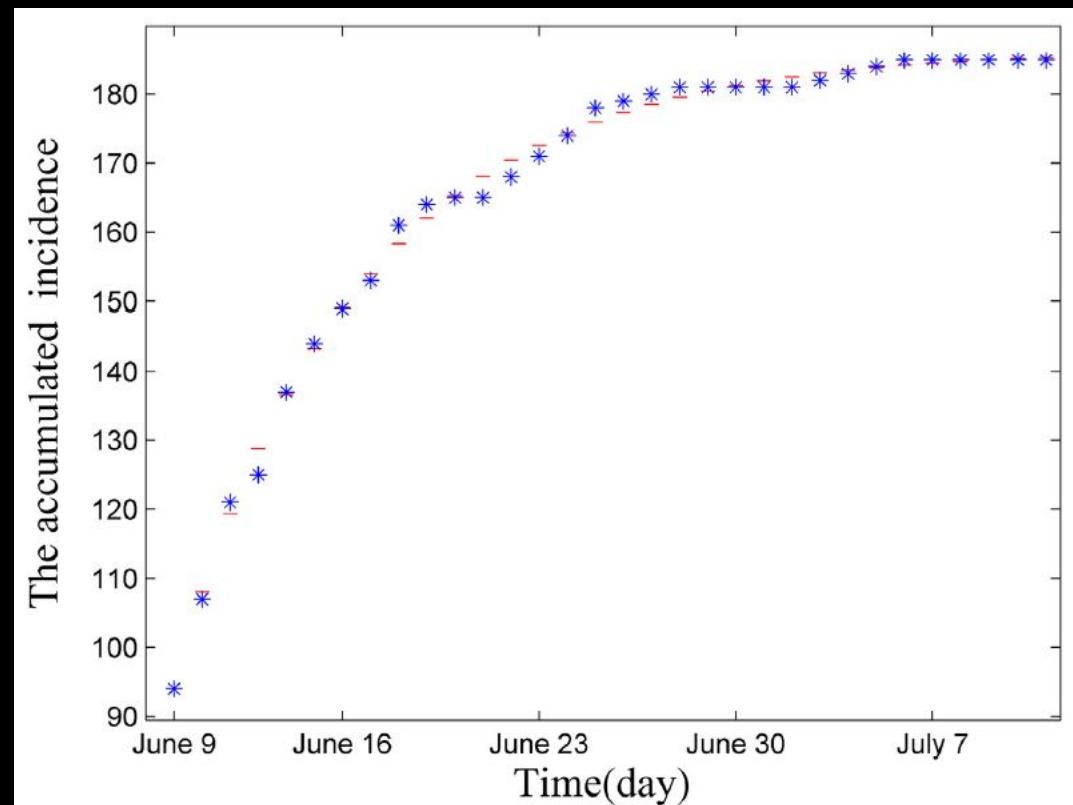
- Isolation or monitoring rates( $I$ )
- Self-protection coefficients( $d$ )

# SEAHIR Model – Model 2(After control)

## ODE Equations

$$\left\{ \begin{array}{l} \frac{dS}{dt} = -\frac{l_1 \beta_1 SA}{N} - \frac{l_2 \beta_2 SI}{N} - \frac{l_3 \beta_3 SH}{N}, \\ \frac{dE}{dt} = \frac{l_1 \beta_1 SA}{N} + \frac{l_2 \beta_2 SI}{N} + \frac{l_3 \beta_3 SH}{N} - \sigma E - d_1 E, \\ \frac{dA}{dt} = (1 - \gamma) \sigma E - k_1 A - d_2 A, \\ \frac{dI}{dt} = \gamma \sigma E - \lambda I - d_3 I, \\ \frac{dH}{dt} = \lambda I - k_2 H - \delta H - d_4 H, \\ \frac{dR}{dt} = k_1 A + k_2 H + \delta H + d_1 E + d_2 A + d_3 I + d_4 H, \end{array} \right.$$

## Fitting curve



# What is Reproduction number( $R_0$ ) ?

$R_0$  : The threshold whether disease will outbreak and be prevalent in the crowd

$R_0 > 1$  : The disease will spread

$R_0 < 1$  : The disease will disappear

Using SIR model,



S : the number of susceptible individuals

I : the total number of infected cases

R : the number of hospitalized cases

$\alpha \cdot S \cdot I$  : Rate of appearance

$\gamma \cdot I$  : Rate of removed

$$\Delta I = \alpha \cdot S \cdot I - \gamma \cdot I \\ = \gamma \cdot (\alpha / \gamma \cdot S - 1) \cdot I$$

Important

$$\alpha / \gamma \cdot S = R_0$$

$R_0$  : criteria=1

# Calculating Reproduction number ( $R_0$ )

## S1 File. Mathematical analysis.

### A. The basic reproduction number $R_0$ of system (1)

Through simple calculation, we can obtain a disease free equilibrium  $E_1 = (S_1, 0, 0, 0, 0, R_1)$ . Then we use the spectral radius of the next generation matrix (the method proposed by the Van Den Driessche in [1]) to get the expression of  $R_0$  of system (1). Firstly, only the infected compartments satisfied by the following system are considered:

$$\begin{cases} \frac{dE}{dt} = \beta_1 \frac{SA}{N} + \beta_2 \frac{SI}{N} + \beta_3 \frac{SH}{N} - \sigma E, \\ \frac{dA}{dt} = (1 - \gamma)\sigma F - \kappa_1 A, \\ \frac{dI}{dt} = \gamma\sigma F - \lambda I, \\ \frac{dH}{dt} = \lambda I - k_2 H - \delta H. \end{cases}$$

And,

$$F = \begin{pmatrix} \beta_1 \frac{S_0 A}{N} + \beta_2 \frac{S_0 I}{N} + \beta_3 \frac{S_0 H}{N} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}, \quad V = \begin{pmatrix} \sigma E & 0 & 0 & 0 \\ k_1 A - (1 - \gamma)\sigma E & \lambda I - \gamma\sigma E & 0 & 0 \\ 0 & 0 & k_2 H + \delta H - \lambda I & 0 \end{pmatrix},$$

where  $F$  denotes the rate of appearance of new infection and  $V$  denotes the rate of transfer of individuals. Calculating the derivative of  $F$  and  $V$  about  $x = (E, A, I, H)$ , respectively. Then substitute initial data  $(S_0, E_0, A_0, I_0, H_0, R_0)$  into variables, we can get:

$$F = \begin{pmatrix} 0 & \beta_1 \frac{S_0}{N} & \beta_2 \frac{S_0}{N} & \beta_3 \frac{S_0}{N} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}, \quad V = \begin{pmatrix} \sigma & 0 & 0 & 0 \\ -(1 - \gamma)\sigma & k_1 & 0 & 0 \\ -\sigma\gamma & 0 & \lambda & 0 \\ 0 & 0 & -\lambda & \delta + k_2 \end{pmatrix},$$

and thus

$$FV^{-1} = \begin{pmatrix} \frac{(1 - \gamma)\beta_1 S_0}{k_1 N} + \frac{\gamma\beta_2 S_0}{\lambda N} + \frac{\gamma\beta_3 S_0}{(k_2 + \delta)N} & \frac{\beta_1 S_0}{k_1 N} & \frac{\beta_2 S_0}{\lambda N} + \frac{\beta_3 S_0}{\delta + k_2} & \frac{\beta_3 S_0}{(\delta + k_2)N} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix},$$

where  $R_0$  is the biggest eigenvalue of matrix  $FV^{-1}$  i.e.  $R_0 = \rho(FV^{-1})$ . The expression of  $R_0$  is as follows:

$$R_0 = \frac{(1 - \gamma)\beta_1 S_0}{k_1 N} + \frac{\gamma\beta_2 S_0}{\lambda N} + \frac{\gamma\beta_3 S_0}{(k_2 + \delta)N}.$$

$F$  : the rate of appearance of new infection

$V$  : the rate of transfer of individuals

$$R_0 = \frac{(1 - \gamma)\beta_1 S_0}{k_1 N} + \frac{\gamma\beta_2 S_0}{\lambda N} + \frac{\gamma\beta_3 S_0}{(k_2 + \delta)N}.$$

# What is Reproduction number( $R_0$ ) ?

In this article,

F : the rate of appearance of new infection

V : the rate of transfer of individuals

$$R_0 = \frac{(1 - \gamma)\beta_1 S_0}{k_1 N} + \frac{\gamma\beta_2 S_0}{\lambda N} + \frac{\gamma\beta_3 S_0}{(k_2 + \delta)N}.$$

$\therefore F/V$

$= R_0$

Using SIR model,



S : the number of susceptible individuals

I : the total number of infected cases

R : the number of hospitalized cases

$\alpha \cdot S \cdot I$  : Rate of appearance

$\gamma \cdot I$  : Rate of removed

$$\Delta I = \alpha \cdot S \cdot I - \gamma \cdot I \\ = \gamma \cdot (\alpha / \gamma \cdot S - 1) \cdot I$$

Important  
 $\alpha / \gamma \cdot S = R_0$

$R_0$  : criteria=1

# What are the Reproduction number( $R_0$ ) values?

## Model 1)

$$R_0 = 4.422$$

# Disease will spread

## Model 2)

$R_e = 0.385$

[ $R_c$  is Model 2's  $R_0$  value]

# Disease will disappear

$R_0 > 1$  : The disease will spread  
 $R_0 < 1$  : The disease will disappear

# Conclusion of research paper

Isolating all the close contacts  
& strengthening the self-protection ability of susceptible are  
the effective control measures

# Data cleaning

MERS infected case data from WHO

MERS-CoV cases in the Republic of Korea as of 21/7/2015*							
Case no.	Date of notification to WHO	Age	Sex	Health care worker	Comorbidities	Date of symptoms onset	Date of first hospitalization
1	20/05/2015	68	M	No	NA	11/05/2015	15/05/2015
2	22/05/2015	63	F	No	NA	19/05/2015	NA
3	22/05/2015	76	M	No	NA	20/05/2015	NA
4	26/05/2015	46	F	No	NA	25/05/2015	NA
5	26/05/2015	50	M	Yes	NA	25/05/2015	NA
6	28/05/2015	71	M	No	NA	24/05/2015	NA
7	29/05/2015	28	F	Yes	NA	26/05/2015	NA
8	29/05/2015	56	M	No	NA	27/05/2015	09/05/2015
9	29/05/2015	79	F	No	NA	20/05/2015	NA
10	29/05/2015	49	F	No	NA	21/05/2015	NA
11	29/05/2015	49	M	No	NA	21/05/2015	NA
12	29/05/2015	46	F	Yes	No	26/05/2015	26/05/2015
13	30/05/2015	35	M	No	NA	20/05/2015	13/05/2015
14	30/05/2015	35	M	No	NA	24/05/2015	25/05/2015
15	01/06/2015	40	M	No	NA	20/05/2015	15/05/2015
16	01/06/2015	45	M	No	NA	22/05/2015	22/05/2015
17	01/06/2015	77	F	No	NA	20/05/2015	30/05/2015
18	02/06/2015	60	M	No	NA	28/05/2015	15/05/2015
19	02/06/2015	40	M	No	NA	23/05/2015	15/05/2015
20	02/06/2015	59	F	No	NA	23/05/2015	NA
21	02/06/2015	39	F	No	NA	27/05/2015	31/05/2015
22	02/06/2015	73	M	No	NA	31/05/2015	NA



	X	date	case.I	cum.I
1	1	20150520	1	1
2	2	20150521	0	1
3	3	20150522	2	3
4	4	20150523	0	3
5	5	20150524	0	3
6	6	20150525	0	3
7	7	20150526	2	5
8	8	20150527	0	5
9	9	20150528	1	6
10	10	20150529	6	12
11	11	20150530	2	14
12	12	20150531	0	14

source : <https://www.who.int/csr/don/25-october-2015-mers-korea/en/>

# Model 1 – Parameter estimation(R code)

```
# 2. Define a mathematical model to fit the data  
  
# Before control  
Stack_function <- function(time, state, parameters) {  
  with(as.list(c(state, parameters)), {  
    N = 49520000  
    dS <- -(beta_1 * (A * S)/N) - (beta_2 * (I * S)/N) - (beta_3 * (H * S)/N)  
    dE <- (beta_1 * (A * S)/N) + (beta_2 * (I * S)/N) + (beta_3 * (H * S)/N) - (1/4.3 * E)  
    dA <- (1-gamma)*1/4.3*E-(1/5*A)  
    dI <- (gamma * 1/4.3 * E) - (1/5 * I)  
    dH = (1/5 * I) - (1/7 * H) - (1/15.16 * H)  
    dR = (1/5 * A) + (1/7 * H) + (1/15.16 * H)  
  
    return(list(c(dS, dE, dA, dI, dH, dR)))  
  })
```

ODE equations

```
# Before control  
Mers_Model_function <- function(data, P) {  
  
  N = 49520000  
  init <- c(S = N-40, E = 30, A = 30, I = 1, H = 16, R = 0)  
  parameters <- c(beta_1 = P[1], beta_2 = P[2], beta_3 = P[3], gamma = P[4])  
  times <- seq(0, 19, by = 1)  
  out <- as.data.frame(ode(y = init, times = times, func = Stack_function, parms = parameters))  
  out$time <- NULL  
  
  return(out)  
}  
  
P <- c(0.8756, 0.7833, 0.4568, 0.0348)  
  
res <- Mers_Model_function(data, P)
```

calculate ODE equations

```
lower <- c(0,0,0,0)  
upper <- c(1,1,1,1)  
library(GenSA)
```

Simulated Annealing(Parameter estimation)

```
nparam = 4  
out_estimation_result <- GenSA(par = par, lower = lower, upper = upper, fn = Eval_function,  
                                   data = parameter_data, control=list(threshold.stop=min.global+tol,  
                                   verbose=FALSE, maxit=max.iteration))  
  
print("SA-driven parameter estimation result:")  
print(out_estimation_result[c("value","par","counts")])
```

# Modeling and Simulation Contents

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## MERS

Result 1) Model\_1 – Estimation result

Result 2) Model\_2 – Estimation result

Result 3) What if there's no control measures continuously?

## COVID-19 (Application)

Result 4) Model\_1 – Estimation result

Result 5) Model\_2 – Estimation result

Result 6) COVID-19 prediction

# MERS Modeling

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Result 1) Model\_1 + Prediction(w/o d,l)

Result 2-1) Model\_2 – Modification X(Estimation result)

Result 2-2) Model\_2 – Modification O(Modified Estimation result)

Result 3) What if there's no control measures continuously?

# Result 1. MERS Model 1 – Parameter estimation result

MERS Model 1(before control)

Black point = Actual Data  
(5/20~6/8)

Red line = Predicted Data

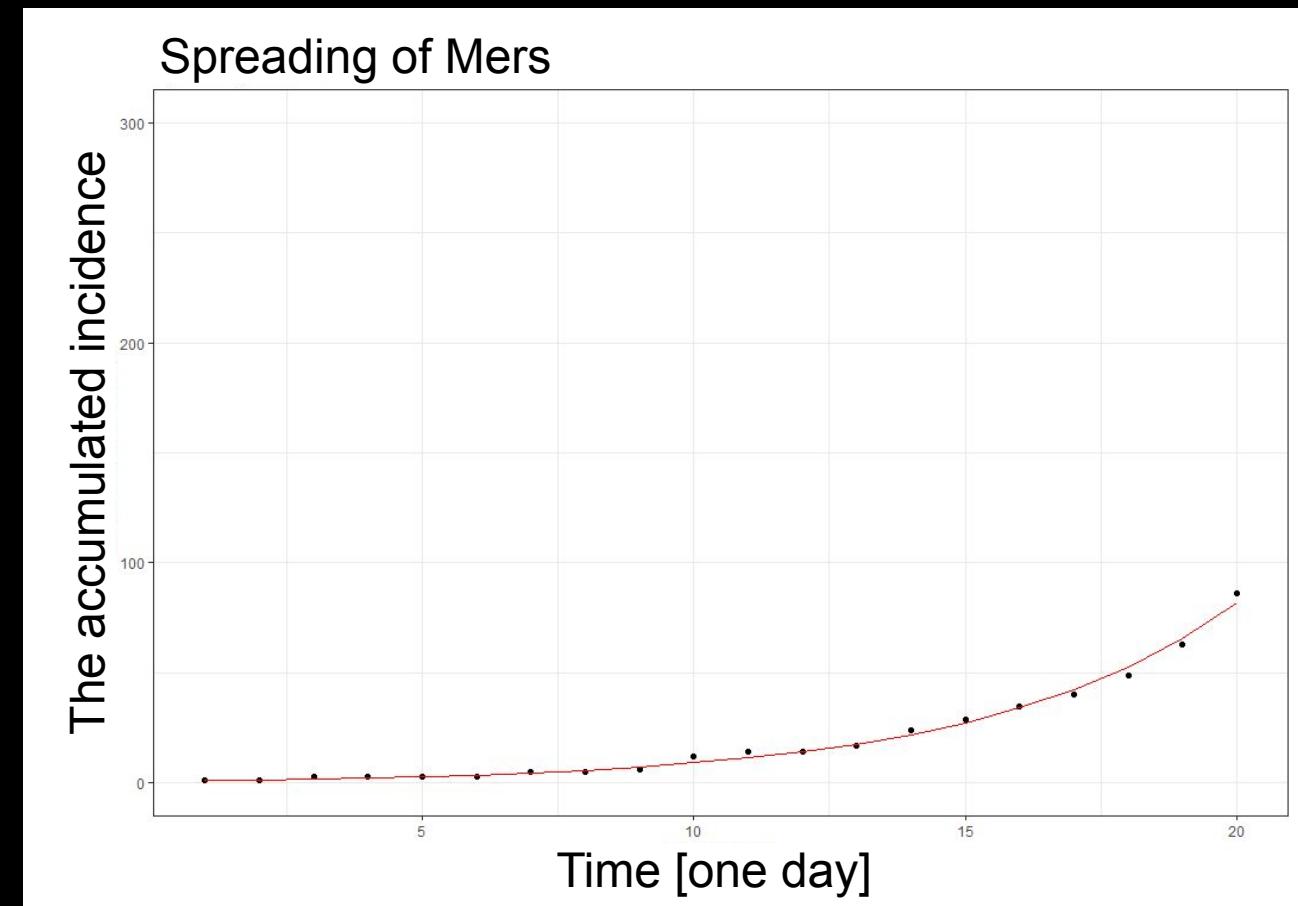
\$par

$\beta_1 = 0.80794175$ ,

$\beta_2 = 0.86679827$ ,

$\beta_3 = 0.01931138$ ,

$\gamma = 0.05311680$



# Result 2. MERS Model 2 – Parameter estimation result

MERS Model 2(after control)

Black point = Actual Data  
(6/9~7/10)

Red line = Predicted Data

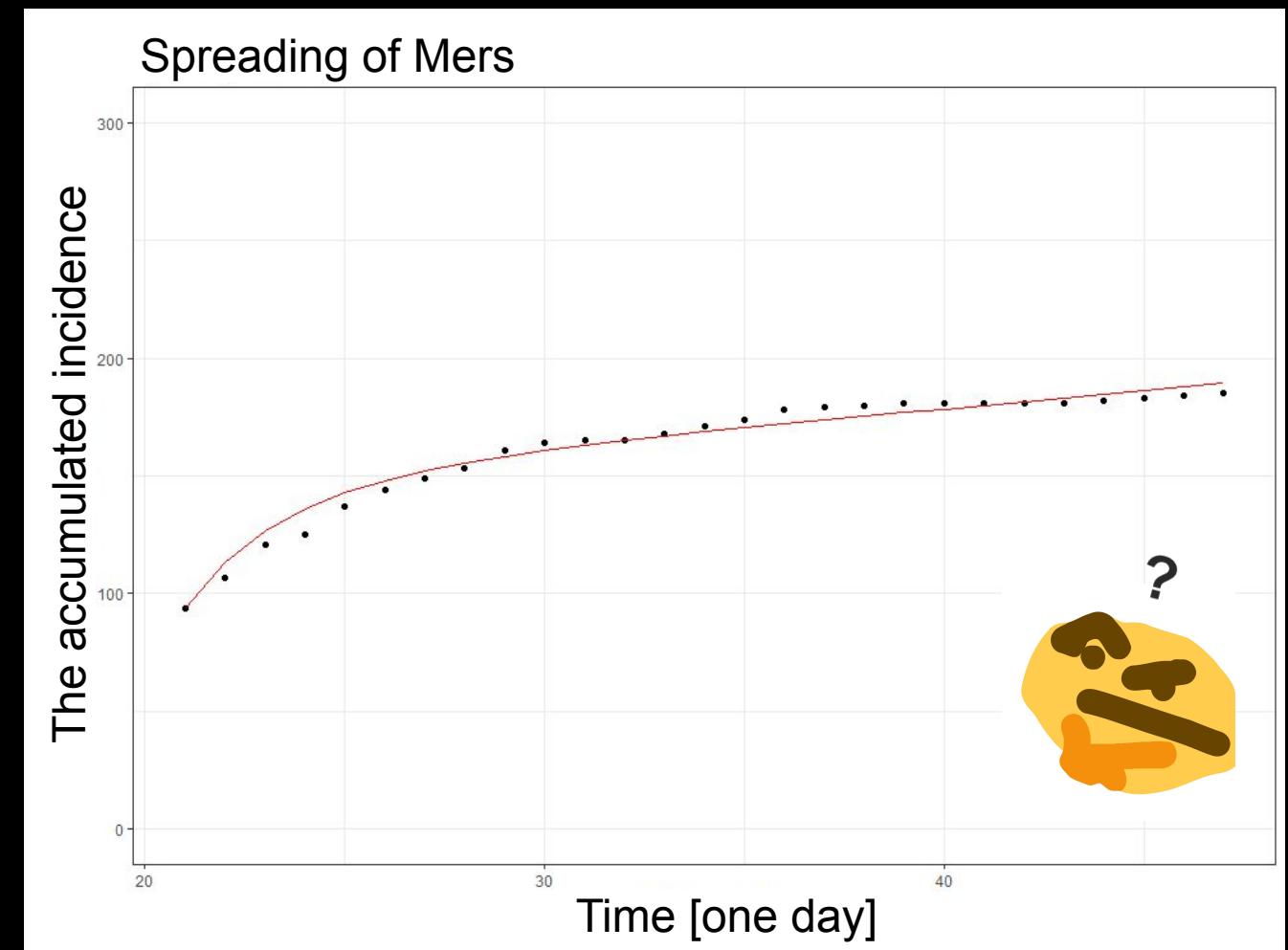
\$par

I1 = 0.46136703

I2 = 0.00000000

I3 = 0.00000000

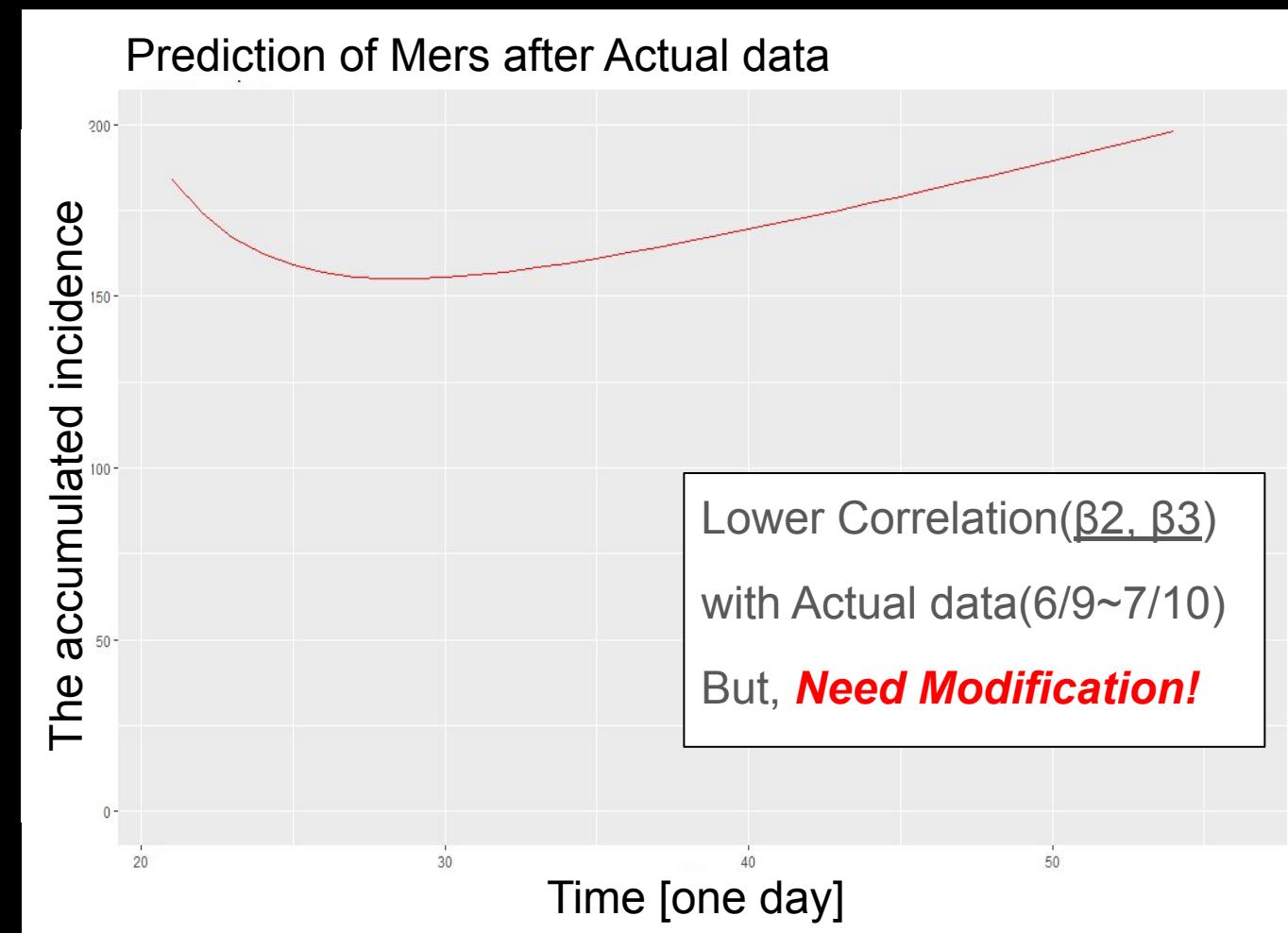
d = 0.05920967



# Result 2. MERS Model 2 – Modification X

MERS Model 2 (Estimated)  
(6/9~7/10)  
Red line = Predicted Data

\$par  
l1 = 0.46136703  
l2 = 0.00000000  
l3 = 0.00000000  
d = 0.05920967

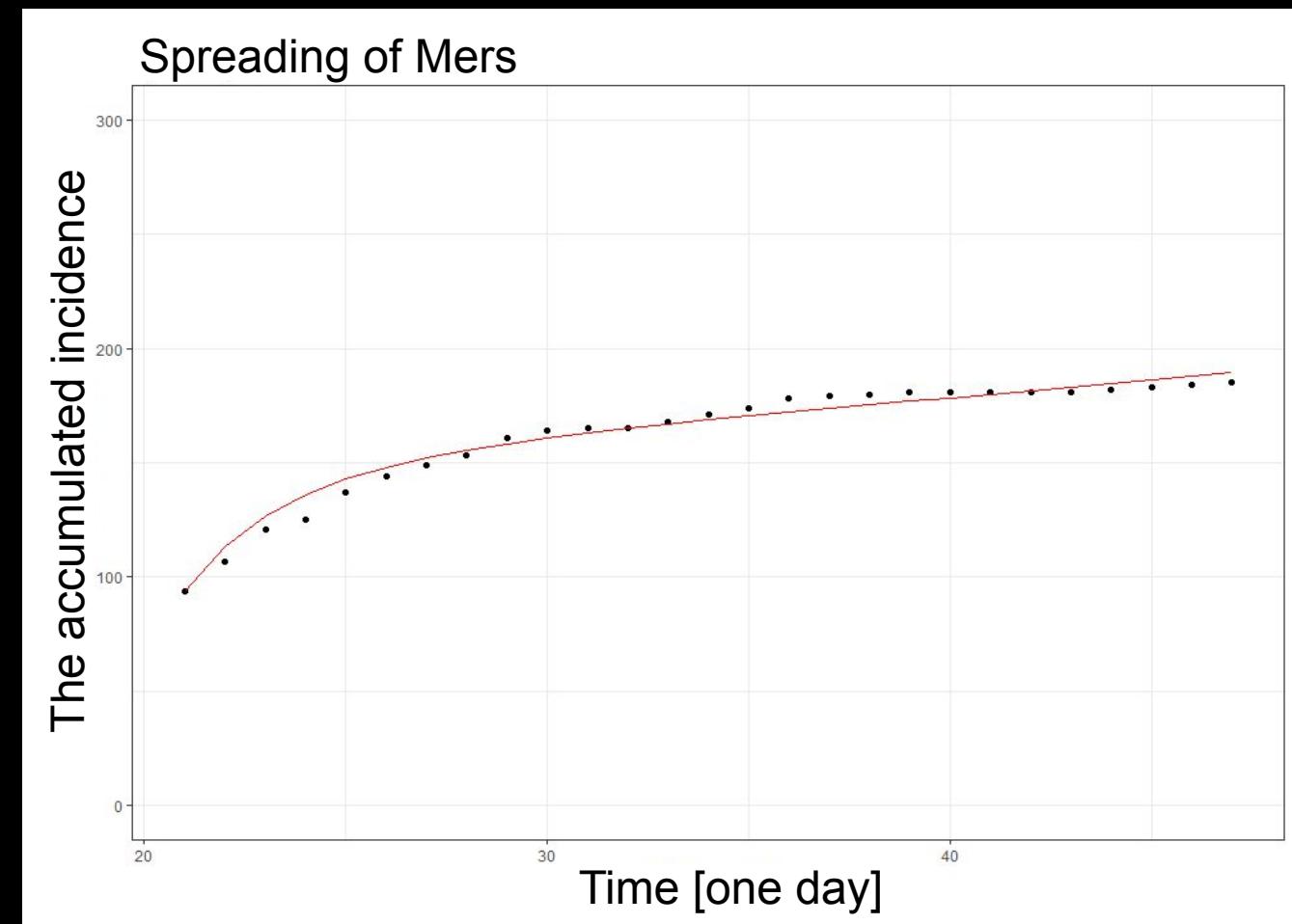


# Result 2. MERS Model 2 – Modification 0

MERS Model 2 (Modified)  
(6/9~7/10)  
Red line = Predicted Data

\$par  
I1 = 0.46136703  
I2 = 0.90000000  
I3 = 0.30000000  
d = 0.05920967  
(I2,I3)

From journal source

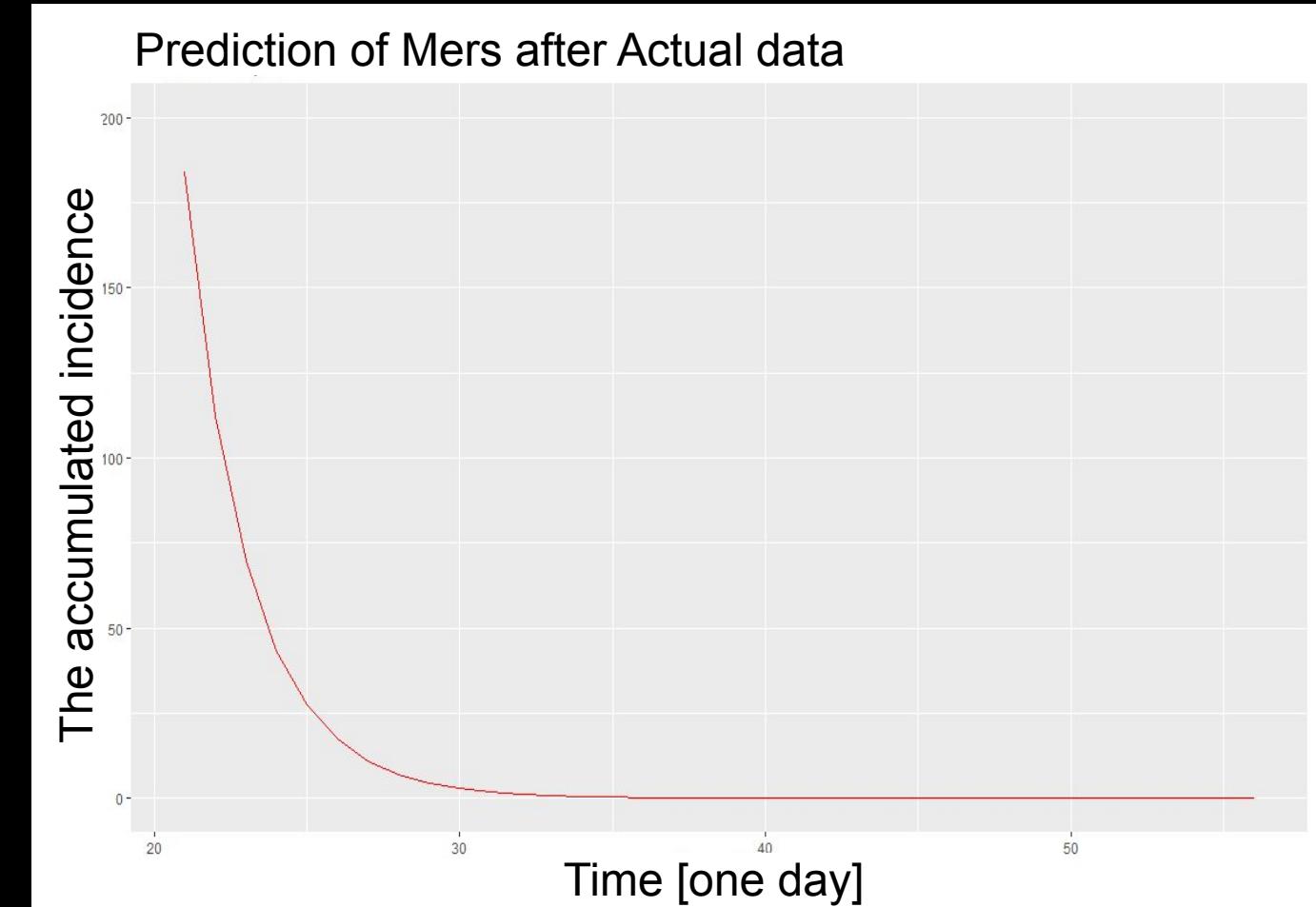


# Result 2. MERS Model 2 – Modification 0

MERS Model 2 (Modified)  
(6/9~7/10)  
Red line = Predicted Data

\$par  
I1 = 0.46136703  
I2 = 0.90000000  
I3 = 0.30000000  
d = 0.05920967  
(I2,I3)

From journal source



# Result 3. MERS Model 1 – Prediction(without d,l)

Q. What if there's no control measures continuously?

MERS Model 1

Red line = Predicted Data

self-protection coefficients

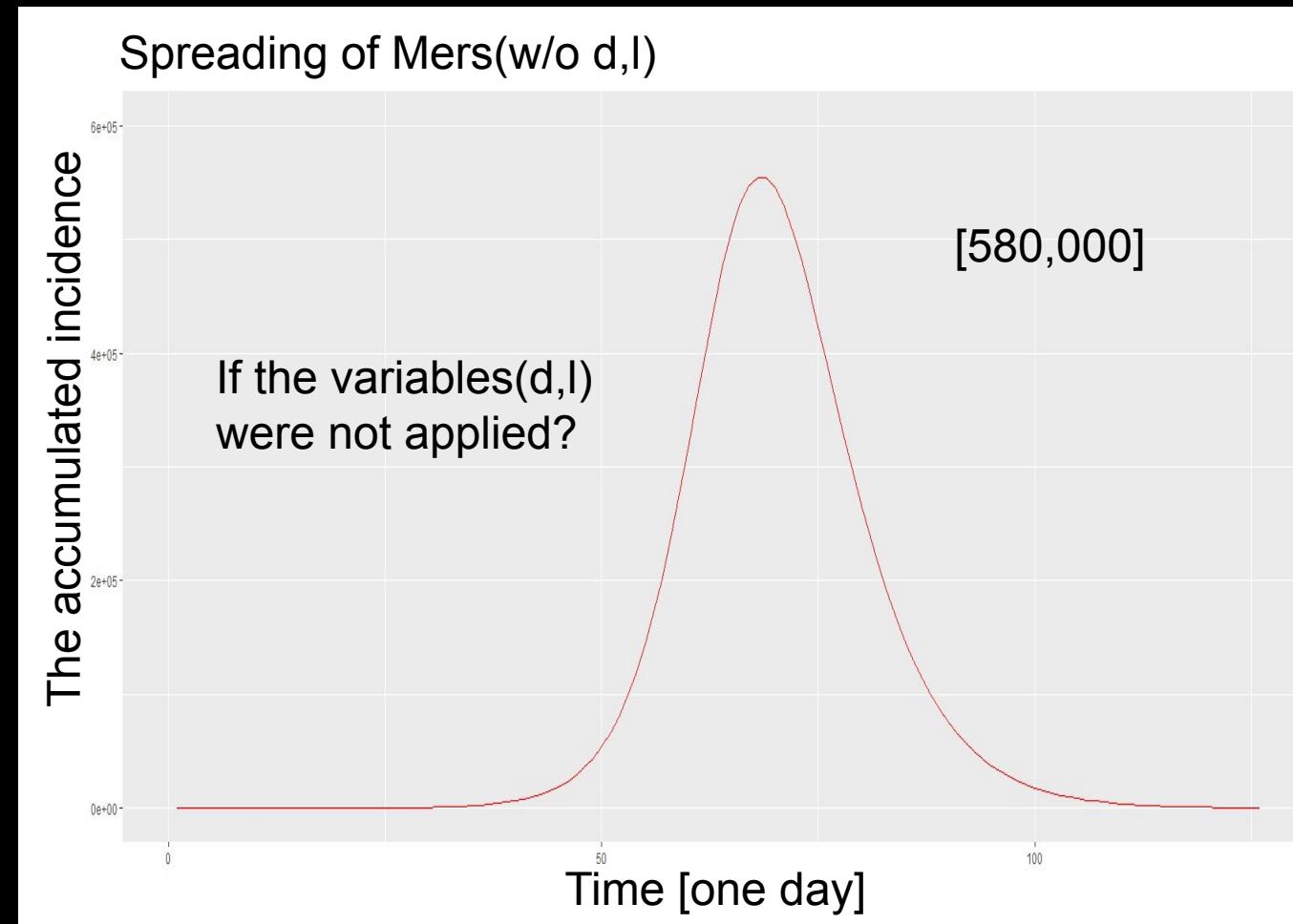
I1 – with asymptomatic cases

I2 – with symptomatic cases

I3 – with hospitalized cases

d – isolation or monitoring

in E, A, I and H compartment



# COVID-19 Modeling

---

COVID-19 (Application)

Result 4) Model\_1 – Estimation result

Result 5) Model\_2 – Estimation result

Result 6) COVID-19 prediction

## Result 4. COVID Model 1 – Parameter estimation result

COVID Model 1(before control)

Black point = Actual Data  
(2/15~3/18)

Red line = Predicted Data

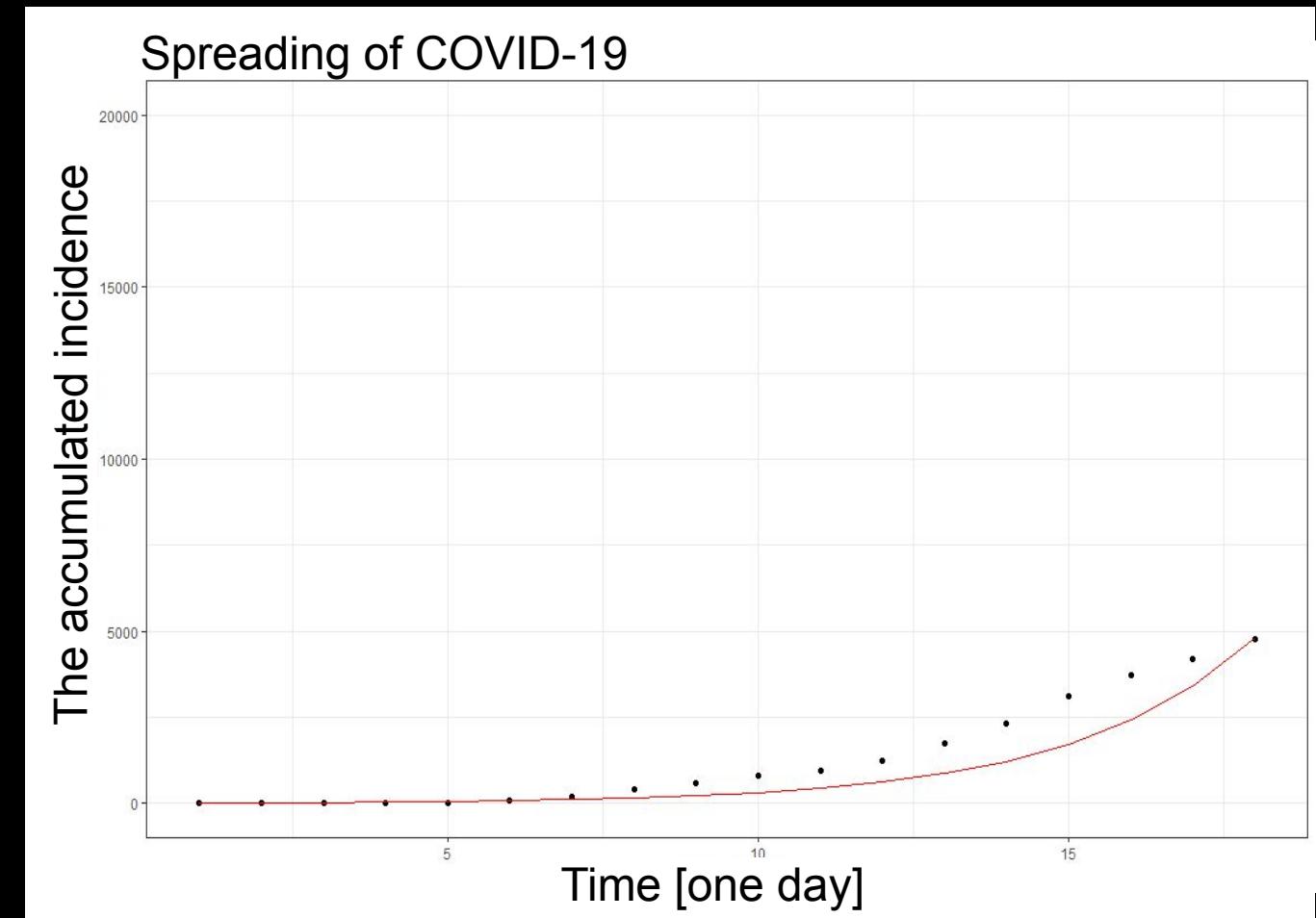
\$par

$\beta_1 = 0.87$

$\beta_2 = 0.88$

$\beta_3 = 0.7$

$\gamma = 0.9$



# Result 5. COVID Model 2 – Parameter estimation result

Mers Model 2(after control)

Black point = Actual Data  
(3/19~4/15)

Red line = Predicted Data

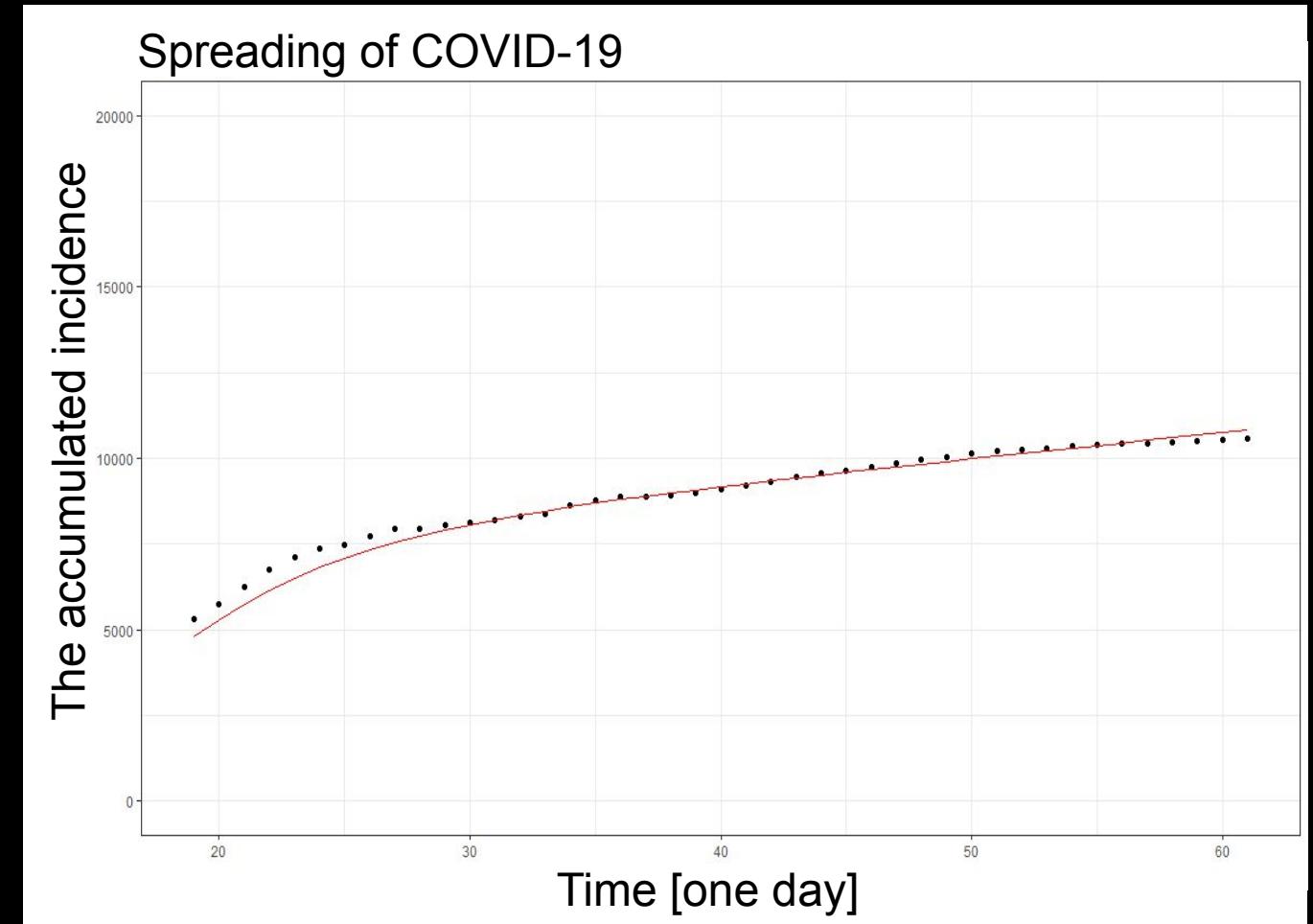
\$par

I1 = 0.78

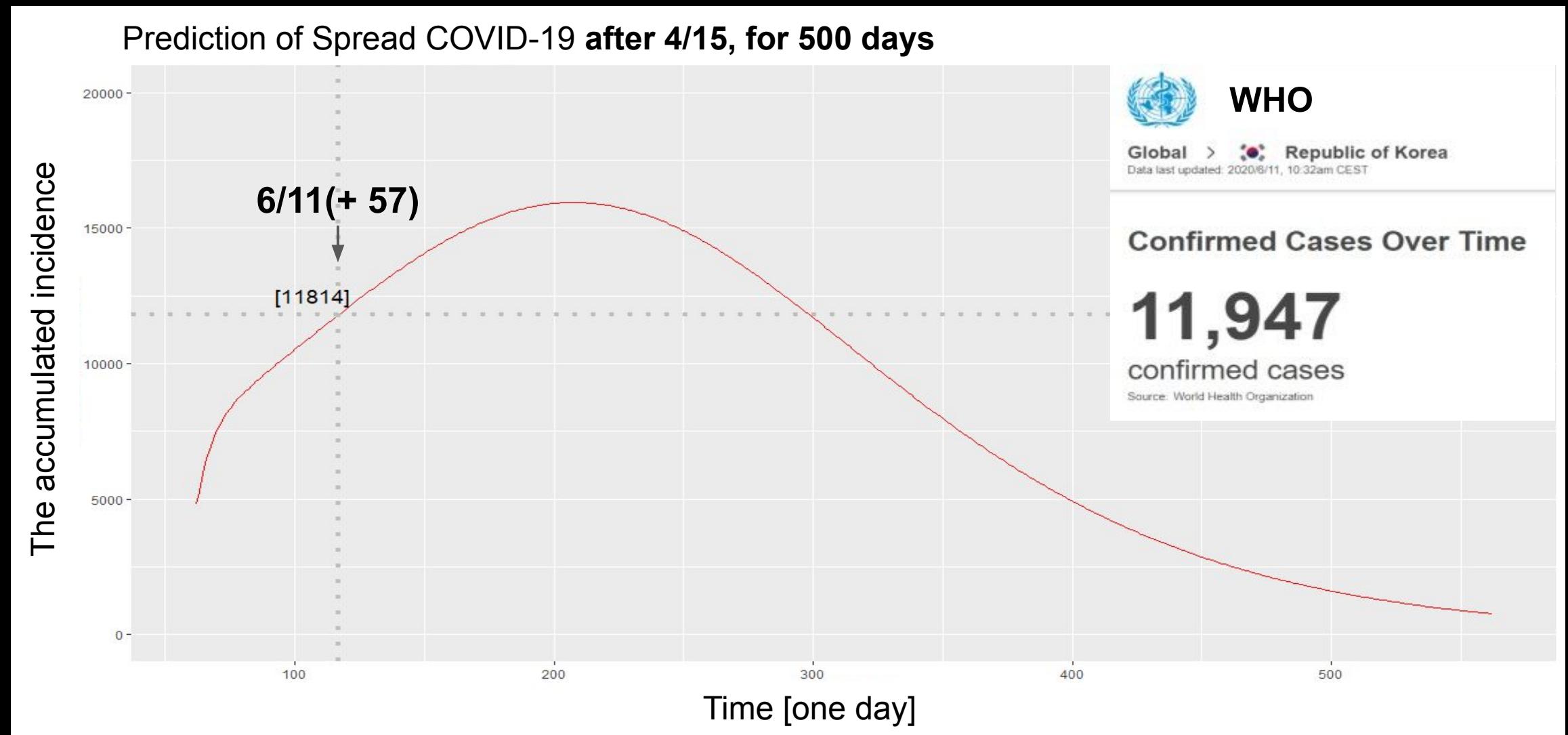
I2 = 1.00

I3 = 1.00

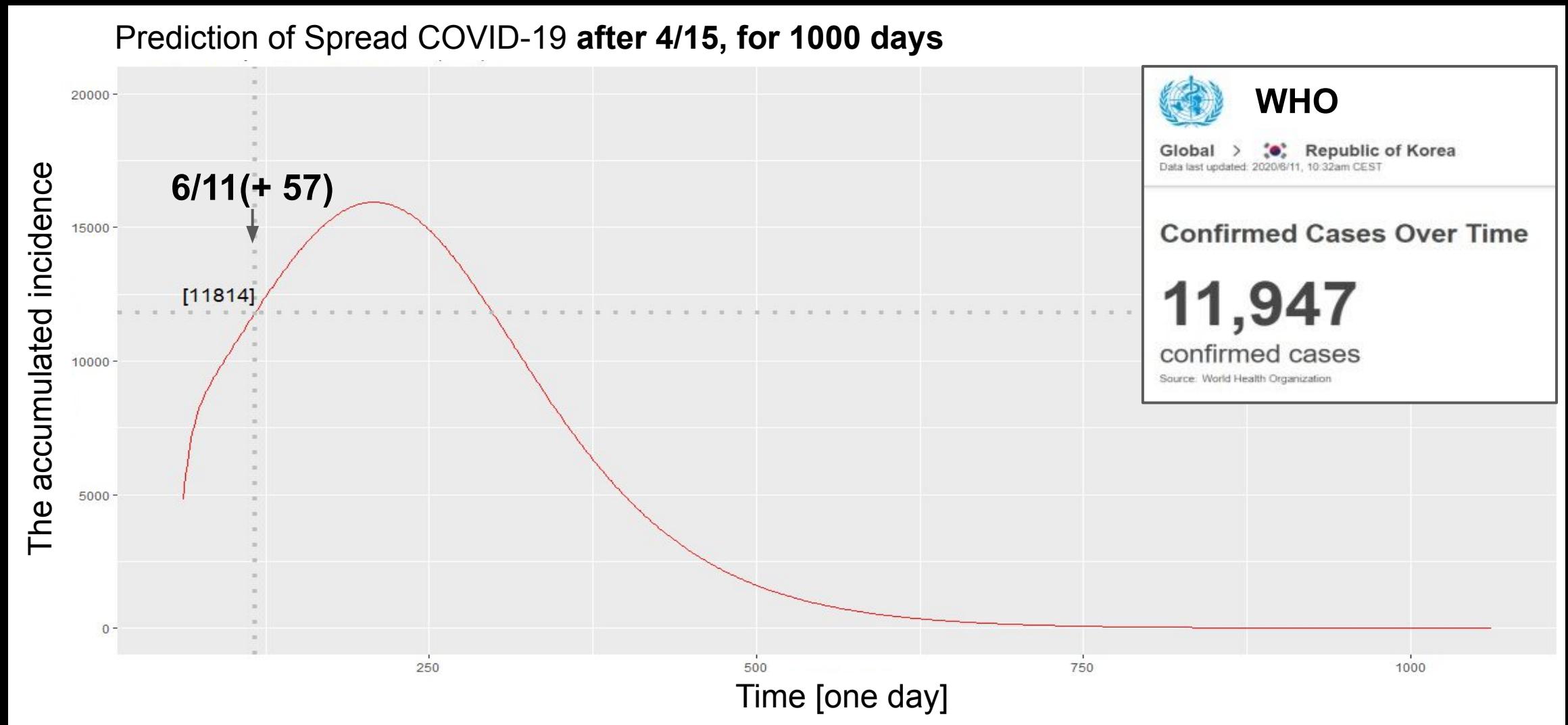
d = 0.24



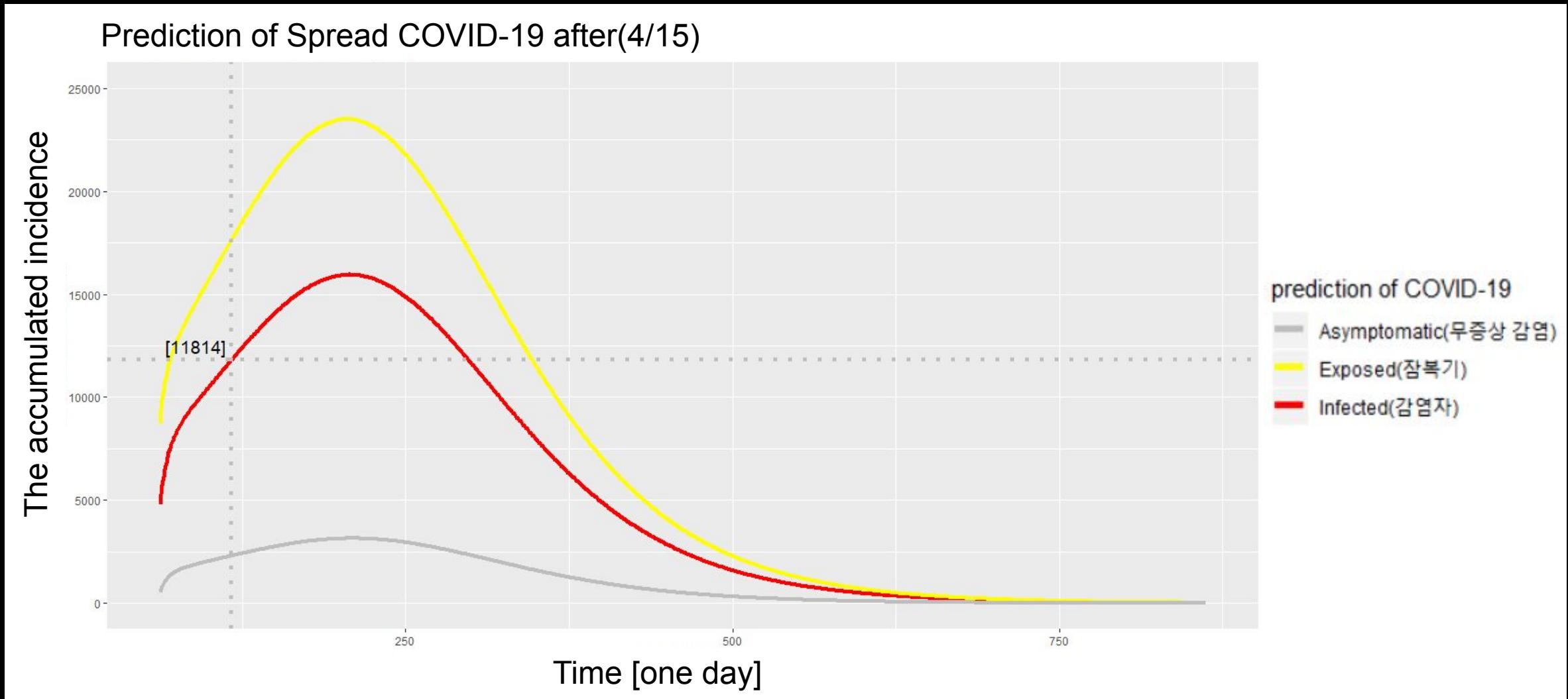
# Result 6. COVID Model 2 – Prediction of Spreading COVID-19



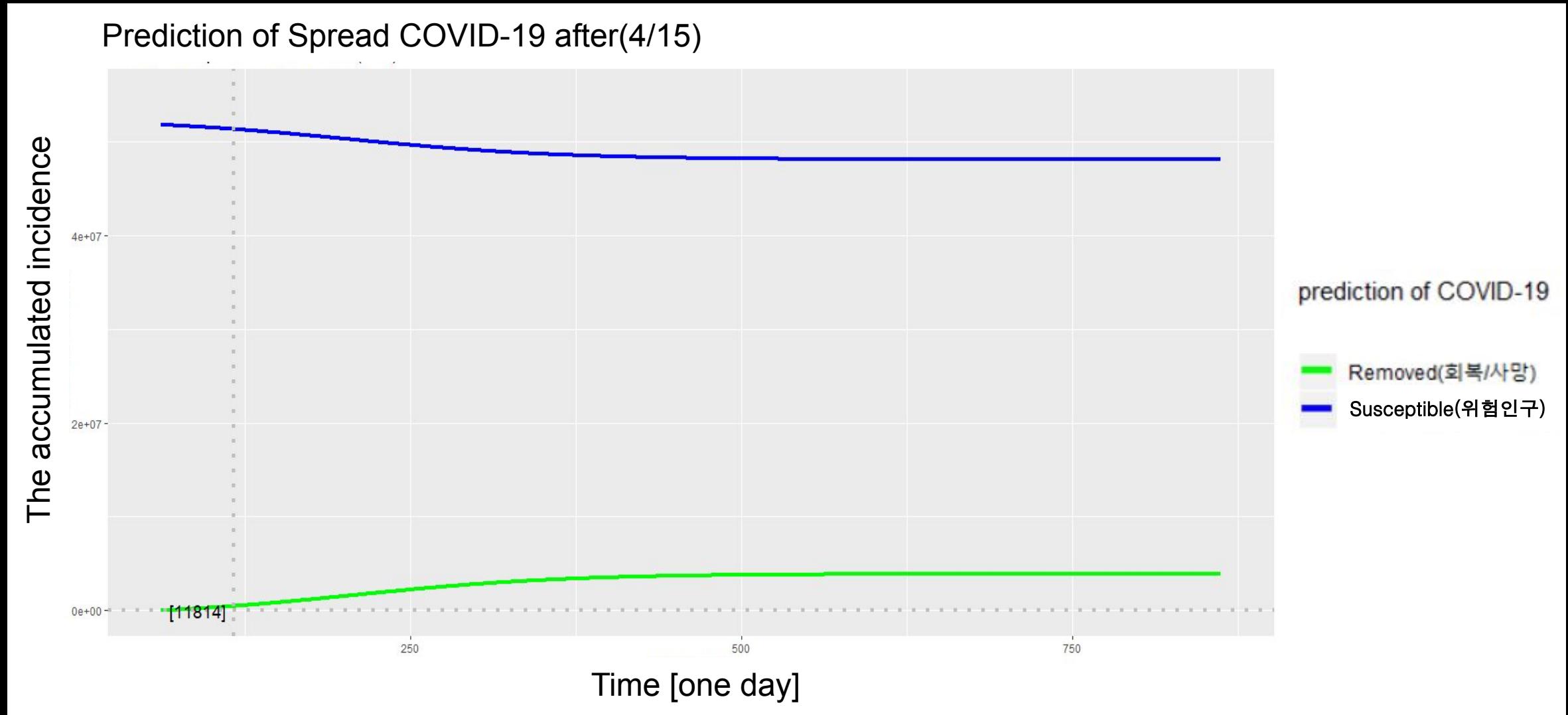
# Result 6. COVID Model 2 – Prediction of Spreading COVID-19



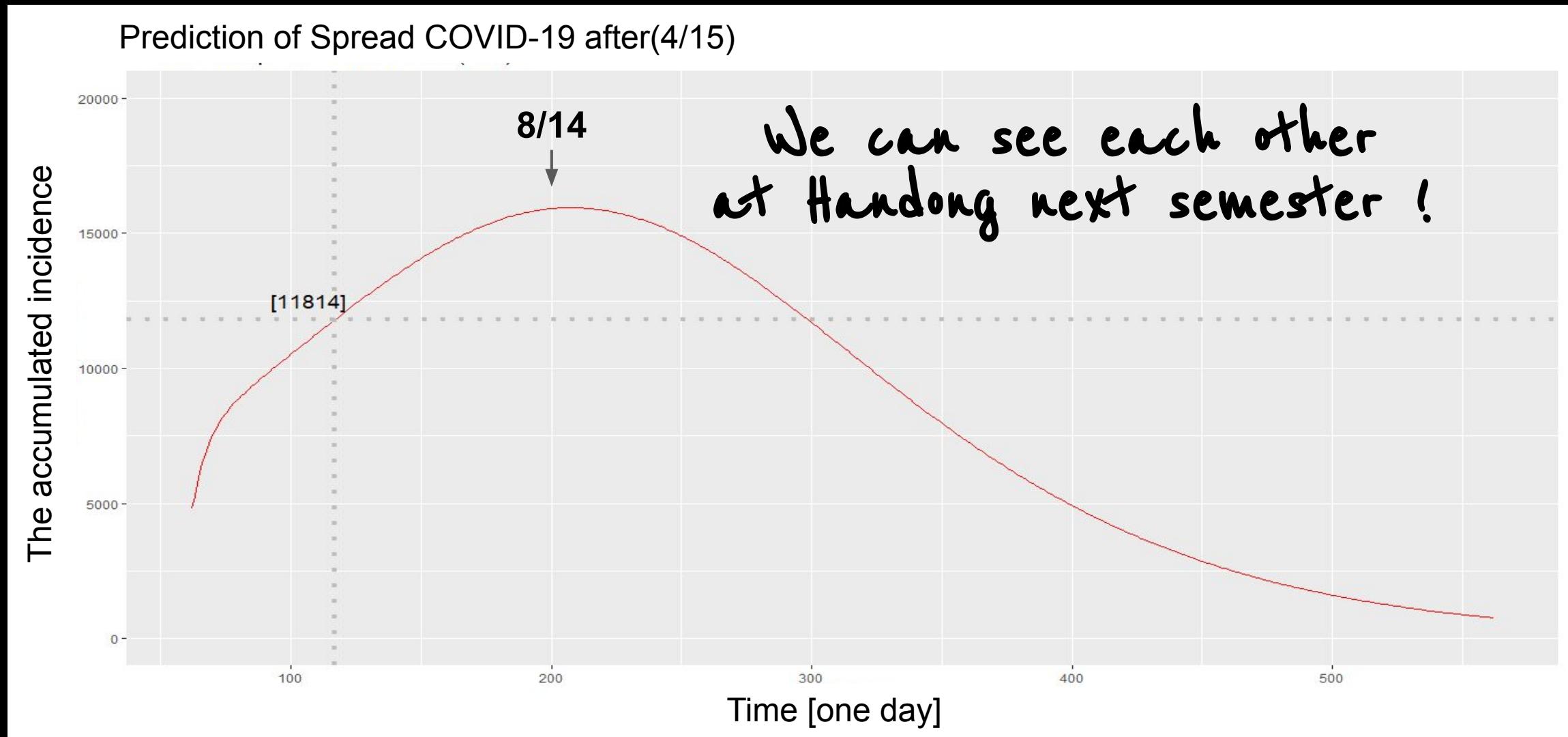
# Result 6. COVID Model 2 – Prediction of Spreading COVID-19



# Result 6. COVID Model 2 – Prediction of Spreading COVID-19



## Result 6. COVID Model 2 – Prediction of Spreading COVID-19





# By using our SEAIHR model,

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- We can predict and prepare demands of commodities such as mask, hand sanitizer.
- We can know which parameters are more significant for decreasing the epidemic spreading.
- We can predict 2020 fall semester will be begin in offline.

# Acknowledgement

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Prof. Ah-Ram Kim ❤️

We appreciate professor Ah-Ram Kim for his advice and feedbacks!

We failed to contact the authors… they didn't answer : (

# Role of Team members

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- Yubin Hong : Make code for modeling, Analyze for modeling result, Apply Mers model to COVID-19
- Danbi Hong : Analyze model equations, Calculate  $R_0$
- Eun Hwangbo : Data cleaning, Make code for modeling



Thank you