Susceptible, Exposed, Infected and Removed (SEIR) model for Coronavirus spread. The Pullman introduction case

by: Omar E. Cornejo, PhD (School of Biological Sciences).
March 11, 2020

Most models I have seen to this date focusing on SARS-CoV-2 are of the SEIR type. Something to be recognized is that there is a lot of variability in the estimates of R_0 ranging from 2 to 3.5 Most of the estimates seem to converge towards $R_0 = 2.5$. So I am going to assume that this is a reasonable estimate. A modified SEIR model from influenza has been used to estimate the number of cases progression in Wuhan[1]:

$$\dot{S} = -\beta SI/N \tag{1}$$
$$\dot{E} = \beta SI/N - \sigma E \tag{2}$$
$$\dot{I} = \sigma E - \gamma I \tag{3}$$
$$\dot{R} = \gamma I \tag{4}$$
$$N = S + E + I + R \tag{5}$$

where β is the transmission rate, σ is the infection rate (development of infection) and it is usually estimated as the inverse of the incubation period, and γ is the recovery rate estimated as the inverse of the infectious period.

For this we need to make reasonable assumptions about incubation period and the infectious period. It has been assumed that $\sigma = 1/5.2$ under the estimation that the incubation period is 5.2 days[2]. In Wuhan, it was estimated that hospitalization period of recovered patients was 12.39$\pm$ 4.77 days[3,4]. For simplicity we assume the ceiling of the infectious period to be then 17.16 and $\gamma = 1/17.16$.

R_0 is usually estimated as the leading eigenvalue from the FV^{-1} matrix that describes the terms for the acquisition of the infections and the transition between states. In the simplest SEIR model that does not consider the age structure we can then simply describe it as:

$R_0 = \frac{\beta\sigma}{\sigma(\gamma+\mu)}$

The transmission rate then can be estimated from the relationship $\beta = R_0\gamma$ from this model. Given that the mean R_0 has been estimated to be 2.5 across multiple studies[1,2,5,6], we can safely assume that $\beta = 2.5/17.16 = 0.146$.

All scenarios were examined using simulations in R 3.6.4 using the odeSolve package to explore numerically the dynamics.

To set the starting point for the simulations we assume that the Susceptible population of Pullman follows the census data available at https://datausa.io/profile/geo/pullman-wa (Figure 1). We will assume that the total number of individuals is 32,382. We perform simulations under three different introduction scenarios, all assuming that exposed individuals travel from the west side to Pullman. The two scenarios assume: i) that 1 exposed individual ($E_b = 1$) introduces the disease to town;and ii) that 10 exposed individuals ($E_b = 10$) introduce the disease to town. (I considered the third scenario that 100 exposed individuals, $E_b = 100$, introduce the disease to town, but it seem to bad).

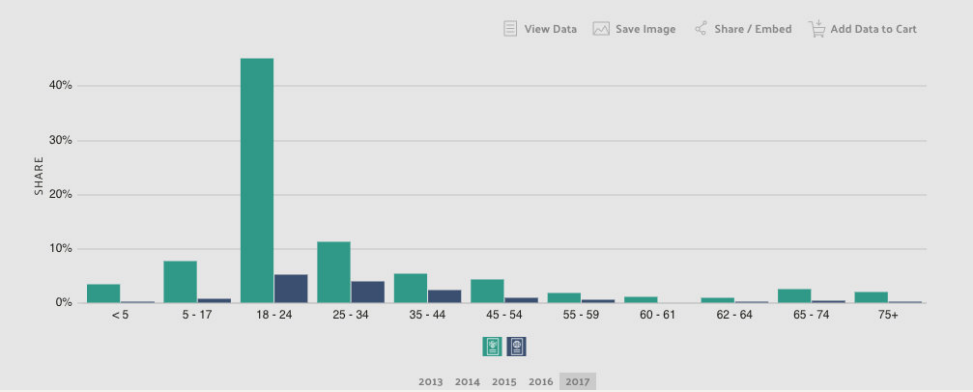

Figure 1. Census data from the town of Pullman

Wang model (assuming no mortality and no age population structure)

Scenario 1: 1 exposed (E) individual arrives to Pullman

Under the assumption that 1 exposed individual arrives to Pullman, we examine the expected dynamics after 120 days and 300 days after introduction. Figure 2 shows that after 120 days after the introduction of a single infected individual we would expect that approximately 1074 individuals would have been exposed (3.32% of the Pullman population). Out of these, we would expect to see 405 infected individuals (1.25% of the Pullman population) and 433 recovered individuals (1.34% of the Pullman population) at day 120 post introduction. This is not unreasonable and consistent with the observed

dynamics in Seattle, Italy, South Korea.

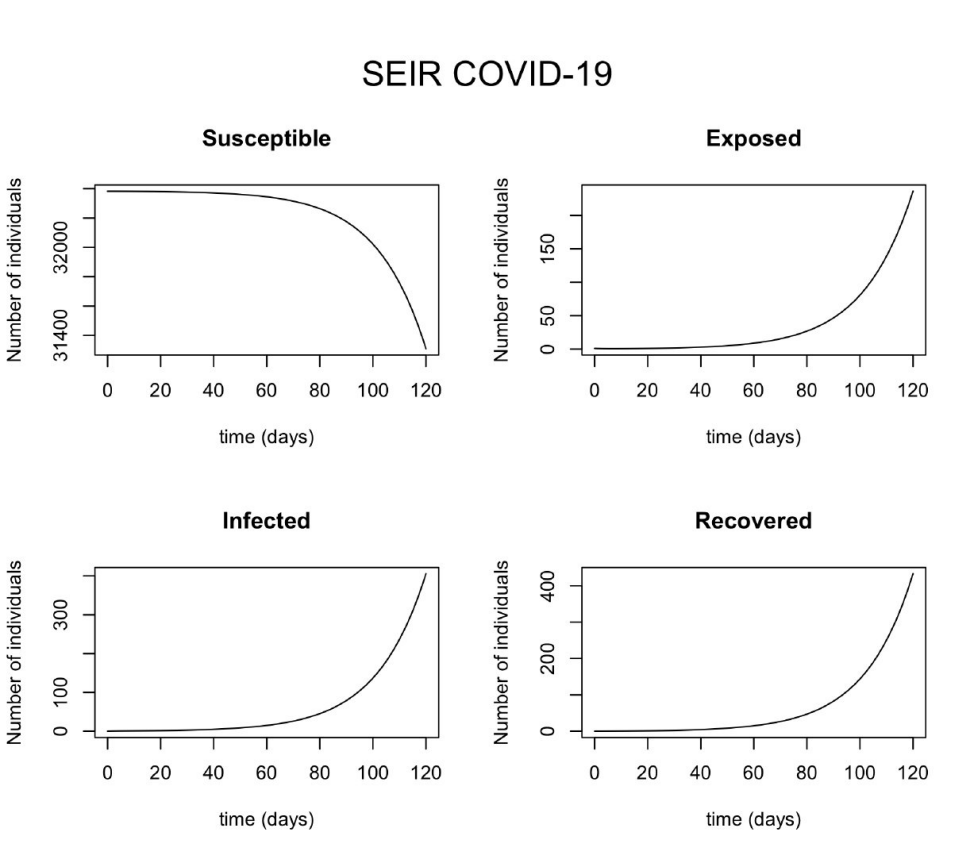

Figure 2. Dynamics of Susceptible, Exposed, Infected, and Recovered individuals during the intial phase of the outbreak caused by 1 exposed individual.

If we allow the simulations to continue for 300 days (ten months) we predict that at the peak of the epidemic we will have 5825 infected individuals (at 193 days after the introduction of the exposed individual), giving you an idea of the potential burden of the number of disease individuals to our hospital resources in town. Now, this could be an unreasonable situation because even in Wuhan, it has been observed that as the epidemic progresses, R_0 has been estimated to decay. The multi-phase analysis of the epidemics has suggested that in these places $R_0 = 1.3$ after the intial introduction[1]. It is unclear to me at the moment if this decay in R_0 is due to mitigation effects of public health measurements or changes in the intrinsic dynamic of the epidemic. In this scenario, after 10 months of transmission 28873 individuals (89%) of the population of Pullman could have been infected.

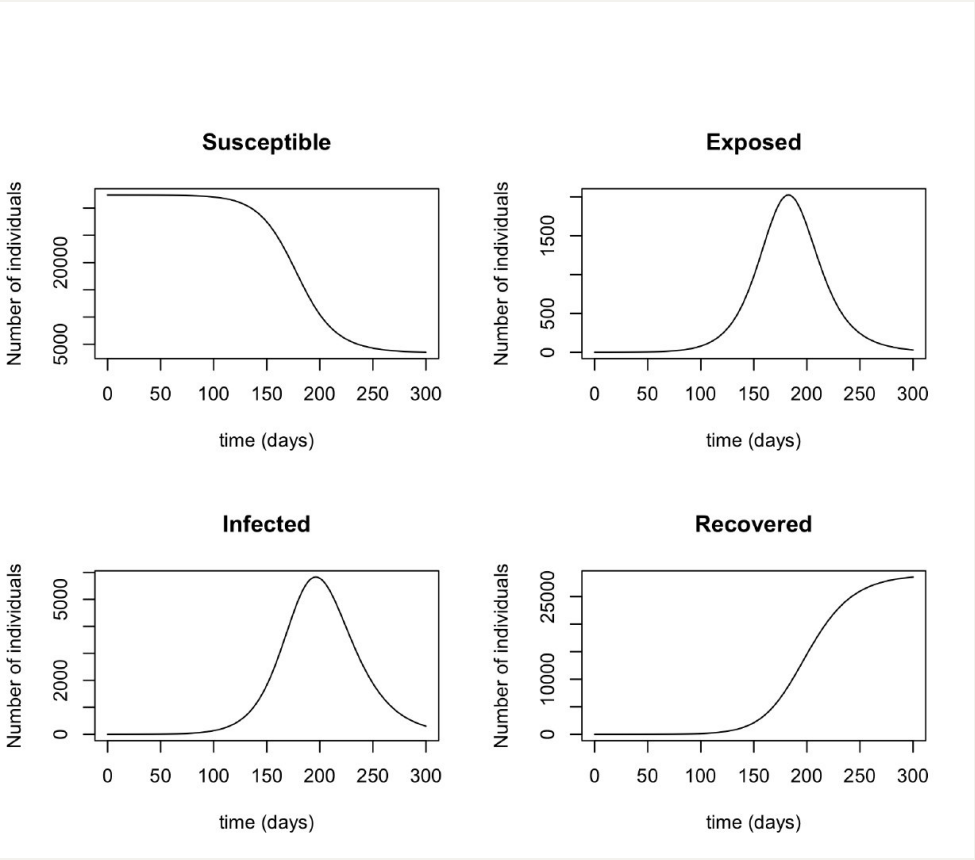

Figure 3. Dynamics of Susceptible, Exposed, Infected, and Recovered individuals for 10 months after introduction after 1 Exposed individual.

Scenario 2: 10 exposed (E) individuals arrive to Pullman

Under the assumption that 10 exposed individuals arrive to Pullman after Spring Break, we examine the expected dynamics after 120 days and 300 days after introduction. Figure 4 shows that after 120 days after the introduction of a single infected individual we would expect that approximately 8071 individuals would have been exposed (25% of the Pullman population). Out of these, we would expect to see 2935 infected individuals (9.1% of the Pullman population) and 3681 recovered individuals (11.4% of the Pullman population) at day 120 post introduction. This is not unreasonable and consistent with the observed dynamics in Seattle, Italy, South Korea.

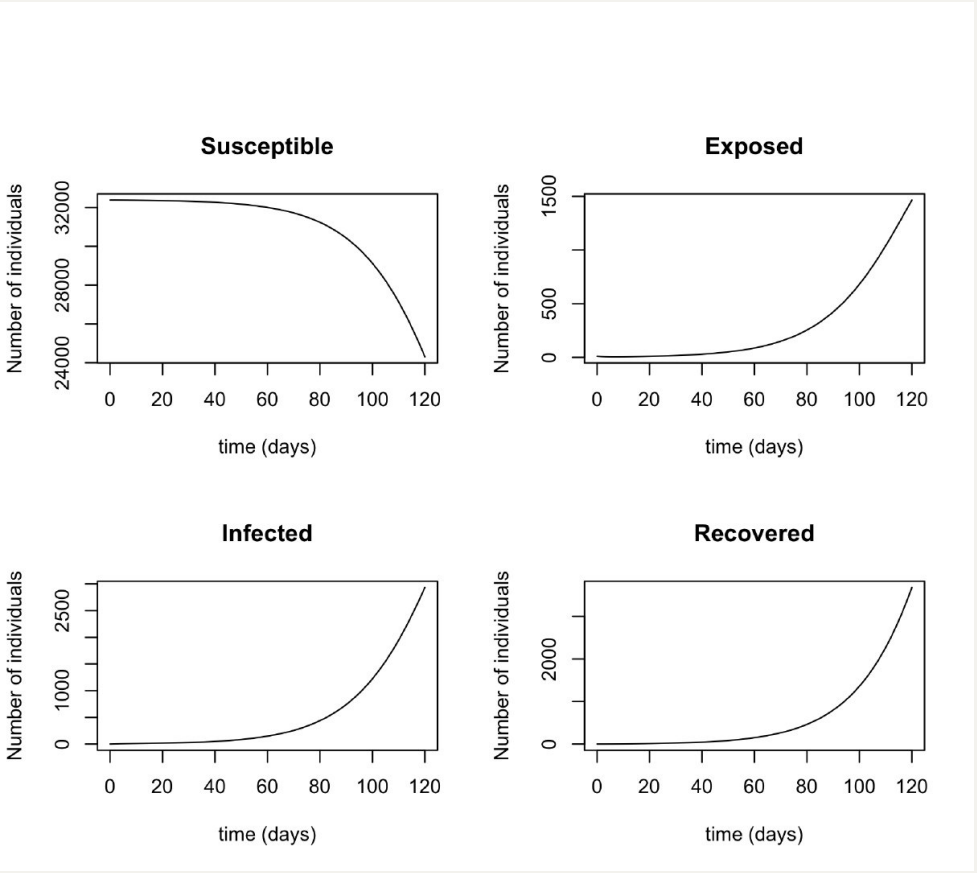

Figure 4. Dynamics of Susceptible, Exposed, Infected, and Recovered individuals during the intial phase of the outbreak caused by 10 exposed individuals.

If we allow the simulations to continue for 300 days (ten months) we predict that at the peak of the epidemic we will have 5832 infected individuals (at 156 days after the introduction of the exposed individual, 37 days earlier than that observed for the case of a single introduction). Now, this could be an unreasonable situation because even in Wuhan, it has been observed that as the epidemic progresses, R_0 has been estimated to decay. The multi-phase analysis of the epidemics has suggested that in these places $R_0 = 1.3$ after the intial introduction[1]. It is unclear to me at the moment if this decay in R_0 is due to mitigation effects of public health measurements or changes in the intrinsic dynamic of the epidemic. In this scenario, after 10 months of transmission 28,974 individuals (89.5%) of the population of Pullman could have been infected (Figure 5).

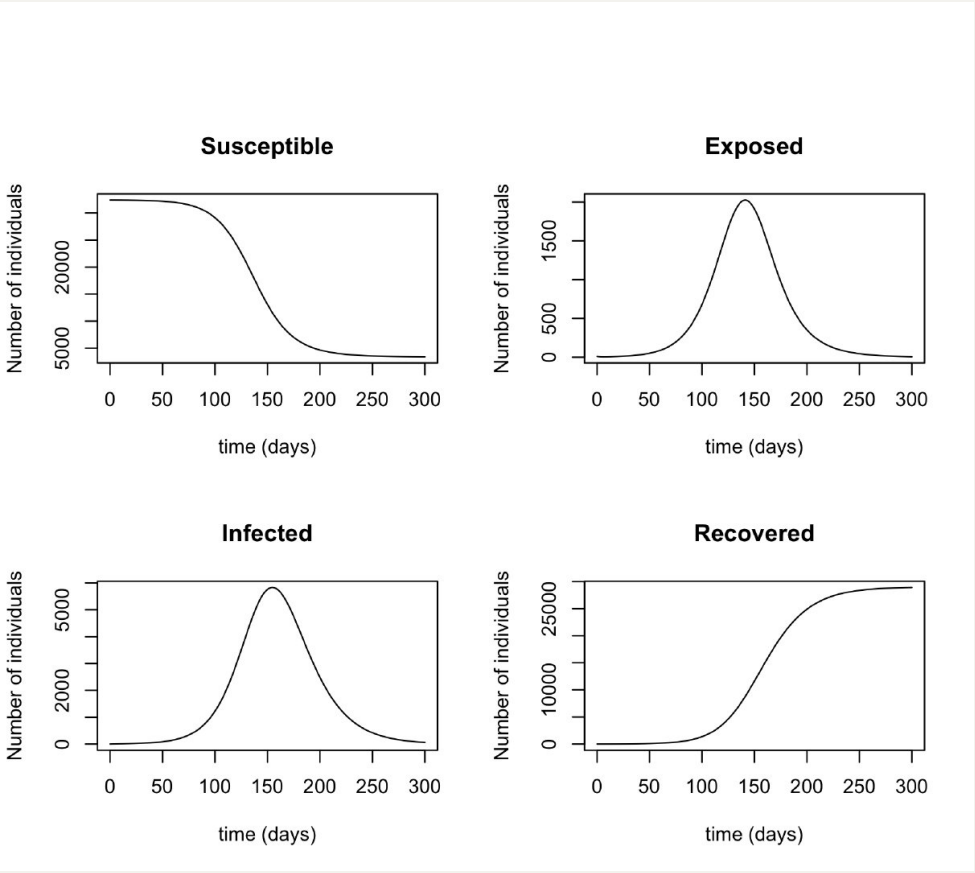

Figure 5. Dynamics of Susceptible, Exposed, Infected, and Recovered individuals for 10 months after introduction after 10 Exposed individuals.

Considerations about the mortality rate associated to SARS-CoV-2 infections

At this point the mortality rate by SARS-CoV-2 seems to be remarkably different between individuals of different ages[7]. In this study, following 72,314 cases in Wuhan 44,672 (62%) were classified as confirmed cases of COVID-19, the number of suspected cases was 16186 (22%), the number of diagnosed cases 10,567 (15%) and the number of asymptomatic 889 (1%). I am going to assume the distribution of fatality rate from[7]:

1. 2.3% (1023 of 44672 confirmed cases)
2. 14.8% in patients aged ⩾80 years (208 of 1408)
3. 8.0% in patients aged 70-79 years (312 of 3918)
4. 49.0% in critical cases (1023 of 2087)

From these, I am going to assume the mortality rate (μ_o) of individuals > 70 year old to be 8% or 11.4% in a 2 months period to model the spread of disease in an age structured population for individuals, and consider the mortality rate (μ_b) for the rest of the population to be 2.3% in a 2 months period in which these observations were done (60 days). The mortality rate for >70 yo would

then be $\mu_o = 0.0013$ *deaths/day* or $\mu_o = 0.0019$ *deaths/day* and the mortality rate of rest of the population is $\mu_b = 0.0004$.

A back of the envelop calculation would allow us to infer that for Scenario 1 (1 Exposed individual infection) we could be facing between 20 - 60 SARS-CoV-2 associated deaths during the epidemic, that is a 2.3% mortality rate. If we structure this by ages NB-70 and >70 we could expect to see 1019 infected individuals between NB-70 and 55 individuals older than 70. Given the higher mortality rate in the elderly population we could see 6 old people daying in the first 120 days of infection in Pullman

I have yet to work on the mitigation impact on these numbers and also my original idea that was looking at an age structured model of the epidemic.

You can see the code for the simulations below.

```
##########################################
## Simple model
##########################################


# case to consider sqrt(2.5*0.0583*(0.0583+0.0004)) =
0.0925. This is a note for Omar
#  original estimation was b = 0.147

parameters <- c(b = 0.147,
  s = 0.192,      #1/5.2
  g = 0.0583,     #1/17.16
  m = 0.0004)

state <- c(X = 32382,
  Y = 1,
  Z = 0,
  W = 0)

N=32382

seir_covid <-function(t, state, parameters) {
  with(as.list(c(state, parameters)),{
    dX <- (-b*X*Z)/N
    dY <- (b*X*Z)/N - s*Y
    dZ <- s*Y - g*Z
    dW <- g*Z
```

```
    # return the rate of change
    list(c(dX, dY, dZ, dW))
  }) # end with(as.list ...
}


times <- seq(0, 120, by = 1)


out_1 <- ode(y = state, times = times, func =
seir_covid, parms = parameters)
colnames(out_1) <-
c("time","Susceptible","Exposed","Infected","Recovered")
head(out_1)

par(oma = c(0, 0, 4, 0))
plot(out_1, xlab = "time (days)", ylab = "Number of
individuals")
#plot(out[, "Susceptible"], out[, "Infected"], pch =
".")
mtext(outer = TRUE, side = 3, "SEIR COVID-19", cex =
1.5)




times <- seq(0, 300, by = 1)


out_1 <- ode(y = state, times = times, func =
seir_covid, parms = parameters)
colnames(out_1) <-
c("time","Susceptible","Exposed","Infected","Recovered")
head(out_1)

par(oma = c(0, 0, 4, 0))
plot(out_1, xlab = "time (days)", ylab = "Number of
individuals")
#plot(out[, "Susceptible"], out[, "Infected"], pch =
".")
mtext(outer = TRUE, side = 3, "SEIR COVID-19", cex =
1.5)
```

```
#######################
##. 10 exposed
#######################

parameters <- c(b = 0.147,
  s = 0.192,      #1/5.2
  g = 0.0583,     #1/17.16
  m = 0.0004)

state <- c(X = 32382,
  Y = 10,
  Z = 0,
  W = 0)

N=32382

seir_covid <-function(t, state, parameters) {
  with(as.list(c(state, parameters)),{
    dX <- (-b*X*Z)/N
    dY <- (b*X*Z)/N - s*Y
    dZ <- s*Y - g*Z
    dW <- g*Z
    # return the rate of change
    list(c(dX, dY, dZ, dW))
  }) # end with(as.list ...
}



times <- seq(0, 120, by = 1)



out_2 <- ode(y = state, times = times, func =
seir_covid, parms = parameters)
colnames(out_2) <-
c("time","Susceptible","Exposed","Infected","Recovered")
head(out_2)

par(oma = c(0, 0, 4, 0))
plot(out_2, xlab = "time (days)", ylab = "Number of
individuals")
#plot(out[, "Susceptible"], out[, "Infected"], pch =
".")
mtext(outer = TRUE, side = 3, "SEIR COVID-19", cex =
1.5)
```

```
times <- seq(0, 300, by = 1)


out_2 <- ode(y = state, times = times, func =
seir_covid, parms = parameters)
colnames(out_2) <-
c("time","Susceptible","Exposed","Infected","Recovered")
head(out_2)

par(oma = c(0, 0, 4, 0))
plot(out_2, xlab = "time (days)", ylab = "Number of
individuals")
#plot(out[, "Susceptible"], out[, "Infected"], pch =
".")
mtext(outer = TRUE, side = 3, "SEIR COVID-19", cex =
1.5)







#####################################
# transmission reduction efforts 2/3*b
#####################################


##########
### after 30 days of introduction
##########


parameters <- c(b = 2*0.147/3,
  s = 0.192,      #1/5.2
  g = 0.0583,     #1/17.16
  m = 0.0004)

state <- c(X = 32376.210,
  Y = 1.6735458,
  Z = 2.8196594,
```

```
  W = 2.296325)

N=32382

seir_covid <-function(t, state, parameters) {
  with(as.list(c(state, parameters)),{
    dX <- (-b*X*Z)/N
    dY <- (b*X*Z)/N - s*Y
    dZ <- s*Y - g*Z
    dW <- g*Z
    # return the rate of change
    list(c(dX, dY, dZ, dW))
  }) # end with(as.list ...
}


times <- seq(0, 90, by = 1)


out_bh_1 <- ode(y = state, times = times, func =
seir_covid, parms = parameters)
colnames(out_bh_1) <-
c("time","Susceptible","Exposed","Infected","Recovered")
head(out_bh_1)

par(oma = c(0, 0, 4, 0))
plot(out_bh_1, xlab = "time (days)", ylab = "Number of
individuals")
#plot(out[, "Susceptible"], out[, "Infected"], pch =
".")
mtext(outer = TRUE, side = 3, "SEIR COVID-19", cex =
1.5)


times <- seq(0, 270, by = 1)


out_bh_1 <- ode(y = state, times = times, func =
seir_covid, parms = parameters)
colnames(out_bh_1) <-
c("time","Susceptible","Exposed","Infected","Recovered")
head(out_bh_1)

par(oma = c(0, 0, 4, 0))
```

```
plot(out_bh_1, xlab = "time (days)", ylab = "Number of
individuals")
#plot(out[, "Susceptible"], out[, "Infected"], pch =
".")
mtext(outer = TRUE, side = 3, "SEIR COVID-19", cex =
1.5)



##########
### after 45 days of introduction
##########

parameters <- c(b = 0.147/2,
  s = 0.192,      #1/5.2
  g = 0.0583,     #1/17.16
  m = 0.0004)

state <- c(X = 32367.428,
  Y = 3.6463758,
  Z = 6.1449310,
  W = 5.780)

N=32382

seir_covid <-function(t, state, parameters) {
  with(as.list(c(state, parameters)),{
    dX <- (-b*X*Z)/N
    dY <- (b*X*Z)/N - s*Y
    dZ <- s*Y - g*Z
    dW <- g*Z
    # return the rate of change
    list(c(dX, dY, dZ, dW))
  }) # end with(as.list ...
}



times <- seq(0, 90, by = 1)



out_bh_1 <- ode(y = state, times = times, func =
seir_covid, parms = parameters)
colnames(out_bh_1) <-
c("time","Susceptible","Exposed","Infected","Recovered")
head(out_bh_1)
```

```
par(oma = c(0, 0, 4, 0))
plot(out_bh_1, xlab = "time (days)", ylab = "Number of
individuals")
#plot(out[, "Susceptible"], out[, "Infected"], pch =
".")
mtext(outer = TRUE, side = 3, "SEIR COVID-19", cex =
1.5)


times <- seq(0, 270, by = 1)


out_bh_1 <- ode(y = state, times = times, func =
seir_covid, parms = parameters)
colnames(out_bh_1) <-
c("time","Susceptible","Exposed","Infected","Recovered")
head(out_bh_1)

par(oma = c(0, 0, 4, 0))
plot(out_bh_1, xlab = "time (days)", ylab = "Number of
individuals")
#plot(out[, "Susceptible"], out[, "Infected"], pch =
".")
mtext(outer = TRUE, side = 3, "SEIR COVID-19", cex =
1.5)`
```