

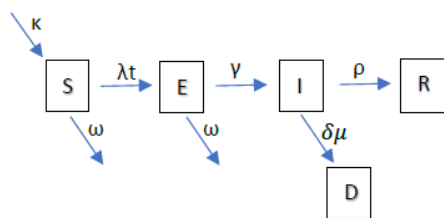
The estimated effect of infectiousness from asymptomatic population and its impact on the outcomes of COVID-19 epidemics in Wuhan, China: a modelling study

Introduction

In December, 2019, the severe acute respiratory syndrome coronavirus 2 (SARS-Cov-2) emerged in Wuhan, China, and quickly swept across other provinces in China and other countries. Several studies have suggested the effect of COVID-19 transmission coming from asymptomatic populations who have been infected by SAR-Cov-2 virus but show none of the signs of COVID-19 symptoms, like cough, fever or breathing difficulties, during incubation period¹⁻³, indicating great contribution of COVID-19 transmission from these asymptomatic group. However, the specific force of infectiousness from asymptomatic COVID-19-infected patients is still unknown. To investigate the impact of asymptomatic infectiousness of COVID-19, this study tried to project different COVID-19 epidemics in Wuhan, China, under different scenarios of asymptomatic infectiousness by building a deterministic compartmental SEIR model with other parameters reflecting reality situation of pandemics in Wuhan, China, and try to estimate the true effect of asymptomatic infectiousness by sensitivity analysis with the reference of reported case data in Wuhan. Also, this study tried to project the counterfactual scenario of without any intervention under different estimates of asymptomatic infectiousness in Wuhan to see how different asymptomatic infectiousness would influence the natural epidemics of COVID-19.

Methods

To reflect the disease development of COVID-19, I constructed a deterministic compartmental susceptible-exposed-infected-recovered (SEIR) model. This model is very basic and simple, with only 5 compartments: susceptible, exposed, infected, recovered and died. All population in Wuhan who never be infected by SARS-Cov-2 would be considered as susceptible. People who start to be infected would go to exposed phase at first which shows no symptoms of COVID-19 and still be contagious. There are movements of population in and out of Wuhan from susceptible group and movement of population only out of Wuhan from exposed group at the starting period of COVID-19 transmission. The rate of being exposed is decided by the force of infection contributed to both the groups of exposed and infected people. After incubation period, people would go from being exposed to infected and be clinically symptomatic. It is assumed that people in infected phase or symptomatic period are more contagious than people in exposed phase or asymptomatic period. People would be recovered after being infected and it is assumed that those who recover from COVID-19 would be immune to it at least till the end of this year 2020. Besides, people who belongs to severe cases in infected phases would go died. The flow diagram and formulas for this SEIR model is shown below.



$$\begin{aligned}dS/dt &= -\beta(I(t) + \theta E(t))S(t) - \omega S(t) + \kappa S(t) \\dE/dt &= \beta(I(t) + \theta E(t))S(t) - \gamma E(t) - \omega E(t) \\dI/dt &= \gamma E(t) - \rho I(t) - \delta\mu I(t) \\dR/dt &= \rho I(t) \\dD/dt &= \delta\mu I(t)\end{aligned}$$

To mimic the real COVID-19 development along with time in Wuhan, this model is fitted with a series of parameters reflecting what have truly happened in Wuhan from the beginning of the COVID-19 transmission. Several parameters vary in different time periods due to the strict quarantine measures conducted in Wuhan after the outbreak of COVID-19. To show the impact of non-pharmaceutical interventions in Wuhan, the basic reproductive number R_0 is set to be different during three periods

based on the estimation from Kucharski et al⁴. R_0 was 2.2 from December 1, 2019 to January 23, 2020 at the beginning of COVID-19 transmission. After the implementation of travel restriction in Wuhan on January 23, R_0 declined to 1.05 and was assumed to further declined to 0.41 after about two weeks due to the comprehensive shutdown and subsequent rigorous quarantine measures. The variation on R_0 directly impact the changes on the per capital rate of an effective contact per day β and force of infection λt .

The rate of being infected from exposed γ is defined by the average incubation period which was estimated from Backer et al⁵. The rate of recovery ρ and death μ are defined by the average time from symptom onset to hospital discharge and average time from symptom onset to death estimated from Sanche et al⁶. In this model I assume that only severe COVID-19 patients would go died, so the number of people to be died per day is also defined by the fraction of severe cases among all cases δ . According to the official news report in Wuhan⁷, the proportion of severe cases dropped from 0.35 to 0.2 after February 14, 2020, so this change would be reflected on δ . There are population movements among susceptible and exposed groups before the travel restriction in Wuhan. During the beginning of COVID-19 transmission period, the daily rate of traveling out of Wuhan ω was 0.014, and the daily rate of entering Wuhan κ was 0.0086. Both these two transition rates were estimated from the travel data on the Baidu Migration server which was in the appendix of Sanche et al⁶. After the travel restriction, Wuhan is assumed to be a totally closed city without any population movement and these two rates would be 0. This model was run from December 1, 2019 to April 28, 2020 which was total 150 days. Each simulation started with 14000000 susceptible individuals which was around the total population in Wuhan in December, 2019⁶, 150 exposed individuals and 50 infected individuals without any recovered and died individuals based on the assumption at the start of COVID-19 outbreak on the first day of December 2019. The specific value and detail of each parameter is shown on the table below.

Parameters	Values	References
Basic reproductive number, R_0	2.2 (2019-12-01 to 2020-01-23), 1.05 (2020-01-04 to 2020-02-07), 0.41 (after 2020-02-08)	Prem ⁸ , Kucharski et al ⁴ Kucharski et al ⁴ Assumed based on Kucharski et al ⁴
Per capital rate of an effective contact per day, β	1.31×10^{-8} (2019-12-01 to 2020-01-23), 6.25×10^{-9} (2020-01-04 to 2020-02-07), 2.44×10^{-9} (after 2020-02-08)	Inferred based on R_0 above
Fraction of infectiousness acquired from asymptomatic compared with symptomatic, θ	0.25, 0.35, 0.45, 0.55, 0.65, 0.75, 0.85	Assumed
Rate of being infected, γ	1/6.4 day ⁻¹	Backer et al ⁵
Rate of recovery, ρ	1/12 day ⁻¹	Sanche et al ⁶
COVID19-specific death rate, μ	1/16.1 day ⁻¹	Sanche et al ⁶
Proportion of severe cases, δ	0.35 (2019-12-01 to 2020-02-14), 0.2 (after 2020-02-15)	Official news report ⁷
Daily transition rate of population exported from Wuhan, ω	0.014(2019-12-01 to 2020-01-23), 0 (after 2020-01-24)	Appendix on Sanche et al ⁶
Daily transition rate of population imported to Wuhan, κ	0.0086(2019-12-01 to 2020-01-23), 0 (after 2020-01-24)	Appendix on Sanche et al ⁶
Initial number of susceptible, S_0	14000000	Appendix on Sanche et al ⁶
Initial number of exposed, E_0	150	Assumed
Initial number of infected, I_0	50	Assumed

Table: parameters of the COVID-19 susceptible-exposed-infected-recovered model

To explore the uncertainty of the true effect of asymptomatic infectiousness during the COVID-19 transmission in Wuhan, I set a parameter θ which is the fraction of infectiousness in exposed group compared to infected group and set it to be ranged from 0.25 to 0.85 by 0.1. I ran this model with totally 7 different θ to project 7 different outcomes of COVID-19 epidemics from December 1, 2019 to April 28, 2020. Then I compared the output results with the cumulated cases from reported COVID-19 data in Wuhan to estimate the true range of θ by sensitivity analysis. After getting 2 plausible θ estimations among all the 7 θ based on data calibration, I ran the model again with these 2 θ within 350 days to see when the COVID-19 transmission will be eliminated under reasonable estimation of the effect of asymptomatic infectiousness.

Besides, I also ran this SEIR model under the counterfactual scenario of without any intervention in 350 days under the different 7 estimates of θ to see how different effects of asymptomatic infectiousness would impact the natural dynamics of COVID-19 transmission. In the counterfactual scenario, the basic reproductive number R_0 is set to be 2.2 all the time. Population movements in and out of Wuhan exist all the time. The proportion of severe cases is constantly 0.35. After getting the output results from the counterfactual scenario, I calculated the numbers of infections averted (NIA) and percent of infections averted (PIA) to see the epidemiological impact of non-pharmaceutical interventions in Wuhan under the deductive effects of asymptomatic infectiousness during the COVID-19 outbreaks.

Results

The simulations showed that the outcomes of the COVID-19 epidemics with non-pharmaceutical interventions in Wuhan would vary dramatically under different effects of asymptomatic infectiousness based on the numbers of the infected, incidence, cumulated cases and death (figure 1). As the fraction of infectiousness in exposed group compared to infected group increases by 0.1, the numbers of the infected, incidence, cumulated cases and death in each day would be around 2 times the corresponding numbers in previous simulation. These output results proved the essentially huge impact effects of asymptomatic infectiousness on the outcomes of the COVID-19 epidemics.

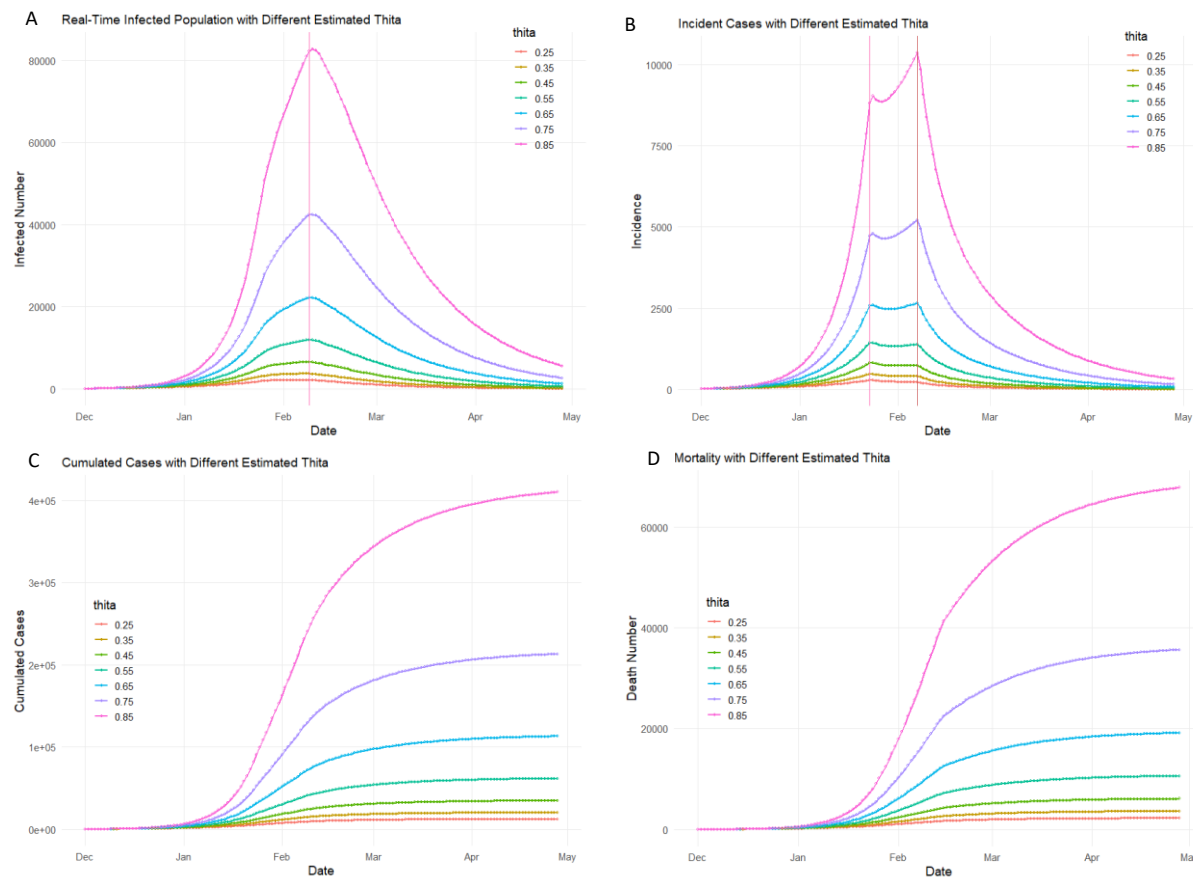


Figure 1: Effects of different asymptomatic infectiousness on the infected (A), incidence (B), cumulated cases (C) and death (D) from December 1, 2019 to April 28, 2020 in Wuhan

Vertical lines on panel A and B represent the dates when most simulations reached the peaks.

Despite the sharp differences on case and death number, the developing trends of the dynamics curves on the infected, incidence, cumulated cases and death under different effects of asymptomatic infectiousness are overall similar along with the time. The peaks of the numbers of the infected and incidence appeared to be around the same dates respectively under different simulations (figure 1 A B). The peak of infected number is mostly appeared on February 9, 2020 in 3 simulations, on February 10, 2020 in 2 simulations and on February 6 and 8, 2020 in 2 simulations. All simulations reached their 2 peaks of incidence cases on January 23 and February 7, 2020 respectively (except that the simulation when θ is 0.55 reached its first peaks on January 24, 2020), which both are the time point of R_0 changing. This showed that the non-pharmaceutical interventions in Wuhan effectively impeded the amplification of COVID-19 transmission.

After fitting the report data of cumulated cases in Wuhan, the fraction of asymptomatic infectiousness compared to symptomatic infectiousness is estimated from 0.45 to 0.55 (figure 2 A). Considering the unreported and missing case data during COVID-19 outbreaks in Wuhan, the fraction of asymptomatic infectiousness compared to symptomatic infectiousness should be close to or even potentially somewhat exceed 0.55. The cumulated cases from reported data in Wuhan was 50333 cases on April 28, 2020, while that from the simulations when θ are 0.45 and 0.55 were 34790 and 61750 cases, respectively. The true curve of cumulated cases in Wuhan should be not as steep as the curve generated by reported data and possibly sitting around the 2 curves generated by these 2 simulations, because on February 12, 2020 there was a surged increase on the incidence which was more than 13000 cases as it suddenly included all the previous cases with COVID-19 symptoms and chest X-ray images but without confirmed positive nucleotide testing due to the changing criteria of case inclusion. Actually, the large amount of incident cases from this date should be distributed among the previous dates to account for the fact of incidence development.

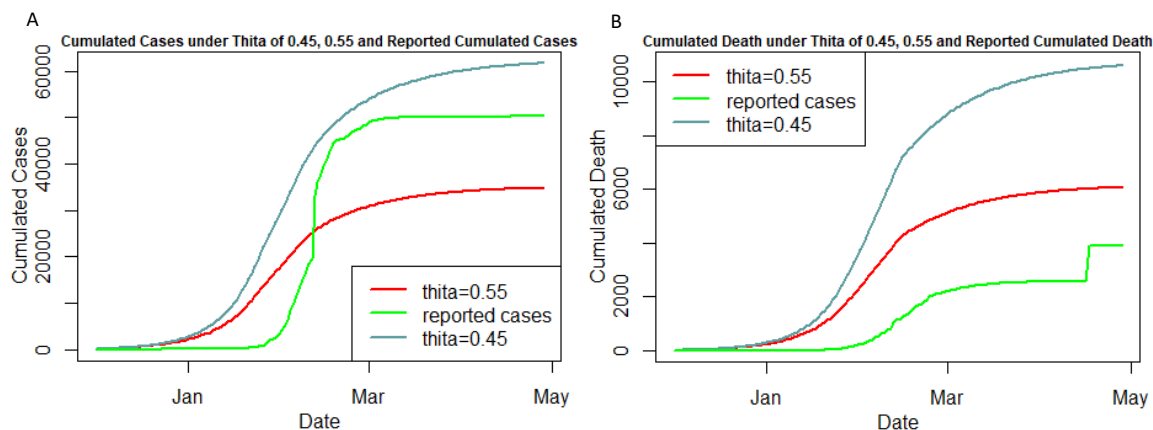


Figure 2: Cumulated cases (A) and death (B) when $\theta = 0.45$ and 0.55 with the corresponding reported data in Wuhan

However, the calibration for cumulated death was not fitted so well (figure 2 B). The cumulated death from reported data in Wuhan was 3869 on April 28, 2020, while that from the simulations when θ are 0.45 and 0.55 were 6070 and 10606 respectively, which were both much more higher than that in reported data. This may due to the imperfect estimation of the parameters about COVID-19 mortality in the previous model. For example, the people in the infected phase that would go to die may not include all the severe cases but extremely severe cases so the proportion δ would be smaller and the simulation of cumulated death would correspond to reported data. Due to the lack of credible information, I did not change this parameter at last, but I tried to run these 2 simulations with a smaller δ which fitted the cumulated death in reported data and saw that the results of cumulated cases were still corresponding to the reported data when θ are 0.45 and 0.55. Hence, it is reasonable to say that the infectiousness

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acquired from the asymptomatic population is around 0.45 to 0.55 times the infectiousness acquired from the symptomatic population.

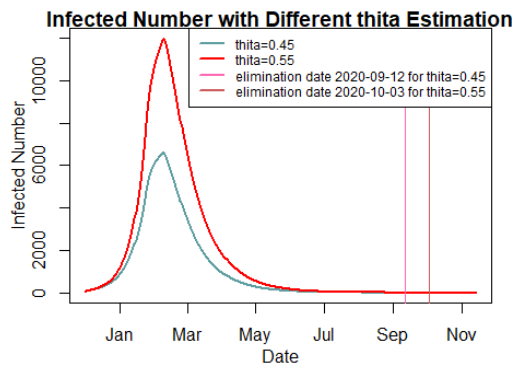


Figure 3: Infected number from December 1, 2019 to November 14, 2020 when $\theta = 0.45$ and 0.55

Assumed the deductive asymptomatic infectiousness above, I found that the COVID-19 transmission in Wuhan would be eliminated between September 12 and October 3, 2020 (figure 3), based on the date when the infected number smaller than 1.

Nevertheless, the simulations under the counterfactual scenario of without any intervention were sharply different with previous simulations considering the quarantine effects in Wuhan (figure 4). All the numbers in the infected, incidence, cumulated cases and death without any intervention are much more higher than those under intervention. What is interesting is that when there is not any intervention the time to reach the

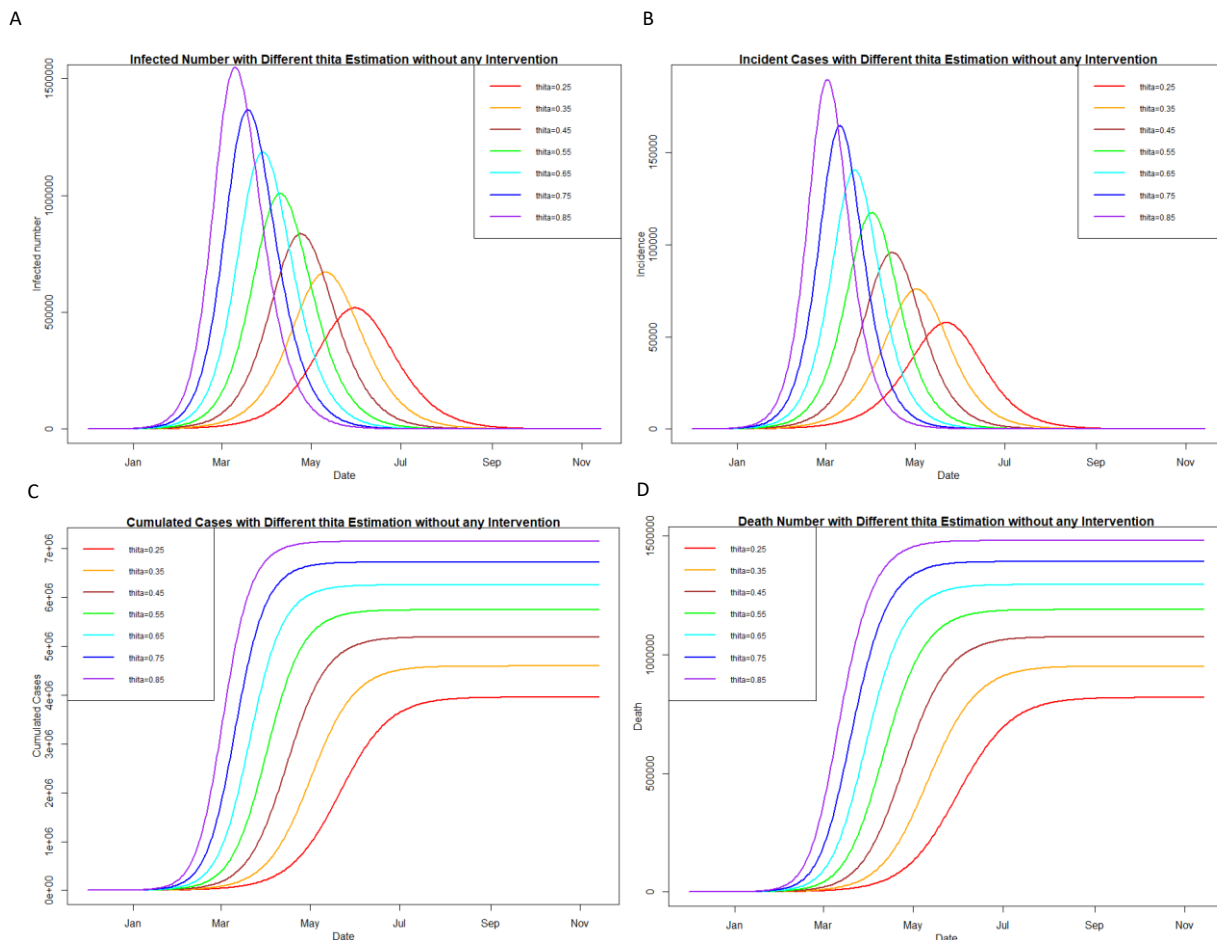


Figure 4: Effects of different asymptomatic infectiousness on the infected (A), incidence (B), cumulated cases (C) and death (D) under the counterfactual scenario of without any intervention from December 1, 2019 to November 14, 2020 in Wuhan

peaks of infected and incidence numbers are totally different among each different effect of asymptomatic infectiousness (figure 4 A B). The larger the effect of asymptomatic infectiousness, the earlier the infected and incidence numbers would reach the peaks, and the shorter period the outbreak

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would last. The NIA comparing the true and counterfactual scenarios when θ is 0.45 is 5157424 and 5684059 when θ is 0.55. The PIA comparing the true and counterfactual scenarios when θ is 0.45 is 99.32% and 98.91% when θ is 0.55. This proved that with the implementation of the rigorous quarantine interventions in Wuhan, the timeline and the magnitude of dynamics of the COVID-19 outbreak and transmission have been controlled really well compared to the counterfactual scenario of without any intervention.

Discussion

This study provided a good estimate of the effect of asymptomatic infectiousness and its impact on the dynamics of the COVID-19 outbreak in Wuhan by sensitivity analysis, while at the same time evaluated the effects of the whole non-pharmaceutical interventions on the control of COVID-19 transmission in Wuhan. The highlights in this study is using time-varying parameters to reflect the implementation of the interventions conducted in Wuhan. However, there are still many limitations in this study. First, this SEIR model is too generous and simple, without considering any risk heterogeneity of being infected like partition on different age groups in many other COVID-19 modeling studies⁸. Second, this model can only be applied based on the assumption that all the people who infected with SARS-Cov-2 would go to the disease progress from being asymptomatic to symptomatic, but a recent study has proved that there was true existence of individuals who did not show any symptom along all the course of the COVID-19 infection checking by posterior antibody testing⁹. Last, some parameters in this study like the proportion of cases which would go to die may still need to be optimized or amended after there are more information supporting the true parameters of COVID-19 transmission in Wuhan.

References

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R code

```
library(EpiModel)

library(ggplot2)

covid19_SEIR <- function(t, t0, parms) {
  with(as.list(c(t0, parms)), {
    ## Derived values
    num <- s.num + e.num + i.num + r.num
    R0 <- 2.2
    if (t >= 55) {
      R0 <- 1.05
    }
    if (t >= 70) {
      R0 <- 0.41
    }

    omega <- 200000/14000000
    kappa <- 0.6*omega

    if (t >= 55) {
      omega <- 0
    }
    beta <- R0/(num*i.dur)
    lambda <- beta * (i.num + thita*e.num)
    gamma <- 1/e.dur
    rho <- 1/i.dur
    severe_prop <- 0.35
    if (t >= 77) {
      severe_prop <- 0.2
    }

    ## Differential equations
    dS <- -lambda*s.num - omega*s.num + kappa*s.num
    dE <- lambda*s.num - gamma*e.num - omega*e.num
    dI <- gamma*e.num - rho*i.num - severe_prop*muI*i.num
    dR <- rho*i.num
    dD <- severe_prop*muI*i.num

    ## Output
    list(c(dS, dE, dI, dR, dD,
          se.flow = lambda * s.num,
          ei.flow = gamma * e.num,
          ir.flow = rho * i.num))
  })
}

param <- param.dcm(e.dur = 6.4, i.dur = 12, thita = c(0.25,0.35,0.45,0.55,0.65,0.75,0.85), muI = 1/16.1)
init <- init.dcm(s.num = 14000000, e.num = 150, i.num = 50, r.num = 0, d.num = 0,
                se.flow = 0, ei.flow = 0, ir.flow = 0)
control <- control.dcm(nsteps = 150, dt = 1, new.mod = covid19_SEIR)

mod <- dcm(param, init, control)

mod
df_covid19 <- as.data.frame(mod)
#Adding the variable of date into the dataframe
df_covid19$date <- format(seq(as.Date("2019-12-01"), as.Date("2020-04-28"), by = "1 day"))
df_covid19$date <- as.Date(df_covid19$date)
#Adding the variable of thita into the dataframe
df_covid19$thita[df_covid19$run == 1] <- 0.25
df_covid19$thita[df_covid19$run == 2] <- 0.35
df_covid19$thita[df_covid19$run == 3] <- 0.45
df_covid19$thita[df_covid19$run == 4] <- 0.55
```


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```
df_covid19$thita[df_covid19$run == 5] <- 0.65
df_covid19$thita[df_covid19$run == 6] <- 0.75
df_covid19$thita[df_covid19$run == 7] <- 0.85
df_covid19$thita <- as.factor(df_covid19$thita)

##Adding the variable of cumulated cases into dataframe
df_covid19$cum_cases[1]<- df_covid19$i.num[1] + df_covid19$ei.flow[1]
df_covid19$cum_cases[151]<- df_covid19$i.num[1] + df_covid19$ei.flow[151]
df_covid19$cum_cases[301]<- df_covid19$i.num[1] + df_covid19$ei.flow[301]
df_covid19$cum_cases[451]<- df_covid19$i.num[1] + df_covid19$ei.flow[451]
df_covid19$cum_cases[601]<- df_covid19$i.num[1] + df_covid19$ei.flow[601]
df_covid19$cum_cases[751]<- df_covid19$i.num[1] + df_covid19$ei.flow[751]
df_covid19$cum_cases[901]<- df_covid19$i.num[1] + df_covid19$ei.flow[901]

for (i in (1:1049)){
  if (df_covid19$thita[i] == df_covid19$thita[i+1]){
    df_covid19$cum_cases[i+1] <- df_covid19$cum_cases[i] + df_covid19$ei.flow[i+1]}
  else if (df_covid19$thita[i] != df_covid19$thita[i+1]){
    df_covid19$cum_cases[i+1] <- df_covid19$i.num[1] + df_covid19$ei.flow[i+1]
  }}

##Draw the pictures of the COVID-19 dynamics from the 7 simulations by ggplot2
p1 <- ggplot(df_covid19, aes(date, i.num, group=thita, color = thita)) +
  geom_line(size = 0.8) +
  geom_point(pch = 21, size = 1) +
  theme_minimal(base_size = 14) +
  theme(
    panel.grid.minor = element_blank(),
    legend.position = c(0.9,0.85),
    plot.margin = margin(3,15,3,3,"mm")
  ) +
  labs(x = "Date", y= "Infected Number",
    subtitle = "Real-Time Infected Population with Different Estimated Thita")
p1

p2 <- ggplot(df_covid19, aes(date, ei.flow, group=thita, color = thita)) +
  geom_line(size = 0.8) +
  geom_point(pch = 21, size = 1) +
  theme_minimal(base_size = 14) +
  theme(
    panel.grid.minor = element_blank(),
    legend.position = c(0.9,0.85),
    plot.margin = margin(3,15,3,3,"mm")
  ) +
  labs(x = "Date", y= "Incidence",
    subtitle = "Incident Cases with Different Estimated Thita")
p2

p3 <- ggplot(df_covid19, aes(date, cum_cases, group = thita, color = thita)) +
  geom_line(size = 0.8) +
  geom_point(pch = 21, size = 1) +
  theme_minimal(base_size = 14) +
  theme(
    panel.grid.minor = element_blank(),
    legend.position = c(0.1,0.5),
    plot.margin = margin(3,15,3,3,"mm")
  ) +
  labs(x = "Date", y= "Cumulated Cases",
    subtitle = "Cumulated Cases with Different Estimated Thita")
p3

p4 <- ggplot(df_covid19, aes(date, d.num, group = thita, color = thita)) +
  geom_line(size = 0.8) +
  geom_point(pch = 21, size = 1) +
  theme_minimal(base_size = 14) +
  theme(
    panel.grid.minor = element_blank(),
    legend.position = c(0.1,0.5),
```

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```
plot.margin = margin(3,15,3,3,"mm")
) +
labs(x = "Date", y= "Death Number",
      subtitle = "Mortality with Different Estimated Thita")
p4

##Define the dates when infected number and incidence reach the peaks
df_covid19$date[which.max(df_covid19$i.num[df_covid19$thita==0.25])] #2020-02-06

df_covid19$date[which.max(df_covid19$i.num[df_covid19$thita==0.35])] #2020-02-08

df_covid19$date[which.max(df_covid19$i.num[df_covid19$thita==0.45])] #2020-02-09

df_covid19$date[which.max(df_covid19$i.num[df_covid19$thita==0.55])] #2020-02-09

df_covid19$date[which.max(df_covid19$i.num[df_covid19$thita==0.65])] #2020-02-09

df_covid19$date[which.max(df_covid19$i.num[df_covid19$thita==0.75])] #2020-02-10

df_covid19$date[which.max(df_covid19$i.num[df_covid19$thita==0.85])] #2020-02-10

df_covid19$date[which.max(df_covid19$ei.flow[df_covid19$thita==0.25])] #2020-01-23

df_covid19$date[which.max(df_covid19$ei.flow[df_covid19$thita==0.35])] #2020-01-23

df_covid19$date[which.max(df_covid19$ei.flow[df_covid19$thita==0.45])] #2020-01-23

df_covid19$date[which.max(df_covid19$ei.flow[df_covid19$thita==0.55])] #2020-01-24

df_covid19$date[which.max(df_covid19$ei.flow[df_covid19$thita==0.65])] #2020-02-07

df_covid19$date[which.max(df_covid19$ei.flow[df_covid19$thita==0.75])] #2020-02-07

df_covid19$date[which.max(df_covid19$ei.flow[df_covid19$thita==0.25])] #2020-02-07

#Add the vertical lines of dates when reaching the peaks
p1 + geom_vline(xintercept = as.Date("2020-02-09"), col="hotpink")

p2 + geom_vline(xintercept = as.Date("2020-01-23"), col="hotpink") +
      geom_vline(xintercept= as.Date("2020-02-07"), col="indianred")

library(nCov2019)#a new package that can crawl the updated COVID-19 reported data

wh <- subset(x['Hubei'], city == 'Wuhan') #creat the dataframe of reported

#Draw the curves of cumulated cases calibrated with reported data
max(df_covid19$cum_cases[df_covid19$thita==0.55]) #help define the ylim

par(mfrow = c(1,1), mar = c(3,3,1,1), mgp = c(2,1,0))
plot(df_covid19$date[df_covid19$thita==0.45],df_covid19$cum_cases[df_covid19$thita==0.45],
      ylim = c(0,61800), type="l", col="red",lwd=2, xlab="Date", ylab="Cumulated Cases")
title(main="Cumulated Cases under Thita of 0.45, 0.55 and Reported Cumulated Cases", cex.main=0.78)
lines(df_covid19$date[df_covid19$thita==0.55],df_covid19$cum_cases[df_covid19$thita==0.55], type="l", col=
"cadetblue",lwd=2)
lines(wh$time[1:150],wh$cum_confirm[1:150], type="l", col="green", lwd=2)
legend("bottomright", legend = c("thita=0.55","reported cases","thita=0.45"),
      col=c("red","green","cadetblue"),lty = 1, lwd = 2)

#Draw the curves of death calibrated with reported data
max(df_covid19$d.num[df_covid19$thita==0.55]) #help define the ylim

par(mfrow = c(1,1), mar = c(3,3,1,1), mgp = c(2,1,0))
plot(df_covid19$date[df_covid19$thita==0.45],df_covid19$d.num[df_covid19$thita==0.45],ylim=c(0,10700),
      type="l", col="red",lwd=2,xlab="Date", ylab="Cumulated Death")
title(main="Cumulated Death under Thita of 0.45, 0.55 and Reported Cumulated Death", cex.main=0.78)
lines(df_covid19$date[df_covid19$thita==0.55],df_covid19$d.num[df_covid19$thita==0.55], type="l", col="cad
etblue",lwd=2)
```

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```
lines(wh$time[1:150], wh$cum_dead[1:150], type="l", col="green", lwd=2)
legend("topleft", legend = c("thita=0.55", "reported cases", "thita=0.45"), col=c("red", "green", "cadetblue"), lty = 1, lwd = 2)

##Change the simulating days to 350
control <- control.dcm(nsteps = 350, dt=1, new.mod = covid19_SEIR)

mod <- dcm(param, init, control)

covid19_SEIR_350 <- as.data.frame(mod)
covid19_SEIR_350$date <- format(seq(as.Date("2019-12-01"), as.Date("2020-11-14"), by = "1 day"))
covid19_SEIR_350$date <- as.Date(covid19_SEIR_350$date)
covid19_SEIR_350$thita[covid19_SEIR_350$run == 1] <- 0.25
covid19_SEIR_350$thita[covid19_SEIR_350$run == 2] <- 0.35
covid19_SEIR_350$thita[covid19_SEIR_350$run == 3] <- 0.45
covid19_SEIR_350$thita[covid19_SEIR_350$run == 4] <- 0.55
covid19_SEIR_350$thita[covid19_SEIR_350$run == 5] <- 0.65
covid19_SEIR_350$thita[covid19_SEIR_350$run == 6] <- 0.75
covid19_SEIR_350$thita[covid19_SEIR_350$run == 7] <- 0.85

#See when the COVID-19 would be eliminated
covid19_SEIR_350$date[which(covid19_SEIR_350$i.num[covid19_SEIR_350$thita==0.45] < 1)[1]] #2020-09-12
covid19_SEIR_350$date[which(covid19_SEIR_350$i.num[covid19_SEIR_350$thita==0.55] < 1)[1]] #2020-10-03

max(covid19_SEIR_350$i.num[covid19_SEIR_350$thita==0.55])

plot(covid19_SEIR_350$date[covid19_SEIR_350$thita==0.45], covid19_SEIR_350$i.num[covid19_SEIR_350$thita==0.45],
     ylim=c(0,12000), type="l", col="cadetblue", lwd=2, xlab="Date", ylab="Infected Number",
     main="Infected Number with Different thita Estimation")
lines(covid19_SEIR_350$date[covid19_SEIR_350$thita==0.55], covid19_SEIR_350$i.num[covid19_SEIR_350$thita==0.55], col="red", lwd=2)
abline(v= as.Date("2020-09-12"), col="hotpink")
abline(v= as.Date("2020-10-03"), col="indianred")
legend("topright", legend = c("thita=0.45", "thita=0.55", "elimination date 2020-09-12 for thita=0.45",
                             "elimination date 2020-10-03 for thita=0.55" ),
      col = c("cadetblue", "red", "hotpink", "indianred"), lty = 1, lwd = 2, cex = 0.75)

#Build the counterfactual model without any intervention
covid19_SEIR <- function(t, t0, parms) {
  with(as.list(c(t0, parms)), {
    ## Derived values
    num <- s.num + e.num + i.num + r.num
    R0 <- 2.2

    omega <- 200000/14000000
    kappa <- 0.6*omega

    beta <- R0/(num*i.dur)
    lambda <- beta * (i.num + thita*e.num)
    gamma <- 1/e.dur
    rho <- 1/i.dur
    severe_prop <- 0.35

    ## Differential equations
    dS <- -lambda*s.num - omega*s.num + kappa*s.num
    dE <- lambda*s.num - gamma*e.num - omega*e.num
    dI <- gamma*e.num - rho*i.num - severe_prop*muI*i.num
    dR <- rho*i.num
    dD <- severe_prop*muI*i.num

    ## Output
    list(c(dS, dE, dI, dR, dD,
          se.flow = lambda * s.num,
          ei.flow = gamma * e.num,
          ir.flow = rho * i.num))
```

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```
  })
}

param <- param.dcm(e.dur = 6.4, i.dur = 12, thita = c(0.25,0.35,0.45,0.55,0.65,0.75,0.85), muI = 1/16.1)
init <- init.dcm(s.num = 1400000, e.num = 150, i.num = 50, r.num = 0, d.num=0,
               se.flow = 0, ei.flow = 0, ir.flow = 0)
control <- control.dcm(nsteps = 350, dt=1, new.mod = covid19_SEIR)

mod <- dcm(param, init, control)

df_nointervention <- as.data.frame(mod)
#Adding the variable of date into the dataframe
df_nointervention$date <- format(seq(as.Date("2019-12-01"), as.Date("2020-11-14"), by = "1 day"))
df_nointervention$date <- as.Date(df_nointervention$date)
#Adding the variable of thita into the dataframe
df_nointervention$thita[df_nointervention$run == 1] <- 0.25
df_nointervention$thita[df_nointervention$run == 2] <- 0.35
df_nointervention$thita[df_nointervention$run == 3] <- 0.45
df_nointervention$thita[df_nointervention$run == 4] <- 0.55
df_nointervention$thita[df_nointervention$run == 5] <- 0.65
df_nointervention$thita[df_nointervention$run == 6] <- 0.75
df_nointervention$thita[df_nointervention$run == 7] <- 0.85

##Adding the variable of cumulated cases into dataframe
df_nointervention$cum_cases[1]<- df_nointervention$i.num[1] + df_nointervention$ei.flow[1]
df_nointervention$cum_cases[351]<- df_nointervention$i.num[1] + df_nointervention$ei.flow[351]
df_nointervention$cum_cases[701]<- df_nointervention$i.num[1] + df_nointervention$ei.flow[701]
df_nointervention$cum_cases[1051]<- df_nointervention$i.num[1] + df_nointervention$ei.flow[1051]
df_nointervention$cum_cases[1401]<- df_nointervention$i.num[1] + df_nointervention$ei.flow[1401]
df_nointervention$cum_cases[1751]<- df_nointervention$i.num[1] + df_nointervention$ei.flow[1751]
df_nointervention$cum_cases[2101]<- df_nointervention$i.num[1] + df_nointervention$ei.flow[2101]

for (i in (1:2449)){
  if (df_nointervention$thita[i] == df_nointervention$thita[i+1]){
    df_nointervention$cum_cases[i+1] <- df_nointervention$cum_cases[i] + df_nointervention$ei.flow[i+1]}
  else if (df_nointervention$thita[i] != df_nointervention$thita[i+1]){
    df_nointervention$cum_cases[i+1] <- df_nointervention$i.num[1] + df_nointervention$ei.flow[i+1]
  }}

##Draw the pictures of the COVID-19 dynamics from the 7 simulations without any intervention
max(df_nointervention$i.num)

plot(df_nointervention$date[df_nointervention$run==1], df_nointervention$i.num[df_nointervention$run==1],
     ylim=c(0, 1500000),
     type="l", col="red", lwd=2, xlab="Date", ylab="Infected number",
     main="Infected Number with Different thita Estimation without any Intervention")
lines(df_nointervention$date[df_nointervention$run==2], df_nointervention$i.num[df_nointervention$run==2],
     col="orange", lwd=2)
lines(df_nointervention$date[df_nointervention$run==3], df_nointervention$i.num[df_nointervention$run==3],
     col="brown", lwd=2)
lines(df_nointervention$date[df_nointervention$run==4], df_nointervention$i.num[df_nointervention$run==4],
     col="green", lwd=2)
lines(df_nointervention$date[df_nointervention$run==5], df_nointervention$i.num[df_nointervention$run==5],
     col="cyan", lwd=2)
lines(df_nointervention$date[df_nointervention$run==6], df_nointervention$i.num[df_nointervention$run==6],
     col="blue", lwd=2)
lines(df_nointervention$date[df_nointervention$run==7], df_nointervention$i.num[df_nointervention$run==7],
     col="purple", lwd=2)
legend("topright", legend = c("thita=0.25", "thita=0.35", "thita=0.45", "thita=0.55", "thita=0.65", "thita=0.75", "thita=0.85"),
     col = c("red", "orange", "brown", "green", "cyan", "blue", "purple"), lty = 1, lwd = 2, cex=0.75)

max(df_nointervention$ei.flow)

plot(df_nointervention$date[df_nointervention$run==1], df_nointervention$ei.flow[df_nointervention$run==1],
     ylim=c(0, 190000),
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```
    type="l", col="red",lwd=2,xlab="Date", ylab="Incidence",
    main="Incident Cases with Different thita Estimation without any Intervention")
lines(df_nointervention$date[df_nointervention$run==2], df_nointervention$ei.flow[df_nointervention$run==
2], col="orange", lwd=2)
lines(df_nointervention$date[df_nointervention$run==3], df_nointervention$ei.flow[df_nointervention$run==
3], col="brown", lwd=2)
lines(df_nointervention$date[df_nointervention$run==4], df_nointervention$ei.flow[df_nointervention$run==
4], col="green", lwd=2)
lines(df_nointervention$date[df_nointervention$run==5], df_nointervention$ei.flow[df_nointervention$run==
5], col="cyan", lwd=2)
lines(df_nointervention$date[df_nointervention$run==6], df_nointervention$ei.flow[df_nointervention$run==
6], col="blue", lwd=2)
lines(df_nointervention$date[df_nointervention$run==7], df_nointervention$ei.flow[df_nointervention$run==
7], col="purple", lwd=2)
legend("topright", legend = c("thita=0.25", "thita=0.35", "thita=0.45", "thita=0.55", "thita=0.65", "thita=0.7
5", "thita=0.85"),
      col = c("red", "orange", "brown", "green", "cyan", "blue", "purple"), lty = 1, lwd = 2, cex=0.75)

max(df_nointervention$cum_cases)

plot(df_nointervention$date[df_nointervention$run==1], df_nointervention$cum_cases[df_nointervention$run==
1], ylim=c(0, 7151400),
     type="l", col="red",lwd=2,xlab="Date", ylab="Cumulated Cases",
     main="Cumulated Cases with Different thita Estimation without any Intervention")
lines(df_nointervention$date[df_nointervention$run==2], df_nointervention$cum_cases[df_nointervention$run==
2], col="orange", lwd=2)
lines(df_nointervention$date[df_nointervention$run==3], df_nointervention$cum_cases[df_nointervention$run==
3], col="brown", lwd=2)
lines(df_nointervention$date[df_nointervention$run==4], df_nointervention$cum_cases[df_nointervention$run==
4], col="green", lwd=2)
lines(df_nointervention$date[df_nointervention$run==5], df_nointervention$cum_cases[df_nointervention$run==
5], col="cyan", lwd=2)
lines(df_nointervention$date[df_nointervention$run==6], df_nointervention$cum_cases[df_nointervention$run==
6], col="blue", lwd=2)
lines(df_nointervention$date[df_nointervention$run==7], df_nointervention$cum_cases[df_nointervention$run==
7], col="purple", lwd=2)
legend("topleft", legend = c("thita=0.25", "thita=0.35", "thita=0.45", "thita=0.55", "thita=0.65", "thita=0.75
", "thita=0.85"),
      col = c("red", "orange", "brown", "green", "cyan", "blue", "purple"), lty = 1, lwd = 2, cex=0.75)

max(df_nointervention$d.num)

plot(df_nointervention$date[df_nointervention$run==1], df_nointervention$d.num[df_nointervention$run==1],
ylim=c(0, 1480000),
     type="l", col="red",lwd=2,xlab="Date", ylab="Death",
     main="Death Number with Different thita Estimation without any Intervention")
lines(df_nointervention$date[df_nointervention$run==2], df_nointervention$d.num[df_nointervention$run==2],
col="orange", lwd=2)
lines(df_nointervention$date[df_nointervention$run==3], df_nointervention$d.num[df_nointervention$run==3],
col="brown", lwd=2)
lines(df_nointervention$date[df_nointervention$run==4], df_nointervention$d.num[df_nointervention$run==4],
col="green", lwd=2)
lines(df_nointervention$date[df_nointervention$run==5], df_nointervention$d.num[df_nointervention$run==5],
col="cyan", lwd=2)
lines(df_nointervention$date[df_nointervention$run==6], df_nointervention$d.num[df_nointervention$run==6],
col="blue", lwd=2)
lines(df_nointervention$date[df_nointervention$run==7], df_nointervention$d.num[df_nointervention$run==7],
col="purple", lwd=2)
legend("topleft", legend = c("thita=0.25", "thita=0.35", "thita=0.45", "thita=0.55", "thita=0.65", "thita=0.75
", "thita=0.85"),
      col = c("red", "orange", "brown", "green", "cyan", "blue", "purple"), lty = 1, lwd = 2, cex=0.75)

##Calculate the NIA and PIA of COVID-19 comparing with having and no intervention
cum_inc_0.45 <- sum(covid19_SEIR_350$ei.flow[covid19_SEIR_350$thita == 0.45]) + covid19_SEIR_350$i.num[1]
cum_inc_0.45_nointv <- sum(df_nointervention$ei.flow[df_nointervention$thita == 0.45]) + df_nointervention
$i.num[1]
NIA_0.45 <- cum_inc_0.45_nointv - cum_inc_0.45
```

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```
PIA_0.45 <- NIA_0.45 / cum_inc_0.45_nointv
cum_inc_0.45 #35215

cum_inc_0.45_nointv #5192639

NIA_0.45 #5157424

PIA_0.45 #0.9932184

cum_inc_0.55 <- sum(covid19_SEIR_350$ei.flow[covid19_SEIR_350$thita==0.55]) + covid19_SEIR_350$i.num[1]
cum_inc_0.55_nointv <- sum(df_nointervention$ei.flow[df_nointervention$thita==0.55]) + df_nointervention
$i.num[1]
NIA_0.55 <- cum_inc_0.55_nointv - cum_inc_0.55
PIA_0.55 <- NIA_0.55 / cum_inc_0.55_nointv
cum_inc_0.55 #62548

cum_inc_0.55_nointv #5746607

NIA_0.55 #5684059

PIA_0.55 #0.9891157
```