MODELING COVID-19 EPIDEMIC TO GUIDE DECISION MAKING

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ABSTRACT

A coronavirus has many crown-like spikes on its surface. Two recent examples of these viruses are SARS-CoV-1 and SARS-CoV-2. The former caused the 2003 outbreak of severe acute respiratory syndrome (SARS), that according to the World Health Organization (WHO), as of July 5, 2013, infected a total of 8,439 people and 812 died worldwide. The latter caused the coronavirus disease 2019 (Covid-19), that the WHO declared a pandemic on March 11, 2020. Unlike the SARS-CoV-1, the SARS-CoV-2 is much more contagious and widespread, and it has adversely affected life in almost every country. The Centers for Disease Control and Prevention (CDC) reported that as of July 24, 2020, there were over 15 million confirmed cases of Covid-19 in the world, among them the US had 4,024,492 cases out of which 72,219 were new cases as of July 25, within a 24- hour period. It reported 143,868 total deaths in the US due to this disease that included 1,113 new deaths during this 24-hour period. Among the US cases, one million new cases were added during July 9-24, 2020, indicating an exponential growth of new Covid-19 cases relative to the timeline of SARS-CoV-1.

One way to understand and predict the impact of Covid-19 is to formulate a mathematical model to predict the spread of illness, hospitalization, death, recovery, etc. based on assumptions about the characteristics of the disease and behavior of individuals. Many institutions, universities, and organizations have formulated mathematical models for this purpose. Some notable organizations for this purpose include the Covid-19 Forecast Hub that hosts over 30 international research groups and their models, the CDC, and the FiveThirtyEight (Best & Boice, July 24, 2020; ABC News Internet Ventures, 2020).

The purpose of this research is to introduce basic terminology about the spread of infectious diseases and to formulate basic epidemic models to analyze Covid-19 to guide managerial decisions.

THE CHARACTERISTICS OF COVID-19 EPIDEMIC

Dr. Gro Harlem Brundtland, Director-General of the WHO (2003), said "We do not mark the end of SARS today, but we observe a milestone: the global SARS outbreak has been contained." He said "SARS is a warning, SARS pushed even the most advanced public health systems to the breaking point. Those protections held, but just barely. Next time, we may not be so lucky. We have an opportunity now, and we see the need clearly, to rebuild our public health

protections. They will be needed for the next global outbreak, if it is SARS or another new infection."

Thirteen years later, Dr. Brundtland's warning came true with the arrival of SARS-CoV-2 virus that causes Covid-19 disease and was first reported on December 31, 2019 (World Health Organization, 2021). Covid-19 has directly or indirectly affected most individuals, organizations, and countries. The economic and social life in most countries was severely affected. This study explores the parameters that govern the dynamics of this infectious disease and should be of interest to public healthcare policy planners, managerial decision makers, and individuals who want to minimize the chance of getting infected by Covid-19 disease.

The CDC reports that seven human coronaviruses have been identified since the mid-1960s and four of which (HKU1, NL63, 229E, and OC43) cause common illness in people while three coronaviruses, namely, MERS-CoV, SARS-CoV, and SARS-CoV-2, have evolved from animals to become human coronaviruses.

On January 21, 2020, the CDC confirmed the first US case of Covid-19 in Snohomish County, Washington, where a 35-year-old man, who had travelled to Wuhan, China, showed up at an urgent care clinic with Covid-19 symptoms (Holshue et al., 2020). The SARS-CoV-2 is a new virus for which people do not have a natural immunity and, at that time, there was no vaccine for it. The Covid-19, the **co**rona **vi**rus **d**isease that originated in 20**19**, caused a public health crisis that has resulted in an economic crisis. Almost every industry was adversely affected by the Covid-19 epidemic. In the US, the economy shrank 5% in the first quarter of 2020 followed by 9.5% in the second quarter.

The economic and business activity could not recover without controlling Covid-19. The government administrators, public health officials, business leaders, school administrators, employees, households, parents, and individuals tried to gain a better understanding of Covid-19 to control its spread so they could return to normal operations. The target audience of this study is everyone who is interested in how an infectious disease like Covid-19 spreads through a population and what measures are useful to minimize its impact and reduce and eliminate this disease.

Basic and Effective Reproductive Rates, R_0 and R_E

The reproductive rate or reproduction number measures the contagiousness of a disease. The spread of an infectious disease is controlled by its reproduction number. The basic reproductive rate, R_0, is the average number of secondary infections caused by an individual in a fully susceptible population. The effective reproductive rate, R_E, is the average number of secondary cases generated by an infected individual in a population where some individuals have been previously infected or immunized so not everyone is susceptible to the disease. R_0 plays a key role in the spread of a disease and in determining the population size that must be vaccinated to attain herd immunity. SARS-CoV-2 virus continues to mutate and spawn new variants and subvariants. WHO names coronaviruses using Greek alphabet. The following presents selected literature on reproduction number for different variants and subvariants of SARS-CoV-2 virus.

Esterman (2022) provides that the basic reproduction numbers, R_0, for various strains of SARS-CoV-2 virus. The ancestral strain in Wuhan, China: R_0 = 3.3. Delta strain that appeared in India: R_0 = 5.1. Omicron BA.1 in Botswana and South Africa: R_0 = 9.5. Omicron BA.2 has R_0 = 13.3. He summarizes the impact of these variants and subvariants as follows:

- *Three subvariants of Omicron (BA.1, BA.2, and BA.3) appeared in late November 2021 in South Africa. In early January 2022, BA.1 rapidly spread across Australia replacing Delta and causing more than 100,000 cases per day at the peak (early January 2021) of the first wave of Omicron. The second Omicron wave was caused by BA.2 and peaked in early April 2022 at more than 60,000 cases a day. Omicron BA.2 was even more transmissible than BA.1.*
- *Omicron BA.4 and BA.5 were detected in South Africa in January 2022 and February 2022 respectively. The third wave in Australia was caused by BA.4 and BA.5 started in July 2022, as BA.4 and BA.5 became the dominant Covid-19 strains. BA.4 and BA.5 are more infectious than previous variants and subvariants and are better able to evade immunity from vaccines and previous infections. BA.4 and BA.5, however, did not cause more sever disease compared with the previous subvariants of Omicron possibly due to previous infections or vaccinations.*

Katella (2022) notes the following characteristics for some variants and subvariants of SARS-CoV-2.

- *Alpha (B.1.1.7) first appeared in Great Britain in November 2020. It was 30%-50% more contagious than the original SARS-CoV-2 strain and created 66% of cases in the US by mid-April 2021. It also caused more severe disease than the original virus.*
- *Beta (B.1.351) appeared in South Africa at the end of 2020 and was 50% more contagious than the original virus. Beta may have caused more severe disease than the other variants, but it did not become the dominant variant in the US.*
- *Delta (B.1.617.2) first appeared in India in late 2020 and spread around the world to become the dominant variant. It was 80%-90% more contagious than the Alpha variant. Starting in June 2021, Delta spread across the US and caused some breakthrough infections among fully vaccinated individuals. More contagious variants of Delta later emerged and infected many people.*
- *Omicron (BA.1) appeared in Botswana and South Africa in late November 2021 and quickly spread across the world. BA.1 was more contagious than Delta but tended to cause less severe disease. In the US in December 2021, Omicron caused daily infections that exceed one million cases. Omicron generated many subvariants including BA.5, BQ.1, BQ.1.1.*

Liu and Rocklöv (2022) conduct extensive literature review of articles publications in Chinese and US journals and conclude that the reproduction number for Omicron is 5.08 which is higher than that of the Delta variants.

Selected Covid-19 Modelling Across the World

The following presents selected model building efforts by researchers to understand the dynamics of Covid-19 in different parts of the world.

Biswas, Khaleque, and Sen (2020), in a pre-print (not peer-reviewed) study use data from China and Italy in an SIR framework. They use a Euclidean network of interactions among

individuals to show that the new infections of Covid-19 are inversely proportional to Euclidean distance (raised to power ~1.85) from the epicenter of the disease. They calculate that the exponent of distance from the epicenter Wuhan is 0.268 for China and from the epicenter Bergamo is 0.383 for Italy. So generally, infections would be larger the closer the individuals are located to the epicenter of this disease and this spatial dependence follows an approximate power law with exponent ~1.85.

Cooper, Mondal, and Antonopoulos (2020) utilize a classical susceptible-infected-removed (SIR) model to study the spread of Covid-19 in China, South Korea, India, Australia, USA, Italy and the state of Texas in the USA. They consider data from January-June 2020. They make predictions regarding various parameters of disease dynamics and the numbers of individuals in S, I, R compartments of the populations until September 2020. They note: "This allowed us to estimate the development of Covid-19 spread in these communities by obtaining estimates for the number of deaths D, susceptible S, infected I and removed Rm populations in time." By comparing recorded data with the results of their predictions they claim that the spread of this disease can be controlled by early implementation of proper restrictions and strong control policies. They make a few statements that are incorrect. Here are our observations on this study.

- The authors utilize a typical closed SIR model where births and deaths (other than those due to COVID-19) can be neglected due to short duration of the study.
- They claim that their total population, N, is not specified or held constant. They specify three compartments of individuals in their three SIR equations so N in their model can be obtained by adding these three compartments. Thus, $N(t) = S(t) + I(t) + R(t)$. Adding their three SIR equations results in $\frac{dN}{dt} = N'(t) = 0$. So, their model requires a constant total population even though the authors do not acknowledge it.
- They claim that unlike in the classic SIR model, the susceptible population does not monotonically decrease in their modified SIR model but can increase to accommodate new surges in infections. Contrary to their claim, however, their equation (1) specifies the typical susceptibles function with a monotonically decreasing slope. $\frac{dS}{dt} = S'(t) = -aS(t)I(t) < 0$. So, the disease incidence, $aS(t)I(t)$, decreases monotonically in their model.
- They acknowledge that deaths and recoveries are not generated directly by their SIR model, so they estimate them separately. A better approach is to model them directly in and extended SIR model. For example, Ndaïrou, Faïçal, Iván Area, Juan J. Nieto, and Delfim Torres (2020) extend the SIR model to directly incorporate the number of deaths, recoveries, reinfections, hospitalizations, serious infections, etc.

- To estimate S, I, and R, they set initial values between 0-1 and scale their variables to fit the data. They set initial conditions of the SIR model as S(0) = 1, and I(0) = R(0) <= 1. This indicates that initially everyone is susceptible, and some people may be infected or removed (recovered or dead). However, although everyone is susceptible to the new pathogen, some people have to be infected at the start of the epidemic, thus S(0) < 1 and I(0) > 0 and R(0) = 0 since the infected individuals will be moved from the susceptible compartment to the infected compartment, while none will have recovered or died at the very beginning of the epidemic.
- They do not specify N(0), the initial population size in the SIR model. However, by definition, N(0) = S(0) + I(0) + R(0). The sum of the components (as fractions) will be one. They do not specify but their approach normalizes N to 1 (or 100%).
- They fit their model to the data by trial-and-error and visual inspection thus introducing bias in their estimates and predictions since the result are not produced automatically by applying the model itself but by active intervention by the researchers to fit the model to results. So different researchers will obtain different results from the same data set.
- They estimate and plot total infections, active infections (I), recoveries (R), deaths (D), and active susceptibles (S) over time for different countries and the state of Texas. Their plots show that the researchers have achieved good approximation in fitting their model to actual data. However, their SIR model does not extend to their data analyses.
- Their theoretical SIR model does not extend to their actual data analysis regarding deaths (D), recoveries (R), and surges based on increasing S and I. This is because their SIR model does not directly incorporate deaths and recovered individuals, nor does it accommodate surges due to increased numbers of usucaptible individuals.
- They state that during a surge, the number of susceptible individuals increases, and the number of infected individuals also increases. They conclude that in the absence of a vaccine, drastic actions should be taken to control the spread of disease in its early stages. So, the disease could be eliminated by reducing the susceptible population to zero.
- They recommend that in the absence of an effective vaccine the authorities should enforce strict measures to the spread of epidemic at its early stages.
- They do not share their code or data, so the readers are unable to replicate their results.

Ndaïrou, Area, Nieto, and Torres (2020) study transmission dynamics of Covid-19 in Wuhan (population about 11 million people) with a modified SIR model. This model utilizes a constant total population size N that is subdivided into eight epidemiological classes: susceptible, exposed, symptomatic and infectious, super-spreaders, infectious but asymptomatic hospitalized,

recovery, and fatality. This model allows for surges in susceptible class and does not require a monotonically decreasing susceptible class of individuals. These authors adjust the Wuhan population of 11 million by dividing by 250 to account for strict lock downs. They simulate results of the model and compare them with actual data and find good approximations of their model performance with actual data. They estimate the basic reproductive number for Wuhan as $R_0 = 0.945$. This is less than 1 indicating that the authorities quickly contained the spread of Covid-19 through strict Zero-Covid measures of quarantine and lock-down of communities with infected individuals. For a preprint (not peer-reviewed) of a study on the index case in Wuhan, China, please refer to Pekar, Worobey, Moshiri, Scheffler, and Wertheim (2020).

THE STUDY

This study takes a mathematical model building approach to generate insights to control Covid-19. This study addresses the following research questions:

- RQ #1. What types of mathematical models are useful in understanding Covid-19?
- RQ #2. What parameters determine the spread of an infectious disease like Covid-19 through the population?
- RQ #3. What proportion of the population will become infected with Covid-19 *if no preventive measures are taken* to stop the spread of this epidemic?
- RQ #4. What level of *vaccine-induced herd immunity* is required to control the disease?
- RQ #5. What steps should individuals and organizations take to control the spread of this disease?

THE SUSCEPTIBLE-INFECTIOUS-RECOVERED MODEL AND ITS VARIATIONS

The following two research questions are addressed here.

- RQ #1. What types of mathematical models are useful in understanding Covid-19?
- RQ #2. What parameters determine the spread of an infectious disease like Covid-19 through the population?

The SIR Model of Epidemics

The SIR model (Kermack & McKendrick, 1927) describes the diffusion of an infectious disease through a susceptible pupation by dividing the population into three different compartments of susceptibles (S), infectious (I), and recovered (R). The relationships among the number of S, I and R can be described as $S \rightarrow I \rightarrow R$. The SIR model may be closed or open where the closed model assumes that the overall population does not change while the open model allows new births and deaths (other than those due to the pathogen).

Closed SIR system

An SIR model can be represented with a deterministic ordinary differential equation (ODE) system given below:

$$\frac{dS}{dt} = -\beta I \frac{S}{N} \qquad equation\ (1)$$

$$\frac{dI}{dt} = \beta I \frac{S}{N} - \gamma I \qquad equation\ (2)$$

$$\frac{dR}{dt} = \gamma I \qquad equation\ (3)$$

- Equation (1) describes the dynamics of the susceptibles compartment in terms of outflow of individuals from the susceptibles compartment to the infectious compartment.
  - β is the probability of disease transmission times the contact rate between susceptible (S) and infectious (I) individuals that independently and randomly mix with one another.
  - $\frac{S}{N}$ is the fraction of encounters with susceptible individuals.
  - βIS is the *incidence rate*, the number of newly infected individuals per unit time.
  - $\beta I \frac{S}{N}$ is the *incidence fraction*. The negative sign in equation (1) represents removal of individuals from the susceptible compartment.
- Equation (2) describes the dynamics of the infected compartment in terms of inflow of individuals from the susceptibles compartment and outflow of individuals to the recovered compartment.
  - Equation (2) describes disease *prevalence*, which is the number of infected individuals at time t.
  - $\beta I \frac{S}{N}$ is the *incidence fraction*. The positive sign in equation (2) represents addition of individuals to the infected compartment.
  - γ represents *the recovery rate.* It is the rate of transition from infectious to recovered.
  - $\frac{1}{\gamma}$ is the average infectious period.

  - γI is the number of individuals who recover per unit of time. The negative sign indicates that these individuals are removed from the infected compartment.
- Equation (3) describes the dynamics of the recovered department.
  - γI is the number of individuals who recover per unit of time. The positive sign indicates that these individuals are added to the recovered compartment.
- N represents population size. N was operationalized by normalizing it to 1 indicating 100% of the population. So, $S + I + R$ would be expressed as fractions.
- $N = S + I + R$.
- N is constant in a closed SIR system, so $\frac{dN}{dt} = 0$. This can be confirmed by adding equations (1)-(3).
- The basic reproductive ratio, R_0, is the expected number of secondary infections from an index case in a randomly mixing pupation. For the SIR model, $R_0 = \frac{\beta}{\gamma}$.
- If $R_0 > 1$, each index susceptible case infects more than one other person so the infection spreads among susceptible population resulting in an expanding epidemic.
- If R_0<1, then each infected individual infects less than one other person on average and the epidemic dies out.

Open SIR System

In an open SIR model, there is "background" death rate (μ) that is balanced by per capita birth rate (μ). In this model, the relationships among the number of susceptibles (S), infectious (I) and recovered (R) can be described as follows:

$$\frac{dS}{dt} = \mu(N - S) - \beta I \frac{S}{N} \quad equation\ (4)$$

$$\frac{dI}{dt} = \beta I \frac{S}{N} - (\mu + \gamma)I \quad equation\ (5)$$

$$\frac{dR}{dt} = \gamma I - \mu R \quad equation\ (6)$$

In the open SIR system, the basic reproductive ratio, $R_0 = \frac{\beta}{\gamma + \mu}$.

ESTIMATING SIR MODEL WITH R SOFTWARE

The following two research questions are addressed here.

- RQ #3. What proportion of the population will become infected with Covid-19 *if no preventive measures are taken* to stop the spread of this epidemic?
- RQ #4. What level of *vaccine-induced herd immunity* is required to control the disease?

The SIR model has been extended to incorporate other aspects like exposed status, hospitalizations, deaths, etc. The model parameters can be estimated from published studies, discussed above, about the behavior of infectious pathogen, SARS-CoV-2.

This system of equations can be solved by numerical integration by using the *deSolve* package in R (R Development Core Team, 2022). *R is an open-source software and environment that can be utilized by the reader to reproduce the results of this study.* The appendix describes how the reader can utilize R to run programs.

The following annotated code is adapted from Bjornstad (2018) to estimate a closed SIR model. The main steps are described below.

1. In an R script, specify a gradient function (sir_mod) containing the following arguments: time t, a vector y representing the state variables (S, I, R, N) of the SIR model, and a variable *parms* containing parameter values (μ, β, and γ, and N).
2. Specify the time points in weeks, and time-increments per week, for example, 26 weeks with 10-increments per week.
3. S + I + R = N and N = 1. So, S, I, R are modeled here as fractions of N.
4. Specify *parms* values, for example, $\mu = 0$, $\beta = 2$ (so disease transmission rate is 2), and $\gamma = 1/2$ (so the infectious period is 2 weeks). For $\beta = 2$ and $\gamma = 1/2$, the basic reproductive rate, $R_0 = \frac{\beta}{\gamma} = 4$.
5. The starting values of the state variables S, R, R. Let 0.1% of the population be infected at the start of the epidemic so, I = 0.1%, S = 0.999, and R = 0.
6. The *ode()* function of the *deSolve* package in R is utilized to solve the system of differential equations. For this purpose the following arguments are entered into the *ode()* function: start (the starting state values of S, I, and R), times, the gradient function, and the parameters.
7. Plot the values of S, I, R, against time as shown in Figure 1(a).
8. Plot R_0 on the horizontal axis, and the corresponding proportion of the population that will ultimately become infected if no preventive measures are taken to stop the spread of the infectious disease. This is shown in Figure 1(b).
9. The following R script was utilized to obtain the results of this study.

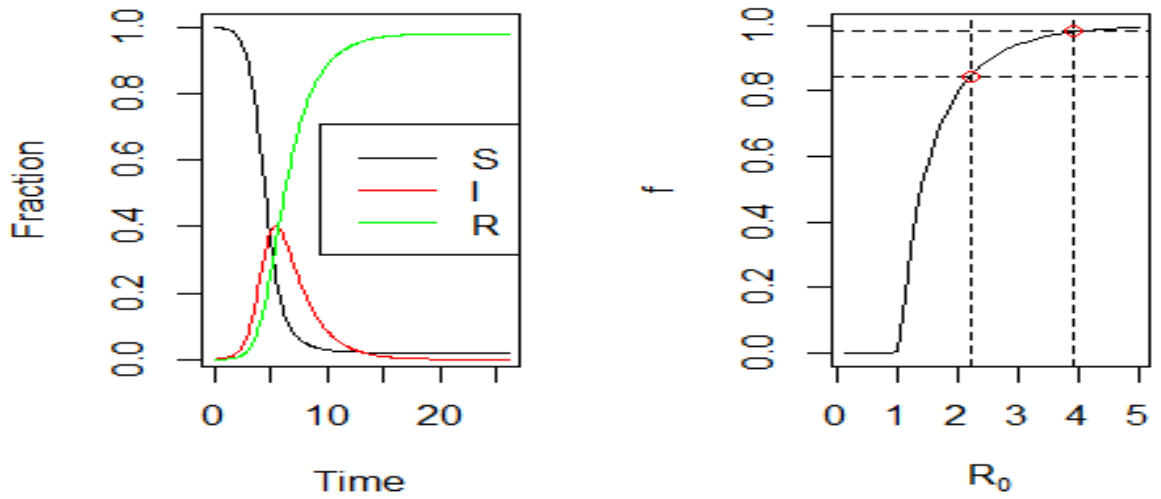
```
# Adapted from Bjornstand, O. N. (2018) Epidemics: Models and Data Using R, Springer.
# Here a # represents a comment and ## represents results generated by R code.

# Closed SIR model, mu = 0
```

```
# load the required package in R
require(deSolve)

## Loading required package: deSolve

# Define the gradient function
sir_mod <- function(t, y, parms){
  S = y[1]; I = y[2]; R = y[3]
  beta = parms["beta"]; mu = parms["mu"]; gamma = parms["gamma"]; N = parms["N"]

  dS = mu * (N-S) - beta * S * I/N
  dI = beta * S * I/N - (mu+gamma) * I
  dR = gamma * I - mu * R
  res = c(dS, dI, dR)
  list(res)
}

times = seq(0, 26, by = 1/10)
parms = c(mu=0, N=1, beta=2, gamma=1/2)
start = c(S=0.999, I=0.001, R=0)

out=ode(y=start, times=times, func=sir_mod, parms=parms)
out=as.data.frame(out)

par(mfrow=c(1,2))
plot(x=out$time, y=out$S, ylab="Fraction", xlab = "Time", type="l")
lines(x=out$time, y=out$I, col="red")
lines(x=out$time, y=out$R, col="green")
legend("right", legend = c("S", "I", "R"), lty = c(1,1,1), col = c("black", "red",
"green"))

# Calculate R0
(R0 <- parms["beta"]/(parms["gamma"] + parms["mu"])) # So R0 = 4.

## beta
##    4

# Calculate the threshold for vaccine-induced herd immunity.
(pc <- 1 - 1/R0) # So 0.75% vaccine cover is required to eliminate the disease.

## beta
## 0.75

# Final epidemic size. Load the rootSolve pacakge in R.
require(rootSolve)

## Loading required package: rootSolve

equil=runsteady(y=c(S= 1-1E-5, I=1E-5, R=0),
                times=c(0, 1E5), func=sir_mod, parms=parms)

# Final epidemic size - rough method
(f <- exp(-R0))
```

```
##     beta
## 0.018316

# For R0 = 4, what fraction of S escape infection?
round(equil$y, 3)

##    S    I    R
## 0.02 0.00 0.98

# The fraction of S that escape infection = 1-f
R0 = seq(0.1, 5, length=50)
betas = R0 * 1/2
f=rep(NA, 50)
for(i in seq(from=1, to=50, by=1)){
  equil=runsteady(y=c(S=1-1E-5, I=1E-5,R=0), times=c(0,1E5), func=sir_mod,
                  parms=c(mu=0, N=1, beta=betas[i], gamma=1/2))
  f[i]=equil$y["R"]
}

# Plot f, the fraction of S that become infected.
plot(R0, f, type="l", xlab = expression(R[0]))
abline(v=2.2, lty=2); abline(v=3.9, lty=2);
abline(h=.845, lty=2); abline(h=.98, lty=2)
points(x=2.2, y = .845, pch = 21, col = "red")
points(x=3.9, y = .98, pch = 21, col = "red")
```

RESULTS AND CONCLUSION

Figure 1 (a): The S, I, and R over time. Figure 1(b): The fraction infected (f) versus R_0



- Figure 1 displays the fraction of susceptibles, infected, and recovered individuals over time in the left panel, and the relationship between the proportion of the pupation that becomes infected with the disease and the basic reproductive rate. It is apparent that a higher proportion of the pupation will become infected as R_0 increases. So, the basic message here is to reduce R_e as much as possible to bring the spread of disease under control. So, every effort must be made to reduce the effective R_e to reduce the fraction of infected individuals in the population.

Esterman (2022) provides R_0 = 3.3 (for the ancestral strain in Wuhan, China); R_0 = 5.1 for Delta that appeared in India; R_0 = 9.5 for Omicron BA.1 in Botswana and South Africa; and R_0 = 13.3 Omicron BA.2. For this study we set the range of $R_0 = 2.2 - 3.9$. Figure 1(b) displays these R_0 values on the horizontal axis and the corresponding proportion of the population that would become infected if no measures are taken to reduce the spread of Covid-19 disease:

1. If $R_0 = 2.2$, at equilibrium only 15.50% of the population escapes infection while 84.50% of the population becomes infected and recovers that includes individual who are impaired health or those who die due to this disease.
2. If $R_0 = 3.9$, at equilibrium only 2% of the population escapes infection while 98% of the population becomes infected and recovers that includes individual who are impaired health or those who die due to this disease.

Clearly these infection numbers are very high and intolerable and call for taking steps to reduce the effect reproductive rate, R_E, that will bring this epidemic under control. Traditional methods of disease surveillance often do not measure cases that are asymptomatic, not diagnosed, or not reported. So, the traditional methods should be supplemented by studies of population-level incidence of Covid-19 based on a national blood sample containing infection-induced SARS-CoV-2 antibodies. One such recent study, published by the CDC, shows that by December 2021, 33.5% (95% CI = 33.1–34.0) of the US population was infected with Covid-19 and by February 2022, 57.7% (95% CI = 57.1–58.3) of the US adults, and about 75% of the US children, were infected by Covid-19 (Clarke, et al., 2022).

Vaccine-Induced Herd Immunity

The threshold for vaccine-induced herd immunity, p_c, can be calculated by p_c = 1 - 1/R_0. So, if $R_0 = 2.2 - 3.9$ then p_c = 54.55% - 74.36% vaccine cover is required to eliminate the disease. This percentage will need to be adjusted for the effectiveness of a vaccine (say it is 50% - 90% effective) and what proportion of the population will take the vaccine.

Taking Steps to Control the Spread of Covid-19

The final research question is addressed here.

- RQ #5. What steps should individuals and organizations take to control the spread of this disease?

The Covid-19 has had a very severally negative impact on the lives of many Americans as they have had to adapt to the new reality of this epidemic. Both non-pharmaceutical and pharmaceutical measurers should be undertaken to control the spread of Covid-19. WHO, CDC, Federal and state governments, The Association of American Medical Colleges, the Center for Health Security, and organizational administrators issues guidelines to guide the behavior of individuals. Table 1 presents some guidelines that were issued in early 2020 and most of them are still valid as a reference for future.

Table 1: Guideline to Reset the US Response to Covid-19

A Road Map to Reset the Nation's Approach to the Pandemic	Resetting Our Response: Changes Needed in the US Approach to Covid-19
Source: Association of American Medical Colleges. Retrieved from https://www.aamc.org/Covidroadmap/roadmap	Source: The Center for Health Security. Retrieved from https://www.centerforhealthsecurity.org/our-work/pubs_archive/pubs-pdfs/2020/200729-resetting-our-response.pdf
Immediate Actions 1. Remedy critical supply and drug shortages. 2. Increase availability and accessibility of testing. 3. Establish national standards on face coverings. 4. Establish and enforce national criteria for local stay-at-home orders and reopening protocols. 5. Establish national criteria for K-12 school reopenings and convene a working group to study different approaches by mid-August. 6. Immediately expand health insurance through COBRA. 7. Begin planning now to prioritize distribution of the SARS-CoV-2 vaccine. 8. Address and resolve health care inequities. 9. Inform, educate, and engage the public. Longer-Term Actions 1. Broaden health insurance. 2. Strengthen the nation’s public health infrastructure.	1. Encourage and, where appropriate, mandate nonpharmaceutical interventions. 2. Close higher risk activities and settings in jurisdictions where the epidemic is worsening and reinstitute stay-at-home orders where healthcare systems are in crisis. 3. Bolster PPE supply chains and stockpiles and make information about the PPE manufacturing base and supply chain publicly available, with the goal of expanding PPE availability. 4. Bolster test supply chains, plan for shortages, and collaborate with states and commercial laboratories to expand capacity and improve test turnaround times. 5. Conduct and make public detailed analyses of epidemiologic data collected during case investigations and contact tracing. 6. Curate and fund a rapid research agenda to cope with major challenges that have arisen. 7. Scale up contact tracing and continue to improve performance. 8. Identify and disseminate best practices for improving the public health response. 9. Plan for a vaccine, including production, allocation, distribution, and community engagement, to ensure a successful rollout. 10. Develop policies and best practices to better protect group institutions.

REFERENCES AND OTHER RESOURCES

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APPENDIX: A BREIF INTRODUCTION TO R LANGUAGE AND ENVIRONMENT

R is an open-source and free software language and environment for statistical analysis, model building, and visualization. R can produce elegant graphs with ease. Ross Ihaka and Robert Gentleman, University of Auckland, developed R in 1991 by utilizing two programming languages -- Scheme and S. Scheme emphasizes simplicity and elegance, and it is a dialect of Lisp language. S language was developed at Bell Telephone Laboratories (Bell Labs) during 1970s and 1980s; it focused on data analysis and emphasized ease of use (Peng, 2022).

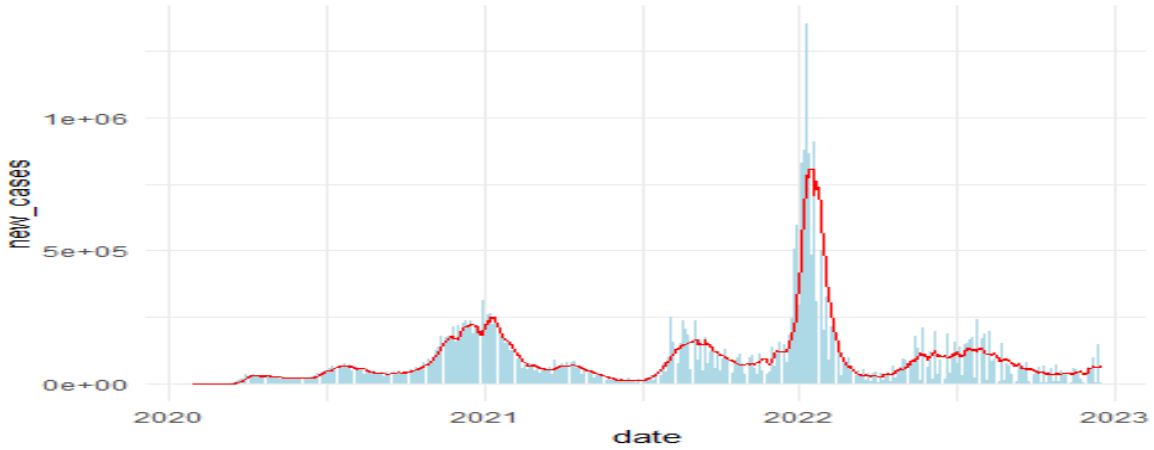
Managers and policy makers interested in exploring and understanding the dynamics of an infectious disease like Covid-19 can do so by using R that they can download and install from https://cran.r-project.org/. Posit (or RStudio) is a popular Integrated Development Environment (IDE) that makes it easier to utilize R and produce high quality output in various formats

(DOCX, HTML, PDF, etc.). Posit is also free and can be download and installed from https://posit.co/. Both R and Posit run on a variety of operating systems including most Unix platforms, Mac OS, and Windows. Many YouTube videos guide beginners to download and install R and Posit (or RStudio) and run R programs (for example, R Programming 101, 2018).

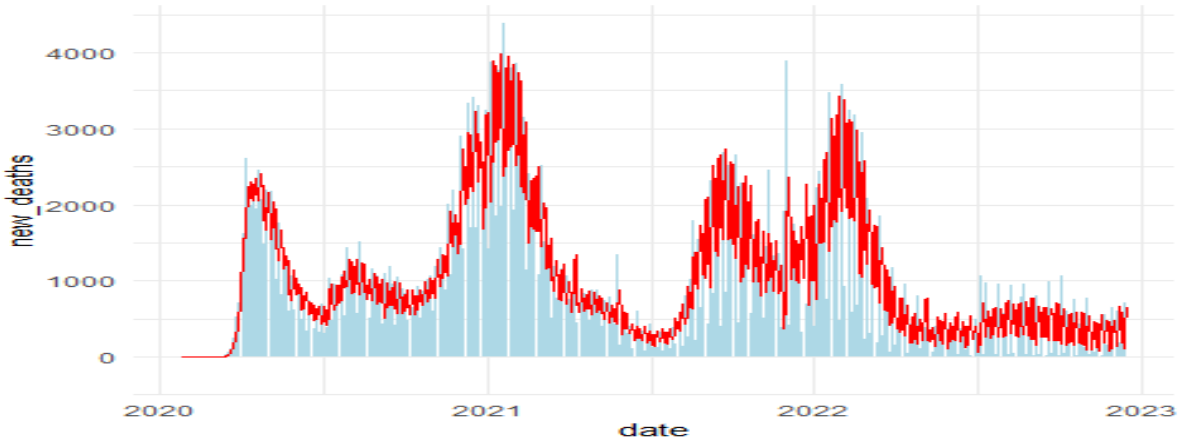
While R is an impressive language and environment for modeling, data analysis, and visualization, its capabilities have been extended by thousands of packages. There are over a hundred R packages for Covid-19 modeling and data analysis (Soetewey, 2020). The following illustrates how to utilize tidycovid19 package in R along with other R packages, to collect and analyze Covid-19 data. The tidycovid19 package provides many functions for downloading, analyzing, and displaying Covid-19 information (Gassen, n.d., Gassen, 2022). Readers can work in the R console or in Posit (or RStudio) to create an R script containing the following R code. China and the US took two different approaches to Covid-19 control, so the following code highlights infections and deaths in these two countries along with analyses about geographic spread of this disease in different regions. The reader will appreciate the ease with which latest Covid-19 data can be accessed, analyzed, and displayed.

```
# R code to obtain, analyze, and display the latest Covid-19 data
# Here a # represents a comment and ## represents results generated by R code.

# set RStudio as the CRAN mirror to download and install R packages
options(repos = c(CRAN = "http://cran.rstudio.com"))

# install an R package called remotes
# install tidycovid19 package: remotes::install_github("joachim-gassen/tidycovid19")

# install an R package called pacman
# load several packages with p_load() function in pacman package
pacman::p_load(tidyverse, tidycovid19, zoo)

# download data with download_merged_data() function in tidycovid19
df <- download_merged_data(cached = TRUE, silent = TRUE)

str(df) # look at the structure of df data file

# print regions
unique(df$region)

## [1] "Latin America & Caribbean " "South Asia"
## [3] "Sub-Saharan Africa "        NA
## [5] "Europe & Central Asia"      "Middle East & North Africa"
## [7] "East Asia & Pacific"        "North America"

# print 3-letter country code
unique(df$iso3c)

# print country names
unique(df$country)

#------------ USA -----------
# new cases aveaged weekly
```

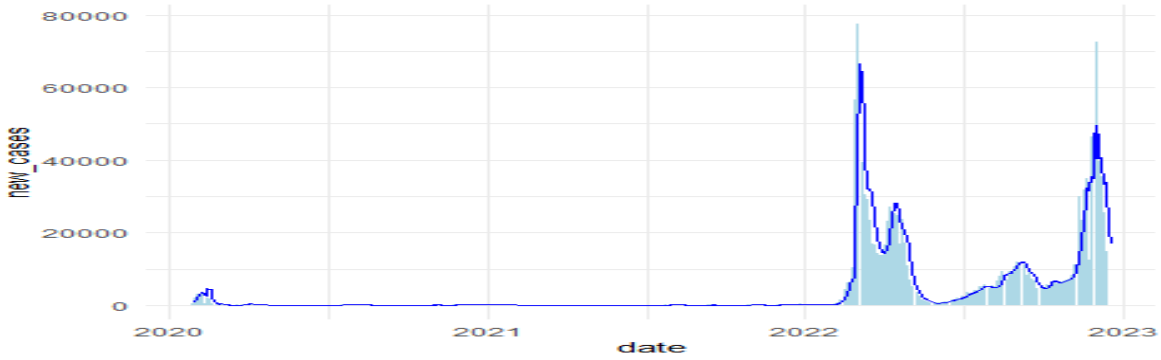
```
df %>% filter(iso3c == "USA") %>%
  mutate(
    new_cases = confirmed - lag(confirmed),
    ave_new_cases = rollmean(new_cases, 7, na.pad=TRUE, align="right")
  ) %>%
  filter(!is.na(new_cases), !is.na(ave_new_cases)) %>%
  ggplot(aes(x = date)) +
  geom_bar(aes(y = new_cases), stat = "identity", fill = "lightblue") +
  geom_line(aes(y = ave_new_cases), color ="red") +
  theme_minimal()
```




```
# new weekly deaths averaged over a month
df %>% filter(iso3c == "USA") %>%
  mutate(
    new_deaths = deaths - lag(deaths),
    ave_new_deaths = rollmean(new_deaths, 4, na.pad=TRUE, align="right")
  ) %>%
  filter(!is.na(new_deaths), !is.na(ave_new_deaths)) %>%
  ggplot(aes(x = date)) +
  geom_bar(aes(y = new_deaths), stat = "identity", fill = "lightblue") +
  geom_line(aes(y = ave_new_deaths), color ="red") +
  theme_minimal()
```

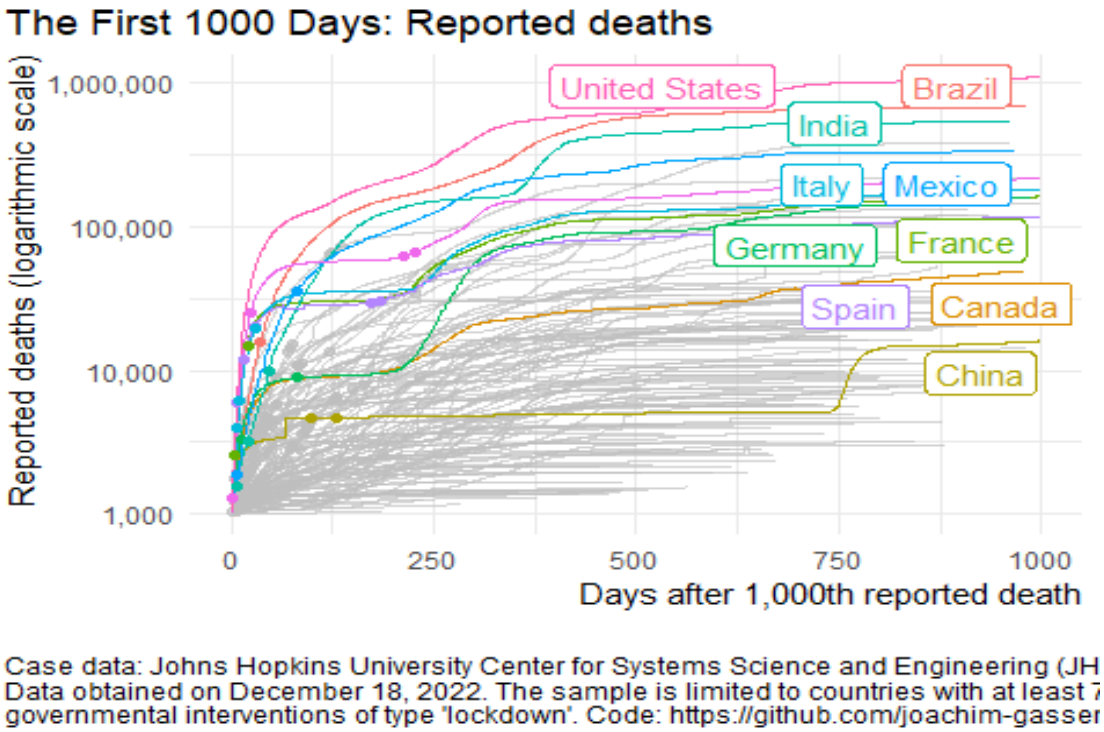


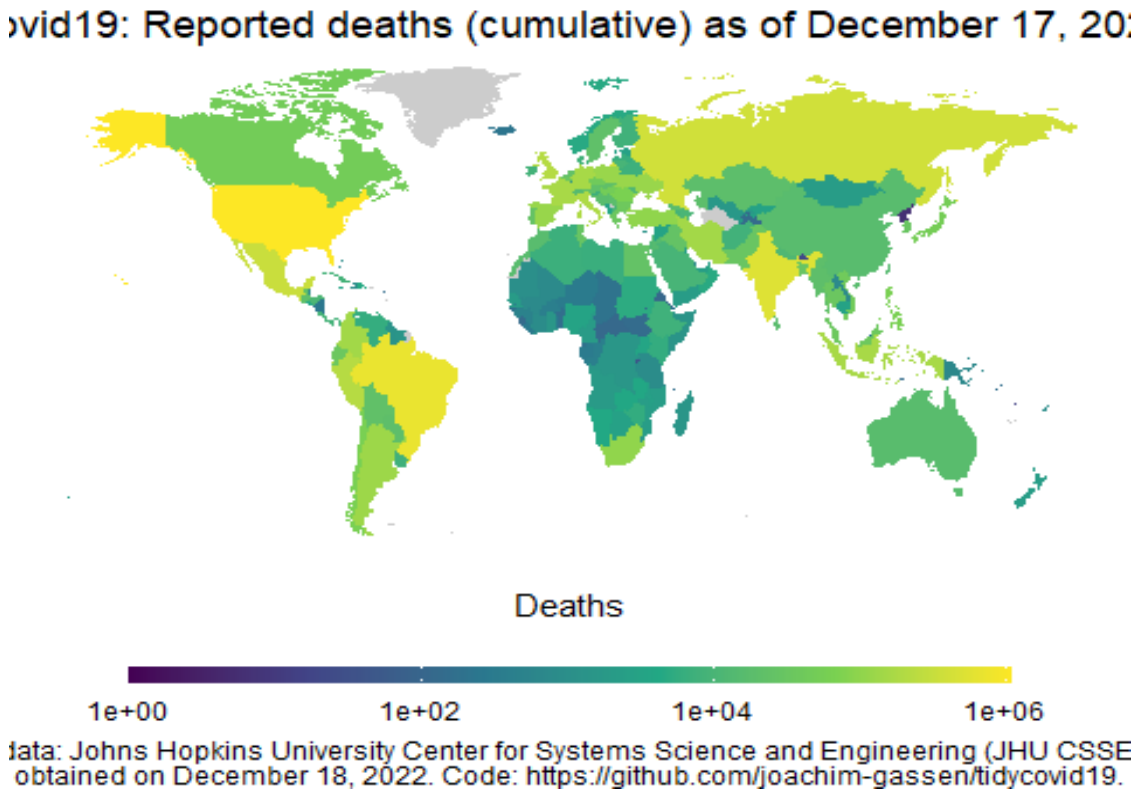

```
#--------- China -----------------
df %>%
  filter(iso3c == "CHN") %>%
  mutate(
    new_cases = confirmed - lag(confirmed),
    ave_new_cases = rollmean(new_cases, 7, na.pad=TRUE, align="right")
  ) %>%
  filter(!is.na(new_cases), !is.na(ave_new_cases)) %>%
  ggplot(aes(x = date)) +
  geom_bar(aes(y = new_cases), stat = "identity", fill = "lightblue") +
  geom_line(aes(y = ave_new_cases), color = "blue") +
  theme_minimal()
```




```
# new weekly deaths averaged over a month
df %>% filter(iso3c == "CHN") %>%
  mutate(
    new_deaths = deaths - lag(deaths),
    ave_new_deaths = rollmean(new_deaths, 4, na.pad=TRUE, align="right")
  ) %>%
  filter(!is.na(new_deaths), !is.na(ave_new_deaths)) %>%
  ggplot(aes(x = date)) +
  geom_bar(aes(y = new_deaths), stat = "identity", fill = "lightblue") +
  geom_line(aes(y = ave_new_deaths), color ="red") +
  theme_minimal()
```

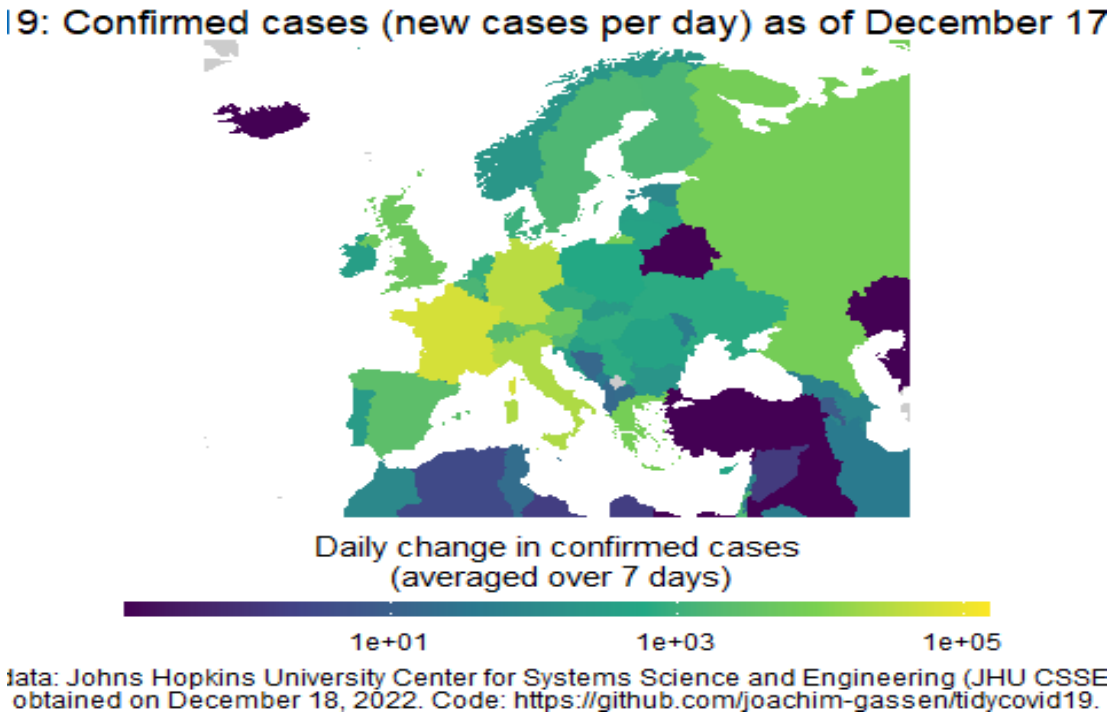

```
#------ many countries ------------------
merged <- download_merged_data(cached = TRUE, silent = TRUE)
plot_covid19_spread(
  merged, highlight = c("BRA", "CAN", "CHN", "DEU", "ESP", "FRA", "GBR", "IND",
"ITA", "MEX", "USA"),
  intervention = "lockdown", edate_cutoff = 1000
)

## Warning: ggrepel: 1 unlabeled data points (too many overlaps). Consider
## increasing max.overlaps
```



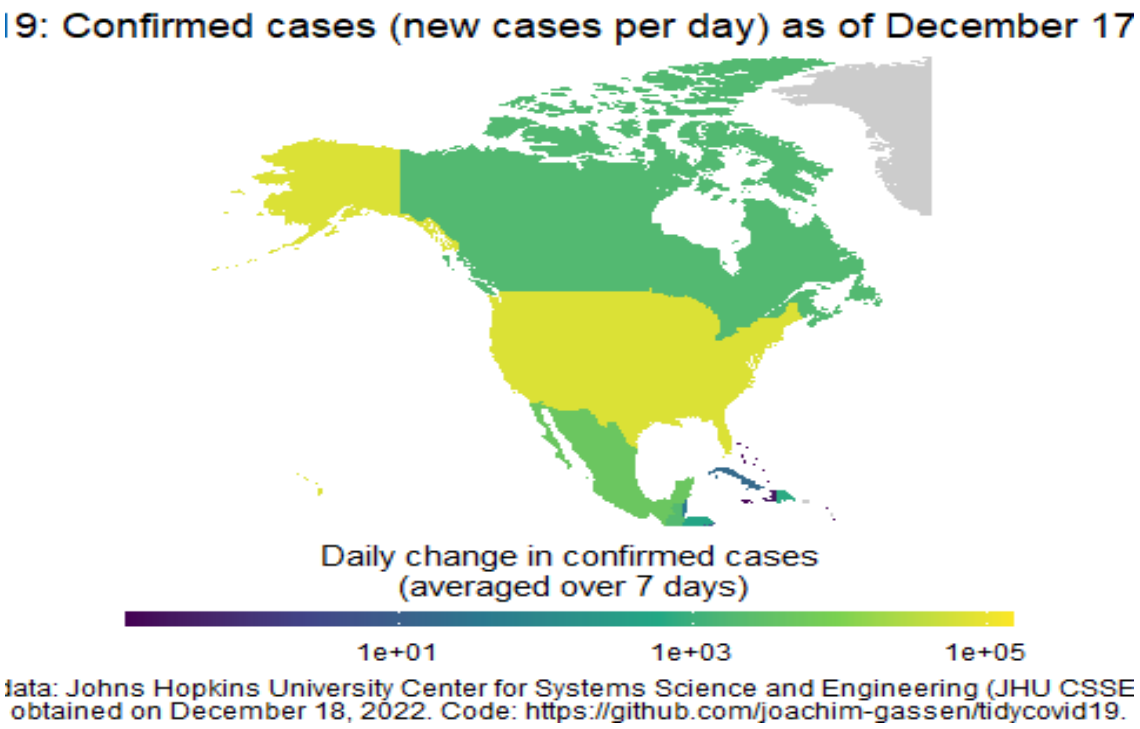


Covid19: Confirmed cases (new cases per day) as of December 17, 2022

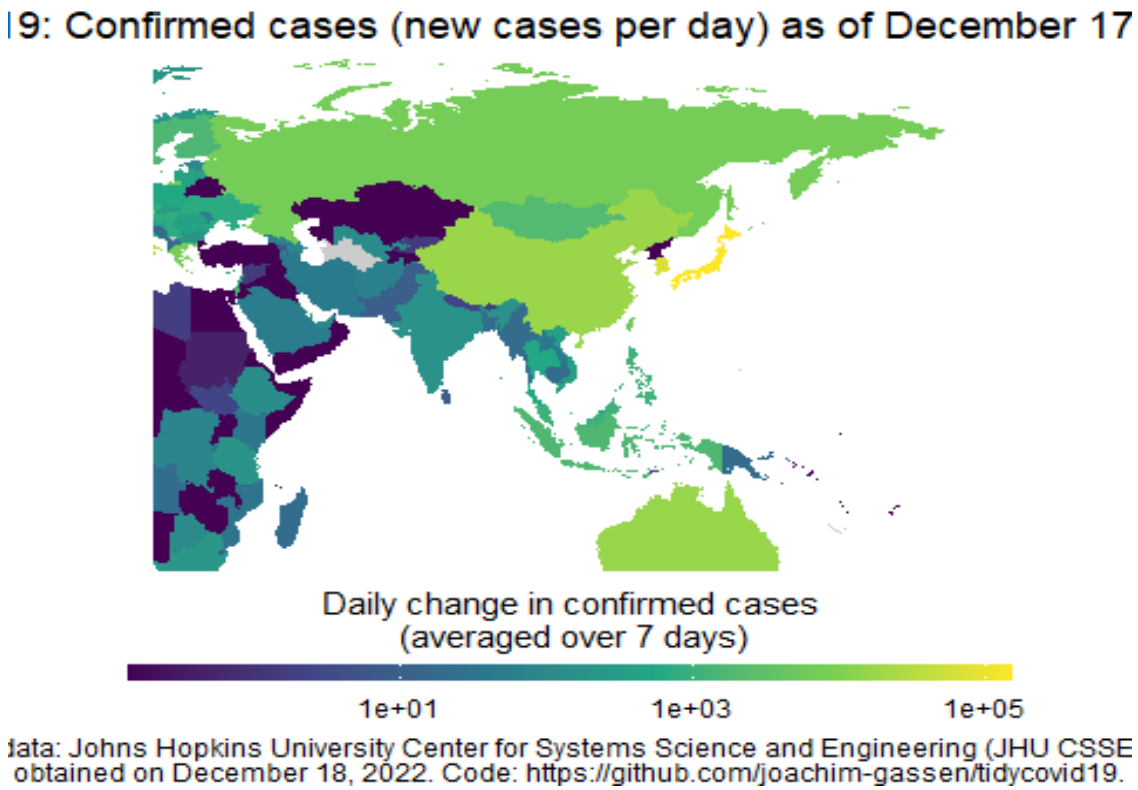
```
# Covid19: Confirmed cases (new cases per day) as of December 17, 2022
map_covid19(merged, type = "confirmed", region = "Europe")
```




```
# Covid19: Confirmed cases (new cases per day) as of December 17, 2022
map_covid19(merged, type = "confirmed", region = "North America")
```




```
# Covid19: Confirmed cases (new cases per day) as of December 17, 2022
map_covid19(merged, type = "confirmed", region = "Asia")
```


9: Confirmed cases (new cases per day) as of December 17
Daily change in confirmed cases
(averaged over 7 days)
1e+01
1e+03
1e+05
lata: Johns Hopkins University Center for Systems Science and Engineering (JHU CSSE
obtained on December 18, 2022. Code: https://github.com/joachim-gassen/tidycovid19.