Biophysics and Physiological Modeling
Chapter 12: COVID-19 and epidemiology (web edition)

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Introduction: going viral …

In this chapter, we'll investigate how the finite difference (FD) approach we developed in **CHAPTER 3** can be used to model the spread of the novel coronavirus that's responsible for the COVID-19 pandemic. Imagine…

> *You've been talking with Esperanza (Espe – a friend studying public health policy and epidemiology) about the marble game and she's intrigued. She thinks that you should be able to apply the finite difference (FD) approach that we've learned in Chapters 3-11 to gain insights into the COVID-19 pandemic. She's heard people on TV say "Without a vaccine everyone who's not immune will eventually get COVID-19. Social distancing will flatten the curve, but ultimately the same number of people will be infected in the end – no matter what we do." She says epidemiological models show that's simply **not true**! Social distancing not only lowers the peak in the infection rate, but it can also reduce the total number infected. It can even prevent the outbreak from occurring at all!*

In **SECTION 12.1** we'll take up Espe's challenge and investigate the simplest possible model of a pandemic. It's an unrealistic **UG model** that predicts "unlimited growth" in the number of infectious people, but it's an important starting point for understanding the pandemic, particularly in the early stages, which we'll call epoch ①. By comparing the UG model with real COVID-19 data for the United States at the beginning of March 2020, we'll discover that it successfully models the infection rate data for the first "19 days" of the pandemic in the US and almost until the end of March 2020. Next, we'll investigate a model that limits the growth of the COVID-19 outbreak by accounting for the finite size of the susceptible population. We'll investigate this **finite population (FP) model** in **SECTION 12.2** and discover the "logistic growth" that it predicts and how social distancing and mask wearing can indeed "flatten the curve" just like the quote Espe mentioned above.

In **SECTION 12.3** we'll add "recovery" to the finite population model, so that infected individuals eventually recover. As we'll discover, adding this simple idea to the epidemiological model makes the difference that Espe was talking about. We'll investigate the resulting **susceptible-infected-recovered model (SIR model)** that was first developed by Kermack and McKendrick way back in 1927. In that model, susceptible individuals can be infected by another infected individual and then recover – that's it! Even though it sounds straight forward, the SIR model's mathematical predictions are surprisingly complex. It's the origin of the epidemiological parameter $\mathcal{R}_0$ (pronounced "R naught") that you may have read about in the news or heard about in the 2011 movie Contagion. It also predicts the concept of "herd immunity" that explains why not all

susceptible people need be infected if social distancing is maintained. For $\mathcal{R}_0 > 1$, the SIR model always predicts that the infection rate curve, $R_i(t)$ will have a characteristic peaked shape that I call the "**exponential dragon**."

In **SECTIONS 12.4 – 12.10** of this **WEB EDITION** of **CHAPTER 12** we'll apply our SIR model to real COVID-19 data in the United States in the period from March 2020 through August 2021. This analysis was done as the data came in day-by-day and is a record of my attempts to find simple models of the COVID-19 pandemic in the United States. Unfortunately, the analysis grew complex and lengthy, but it did result in a peer-reviewed journal article [Nelson 2021]. For completeness, that full investigation is included here in this **WEB EDITION** of **CHAPTER 12**.

In **SECTION 12.4**, we'll apply our SIR model to real COVID-19 data in the United States in the first two weeks of April 2020 and discover that just like meteorological modeling, epidemiological modeling can suffer from the **butterfly effect** (sensitive dependence on initial conditions), which explains why predictions made during the initial exponential growth period were all wrong. In **SECTION 12.5** we'll use data from the first two weeks of April 2020 to predict the infection rate in the US for the next month and beyond to discover that the SIR model does an excellent job of predicting the infection rate until at least Memorial Day (May 25), which we'll call epoch ②. We'll also talk about how implementing social distancing just 7 days earlier could have saved over 82,000 lives and 1.3 million people from COVID-19 infections by Memorial Day 2020. It's an important **public health policy** lesson.

In **SECTION 12.6** we'll investigate modeling the transition from epoch ① to epoch ② by changing the "infection rate coefficient" using a "Gaussian transition function" and assume that all the other SIR model parameters remain unchanged. Once we've successfully done that, we'll change the infection rate coefficient for the US as a whole to that observed in New York City after they implemented social distancing and mask wearing etc. We'll then discover how many infections and lives could have been saved – if the rest of the United States had followed NYC's lead.

In **SECTION 12.7** we'll model the effects of lifting social distancing guidelines prematurely. As we'll discover, this period of **relaxed social distancing** (epoch ③) instigated what became known as the summer surge. The resulting growth in infection was only moderated when the US returned to **stricter social distancing** in epoch ④.

As we'll discover in **SECTION 12.8**, the next epoch ⑤ of the pandemic was caused by a return to **relaxed social distancing** for an extended period. I'll call epoch ⑤ the fall dragon because it was the first time that the infection rate exhibited a peak corresponding to the exponential dragon of the SIR model. The fall dragon was the first time in the pandemic that the model population size became a constraining parameter in the fitted model.

During epoch ⑤, COVID-19 vaccines were approved by the FDA for use in the United States and in **SECTION 12.9** we'll develop and validate a simple modification of the SIR model that's able to include published vaccination data. As we'll discover, this SIRV model is able to successfully model the published infection rate data from the beginning of the pandemic up to May 31, 2021 by adding an epoch ⑥ corresponding to a smaller exponential dragon caused by a substantial further reduction in social distancing.

Epoch ⑦ of the pandemic began after May 31, 2021 and resulted in what became known as the "**delta peak**," because it was caused primarily by the newly dominant delta variant of COVID-19. As we'll discover in **SECTION 12.10**, the beginning of the delta peak could be successfully modeled by an exponential dragon predicted by the SIRV model up until about August 12, 2021, albeit with an extremely high infection rate constant [Nelson 2021]. While the fitted model successfully predicted that a peak would occur soon after August 12, 2021, the behavior of the model during and after the peak did not match the published data at all – most likely because the delta variant did not behave like the previous variants of COVID-19 (mostly alpha). The most likely explanation is that the assumption of permanent immunity was no longer valid during epoch ⑦.

In **APPENDIX 12.A**, we compare our SIR model with one that was used in mid-April 2020 to help hospitals and public health officials with hospital capacity planning in the Penn Medical system.

Modeling the pandemic

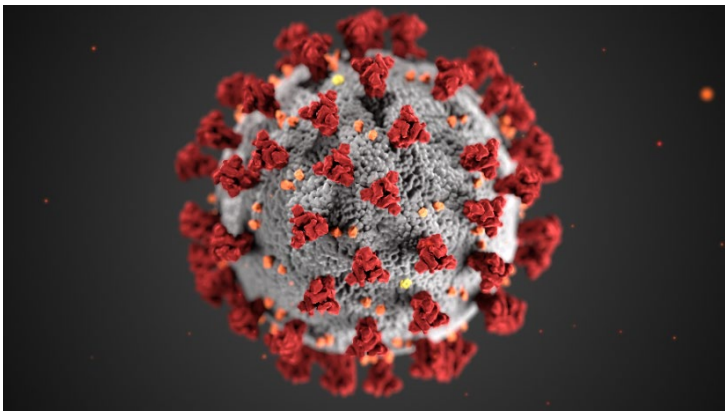


Fig.12.01 Image 23311 from the CDC [2020] – Caption: This illustration, created at the Centers for Disease Control and Prevention (CDC), reveals ultrastructural morphology exhibited by coronaviruses. Note the spikes that adorn the outer surface of the virus, which impart the look of a corona surrounding the virion, when viewed electron microscopically. A novel coronavirus, named Severe Acute Respiratory Syndrome coronavirus 2 (SARS-CoV-2), was identified as the cause of an outbreak of respiratory illness first detected in Wuhan, China in 2019. The illness caused by this virus has been named coronavirus disease 2019 (COVID-19).

Okay, so you've seen Fig.12.01 before, heard a lot about the **COVID-19 pandemic**, and how **social distancing** and **mask wearing** can **flatten the curve** to slow down the spread of the disease.

You've probably even seen a graphic like Fig.12.02 illustrating how social distancing slows the spread of infection to keep the peak number of cases below the capacity of the medical system.

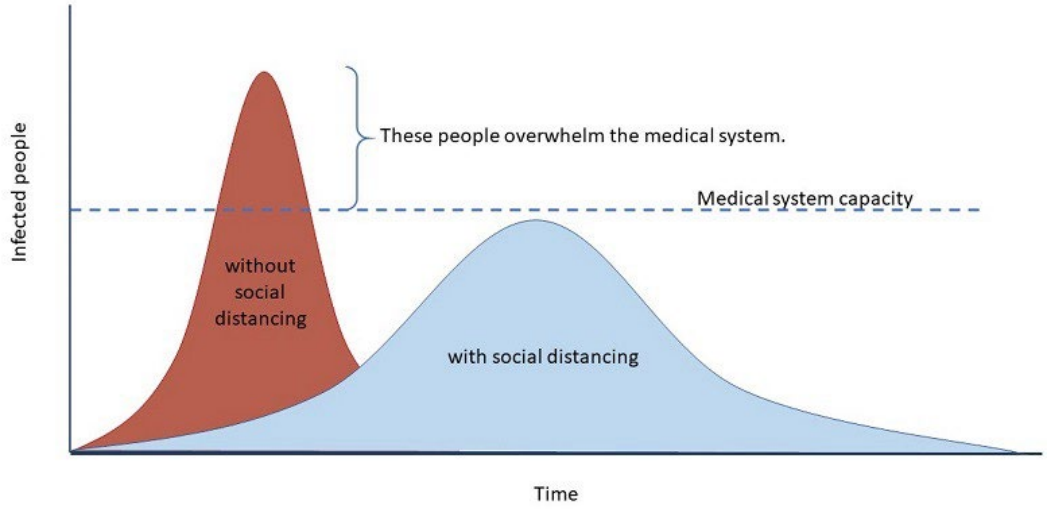


Fig.12.02 Illustration of how social distancing slows spread of infection to keep peak number of cases below the capacity of the medical system (dateline March 10, 2020). [Credit: Nancy R. Gough, BioSerendipity, LLC; This work is licensed under a Creative Commons Attribution-ShareAlike 4.0 International License.] [Gough 2020]

Fig.12.02 is a good journalistic graphic illustrating the effect, but when I first saw it (and others like it), I was struck by the rather simple shape of the curves – they both looked like bell-normal or **Gaussian** curves (**CHAPTERS 8** and **10**) to me. Also, if you've been paying attention to these materials, you should have noticed that the graphic is not a properly formatted scientific graph for real data. The main reason is that the axes don't have numbers or units. That's okay if you're just trying to get across the general idea of **social distancing** – but as a scientific modeler you should want more …

During our extended spring break in 2020, I thought that *now* (March 13, 2020) would be a great time to investigate whether the finite difference methods that we've been developing using this **BIOPHYSICS AND PHYSIOLOGICAL MODELING** (**BPM**) book can be applied to epidemiology and the idea that social distancing [Gough 2020] will help slow the spread of the disease. Let's see what we can discover…

12.1 The outbreak – exponential growth

Initial infections – exponential growth

We can modify the marble game model from **BPM CHAPTERS 1-3** (available online for free at Circle4.com) to provide a starting point for modeling the spread of COVID-19. The simplest model that we'll consider is only realistic during the initial phase of infection and predicts the worst possible case for the epidemic. Fig.12.03 shows a **finite difference** (**FD**) diagram (**CHAPTER 3**) of this worst-case model, which we'll call the **unlimited growth** (**UG**) **model**.

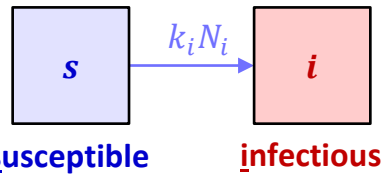


Fig.12.03 FD diagram of a two-box epidemiological model. The two boxes in this **unlimited growth** (**UG**) **model** represent the two parts of the model population. Box s represents people that are susceptible to the disease. Box i represents people that are infectious.

The two boxes in Fig.12.03 represent all the possible states of the **model population**. The criterion for being in the model population is simply that an individual can be infected – and that their infection is reported – if they're exposed.
Note: Unlike most of the FD diagrams we've talked about in this **BPM BOOK**, the two boxes in Fig.12.03 don't represent physical locations – they're conceptual boxes that we're using to characterize subsets of the model population. Our model assumes that all people in the model population (both susceptible and infectious) interact with each other at a constant rate during the time period under consideration.

The UG model assumes that the **infection rate** R_i is given by

$$R_i = k_i N_i \tag{12.1}$$

where N_i [=] 1 is the number of infectious people, the **number infectious**, and k_i [=] 1/d is the **infection rate constant** with units of "per day per infectious person." The idea behind the UG model and equation (12.1) is that an infectious person wanders randomly throughout the model population, just like a molecule in aqueous solution, infecting others with a rate characterized by an infection rate constant k_i. An infection rate constant of $k_i = 0.25\ \text{d}^{-1}$ means that an infectious person infects 0.25 susceptible people per day (or one susceptible person every 4 days), on average, causing them to ''jump'' from box $s \rightarrow i$ when they become infectious – usually some days after contact with the infectious person.

The observed infection rate R_i per day is a number that's published by country at the European Centre for Disease Prevention and Control as **new confirmed cases** (per day) [ECDC 2020]. Those data don't match up with the model exactly, but they're the best data that I could find as of March 16, 2020. What we'd really like to know is the total number of infectious people – regardless of whether they're showing any symptoms or whether they've been officially diagnosed, but those data aren't available.

About what you discovered: a note on notation

I chose to use the symbol N_i for the number infectious to make the notation in this **CHAPTER 12** match what we've done in the rest of this **BPM BOOK**. Epidemiologists prefer using the single uppercase letter I instead of N_i. They also prefer to use Greek letters for the rate constants so that

equation (12.1) would be written as $R_i = \beta I$. We'll stick with using the chemistry k with a descriptive subscript for rate constants and N with a descriptive subscript for numbers in the boxes of the model. N without a subscript will be the total number in the model population. Hence, for the UG model we can write $N = N_s + N_i$ which matches equation (1.1) of the marble game, i.e., $N = N_1 + N_2$. That way, the notation in this **CHAPTER 12** will match all the myriad other models that we've developed based on the marble game. ❑

Let's see what the worst-case FD model of Fig.12.03 predicts …

Unlimited growth

The FD model of Fig.12.03 is just about as simple as it can be, but it has one major difference from all the other models that we've talked about in this **BPM BOOK**. That difference is that the infection rate $R_i = k_i N_i$ (12.1) depends on the **number infectious** N_i – rather than the **number susceptible** N_s, i.e., the FD equation for the change δN_i in the number infectious is

$$\delta N_i = +k_i N_i \delta t \tag{12.2}$$

where the timestep δt [=] d (has units of days). The plus sign + in equation (12.2) is not really necessary, but I included it for dramatic effect! Let me explain … Unlike drug elimination (**CHAPTERS 2** and **4**) – where the rate of *decrease* in the drug concentration depends on the amount already there – the rate of *increase* in the number infectious N_i depends on the number that are already infectious. The change δN_i is always positive, which makes the number infectious N_i always increase. The rate of infection $\delta N_i / \delta t$ is proportional to N_i the number infectious so that the bigger N_i, the bigger the infection rate. In the UG model, there's no limit to the increase, which is why we're calling the FD model of Fig.12.03 the **unlimited growth** (**UG**) **model**.

Data on the spread of COVID-19 is usually reported as the "new infection rate" or "new confirmed cases per day," which corresponds to the infection rate R_i, hence it's convenient for us to formulate our model using that **metric**. Hence, we can write equation (12.2) as

$$\delta N_i = R_i \delta t \tag{12.3}$$

where R_i is given by equation (12.1). Combining this equation (12.3) with the corresponding **FD update equation** (3.31) gives us the following **condensed FD instruction**

$$N_i^{\text{new}} = N_i^{\text{old}} + R_i^{\text{new}} * \delta t \tag{12.4}$$

for predicting the new number infectious N_i^{new} from the old number infectious N_i^{old} after a timestep δt, by adding the change in the number infectious $\delta N_i^{\text{new}} = R_i^{\text{new}} * \delta t$, where $R_i^{\text{new}} = k_i * N_i^{\text{old}}$ from equation (12.1).

Q.12.01 **(a)** Using equations (12.1) and (12.4) *write out* a complete FD algorithm, including unit checks, to calculate the infection rate $R_i(t)$ and number infectious $N_i(t)$ using a timestep of $\delta t = 1$ d, an infection rate constant of $k_i = 0.3\ \text{d}^{-1}$ (where d^{-1} is pronounced "per day"), and an initial number infectious of $N_i(t = 0) = N_0 = 10$.
(b) By hand, calculate steps 0, 1, and 2 of your finite difference algorithm and *record* your answer in the form of an FD output table.
Hint: As usual, you should do parts (a) and (b) of this question together. It's easier that way.
Note: I go over the how to do these questions in the YouTube video https://youtu.be/gLao39Wcf3Y [Nelson 2020a] for this **SECTION 12.1**.

About what you discovered: the infection rate constant k_i

It's important to note that the infection rate constant has a simple interpretation. The value of $k_i = 0.3\ \text{d}^{-1}$ in Q.12.01 means that an infectious person infects 0.3 susceptible people per day (on average) while they are infectious in our UG model. ❑

Q.12.02 **(a)** Open the preformatted spreadsheet BPM.Ch12_Unlimited_growth.xlsx and fill in the blank cells with your algorithm and check that you get *exactly* the same results that you calculated by hand in Q.12.01(b). The spreadsheet should automatically plot both the new infection rate $R_i(t)$ and the number infectious $N_i(t)$. As always, you then need to reduce the timestep δt and add enough steps so that the curves reach day $t = 19$ d. *Record* your graph for the number infectious N_i as a function of time.
Reminder: As usual, the timestep parameter δt should be made small enough that it doesn't affect the model.
(b) Make a copy of each of the two graphs and change the vertical axis of each graph to a **Logarithmic scale** (**CHAPTER 2**). *Record* your semi-log graph for the new infection rate $R_i(t)$.
(c) *Briefly describe* what you can conclude from the shapes of the resulting semi-log graphs.

Q.12.03 **CALCULUS QUESTION** **(a)** Using calculus, *show that* the analytical solution to FD equation (12.2) for $N_i(t)$ in the limit that $\delta t \to 0$ is:

$$N_i = N_0 e^{k_i t} \tag{12.5}$$

where N_0 is the initial number infectious N_i at time $t = 0$. Your answer should use a format similar to the "Calculus can be useful" AWYD in **CHAPTER 3**.
(b) By taking the derivative of equation (12.5), *show that* the analytical solution for $R_i(t)$ is

$$R_i = k_i N_0 e^{k_i t} \tag{12.6}$$

Q.12.04 **DISCUSSION QUESTION** By substituting equation (12.5) into equation (12.1), *show that* the analytical solution for R_i as a function of time is equation (12.6).
Hint: Okay, this is not a trick question. It really is that easy!

About what you discovered: Proportional change once again

In Q.12.02, Q.12.03 and Q.12.04 you showed that the initial **unlimited growth model** of the spread of an infection like COVID-19 is another example of proportional change. The only major mathematical difference between equations (12.5) and (12.6) and equations (3.17), (4.9), (4.21), (9.18) and (11.74), is that our unlimited growth model has a *positive* rather than a *negative* exponent, which means that it describes **exponential growth** instead of **exponential decay**.

Your answer to Q.12.02(a) should look something like Fig.12.04. It shows the characteristic exponential growth that's expected for an unlimited growth model. Fig.12.05 shows the same model data on a semi-log graph. The fact that it's a straight line, indicates the **exponential dependence** of the number infectious N_i on time t (**CHAPTER 2**).

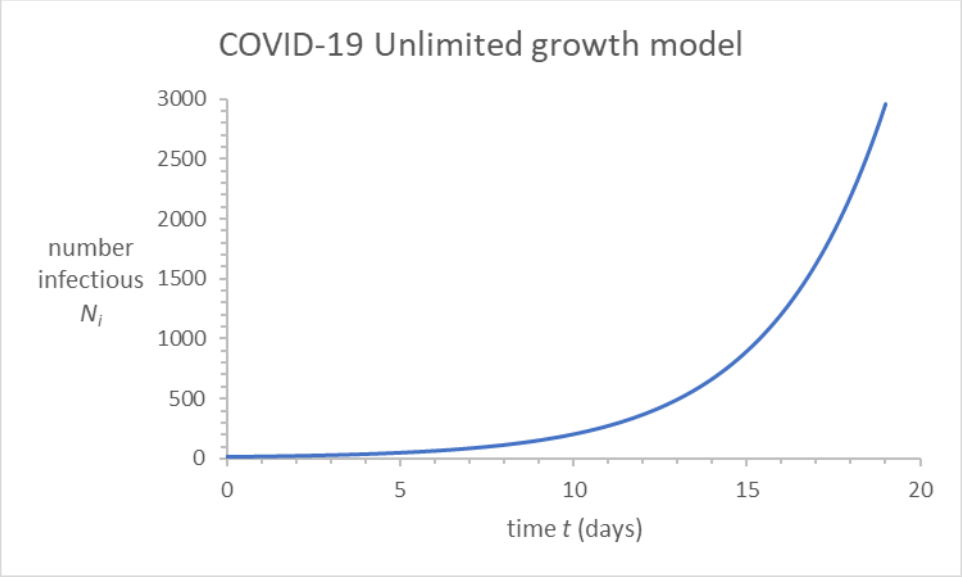


Fig.12.04 Excel chart showing the exponential growth of the number infectious N_i according to our unlimited growth model of COVID-19.

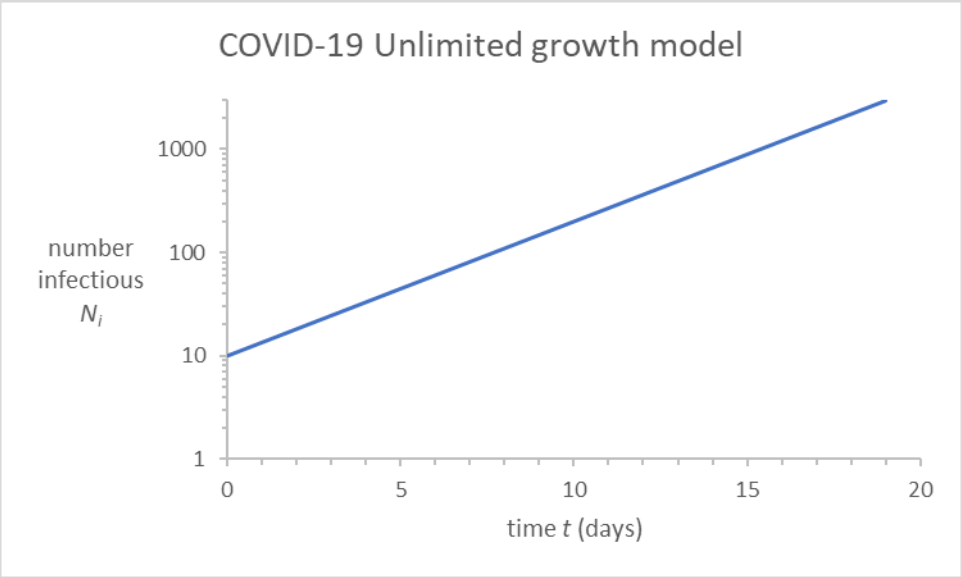


Fig.12.05 Excel semi-log chart showing the exponential growth of the number infectious N_i according to our unlimited growth model of COVID-19. **Note:** This figure is not the same as your answer to Q.12.02(b).

In Q.12.04 you confirmed that equation (12.5) is consistent with our model, by showing that our model's generating equation (12.1) successfully predicts the mathematical form (12.6) predicted by equation (12.5) using calculus in Q.12.03.

Note: It's important to realize that time $t = 0$ in the model is not the time of the first case of COVID-19, I chose an initial infectious number of $N_0 = 10$ for reasons that should become clear when we compare the model with the published number of confirmed new cases per day for the US.
Also note: Equation (12.1) is the reason that the graphs of both $N_i(t)$ and $R_i(t)$ show exponential growth. Equation (12.1) states that the rate of new infections R_i is **proportional** to the number already infectious N_i – another example of **proportional change**. ❑

Doubling time

The **doubling time** t_d is the time it takes for the number infectious N_i to double.

Q.12.05 **(a)** By substituting $N_i = 2N_0$ and $t = t_d$ into equation (12.5), *show that* the doubling time is predicted to be

$$t_d = \frac{\ln 2}{k_i} \tag{12.7}$$

(b) Using equation (12.7) *calculate* the doubling time for the unlimited growth model of COVID-19 spread in Q.12.01 with $k_i = 0.3\ \mathrm{d}^{-1}$.

About what you discovered: doubling time

The **doubling time** that you calculated in Q.12.05(b) ($t_d = 2.3$ days) tells us how long it takes for the number of infectious people to double in the unlimited growth model of Fig.12.03. It's analogous to the to the half-life $t_{½}$ that we discussed at length in **CHAPTER 2** and **CHAPTER 4**. Unfortunately, there's a rather dramatic difference. After each half life, the number of drug molecules (or radioactive nuclei) *decreases* to half its previous value, whereas after each doubling time, the number infectious *doubles*. If you've never studied exponential growth before, you'll probably be surprised by the **explosive** consequences of such a model. The doubling and repeated redoubling predict a pattern that's *always* unsustainable! Let's see what we can discover … ❑

Q.12.06 DISCUSSION QUESTION **(a)** Open your spreadsheet answer to Q.12.02, and *save* a fresh copy of it for this question – a good filename is BPM.Q.12.06(a).xlsx. Then *extend* the graph out from 19 days to 30 days. *Record* R_i the number of new infections predicted for day 30 and the number infectious N_i.

(b) *Compare* your spreadsheet predictions with the predictions of equations (12.6) and (12.5) for day $t = 30$ d of the model.

1st Hint: Your numbers won't be exactly the same as each other, but if there's a significant difference you'll have to decrease the timestep δt – you should have already done that when you answered Q.12.02(a) … Recall, as we discovered in **CHAPTER 3**, if the timestep δt is too big, the FD model will not give accurate results. Because of its nature, FD equation (12.2) is one that requires a smaller-than-you-might-expect timestep – it's another example of a **stiff equation** (**CHAPTER 11**).

2nd Hint: As always, you should also use what you learned about making quantitative comparisons in the "talking numbers" AWYD in **CHAPTER 2**. You might find the preformatted spreadsheet BPM.Ch02_Talking_numbers.xlsx useful.

(c) Extend the graph out from 30 days to 60 days. *Record* R_i the number of new infections predicted for day 60 and the number infectious N_i.

(d) *Compare* your spreadsheet predictions with the predictions of equations (12.6) and (12.5) for day $t = 30$ d of the model.

Don't freak out: The huge number on day 60 is reliant on the assumption of unlimited growth and that no individual ever recovers from the disease and that there's no social distancing or mask wearing and no quarantine of the exposed or isolation of the infectious. We'll get to all of that soon … but it's important to understand just how devastatingly explosive unrestricted **exponential growth** really is.

About what you discovered: exponential growth has explosive consequences

Another example of exponential growth is a nuclear explosive device. **Induced nuclear fission** of **uranium 235** (**^{235}U**) occurs when a ^{235}U nucleus is hit by a neutron. The ^{235}U nucleus randomly splits (**fissions**) into smaller parts, and on average releases about 2.5 more neutrons and a great deal of energy. If this occurs deep inside a mass of pure uranium 235, then each neutron is likely to collide with another ^{235}U nucleus, which in turn will produce 2.5 more neutrons … a **chain reaction** then ensues. If we made an FD model of this process, we'd get a similar exponential

growth curve to Fig.12.04. However, the timescale would be much, much shorter. The exponential growth continues until the ^{235}U mass blows apart from all the energy released (a **nuclear fizzle**) or all of the ^{235}U nuclei are split apart releasing the maximum amount of energy – a **nuclear explosion**. You might be interested to know that the critical mass required to initiate this kind of unlimited fission is about 52 kg, which corresponds to a sphere of pure ^{235}U about 17 cm in diameter. This doesn't sound like very much – but thankfully separating the rare ^{235}U nuclei from naturally occurring uranium (mostly ^{238}U) is *extremely* difficult!

Regular chemical explosives, used in mining etc., also rely on a rapid chain reaction that releases energy. The main difference is that nuclear reactions release about one million times more energy! Yet another example of exponential growth – that you may already have heard of – is bacterial growth in an infinite medium. If the medium is not infinite, then the bacterial growth is only exponential initially and it slows down when resources become scarce. We'll be modeling this limitation in **SECTION 12.2**. ❑

Q.12.07 **DISCUSSION QUESTION** Add a **Theory table** (**CHAPTER 2**) to your spreadsheet from Q.12.02 to plot the analytical equation (12.5) out to 19 days.
(a) *Record* a graph that clearly shows both the FD model and the analytical solution (12.5).
(b) *Briefly discuss* what you can conclude about the equivalence of our FD model and the analytical solution (12.5) for exponential growth.

Comparison with reported data … day-19

Okay, so now that that we've investigated the properties of the unlimited growth model, let's see how well it does in predicting the real COVID-19 data in the US. If you're interested in other countries, the data are also available at Our World in Data the Our World in Data (EOWID) [OWID 2022c]bas **new confirmed cases** (per day).

Q.12.08 **DISCUSSION QUESTION** Open the preformatted spreadsheet BPM.Ch12_USA_day-19.xlsx. It contains data reported at the ECDC as **new confirmed cases** (per day) in the USA in the 19 days following Feb 26 2020.
(a) Add an **Exponential trendline** to the graph and check the options for **Display Equation on chart** and **Display R-squared value on chart**. After making sure that the chart is formatted properly, *record* your graph.
(b) *Record* the model parameters that you can obtain from the Excel trendline equation in the graph by comparing it with equation (12.6).
Hint: You'll need to determine k_i first before you calculate N_0.
(c) Before you read the following AWYD, *briefly discuss* what you can conclude about the applicability of the unlimited growth model from the graph you just made.

About what you discovered: … not so fast – don't jump to conclusions!

Your answer for Q.12.08(a) should look something like Fig.12.06. Most people looking at Fig.12.06 would (quite reasonably) have the optimistic view that the data for the last 5 days appear

to be below the predictions of the exponential model, but there's a problem with that conclusion that you may have forgotten from **CHAPTERS 4** and **6** – Excel doesn't actually do a proper least-squares fit when it does an "**exponential trendline**." Let's see what we can discover …

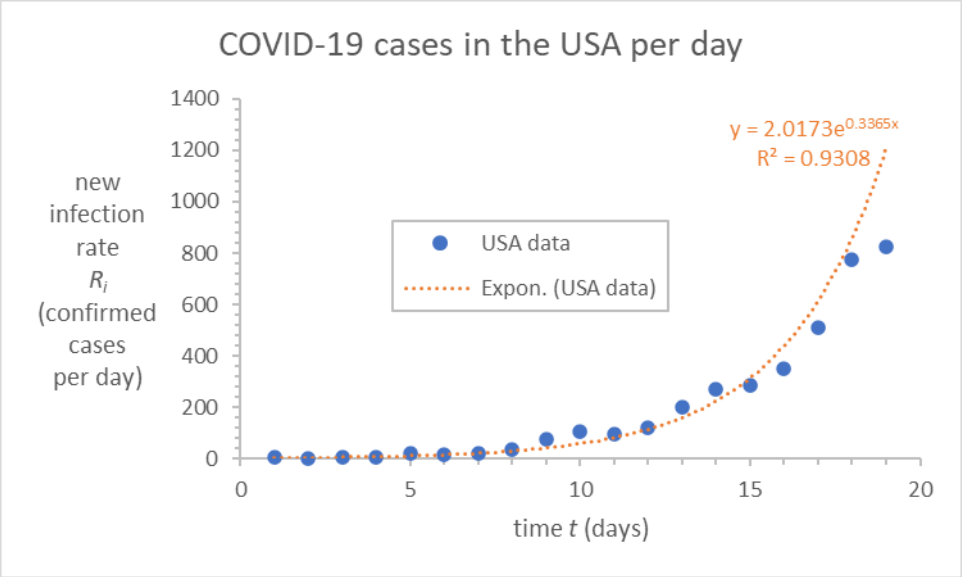


Fig.12.06 Excel chart comparing the exponential growth model of equation (12.6) with reported data for the USA in the 19 days since February 26, 2020. The dotted line is an Excel "exponential trendline" fit. Data source ECDC [2020].

❑

Q.12.09 **DISCUSSION QUESTION** Using what you learned in **CHAPTER 6**, fill in the three empty columns of the experimental data table labeled **USA new infections starting 2/27/2020 (ECDC)** to do a proper least-squares fit to the USA data. The **UG** column should calculate the theoretical (expected) infection rate R_i using equation (12.6). The residuals r should be calculated using equation (4.12), the r^2 column should be calculated by squaring the residuals and the **quality of fit** Q should be calculated using equation (6.11).

Note: I go over the how to do these questions in the YouTube video https://youtu.be/gLao39Wcf3Y for this **SECTION 12.1** [Nelson 2020a].

(a) Before you do anything else, delete the Excel trendline and add a series to your graph to show the prediction of equation (12.6). *Record* your graph showing the comparison with the unlimited growth (**UG**) model with the parameters $N_0 = 6$ and $k_i = 0.34$, which should already be in the spreadsheet.

(b) Using the techniques we learned in **CHAPTER 6**, use Excel's **Solver** to do a least-squares fit to equation (12.6) and record your **least-squares fit** to the USA data up to day 19 of the COVID-19 epidemic in the US. *Record* your graph showing the least-squares fit to the USA data.

About what you discovered: scientists need to be objective

As we discussed **CHAPTER 5**, it's important for scientists to question everything [tomtom5418 2012], including our own optimistic expectations. You should always do a sanity check when you

look at any graph including a fit to data. The fact that the last five data points in Fig.12.06 are lower than the "exponential trendline" fit should make you prick up your scientific ears. What's going on? Why are the last 5 days different? Are we doing this right? As we've learned from the marble game, there's always some kind of unpredictability in real world data. The least-squares fit in Fig.12.07 shows that the USA data are more evenly spread around the prediction – but that's precisely what a least-squares fit does! The question is not whether there's an even spread but whether there are **systematic deviations**. That can be answered best with a residuals graph (**CHAPTER 4**). But in the case of exponential growth or decay we can also gain the same insights from a semi-log graph …

Note: This section was written at USA day 19 (March 16, 2020). As of this writing, I have no idea of what's going to happen next … my sincere hope is that social distancing etc. will slow the rate of infection by reducing k_i in the US … the data from China seem encouraging – that k_i can be reduced – but the future is the undiscovered country … in the meantime, let's see what our modeling approach can tell us about what to expect in the future.

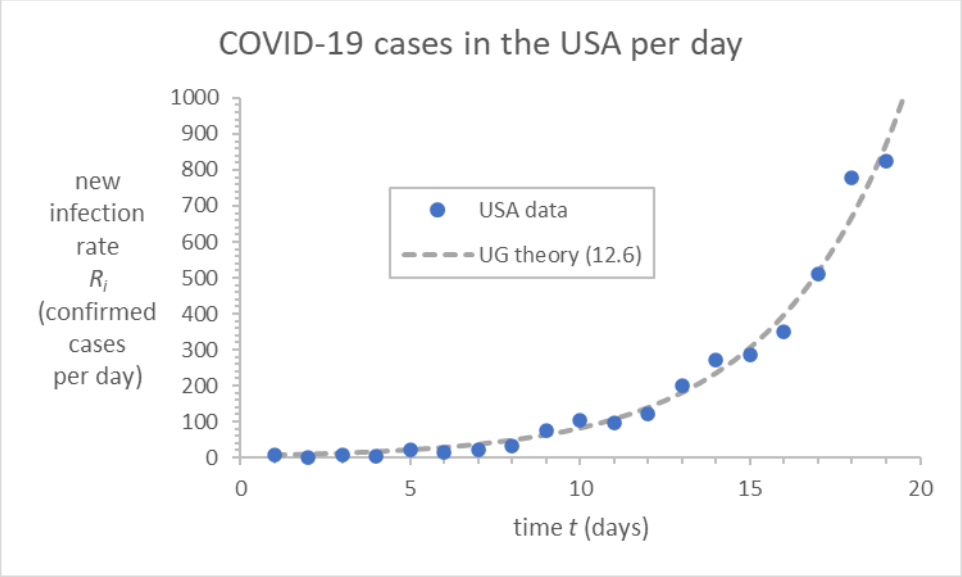


Fig.12.07 Excel chart comparing the exponential growth model of equation (12.6) with reported data for the USA in the 19 days since February 26, 2020. The dotted line is a more scientific **least-squares fit** to the USA data for the "first 19 days." The fitted model parameters are $N_0 = 23$ and $k_i = 0.26\ \mathrm{d}^{-1}$. Data source ECDC [2020].

❑

Semi-log graphs – a different perspective

Q.12.10 DISCUSSION QUESTION **(a)** Change the vertical axis of your graph from Q.12.08(a) to a **Logarithmic scale**. *Record* your graph.

(b) Change the vertical axis of your graph from Q.12.09(b) to a **Logarithmic scale**. *Record* your graph.

(c) As we discovered in **CHAPTERS 4** and **6**, there's a technical difference between the least-squares fit to an exponential function (Q.12.09) Fig.12.07 and Excel's exponential

trendline fit in (Q.12.08(a)) Fig.06 – see the "exponential fit technicality" AWYD in **CHAPTER 4**. *Briefly explain* any differences you see.

About what you discovered: technicality – bias in Excel's exponential trendline

Fig.12.08 shows a semi-log graph that shows a combination of your answers to Q.12.10(a) and (b) (you weren't expected to make this combined graph). The **LS fit** is the same fit as in Fig.12.07. It minimizes the sum of the squares of the residuals in the graph of Fig.12.07. As we discovered in **CHAPTERS 4** and **6**, Excel's **exponential trendline** is actually a linear regression to the log of the data that minimizes the sum of the squares of the residuals of the log values – when it's rescaled as shown in Fig.12.08, which makes all the residuals equally important when viewed on a semi-log graph like Fig.12.08. In contrast, the **LS fit** in Fig.12.08 makes all the residuals equally important when viewed on an unscaled (linear scale) graph like Fig.12.07.

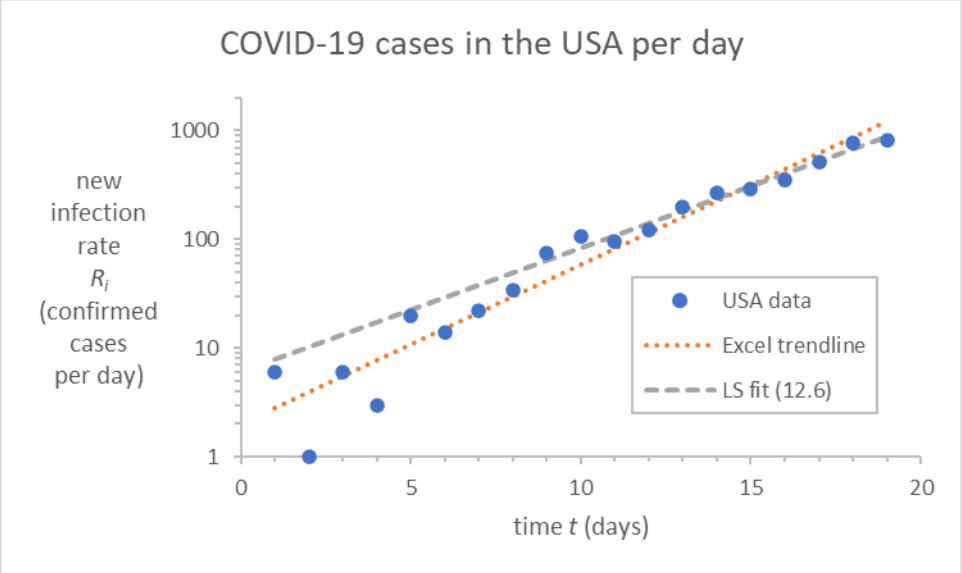


Fig.12.08 Excel semi-log chart comparing the exponential growth model of equation (12.6) with reported data for the USA in the 19 days since February 26, 2020. The dotted line is Excel's "exponential trendline" and the dashed line is a more scientific **least-squares fit** to the USA data for the "first 19 days." The fitted model parameters are $N_0 = 6.0$ and $k_i = 0.34\ \mathrm{d}^{-1}$ for the Excel trendline and $N_0 = 23$ and $k_i = 0.26\ \mathrm{d}^{-1}$ for the LS fit. Data source ECDC [2020]. **Note:** You weren't expected to combine the graphs for Q.12.10(a) and (b) to make Fig.12.08.

The net result is that the Excel **exponential trendline** is biased toward the low values early on and the **LS fit** is not. However, because of the shape of the exponential curve, any deviations from the model at high R_i will produce larger absolute residuals, if there's a fixed percentage measurement variability. That will make the LS fit on a semi-log plot *appear* to be biased towards the large numbers at later times. This means that if social distancing is flattening the curve, then the first indication should be a decrease in the LS-fitted infection rate constant k_i … ❑

12.2 Finite population (FP) model

Finite population model

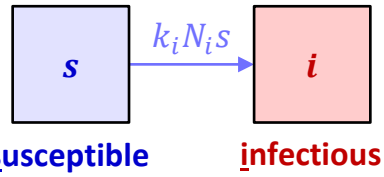


Fig.12.09 FD diagram of a two-box epidemiological model exhibiting limited growth. The two boxes in this **finite population** (**FP**) **model** represent the two parts of the model population that can be affected by the disease. Box s represents the portion susceptible to the disease. Box i represents the portion infectious. Lowercase s is the fraction of the model population that are still susceptible to infection.

One of the problems with our **unlimited growth model** is that the spread of the disease is – well – unlimited! The obvious way to overcome that limitation is to change the model so that it considers the **finite** nature of the susceptible **population**. For example, if you're modeling the situation in New Zealand, the total number infectious N_i can't possibly ever be more that 4.8 million – the total population of New Zealand (as of March, 2020).

Fig.12.09 shows a two-box model that modifies the **infection rate** R_i to be

$$R_i = k_i N_i s \tag{12.8}$$

where k_i [=] 1/d is the **infection rate constant** with units of "per day per infectious person," N_i [=] 1 is the number of infectious people and s [=] 1 is the **susceptible fraction** (note the lowercase "s") of the population *defined* by

$$s \equiv \frac{N_s}{N} \tag{12.9}$$

where N_s is the **number susceptible** and N (with no subscript) is the total number of people in the **model population**, where

$$N = N_s + N_i \tag{12.10}$$

The idea behind equation (12.8) can be understood by thinking about the GlowScript sim MarbleGame once it reaches equilibrium at about $t \approx 2$ ms. The marbles are then evenly spread out throughout the two boxes. If the marbles represent people, infections occur when they get close together. If we assume that encounters between people occur at a constant rate, then the **probability** that an infectious person interacts with a susceptible person (as opposed to another infectious person) is simply s the fraction of the model population that's susceptible. In other words, s is the fraction of people that an infectious person encounters that are still susceptible to the virus (that's what equation (12.9) *defines* as the **susceptible fraction**).

A logical consequence of equation (12.8) is that at the beginning of the epidemic, the susceptible fraction is close to one as $N_s \approx N$ so that

$$s = \frac{N_s}{N} \approx \frac{N}{N} = 1 \tag{12.11}$$

and equation (12.8) reduces to equation (12.1). (Yes, you should go back and reread equations (12.8) and (12.1) to make sure you understand why.) As the epidemic progresses, the susceptible fraction s will decrease – eventually going to zero – once the whole model population is infectious and $s = 0$. When that happens, the infection rate R_i also goes to zero. Hence, equation (12.8) makes the infection rate R_i **proportional** to the susceptible fraction s, so that as the susceptible fraction s get smaller the infection rate R_i gets proportionally slower.

Q.12.11 **(a)** Substitute the definition (12.9) of s into equation (12.8) and solve equation (12.10) for N_s to *show that* our **finite population model** can be calculated using the following algorithm instructions

$$R_i^{\text{new}} = k_i * N_i^{\text{old}} * N_s^{\text{old}}/N \tag{12.12}$$

$$N_i^{\text{new}} = N_i^{\text{old}} + R_i^{\text{new}} * \delta t \tag{12.4}$$

and

$$N_s^{\text{new}} = N - N_i^{\text{new}} \tag{12.13}$$

(b) Using equations (12.12), (12.4) and (12.13) *write out* a complete FD algorithm, including unit checks, to calculate the infection rate $R_i(t)$ and the number infectious $N_i(t)$, for a model population of $N = 1000$ individuals using a timestep of $\delta t = 1$ d, an infection rate constant of $k_i = 0.3\ \text{d}^{-1}$, and an initial number infectious of $N_0 = 1$.
(c) By hand, calculate steps 0, 1, and 2 of your finite difference algorithm and *record* your answer in the form of an FD output table.
Hint: As usual, you should do parts (b) and (c) of this question together. It's easier that way.

Q.12.12 **(a)** Open the preformatted spreadsheet BPM.Ch12_Finite_population.xlsx and fill in the blank cells with your algorithm and check that you get *exactly* the same results that you calculated by hand in Q.12.11(c). The spreadsheet should automatically plot both the new infection rate R_i and the number infectious N_i and the number susceptible N_s as a function of time. As always, you then need to reduce the timestep δt and add enough steps so that the curves visually reach a steady state at the end of the model. *Record* your graph for the new infection rate R_i as a function of time.
Hint: The preformatted spreadsheet charts extend to row **5003** for a good reason.
(b) *Briefly explain* why the model curve for the infection rate R_i has a peak whereas the number infectious N_i always increases.

Social distancing Social distancing – flattening the curve

It seems obvious that if *everybody* has fewer physical interactions – **social distancing** – that will lower the rate that infectious people interact with susceptible people. We can account for that effect in our finite population model by reducing the infection rate constant k_i. In other words, if we reduce the rate of social interaction between *all* people in the population, then the infection rate constant k_i should be reduced proportionally.

Q.12.13 **DISCUSSION QUESTION** **(a)** To see the effect of social distancing on the FP model, change the infection rate constant to $k_i = 0.15\ \mathrm{d}^{-1}$ (i.e., one half of the original model), then extend your graph in time until the graphs once again reach a steady state at the end of the model. *Record* your graph for the new infection rate R_i as a function of time.
Hint: You can use a longer timestep δt than in Q.12.12.
(b) Change the infection rate constant to $k_i = 0.075\ \mathrm{d}^{-1}$ (i.e., one quarter of the original model). *Record* your graph for the new infection rate R_i as a function of time.
(c) *Briefly describe* how decreasing the infection rate constant (by social distancing, mask wearing etc.) affects the model by discussing the timing and magnitude of the peak value in the new infection rate R_i.
(d) *Briefly explain* if you think this is a good example of the effect of **social distancing**. as illustrated in Fig.12.02?

Q.12.14 **(a)** Change the infection rate constant back to $k_i = 0.3\ \mathrm{d}^{-1}$, and then increase the model population to $N = 10{,}000$, and then $N = 1{,}000{,}000$. *Briefly describe* how changing the population size changes the model by discussing the magnitude and peak value of the new infection rate R_i.
(c) Does everyone in the model population still become infectious in this FP model? *Briefly explain* if social distancing etc. or changing the population size has an effect on the fraction susceptible $s = N_s/N$ at the end of the model.
(c) Change the model population to $N = 3.3 \times 10^8$, the estimated total population in the US in mid-April, 2020. *Briefly describe* what you can conclude about the FP model's predictions.
Reminder: You can enter $N = 3.3 \times 10^8$ into Excel as **3.3e8**.

About what you discovered: social distancing – flattening the curve

Fig.12.10 shows a graph that shows a combination of your answers to Q.12.12(a) and Q.12.13(a) (you weren't expected to make this combined graph or use the **Area Chart** format that I used in Excel).

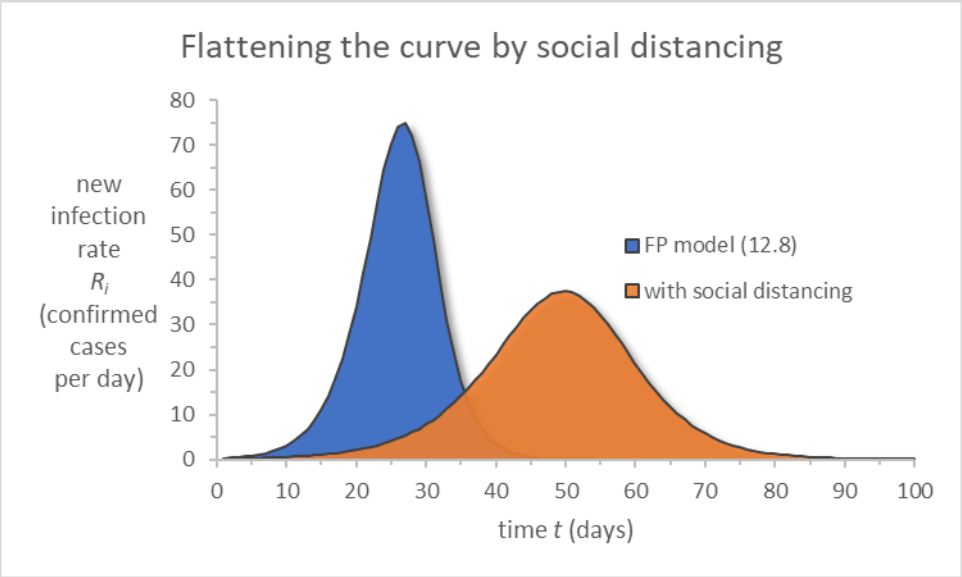


Fig.12.10 Excel area chart showing the predictions of the finite population (FP) model (12.8) for a model population of $N = 1000$, an infection rate constant of $k_i = 0.3\ \mathrm{d}^{-1}$, an initial number infectious of $N_0 = 1$ and a timestep of $\delta t = 1$ d (this is way too big!). The "with social distancing" curve shows the effect of reducing the infection rate constant by a factor of 2 on day 0 to $k_i = 0.15\ \mathrm{d}^{-1}$ by implementing **social distancing** etc. **Q.** This graph looks like Fig.12.02, but is this graph showing the same thing? … As a scientist, you should be taking note!

If you answer **CHALLENGE CALCULUS QUESTION** Q.12.17 (below), you might be able to show why it appears that $R_i^{\max} \propto k_i$ and that the time of the peak is inversely proportional to k_i. ❑

Q.12.15 **(a)** *Briefly describe* the similarities between our figure Fig.12.10 and the example of social distancing at the beginning of this chapter (Fig.12.02).
(b) *Briefly describe* any differences between our figure Fig.12.10 and the example of social distancing at the beginning of this chapter (Fig.12.02).

Q.12.16 Before reading ahead, *briefly describe* what you think the main limitations of the two-box **finite population model** are. Think about what happens in real life, no points off if you don't come up with the same things that I did. Thinking critically about models and their limitations is one of the main skills that we've been developing. Maybe you'll come up with something better than I did. I hope so …

Q.12.17 **CHALLENGE CALCULUS QUESTION** Can you *derive* an analytical equation for $N_i(t)$ and $R_i(t)$ predicted by the FP model? As of this writing, I have no idea whether that's even possible!

About what you discovered: Flatten the curve – but not reducing the number infected

As our FP model shows in Fig.12.10, social distancing will flatten the curve thereby reducing the peak infection rate preventing hospitals from being overwhelmed by the rate of new infections. However, the FP model also predicts that the all susceptible individuals will eventually be infected

– that's what you discovered in Q.12.14. It also explains why the areas under the two curves in Fig.12.10 and Fig.12.02 are the same. That idea can be summarized by

$$N_\infty = \int_{-\infty}^{\infty} R_i \mathrm{d}t = N \tag{12.14}$$

which defines N_∞ (pronounced "N infinity") as the cumulative total number infected as $t \to \infty$ (in the FP model). You don't need to have calculus to understand equation (12.14). As we discovered in **CHAPTER 8**, the integral in the middle of equation (12.14) reads "the area under the $R_i(t)$ curve from $t = -\infty$ to $t = \infty$," i.e., "for all time." In **CHAPTER 8** we also learned how to calculate that area using Excel rather than calculus. Equation (12.14) also includes the prediction of the FP model that $N_\infty = N$, i.e., that everyone in the model population will eventually get infected.

I recently (in mid-April 2020) have seen journalists and medically qualified commentators on cable TV make similar predictions about social distancing. To quote one well-respected journalist

> "*… the whole point of flattening the curve is you're actually not reducing the number of people who will eventually get infected and sick until we get a cure or a vaccine. You're spreading it out over a longer period of time, so the health care system can handle it.*"

While that is what the FP model predicts, the "SIR model" *shows that* that prediction is not correct. In the next section, we'll investigate the SIR model, which predicts that social distancing and mask wearing etc. not only lowers the peak in the infection rate, but it reduces the cumulative total number infected in the outbreak, or – if implemented early enough – can even prevent the outbreak from occurring at all! Let's see what we can discover … ❑

12.3 SIR model

Epidemiological modeling

The main problem with our finite population model is that people don't recover – ever. In other words, anyone who's infected always remains infectious! Clearly, that's not realistic, people do recover from COVID-19 and hence stop being infectious after a period of time. Fig.12.11 shows an FD diagram of an epidemiological model that's quite famous and is known as the **susceptible-infected-recovered model** or **SIR model**, for reasons that should be obvious when you look at Fig.12.11.

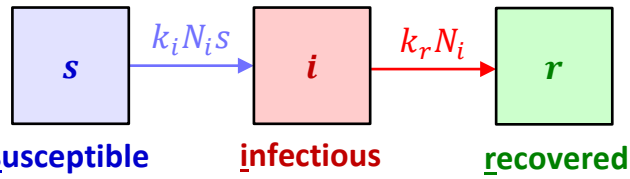


Fig.12.11 FD diagram of the SIR epidemiological model. The three boxes represent the three parts of the model population that can be affected by the disease. Box s represents the portion that's susceptible to the disease. Box i represents the portion infectious. Box r represents the portion that's recovered from the infection (or died). Sometimes this box is labeled removed – as in removed from consideration.

The three boxes in Fig.12.11 represent the possible states of people in the model population. Just like the previous UG and FP models, the criterion for being in the **model population** is that an individual can be infected and that their infection will be officially reported. That means that we're excluding any individuals who could be infected but only get mild or asymptomatic cases and are not tested so that their cases are not officially reported. It's currently estimated (mid 2020) that only between 10-50% of cases are officially reported in the US (more on this topic later).

Many features of the SIR model are the same as the finite population (FP) model. The **number susceptible**, is represented by N_s. Lowercase s represents the **susceptible fraction** defined by equation (12.9). The **number infectious** is represented by uppercase N_i. The **number recovered** is represented by N_r. It's the number of individuals in the model population that have been infected – but have now recovered and are no longer infectious and are further assumed to be immune to the disease forever. The symbol N_r more correctly stands for the **number removed** from the susceptible or infectious boxes. In addition to recovering, individuals can be removed from the number infectious by being isolated from the susceptible portion of the population and they can be removed by death. All of those individuals are represented by box r. We also have a relationship with the total number N in the model population and it spells out the initials of the SIR model in the subscripts of the bookkeeping equation (12.15)

$$N = N_s + N_i + N_r \tag{12.15}$$

It's called the **bookkeeping equation** because it reflects that the fact that all the numbers must add up to the model population size N.

The model is still extremely simplified. It assumes that humans behave just like the molecules in the **marble game**, i.e., they **randomly walk** around and have random interactions with anyone in the whole **population** – just like the molecules we studied in **CHAPTER 10**, and as shown in the GlowScript sim MarbleGame. In other words, we're assuming that the individuals in the population are just like the Green day song "Boulevard of Broken Dreams" – they walk alone until they find someone and either get infected (if they're in box s) or infect the person they found (if they're in box i). In this model, we're assuming that recovered (removed) individuals (box r) can't infect anyone and that they're now permanently immune from infection. That's a lot of

obviously over-simplified assumptions, but it does give us an easy-to-understand model of how an epidemic spreads. It's worthwhile restating at this point that we're only trying to understand the basics of epidemiology with our SIR model. After we understand the basic model and what it explains, then we can start thinking about improving the model to make it more realistic. As we've discovered over and over in this book, simple models often do way better than you might reasonably expect. Let's see what we can discover …

Now that we've talked about the main limitations of the SIR model, let's talk about how it works and what insights it provides. The first thing about the model that you should notice is that the only thing that can happen to susceptible people is that they become infectious! The first question you might then ask is – "What's the likelihood that they don't *ever* get infected?" That's exactly the kind of question that the model is designed to elucidate. However, before we can get to that question, we'll need to get the model working and see what it tells us.

Now that we've described the boxes and how they represent the three possible states of the model population, we can now talk about the arrows between boxes in Fig.12.11. The first arrow from box $s \to i$ represents the rate of infection. That **infection rate** $R_i = k_i N_i s$ is given by equation (12.8) – the exact same equation that we used for the finite population model of Fig.12.09.

The second arrow from box $i \to r$ represents the rate of recovery. That **recovery rate** is given by

$$R_r = k_r N_i \tag{12.16}$$

where k_r [=] d^{-1} is the **recovery rate constant** (note the r subscripts in R_r and k_r). Equation (12.16) means that the probability of any infectious person recovering is a constant – independent of everything, including how long they've been infectious (and hence been in box i). That's a good assumption for radioactive decay or drug elimination because each drug molecule in your blood stream has an even chance of being diverted into the kidneys each time ($\sim$20 s) it flows by them, but infectious people are more complicated than drug molecules. The real recovery process takes time, and it depends on the individual and how long they've been infected. The model also includes the unrealistic possibility that an individual can recover on the same day that they become infectious! It's worse than you might first think, because the most likely time for recovery in the **Poisson process** implied by equation (12.16) is … immediately! However, if you consider the number of people in box i as a whole, then it seems reasonable that the overall recovery rate depends directly on the number infectious N_i. The main advantage of equation (12.16) is that it's easy to understand and it gives us a simple way to predict the recovery rate R_r based solely on the number infectious N_i (12.16). Hence, we don't have to keep track of each individual and how long they've been infected, which would be difficult to do in Excel … remember … we're only trying to understand the basics of epidemiology with our SIR model.

Another advantage of the SIR model (Fig.12.11) and equation (12.16) is that the **mean residence time** (**CHAPTER 2**) in box i can be predicted by equation (2.4), which translates to

$$\tau_i = \frac{1}{k_r} \tag{12.17}$$

where τ_i, "tau i" (see the Greek letters go green! [Nelson 2013]) is the **mean infectious time**, which can be approximated by a quantity that can be measured clinically – the mean (or average) "recovery time."

Q.12.18 **(a)** Using Fig.12.11, *show that* the change δN_i in the number infectious N_i during a short time δt is given by

$$\delta N_i = (R_i - R_r)\delta t \tag{12.18}$$

where R_i is given by equation (12.8) and R_r is given by equation (12.16). Then *show that* the change δN_r in the number recovered N_r is

$$\delta N_r = R_r \delta t \tag{12.19}$$

(b) Combining the relevant equations, including the bookkeeping equation (12.15), *show that* our **SIR model** can be calculated using the following algorithm instructions

$$R_i^{\text{new}} = k_i * {N_i}^{\text{old}} * N_s^{\text{old}}/N \tag{12.12}$$

$$R_r^{\text{new}} = k_r * {N_i}^{\text{old}} \tag{12.20}$$

$${N_i}^{\text{new}} = {N_i}^{\text{old}} + (R_i^{\text{new}} - R_r^{\text{new}}) * \delta t \tag{12.21}$$

$$N_r^{\text{new}} = N_r^{\text{old}} + R_r^{\text{new}} * \delta t \tag{12.22}$$

and

$$N_s^{\text{new}} = N - {N_i}^{\text{new}} - N_r^{\text{new}} \tag{12.23}$$

(c) Using equations (12.12), (12.20) – (12.23) *write out* a complete FD algorithm, including unit checks, to calculate $R_i(t)$, $R_r(t)$, $N_i(t)$, $N_r(t)$, and $N_s(t)$ i.e., everything you'll need to calculate how the number of infectious people N_i changes with time t for a model population of $N = 1000$ individuals using a timestep of $\delta t = 1$ d, an infection rate constant of $k_i = 0.36\ \text{d}^{-1}$, an initial number infectious of $N_0 = 1$, zero recovered and a mean infectious time of $\tau_i = 16$ d.

Hint: You'll need to rearrange equation (12.17) to obtain an equation (12.35) for the **calculated parameter** k_r in terms of the mean infectious time τ_i.

(d) By hand, calculate steps 0, 1, and 2 of your finite difference algorithm and *record* your answer in the form of an FD output table.

Hint: As usual, you should do parts (c) and (d) of this question together. It's easier that way.

Q.12.19 **(a)** Open the preformatted spreadsheet BPM.Ch12_SIR_model.xlsx and fill in the blank cells with your algorithm and check that you get *exactly* the same results that you calculated by hand in Q.12.18(d). The spreadsheet should automatically plot all three of $N_s(t)$, $N_i(t)$ and $N_r(t)$ and the both the new infection rate $R_i(t)$ and the recovery rate $R_r(t)$ as a function of time. As always, you then need to reduce the timestep δt to be small enough and add steps so that the curves visually reach a steady state at the end of the model. *Record* your graph of N_s, N_i and N_r as a function of time.
Note: You should be sure to save separate copies of your spreadsheet answers to this Q.12.19, and Q.12.20(a)-(d), we'll be needing them again later.
(b) *Record* your graph of the new infection rate R_i and the recovery rate R_r as a function of time.
(c) Carefully investigate what happens at the end of the model, e.g., at day 150 or 200. *Briefly discuss* what happens to the values of N_s, N_i and N_r at the end of the model. Does everyone in the model population still become infectious in this SIR model?
(d) *Briefly compare* the shape of the $R_i(t)$ curve with the equivalent curve in Fig.12.10 for the FP model.
(e) *Briefly compare* the shape of the $N_i(t)$ curve with the curves in Fig.12.10 and Fig.12.02 and *briefly discuss* what you can conclude about the meaning of the axis label "Infected people" in Fig.12.02.
(f) *Briefly explain* why the graph for $N_i(t)$ has a faster rise to the peak at about $t \approx 22$ d than the subsequent decline.
Hint: We discussed a similar-but-different situation in Q.6.9(b).
(g) *Briefly explain* why the graphs for $N_i(t)$ and $R_r(t)$ appear to have exactly the same shape. Note that they don't have the same magnitude – and even more importantly – they have different units because they're *not* the same kind of thing.
Hint: Your answer should include one of the new equations in this section.

About what you discovered: SIR model – infectious people recover

Your answers to Q.12.19(a) and Q.12.19(b) should look something like Fig.12.12. As you noted in Q.12.19(d), the curve for the number infectious is asymmetric with a faster rise than decline. The reason for the two time scales is that the infection rate constant $k_i = 0.36\ \text{d}^{-1}$ is significantly bigger than the recovery rate constant $k_r = 0.0625\ \text{d}^{-1}$. Based on the rates we can estimate an infection time constant of $1/k_i = 2.8$ d and a mean infectious time of $\tau_i = 1/k_r = 16$ d. The shapes of the $N_i(t)$ and $R_r(t)$ curves really are identical. $N_i(t)$ and $R_r(t)$ are **proportional** because the recovery rate is related to the number infectious by $R_r = k_r N_i$ (12.16).

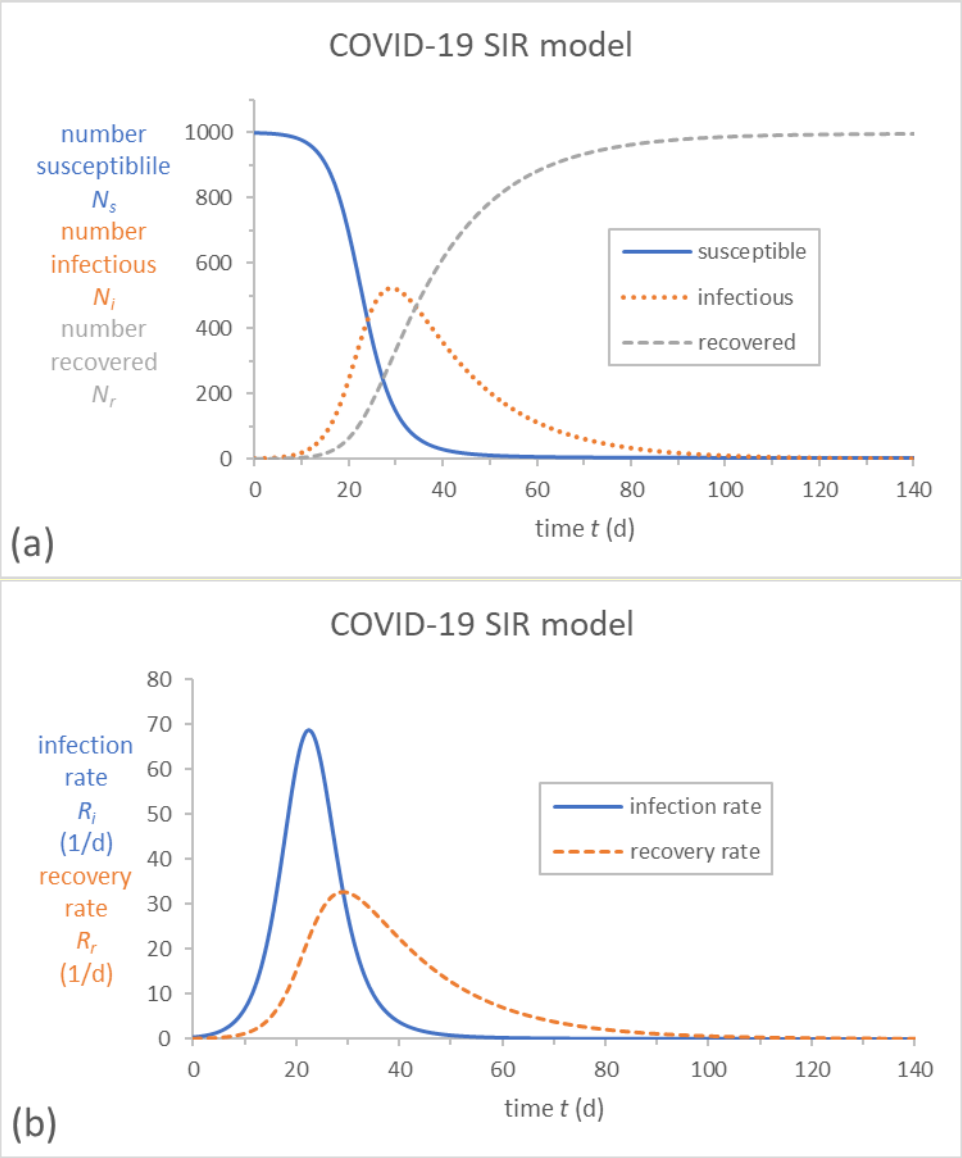


Fig.12.12 Excel charts showing the predictions of the SIR model (Fig.12.11) for a model population of $N = 1000$, an infection rate constant of $k_i = 0.36\ \mathrm{d}^{-1}$, an initial number infectious of $N_0 = 1$ and a timestep of $\delta t = 0.01$ d. Chart **(a)** shows the numbers in the three boxes s, i and r of the SIR model. Chart **(b)** shows the shows the exponential dragon predicted for the infection rate infection rate R_i (solid blue line) and the recovery rate R_r (dashed orange line). **Note:** because of equation (12.16), the recovery rate R_r is directly proportional to the number infectious N_i.

A universal feature of the SIR model is that it predicts an "**exponential dragon**" in the infection rate $R_i(t)$ – see Fig.12.12(b). The duration of the exponential dragon is determined by the value of the infection rate constant k_i. As we'll discover, the peak of the exponential dragon exhibits a characteristic inverted vee shape on a semi-log plot. The idea of using a dragon analogy for explosive exponential growth was inspired by the expression ''tickling the dragon's tail'' that's based on a remark by Richard Feynman about the dangers of some ill-advised early nuclear experiments in which exponential growth had the potential for similar catastrophic consequences [Nelson 2021]. ❑

Social distancing in the SIR model

The effect of social distancing can be added to the SIR model using the same rationale we used for the FP model. Let's see what we can discover …

Q.12.20 DISCUSSION QUESTION **(a)** To see the effect of social distancing on the SIR model, change the infection rate constant to $k_i = 0.18\ \mathrm{d}^{-1}$ (i.e., about one half of the original model), then extend your graph in time until the graphs once again visually reach a steady state at the end of the model. *Record* your graph for the new infection rate R_i as a function of time.

Note: You should *save* separate copies of your spreadsheet answers to Q.12.19, and Q.12.20(a)-(d), we'll be needing them again later.

(b) Change the infection rate constant to $k_i = 0.09\ \mathrm{d}^{-1}$ (i.e., about one quarter of the original model). *Record* your graph for N_s, N_i and N_r as a function of time.

Hint: You can use a longer timestep δt if the graphs change more slowly.

(c) Change the infection rate constant to $k_i = 0.0625\ \mathrm{d}^{-1}$ (i.e., the same as k_r). *Record* your graph for the new infection rate R_i as a function of time.

Hint: See the hint for part (b).

(d) Change the infection rate constant to $k_i = 0.045\ \mathrm{d}^{-1}$ (i.e., about one eighth of the original model). *Record* your graph for the new infection rate R_i as a function of time.

Hint: See the hint for part (b).

(e) Carefully investigate what happens at the end of the model when the values of N_s, N_i and N_r reach a steady state. *Briefly discuss* what happens to the values of N_s, N_i and N_r at the end of the models with different infection rate constant k_i values. Does everyone in the model population still get infected in these SIR models?

(f) *Briefly describe* what happens to the timescale of the outbreak as k_i is reduced by social distancing.

About what you discovered: social distancing in the SIR model

Fig.12.13 shows the predictions of our SIR model with $k_i = 0.085\ \mathrm{d}^{-1}$, $\tau_i = 1/k_r = 16\ \mathrm{d}$ and $N = 1000$. (Note, this graph is not an answer to any one of your answers to Q.12.20.) This graph confirms what Espe said at the beginning of this chapter – that social distancing not only flattens the curve, but it can substantially reduce the cumulative total number infected in the outbreak. In Fig.12.13 the percentage of the model population that ultimately get infected is about 48% (obtained from the number recovered at the end of the graph). You can confirm my graph by putting $k_i = 0.085\ \mathrm{d}^{-1}$ into the spreadsheet you used for Q.12.20(d).

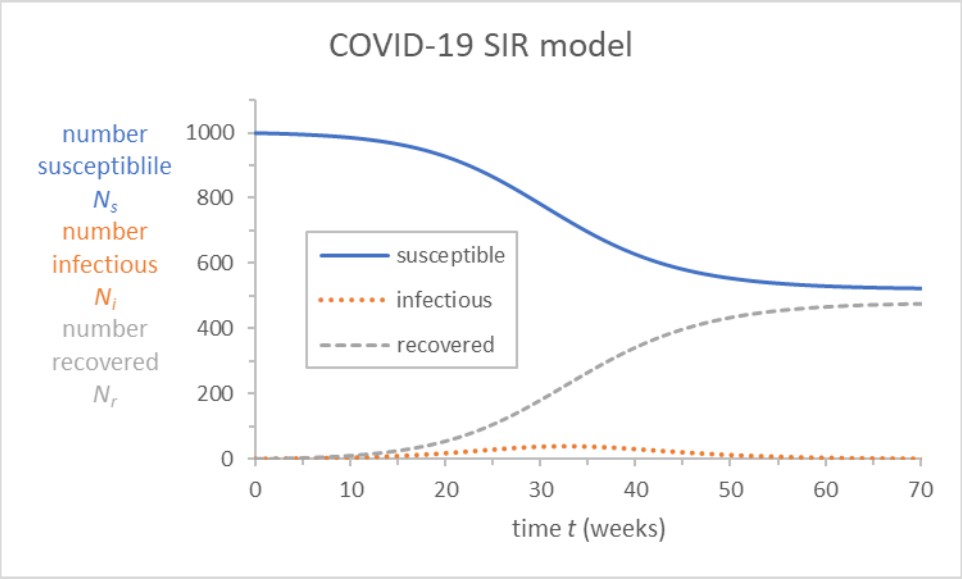


Fig.12.13 Excel chart showing the predictions of the SIR model (Fig.12.11) for a model population of $N = 1000$, an infection rate constant of $k_i = 0.085$ d^{-1}, an initial number infectious of $N_0 = 1$ and a timestep of $\delta t = 0.02$ d. **Note:** the cumulative total infected N_∞ is about 48 % of $N = 1000$.

Okay, so that's all well and good, but there's a catch – a long one – that you discussed in your answer to Q.12.20(f). The timescale of the model outbreak shown in Fig.12.13 is surprisingly long. I changed the units of time t in Fig.12.13 to weeks to make that easier to see. The duration of the outbreak is depressingly long in this model … over a year! ❑

Changing the starting point

Q.12.21 **(a)** Change the infection rate constant back to $k_i = 0.36$ d^{-1} and the timestep to $\delta t = 0.01$ d, then increase the total model population to $N = 10{,}000$. Set the initial number infected to $N_0 = 1$ then change it to $N_0 = 10$. *Briefly describe* how changing the initial number infected N_0 changes the model by discussing what happens to the magnitude of the peak in $N_i(t)$ and the change in the time of the peak in $N_i(t)$.
Hint: After you make the change, you can use **Undo** (Ctrl+Z) and **Redo** (Ctrl+Y) to switch between them – look at the graphs as they change to get a visual idea of the comparison.
(b) *Briefly describe* how the magnitude and time of the peak value of the new infection rate $R_i(t)$ changes when you change the initial number infected from $N_0 = 1$ to $N_0 = 10$.
(c) Use the same technique for $N_0 = 100, 1000, 5000$. *Briefly summarize* what you discovered. Focus on how the model is changed at comparable times relative to the peaks in the infection and recovery rates.
(d) *Briefly describe* what happens to the SIR model when $N_0 = 0$ and $N_0 = 10{,}000$.

About what you discovered: changing the starting point

As you discovered in Q.12.21, the basic effect of increasing the initial number infected is to change the starting point of the model. This suggests that we can skip over the slow initial period of growth in the number infected by simply starting with a higher initial number infected N_0. You

should have discovered that this approximation (of skipping over the initial infections and recoveries) works best if the **initial fraction infectious**

$$i_0 = \frac{N_0}{N} \tag{12.24}$$

is small, i.e., $i_0 \ll 1$. As you discovered in Q.12.21(c) even $i_0 = 0.1$ is small enough for the model to still be basically the same as before, just skipping the initial growth in N_i. ❑

The effect of population size

Q.12.22 **(a)** Change the infection rate constant back to $k_i = 0.36\ \mathrm{d}^{-1}$, then change the total model population to $N = 100$. *Set* the initial number infected to $N_0 = 1$. Then change the model population to $N = 1000, 10^4, 10^5, 10^6, 10^7, 10^8, 10^9$. *Briefly describe* how changing the population size N changes the model by discussing the magnitude and time of the peak in the number infectious N_i.
Hint: After making all the changes, you can use **Undo** (Ctrl+Z) and **Redo** (Ctrl+Y) to cycle between them – look at the graphs as they change to get a visual idea of the comparison.
(b) Make a fresh copy of your spreadsheet for this question. Make the initial fraction infectious i_0 a parameter and change the instruction for N_i in step zero to be

$$N_i^{\text{new}} = N * i_0 \tag{12.25}$$

Note: Equation (12.25) should remind you of what we did with x_0 in our first algorithm of the marble game in **CHAPTER 2**.
Set the initial fraction infected to $i_0 = 0.001$, or one in a thousand, then change the model population to $N = 100$, then $N = 1000, 10^4, 10^5, 10^6, 10^7, 10^8, 10^9$. *Briefly describe* how changing the population size N changes the model with the initial fraction infraction i_0 held constant by discussing the magnitude and time of the peak in the number infectious N_i.
(c) Compare the time of the peak in the number infectious with your answers to part (a). What value of N does it correspond to? It should be one of $N \in \{1000, 10^4, 10^5, 10^6, 10^7, 10^8, 10^9\}$. *Briefly explain* why.

About what you discovered: scaling the SIR model – size doesn't really matter

As you discovered in Q.12.22, model populations of all sizes in the SIR model behave in a similar manner if they start with the same initial fraction infectious i_0. This suggests that we can change the units of N_s, N_i and N_r in the model to **percentages** (or fractions) and model a population of any size. That's what you'll often find if you search for the SIR model online. Obviously, treating the whole of the US as one model population is an oversimplification, but as we've discovered, much can be learnt from simplified models. However, we must always keep in mind that there are

limitations to any model – particularly when we're trying to understand a human population. People aren't molecules. ❑

Q.12.23 **MATH QUESTION** For the mathematically inclined. *Prove* that the SIR model can be divided by any constant number without affecting the relative values of N_s, N_i and N_r and hence *show that* we can simply set the model population size to $N = 100$ and then interpret N_s, N_i and N_r as the **percent susceptible**, **percent infectious** and **percent recovered**, respectively of the model population – whatever size it is – and without changing the model parameters k_i, τ_r That then *shows that* if $N = 100$, we can simply think of N_0 as the **initial percent infectious**.

Finding the peak in the $N_i(t)$ curve

Q.12.24 **(a)** Carefully inspect your $R_i(t)$ and $R_r(t)$ graphs for Q.12.19, Q.12.20(a) and Q.12.20(b). There's something interesting that always happens to $R_r(t)$ when $R_i(t)$ crosses over it. *Briefly describe* what you discovered.
(b) Before reading ahead, see if you can *explain* what you observed. No points off if you can't. The purpose of simple models is to give us questions like this to answer. They might just be mathematical curiosities, or they might provide us with important insights into epidemiological modeling with the SIR model.
Hint: Recall that equation (12.16) predicts that $R_r = k_r N_i$, so that the shape of the $R_r(t)$ curve is the same as the shape of the $N_i(t)$ curve.

If we're interested in understanding how to **flatten the curve**, then obviously we'd like to understand as much as we can about what's happening in the model when the number infectious N_i peaks. The discovery you made in Q.12.24 is central to that understanding. Before we get into the math, let's talk about the FD diagram of the SIR model – it provides us with the essential conceptual understanding of how the SIR model works. Let's take the time now to look once again at Fig.12.11, and see what we can discover…

Q.12.25 **(a)** Look carefully at box i in Fig.12.11. It has two arrows touching it. The arrow on the left represents the infection rate $R_i = k_i N_i s$, which increases the number infectious. The arrow on the right represents the recovery rate $R_r = k_r N_i$, which decreases the number infectious. If the number infectious is increasing, *write* the corresponding mathematical relationship between R_i and R_r.
Hint: Your answers for parts (a)-(c) should be one of $R_i < R_r$, $R_i = R_r$, or $R_i > R_r$.
(b) If the number infectious is decreasing *write* is the mathematical relationship between R_i and R_r.
(c) If the number infectious is momentarily constant *write* is the mathematical relationship between R_i and R_r.

(d) Looking at the shapes of your spreadsheet $N_i(t)$ curves for Q.12.19, Q.12.20(a) and Q.12.20(b), *briefly describe in words* the point in time all those $N_i(t)$ curves that corresponds to $R_i = R_r$.
Hint: A good answer would fill in the blank – "The point in time where $R_i = R_r$ corresponds to the ____ of the $N_i(t)$ curve." (It's important to note that this is not the peak in R_i, but the peak in N_i.)

Okay, so now that we know that the peak in the number infectious $N_i(t)$ corresponds to

$$R_i = R_r \tag{12.26}$$

let's see what we can discover …

Q.12.26 By substituting equations (12.8) and (12.16) into equation (12.26), *show that* the value of the fraction susceptible s at the peak in N_i is given by

$$s_p = \frac{k_r}{k_i} = \frac{1}{\mathcal{R}_0} \tag{12.27}$$

where $\mathcal{R}_0$ is given by

$$\mathcal{R}_0 = \frac{k_i}{k_r} = \frac{1}{s_p} \tag{12.28}$$

Note the use of uppercase script $\mathcal{R}$ to differentiate $\mathcal{R}_0$ from all the other "R"s that we've used so far. This quantity $\mathcal{R}_0$ (pronounced "R naught") is the same one that you might have heard about on TV or read about online. It's called the **basic reproduction number**. Let's see what we can discover about it using our SIR model… but before we do that, let's first talk about s_p, which is the **fraction susceptible at the peak in $N_i(t)$**. It's going to tell us a great deal more than I first expected…

Testing equation (12.27) – predicting the peak

Q.12.27 **(a)** *Briefly compare* the predictions of equation (12.27) with your model data for Q.12.19, Q.12.20(a), Q.12.20(b) and Q.12.20(c).
Hint: You might find the preformatted spreadsheet BPM.Ch02_Talking_numbers.xlsx useful.
(b) *Briefly compare* the predictions of equation (12.27) with your model data for Q.12.20(d). Can you explain what's going on with the model and why equation (12.27) for s_p doesn't apply to the SIR model of question Q.12.20(d)?

About what you discovered: s_p the susceptible fraction at peak number infectious

The **calculated parameter** s_p tells us the fraction of the model population that have *not* been infected at the time t_p of the peak in the number infectious $N_i(t)$. Hence, the value of s_p is a

measure of the intensity of the outbreak. The smaller s_p, the fewer susceptible people are left at time t_p. The larger s_p, the more susceptible people are left at the peak in $N_i(t)$. Hence, s_p gives us a good measure of how much the curve has been **flattened**. The larger s_p is – the flatter the curve in the SIR model. In other words, equation (12.27) gives us a simple way to predict how changing either the infection rate constant k_i or the recovery rate constant k_r **flattens the curve**. ❑

Herd immunity

After the peak, the SIR model predicts that the number infectious N_i will steadily decline because the rate of infection R_i is less than the rate of recovery R_r. This can be related to an epidemiological concept that you might have heard about – **herd immunity**. One way to see how the two concepts are related is to consider the quantity $1 - s_p$, which is the cumulative fraction that have been infected at time t_p. Let's see how that works…

But before we do that, let's *define* the **fraction infectious** i as

$$i \equiv \frac{N_i}{N} \tag{12.29}$$

and the **fraction recovered** as

$$r \equiv \frac{N_r}{N} \tag{12.30}$$

We can then define i_p as the fraction infectious at time t_p and r_p as the fraction recovered at time t_p. It's then easy to use equation (12.15) to show that

$$s_p + i_p + r_p = 1 \tag{12.31}$$

so that $1 - s_p = i_p + r_p$. Hence, the quantity $1 - s_p$ is the sum of $i_p + r_p$, which is simply the cumulative total number of people that have previously been infected at time t_p. Now, our SIR model assumes that individuals who've been infected once can't be infected again. Hence, anyone that's already been infected is considered immune in our SIR model. As a result, the fraction of the model population that are immune at any time can be written as

$$h = i + r = 1 - s \tag{12.32}$$

where h is the **fraction immune**, or the **immune fraction** of the model population.

Once the fraction immune h reaches

$$h_p = 1 - s_p = 1 - \frac{1}{\mathcal{R}_0} \tag{12.33}$$

then the recovery rate R_r is larger than the infection rate R_i and the disease will be in decline and eventually die out. The fraction h_p is the **herd immunity threshold**. If the fraction immune is greater than or equal to h_p, i.e., if

$$h \geq h_p \tag{12.34}$$

then the disease will be in decline rather than growing as indicated by whether $N_i(t)$ decreases or increases, respectively.

1st Note: Epidemiologists would say that the disease is being **eliminated**, when equation (12.34) is true. They're using that word in the same sense that we did for **drug elimination** in **CHAPTERS 2** and **4**.

2nd Note: As of April 2020, it's uncertain whether recovering from COVID-19 imparts **permanent immunity** to further infection by the novel SARS-CoV-2 coronavirus.

Q.12.28 Let's test the predictions of (12.34).

(a) *Show that* the SIR model parameters k_r and k_i can be calculated from N, τ_i, and $\mathcal{R}_0$ using equations

$$k_r = \frac{1}{\tau_i} \tag{12.35}$$

and

$$k_i = k_r \mathcal{R}_0 \tag{12.36}$$

and that the initial values of N_s and N_r in $Step\ 0$ can be calculated using

$$N_r^{\text{new}} = \frac{N}{\mathcal{R}_0} \tag{12.37}$$

$$N_r^{\text{new}} = N - N_i^{\text{new}} - N_s^{\text{new}} \tag{12.38}$$

(b) *Write out* a complete FD SIR algorithm, including unit checks, to calculate how the number of infectious people N_i changes with time t in days for a model population of $N = 1000$ individuals using a timestep of $\delta t = 100$ d, a mean infectious time of $\tau_i = 16$ d, a basic reproduction number of $\mathcal{R}_0 = 2.5$, and an initial number infectious of $N_0 = 1$.

(c) By hand, calculate step 0, 1 and 2 of your finite difference algorithm and *record* your answer in the form of an FD output table.

Hint: As usual, you should do parts (b) and (c) of this question together. It's easier that way.

Q.12.29 **(a)** Open the preformatted spreadsheet BPM.Ch12_Herd_immunity.xlsx and check that it calculates your algorithm instructions *exactly*. The spreadsheet automatically plots all three of N_s, N_i and N_r and the both the new infection rate R_i and the recovery rate R_r as a function of time. As always, you then need to reduce the timestep δt to be small

enough and add steps so that the curves visually reach a steady state at the end of the model. *Record* your graph of N_s, N_i and N_r as a function of time.
(b) *Record* your graph of the new infection rate R_i and the recovery rate R_r as a function of time.
(c) Change the initial number infectious to the maximum possible with $h = h_p$, i.e., $N_0 = 600$ for $\mathcal{R}_0 = 2.5$. In both charts, you'll also need to **[Reset]** the **Axis Options > Maximum** to **[Auto]** and you can change the timestep δt to a smaller value. I chose $\delta t = 0.01$ d. *Record* your graph of N_s, N_i and N_r as a function of time.
(d) *Record* your graph of the new infection rate R_i and the recovery rate R_r as a function of time.
(e) *Briefly explain* how the rather dramatic decrease in the number susceptible N_s and the corresponding increase in the number recovered N_r are consistent with our definition of what **herd immunity** means.

Q.12.30 *Show that* the number infectious $N_i(t)$ always decreases if the immune fraction $h \geq h_p$ by showing that equation (12.18) can be written as

$$\delta N_i = k_i N_i s - k_r N_i \delta t = (k_i s - k_r) N_i \delta t \tag{12.39}$$

and for $h \geq h_p$ (or $s \leq s_p$), δN_i is less than zero, which means that $N_i(t)$ always decreases in the SIR model independent of the current value of N_i.

About what you discovered: herd immunity doesn't mean no-one gets sick

As you discovered in Q.12.29 **herd immunity** doesn't mean that nobody gets sick. It only means that the number infectious $N_i(t)$ won't increase with time. Unfortunately, while $N_i(t)$ is decreasing additional people will continue to get infected.

However, if there is a vaccine for a disease, then equation (12.34) tells us the minimum fraction that must be effectively immunized (or already be immune) to provide **herd immunity** to the whole population. Herd immunity is especially important for highly contagious diseases like measles, particularly when infants younger than 9 months aren't typically given the vaccine and hence rely on herd immunity for their wellbeing.

Note: The $\mathcal{R}_0$ for COVID-19 depends on how much social distancing is being practiced … more later … ❑

Q.12.31 **RESEARCH QUESTION** Pick a highly infectious disease with a high $\mathcal{R}_0$ such as measles and use the SIR model to *investigate* the consequences of a portion of the population not vaccinating their children. After taking into account the effectiveness of the vaccine, determine what fraction of the population can decline vaccination without affecting herd immunity and *report* your conclusions.

Fraction uninfected after the outbreak ends s_∞

Let's define s_∞ (pronounced "s infinity") to be the steady-state value of the susceptible fraction s in the SIR model at long times (when $t \to \infty$), i.e., after the outbreak has subsided. Because s is the fraction of the model population that haven't been infected, the value of s_∞ is of great interest to public health officials (and the rest of us). It tells us the fraction of the susceptible people that survived the outbreak without being infected. Our FD implementations of the SIR model already make predictions for s_∞. Let's summarize what we've already predicted.

Q.12.32 *Summarize* the inputs and outputs of the SIR model by making a table of k_i, k_r, s_p, h_p, $\mathcal{R}_0$, $N_s(t=\infty)$, s_∞, $1-s_\infty$ and the quantity

$$y = \mathcal{R}_0(1 - s_\infty) + \ln s_\infty \tag{12.40}$$

You should open a fresh Excel spreadsheet and *record by hand* the values from the spreadsheets you saved for Q.12.19 and Q.12.20(a)-(d) in the form of a table.
Hint: You can use Excel to calculate s_p from k_i and k_r using equation (12.27), $\mathcal{R}_0$ can be calculated from s_p using equation (12.28), and y can be calculated using equation (12.40), but you'll need to look up the value of $N_s(t=\infty)$ in the last row of your SIR model spreadsheets and then calculate the value of s_∞ using the definition (12.9) of s. You should have rows in your table for each of $k_i \in \{0.36, 0.18, 0.09, 0.0625, 0.045\}$ 1/d.
(a) *Record* your Excel table. You can copy and "paste as picture" into Word.
(b) *Briefly describe* what you discovered about the currently mysterious quantity y that's defined by equation (12.40).

The basic reproduction number $\mathcal{R}_0$

As we just discovered, s_p tells us how much the curve has been flattened. Inversely, the **basic reproduction number** $\mathcal{R}_0$ tells us the intensity of the outbreak. Made famous in the 2011 movie Contagion, $\mathcal{R}_0$ is probably the single-most discussed parameter of epidemiological models including our simple SIR model. What you've probably heard is that $\mathcal{R}_0$ is the average number of infections caused by a single infectious person at the beginning of the outbreak. Fig.12.14 shows my version of a type of schematic diagram that you may have seen elsewhere.

I wasn't focused on the parameter $\mathcal{R}_0$ when I started working on this chapter. It didn't occur to me that such a simple concept would provide such a deep insight into the rather complicated SIR model that we've been working on. I was wrong! Let's see what *you* can discover …

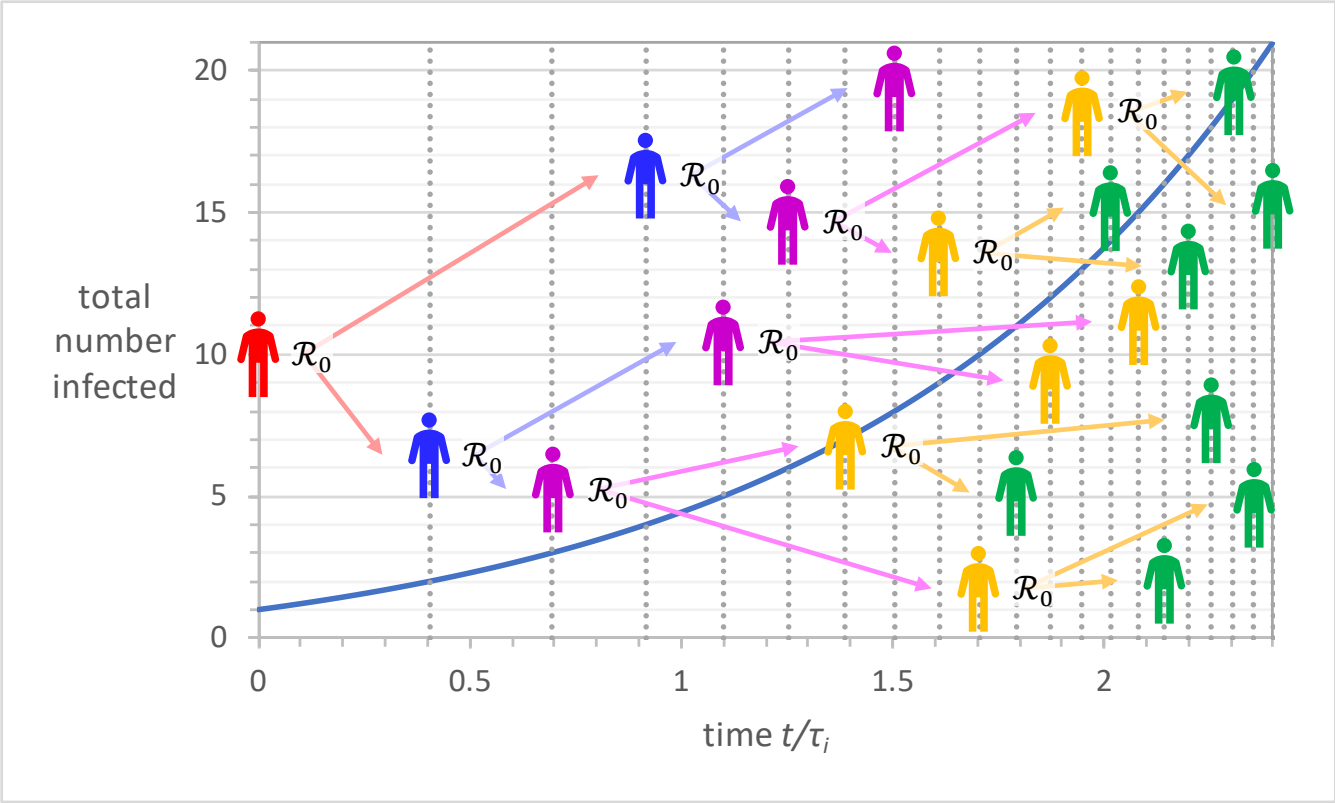


Fig.12.14 Schematic diagram illustrating the meaning of $\mathcal{R}_0$. As shown, if $\mathcal{R}_0 = 2$, one person infects two additional people (on average), each of whom then each infects another two people (on average) so that $2 \rightarrow 4 \rightarrow 8 \rightarrow 16 \rightarrow 32 \rightarrow 64$ ... which is explosive exponential growth. **Note:** Each infectious individual infects others at random times. The superimposed graph shows the **total number infected** predicted by the SIR model with $\mathcal{R}_0 = 2$ (note this is $N_i + N_r$ not N_i). The dotted vertical lines indicate the ensemble average prediction for the time of the next infection. Hence, there's only one person per dotted line in the figure. **Note:** The diagram shows every infectious person infecting exactly two others. In reality, some infectious people infect zero others, while some infectious people are **super-spreaders** that infect many more than the ensemble average of $\mathcal{R}_0 = 2$.

Q.12.33 **(a)** According to Fig.12.14, $\mathcal{R}_0$ is the average total number of people infected per infectious person. That is, each person (on average) infects $\mathcal{R}_0$ other people at the beginning of the outbreak. Now, a person can only infect someone else while they're actually infectious. As we already know, the average time that they're infectious is the mean infectious time τ_i. Using the number $\mathcal{R}_0$ [=] 1 and the time τ_i [=] d, *write out* a mathematical expression for the average rate [=] d^{-1} that an infectious person infects susceptible individuals in an otherwise completely susceptible model population ($s \approx 1$) according to our SIR model.

(b) *Briefly identify* the parameter in the SIR model that corresponds to your answer to part (a). Write the symbol of the parameter – which first appeared in the UG model – and its name.

About what you discovered: how the popular concept of $\mathcal{R}_0$ is related to k_i

Q.12.33 could have been worded "If you divide $\mathcal{R}_0$ by τ_i what do you get?" – but maybe that would have been too easy! It took me a while to realize what you discovered in Q.12.33, i.e., that the popular explanation of $\mathcal{R}_0$ precisely matches our definition of $\mathcal{R}_0$ in equation (12.28).

Using the language of math, my answer to Q.12.33 is

$$\frac{\mathcal{R}_0}{\tau_i} = \frac{\left(\frac{k_i}{k_r}\right)}{\left(\frac{1}{k_r}\right)} = \frac{k_i}{k_r} k_r = k_i \tag{12.41}$$

or

$$\mathcal{R}_0 \equiv k_i \tau_i = \frac{k_i}{k_r} \tag{12.42}$$

where k_i is the infection rate constant (Fig.12.03) that we've been using since the beginning of this **CHAPTER 12**. Note, in equation (12.41) I used the definition of $\mathcal{R}_0 \equiv k_i/k_r$ (12.28) and the SIR model equation (12.17), which says that $\tau_i = 1/k_r$. Maybe you thought that equation (12.42) was obvious – and with hindsight – it is, but it took me a couple of hours to realize how the popular description of $\mathcal{R}_0$ relates to our FD implementation of the SIR model.

A key feature of Fig.12.14 that clarifies a conceptual problem I was having with the popular explanation of $\mathcal{R}_0$ is that the infections occur at random intervals during the infectious period. That means that tertiary infections (purple) can occur before patient zero (red) is no longer infectious. My problem was that I was trying to use a "generational" description of infections (which I saw all over the internet) – in which all the infections only occur at the end of the generation. That isn't consistent with the **Poisson process** of infection implied in the SIR model and even in the UG model of Fig.12.03 – where the probability density for an infectious person infecting someone else is constant – until they're no longer infectious, i.e., transmission of the virus occurs throughout τ_i not just at the end.

Interestingly, I wrote the AWYD "exponential growth has explosive consequences" (after Q.12.06) before I first derived equation (12.42). I now think it's ironic that the "2.5 neutrons per ^{235}U nucleus" mentioned there is completely analogous to the $\mathcal{R}_0 = 2.5$ that you'll see sometimes online as an estimate for COVID-19 (as of mid-March 2020). ❑

Q.12.34 Removing a single person from the web of infections in Fig.12.14 can produce quite dramatic results.
(a) For example, *count* how many infections would be prevented in Fig.12.14 if the first purple person (the third infected overall) stayed at home and wasn't infected because of social distancing? *Briefly compare* that number saved with the original number infected (21).

(b) *Fill in the blank*: Because of the initial exponential growth in the SIR model, the number of infections prevented by a single person staying home grows _____ over time.
Hint: Your answer to part (b) could be turned into a public service announcement – "Social distance now – it **exponentially decreases** the spread of COVID-19."

Q.12.35 We're now going to reproduce the graph in Fig.12.14. Using your spreadsheet from Q.12.29(a), or by reopening the preformatted spreadsheet BPM.Ch12_Herd_immunity.xlsx, set the model population size to $N = 3.3 \times 10^8$ (the estimated population of the U.S. in April 2020), mean infectious time to $\tau_i = 16$ d, a basic reproduction number of $\mathcal{R}_0 = 2$, an initial number infectious of $N_0 = 1$. You'll also need to change the instruction for N_r in $Step\ 0$ to be

$$N_r^{\text{new}} = 0 \tag{12.43}$$

and the instruction for N_s in $Step\ 0$ to be equation (12.23). Then *reduce* the timestep δt to be small enough and add steps to get to $t = 40$ d. You'll then need to add columns for the dimensionless time t/τ_i and the total number infected $N_i + N_r$. Add a chart to plot the total number infected versus dimensionless time t/τ_i and change the axis options to match Fig.12.14.
(a) *Record* your graph.
Hint: You don't need to add the dotted vertical lines shown in Fig.12.14.
(b) *Record* the time t and dimensionless time t/τ_i that the total number infected $N_i + N_r$ reaches 21.
(c) *Briefly describe* how you could add the vertical lines.
Hint: We talked about how draw any shape in an Excel graph in **CHAPTER 2**.

Q.12.36 **(a)** By substituting equations (12.8) and (12.16) into equation (12.18), *show that* the SIR model predicts that

$$\delta i = (k_i s - k_r) i \delta t \tag{12.44}$$

where the **fraction infectious** i is *defined* by equation (12.29).
(b) Using FD diagram Fig.12.11, *show that* the FD equation for the fraction infectious is

$$\delta s = -k_i i s \delta t \tag{12.45}$$

(c) By dividing equation (12.44) by equation (12.45), *show that*

$$\delta i = \left(\frac{k_r}{k_i s} - 1\right) \delta s \tag{12.46}$$

(d) **CALCULUS QUESTION** Using calculus, *show that* the analytical solution to FD equation (12.46) for the **final fraction susceptible** s_∞ in the limit that $\delta s \to 0$ is:

$$\mathcal{R}_0(1 - s_\infty) + \ln s_\infty \approx 0 \tag{12.47}$$

where $s \approx 1$ at the beginning of the model and $s = s_\infty$ as $t \to \infty$ at steady state. Also, $i \approx 0$ at the beginning of the model and $i = 0$ at steady state. $\mathcal{R}_0$ is defined by equation (12.42). Your answer should use a format similar to the "Calculus can be useful" AWYD in **CHAPTER 3**.

About what you discovered: the basic reproduction number $\mathcal{R}_0$

Equation (12.47) is a relationship between the **basic reproduction number** $\mathcal{R}_0$ and the **final fraction susceptible** s_∞ [Jones 2007]. There are two unknowns in equation (12.47), so if you know one, e.g. $\mathcal{R}_0$, then the relationship allows us to find the other, e.g., s_∞ – but there's a catch! – one that you might not have seen before… As far as I know, equation (12.47) can't be solved using basic functions for s_∞, so you can't plug and chug to find s_∞ on your calculator – even if you know $\mathcal{R}_0$. Getting into the methods that can be used to solve this equation (such as the **Newton-Raphson method** – yes, it's that Newton again!) is beyond the scope of this chapter. However, the good news is that we've already confirmed the validity of equation (12.47) with our FD implementation of the SIR model as shown in Table 12.1, which came from my answer to Q.12.32.

My numbers for s_∞ might be a little different from yours, because I used a spreadsheet with **32000** rows! I also used as small a timestep as possible to minimize the finite timestep errors (**CHAPTER 3**). Also, in the $k_i = 0.045$ row of Table 12.1 I entered values of $s_p = 1$ and $h_p = 0$ because the values calculated using equations (12.27) $s_p = 1.3889$ and (12.33) $h_p = -0.3889$ don't make any physical sense as both s_p and h_p represent a *fraction* of the model population.

Table 12.1 Inputs and outputs for the SIR model

k_i (1/d)	k_r (1/d)	s_p	h_p	$\mathcal{R}_0$	s_∞	y
0.36	0.0625	0.1736	0.8264	5.76	0.00320	-0.004
0.18	0.0625	0.3472	0.65278	2.88	0.06820	-0.002
0.09	0.0625	0.6944	0.3056	1.44	0.4571	-0.001
0.0625	0.0625	1	0	1	0.9559	-0.001
0.045	0.0625	1	0	0.72	0.9964	-0.001

The values for y in Table 12.1 are remarkably close to zero – validating that $y \approx 0$ and equation (12.47), particularly when you take into account the assumption used in deriving equation (12.47) and hence (12.40), which is that the model is starts out with $s \approx 1$ so that the fraction infectious i is vanishingly small, i.e., $i \approx 0$ at the beginning of the model. The value we actually used was $i = 0.001$, i.e., one in a thousand, which appears to match the value of y for the smaller values of k_i in Table 12.1. ❑

Now that we've investigated the basic properties of the SIR model, we're ready to investigate how well it does in analyzing and predicting real COVID-19 data in the US. In this **WEB EDITION** of **CHAPTER 12** we'll start doing that in the next section. Let's see what we can discover by analyzing the data as it came in day-by-day in chronological order … In the condensed **CHAPTER 12** of the published book, we'll take a much simpler approach …

12.4 Exponential growth

Relating the SIR model to initial infection rate data – exponential growth

At the beginning of the outbreak, the SIR model predicts an exponential growth that can be used to find some of the parameters of the model – assuming conditions for disease transmission etc. don't change, e.g., by increased social distancing or testing, or seasonal variations etc. During that initial exponential growth period, the fraction susceptible is close to one, i.e., $s \approx 1$. As we discovered in Q.12.21, that's a reasonable approximation so long as $i_0 \lesssim 0.1$ – see the "changing the starting point" AWYD after Q.12.21.

Q.12.37 **(a)** By substituting equation (12.8) and equation (12.16) into equation (12.18), and assuming that $s \approx 1$ during the initial phase of the outbreak, *show that* the change in the number infectious is given by

$$\delta N_i = (k_i - k_r) N_i \delta t \tag{12.48}$$

or

$$\delta N_i = k_g N_i \delta t \tag{12.49}$$

where

$$k_g = k_i - k_r \tag{12.50}$$

is the net **growth rate constant** for the initial phase of the outbreak.

Q.12.38 **CALCULUS QUESTION** **(a)** Using calculus, *show that* the analytical solution to FD equation (12.49) in the limit that $\delta t \to 0$ is:

$$N_i = N_0 e^{k_g t} \tag{12.51}$$

where N_0 is the initial number infectious at the time that we'll call $t = 0$. We're also assuming that the susceptible fraction is still $s \approx 1$ at that time. Your answer should use a format like the "Calculus can be useful" AWYD in **CHAPTER 3**.

(b) By taking the derivative of equation (12.51), *show that* the analytical solution for $\mathrm{d}N_i/\mathrm{d}t$ as a function of time is

$$\frac{\mathrm{d}N_i}{\mathrm{d}t} = k_g N_0 e^{k_g t} \tag{12.52}$$

where

$$\frac{dN_i}{dt} = R_i - R_r = k_g N_i \tag{12.53}$$

Q.12.39 DISCUSSION QUESTION By *substituting* equation (12.51) into equation (12.53), *show that* the analytical solution for $dN_i/dt = R_i - R_r$ as a function of time is equation (12.52). **Hint:** This is not a trick question. It really is that easy!

We now want to see how to make the SIR model match up with the UG model, so that we can use the same approach that we used in Q.12.09 to successfully fit the model to the initial USA data. We can't use equation (12.52) directly because as equation (12.53) states dN_i/dt is not the same as R_i. To avoid confusion with the parameters of the SIR model and the UG model, let's rewrite the UG model infection rate (12.6) as

$$R_i = k_u N_u e^{k_u t} \tag{12.54}$$

where k_u is the infection rate constant for the UG model and N_u is the initial number infectious in the UG model.

Q.12.40 DISCUSSION QUESTION By substituting equation (12.51) into equation (12.8) with $s \approx 1$, *show that* the *initial* new infection rate in the SIR model is given by

$$R_i = k_i N_0 e^{k_g t} \tag{12.55}$$

The reported data correspond to R_i. Hence, in order to make the two models predict the same new infection rate R_i, the new infection rates in equations (12.54) and (12.55) should be equal, so that

$$R_i = k_i N_0 e^{k_g t} = k_u N_u e^{k_u t} \tag{12.56}$$

The only way equation (12.56) can be true, is if the arguments of the exponential function are the same, i.e., $k_g t = k_u t$, so that

$$k_u = k_g = k_i - k_r \tag{12.57}$$

we also need the prefactors in to be the same in equation (12.56), i.e., we need

$$k_i N_0 = k_u N_u \tag{12.58}$$

Q.12.41 DISCUSSION QUESTION (a) By substituting equation (12.57) into (12.58), solving for N_0 and substituting in equation (12.50), *show that* the *initial* predictions of the SIR model will match the predictions of the UG model if we set the initial number infectious in the SIR model to

$$N_0 = \frac{k_i - k_r}{k_i} N_u \tag{12.59}$$

Hence, we can use the same procedure we used in Q.12.09 to find k_u and N_u using a fit to a simple exponential function for R_i (12.54).
(b) *Show that* we can then find the SIR model infection rate constant k_i using

$$k_i = k_u + k_r \tag{12.60}$$

and we can then find N_0 from N_u using equation (12.59).

Technical note: We could fit equation (12.55) directly to the published data, but that would require us to make a guess as to $\tau_i = 1/k_r$ before we started the fit. We'd then have to redo the fit if we changed τ_i. In what follows, you'll discover that the advantage of the above approach is that we can adjust the mean infectious time τ_i and see how it affects the model – without having to redo the fit to the reported data. ❑

About what you discovered: Fitting the SIR model to initial outbreak data

What you discovered in Q.12.41 means that if we make an estimate of the mean infectious time τ_i and N, we can then see what the SIR model predicts and have it be automatically fit to the initial exponential growth part of the outbreak. We'll start by using that approach to see what the prediction of the SIR model is using our existing fit of the UG model to the first 19 days of the COVID-19 outbreak in the US. ❑

The effect of the mean infectious time τ_i

The value of $\tau_i = 16$ d that we've been using comes from the worse-case value I could find online in mid-March 2020. A Wolfram notebook shows a "mean recovery time" of 15.9 days (accessed Apr. 19, 2020) [Wolfram 2020] that I rounded up to 16 days and assumed that it was the same as the mean infectious time. That's probably an overestimate if mild cases of COVID-19 stop being infectious earlier than more severe cases. If you look online, you'll find all kinds of numbers that relate to the mean infectious time, one example that's roughly equivalent is the "average recovery time" for COVID-19.

Q.12.42 *Find three* values that you can use as estimates for the mean infectious time for COVID-19. *Report* the most reliable numbers you found. Don't forget to include references including a URL. Remember, in our model we're most interested in the **mean infectious time** – the average time that an individual is infectious.
1st Note: We're not interested in the incubation time in our model. You can think of the incubation time as being the time it takes an individual to "jump" from box $s \to i$. Compare this with the fact that jumps in the marble game caused by random Brownian motion also take a finite amount of time (**CHAPTER 10**).
2nd Note: The best information for our model should technically include infectious individuals that aren't symptomatic – they're the ones that are thought to be most responsible for the spread of the virus. What can you discover?

In addition to uncertainty about the value of τ_i, there's also the fact that known infectious people are usually isolated from the rest of the population. That's why the "R" in the SIR model is often said to stand for **removed** – as in removed from the number infectious, which has the same effect as **recovered** as long as they don't interact with anyone in box s before they stop being infectious. There are also individuals removed from the number infectious due to death. Hence, given the uncertainties, it's important for us to understand the effect of changing τ_i the mean infectious time in our model.

An additional uncertainty, particularly in the United States during April 2020, is that generally only people with severe symptoms are being tested for COVID-19. The easiest way to account for that is to reduce the model population number N so that it only reflects individuals in the real population that would exhibit severe symptoms if infected. For example, if only one in ten people infected exhibit severe symptoms and hence get tested, then we could reduce the model population for the U.S. from $N = 3.3 \times 10^8$ to $N = 3.3 \times 10^7$ or 33 million. We'll investigate the effect of changing this parameter N and the parameter τ_i after we have a more realistic fit to the published data later in this **SECTION 12.4** and again in **SECTION 12.5**.

Fitting USA data for early March 2020

Q.12.43 Open the preformatted spreadsheet BPM.Ch12_Exponential_dragon.xlsx. Note that there are two main tables – the **SIR model table** is for the FD implementation of the SIR model and the **USA new infections starting 2/27/2020 (ECDC)** table has the new infections data in the US for the first 19 days reported by the ECDC that you analyzed in Q.12.08, Q.12.09 and Q.12.10 together with data up to day 35. The **Param$** column **J** for that table has the parameters for the least-squares fit of the UG model to the day-19 data that you conducted in Q.12.09. However, we're using the symbol k_u for the UG infection rate constant and N_u for the UG model initial number infected to avoid confusion with the SIR model parameters k_i and N_0 (in **Param$** column **A**). t_d is the doubling time for the UG model that's calculated using equation (12.7) with k_i replaced with k_u, i.e.,

$$t_d = \frac{\ln 2}{k_u} \tag{12.61}$$

The chart to the right of the **USA new infections** table shows the prediction of the UG model for the next 16 days (solid line) using the parameters k_u and N_u, and the corresponding data published by the ECDC for new confirmed cases per day until April 1, 2020 as a semi-log graph.

(a) *Run* Excel's **Solver** with a **Set Objective** of **J7**, the cell for the quality of fit Q; the **To:** radio button set to ⊙ **Min**; and **By Changing Variable Cells:** set to **J3,J5**, the cells for UG model parameters k_u and N_u. *Record* your semi-log $R_i(t)$ graph.

(b) *Briefly comment* on how well the UG model does in predicting the next 16 days. *Describe* any systematic deviation between the model predictions and the reported data for those 16 days.
(c) Make a copy of the graph and change the vertical R_i-axis to a linear scale, i.e., uncheck the box for **Logarithmic scale** in the **Axis Options**. *Briefly describe* what new insights this new perspective provides about the predictions of the UG model.

Q.12.44 The **Param$** column **A** for the **SIR model table** has places for the SIR model parameters. I've already inputted $N = 3.3 \times 10^7$ (33 million) for the model population size, $\delta t = 0.015$ d for the timestep and $\tau_i = 16$ d for the mean infectious time. The recovery rate constant is calculated using $k_r = 1/\tau_i$. *Fill in the blank cells* in the rest of the **Param$** column **A** using equations (12.60), (12.59) and (12.42).
(a) *Record* the values calculated by the spreadsheet for k_i, N_0, and $\mathcal{R}_0$.
(b) *Briefly comment* on how those values compare with the values we used in **SECTION 12.3**.
(c) Change the parameter τ_i from 16 days to 8 days, 4 days, 2 days and 1 day and *record* the values of for τ_i, k_r, k_i, N_0, and $\mathcal{R}_0$ in the form of a table.
Hint: You can use Excel to make the table.
(d) *Briefly discuss* how changing the mean infectious time parameter τ_i changes the basic reproduction number $\mathcal{R}_0$.

Q.12.45 Change the mean infectious time back to $\tau_i = 16$ d, then *fill in the blank cells* in the **SIR model table** with your SIR algorithm from Q.12.18(c), or the model answer BPM.Ch12_SIR_algorithm.pdf. Once you've filled in the first step, you can then use the left-double-click copy method to populate the rest of the table. The spreadsheet should then automatically plot the new infection rate $R_i(t)$ predicted by the SIR model– one graph showing the first 35 days and the second showing the first 80 days.

Once you've filled in the first step, you can then use the left-double-click copy method to populate the rest of the table. The spreadsheet should then automatically plot the new infection rate $R_i(t)$ predicted by the SIR model.

(a) *Record* your $R_i(t)$ graph for the first 80 days.
(b) *Record* the value and time of the peak infection rate per day R_i^{peak}.
Note: Don't freak out, the US people didn't let this happen, but it's important to know what the SIR model predicts … if there's no social distancing at all.
(c) *Briefly describe* why R_i^{peak} doesn't occur at t_p, the time of the peak in $N_i(t)$, which we discussed at some length in **SECTION 12.3**.
Hint: Looking at Fig.12.12 should help you formulate your answer.

Q.12.46 As you discovered in Q.12.44(c) and (d) changing the value of the mean infectious time τ_i can have a dramatic effect on the basic reproduction number $\mathcal{R}_0$. Let's see if it has a similar dramatic effect on the peak infection rate.

(a) Add two new columns to the table you made for Q.12.44(c) – one for the time of the peak infection rate and another for the value of R_i^{peak}. Change the mean infectious time to $\tau_i = 8$ d, $\tau_i = 4$ d, $\tau_i = 2$ d and $\tau_i = 1$ d. While you're doing that, pay attention to what happens to the fitted line in the 35-day graph of $R_i(t)$. *Briefly describe* what happens to the fitted line as you change τ_i.

(b) *Briefly explain* why the fit to the initial exponential growth using the UG model doesn't change as you adjust τ_i.

(c) *Record* your updated table including the time and magnitude of the peak infection rate R_i^{peak}.

(d) *Briefly summarize* what can you conclude about the sensitivity of the model predictions for $R_i(t)$ to the parameter τ_i.

Once the UG model has been fitted to the initial exponential growth, there's not much wiggle-room left in the SIR model (we're assuming no change in social distancing or testing and no seasonal variations etc.). In Q.12.46 we investigated the effect of changing the mean infectious time τ_i. There's only one other adjustable parameter left in the SIR model – the size N of the model population. Let's see what we can discover …

Q.12.47 Change the mean infectious time back to $\tau_i = 16$ d. Then investigate changing the size of the model population. First try $N = 3.3 \times 10^8$ the current estimate of the entire US population (330 million, it's ten times the previous model population size). I recommend you enter that number into Excel as **3.3e8**. Then try a model population size of $N = 3.3 \times 10^6$, which would assume that only one in one hundred US residents are susceptible to the COVID-19 disease and would show up in the published R_i data if infected.

(a) *Record* the time and value of the peak infection rate per day R_i^{peak} for $N = 3.3 \times 10^8$ and $N = 3.3 \times 10^6$. Report your answer as a table for N, time, and R_i^{peak} for $N \in \{3.3 \times 10^8, 3.3 \times 10^7, 3.3 \times 10^6\}$.

(b) *Briefly summarize* what you discovered about the effect of changing N in the SIR model.

Note: We've already talked about this, but it's worthwhile going over it again in this context.

(c) In the absence of a vaccine for COVID-19, *briefly explain* if you think it's reasonable to reduce the model population size for the US to a number outside the range we investigated in parts (a) and (b).

(d) Change the model population size back to $N = 3.3 \times 10^7$ then make a copy of the 80-day graph of $R_i(t)$ and change the vertical R_i-axis to a log scale, i.e., check the box for **Logarithmic scale** in the **Axis Options**. Then extend the SIR model table in time (you can

increase δt) until the new infection rate gets back to about one new case per day. *Record* your semi-log graph of graph of $R_i(t)$.

(e) *Briefly describe* what new insights this new perspective provides about the shape of the peak in the SIR model $R_i(t)$ curve.

Hint: Recall that a straight line on a semi-log graph indicates **exponential growth** if the slope (rise over run) is positive and **exponential decay** if the slope is negative.

(f) While monitoring the semi-log plot, cycle through the mean infectious times $\tau_i \in \{16, 8, 4, 2, 1\}$ d and pay to attention how the inverted vee Λ of the peak shifts. Also pay attention to the shape of the tail of the curve. Once again you can use **Undo** (Ctrl+Z) and **Redo** (Ctrl+Y) to cycle between the five values of τ_i. *Briefly summarize* what you discovered.

About what you discovered: the exponential dragon

As you discovered in Q.12.46 and Q.12.47, the peak in the new infection rate $R_i(t)$ remains with all the reasonable choices for τ_i. That's because the exponential doubling time t_d (that we obtained from the fit to the UG model for the first 19 days) doesn't depend on what value we choose for the mean infectious time parameter τ_i. This exponential fit produces the **dragon**'s head peak predicted by the SIR model shown in Fig.12.15(a). This can be seen more mathematically in the semi-log graph of Fig.12.15(b) where the initial straight-line portion indicates the **exponential growth** predicted by both the UG model and the SIR model. As you discovered in Q.12.47(f), the shape of the inverted vee (Λ) of the dragon's head in Fig.12.15(b) also doesn't depend on the τ_i parameter or the model population size. It only depends on the **exponential growth constant** $k_u = k_g = k_i - k_r$ (12.57), which can also be characterized by the **doubling time** t_d, in an analogous manner to how the **drug elimination constant** k_e from **CHAPTER 2** and **CHAPTER 4** is characterized by the drug **half-life**. The slope of the **exponential tail** of the **dragon** is determined by τ_i as shown more clearly in Fig.12.15(b).

As you discovered in Q.12.47(a), the height of the dragon's head is proportional to the choice of the model population size, e.g., if the entire US population (3.3×10^8) is included in the model population the peak grows to nearly $R_i^{\text{peak}} \approx 2 \times 10^7$ d^{-1}! This can be compared with the actual value for the US in early April 2020 of about $R_i \approx 30{,}000$ d^{-1}, which was reduced due to social distancing and mask wearing in the US.

It's important to note that the exponential dragon you discovered in Q.12.43 to Q.12.47 applies to an SIR model in which there's no social distancing in effect. We'll get to how social distancing has affected the data in the beginning of April 2020 after we complete Q.12.49.

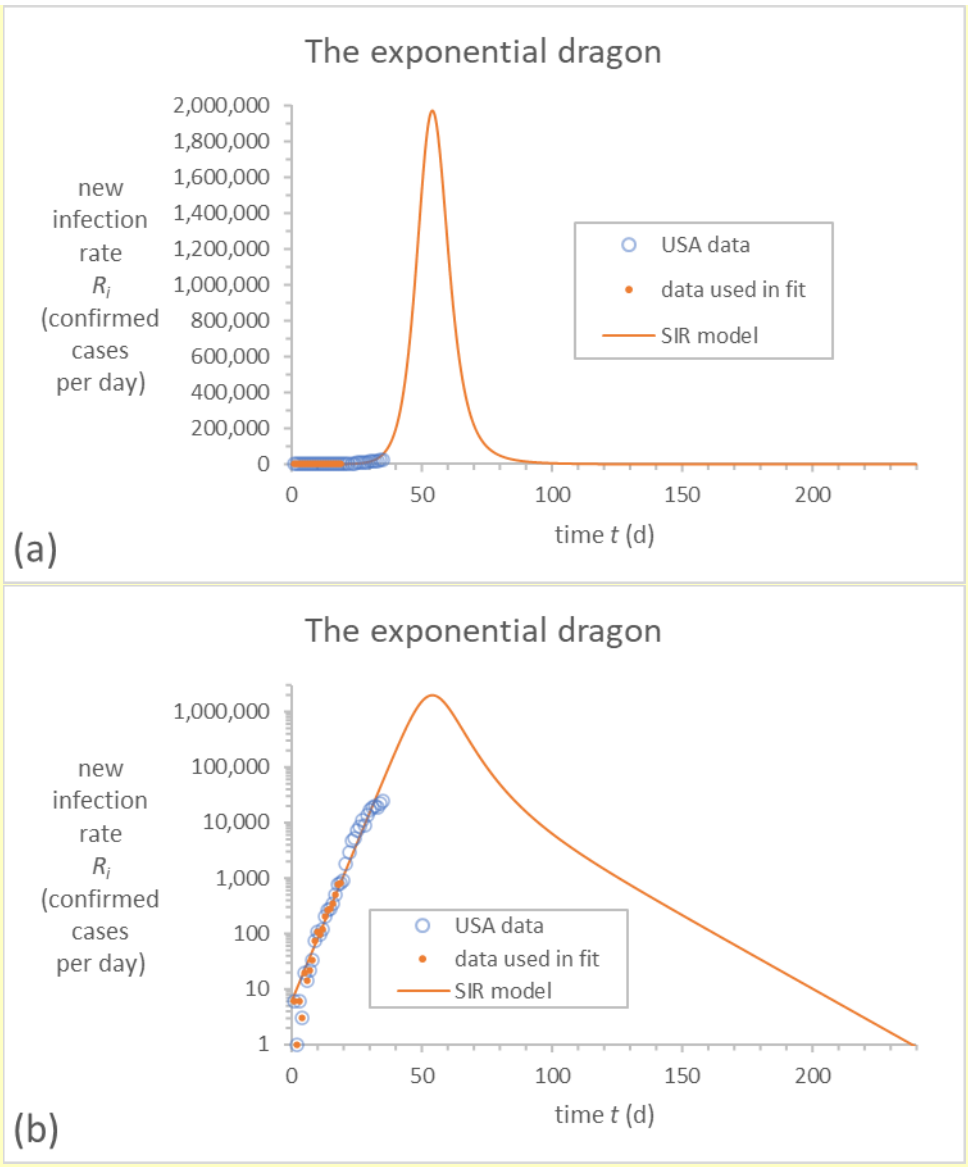


Fig.12.15 Excel chart showing the predictions of the SIR model (Fig.12.11) when fitted to the initial exponential growth during the first 19 days of the outbreak. The exponential growth has fitted parameters of $k_u = 0.2616\ \text{d}^{-1}$ and $N_u = 23.23$, resulting in a doubling time of $t_d = 2.65$ d. The only adjustable parameters remining in the SIR model are the mean infectious time $\tau_i = 16$ d and the model population size $N = 3.3 \times 10^7$. **(a)** The head of the dragon on a linear-scale plot. **(b)** Semi-log graph illustrating the dragon's exponential head and accentuating its long exponential tail, which isn't apparent in the linear-scale graph. Data source ECDC [2020].

Note: The idea of using a dragon analogy for explosive exponential growth was inspired by the expression "tickling the dragon's tail" that's based on a remark by Richard Feynman [Nelson 2021] about the dangers of some ill-advised early nuclear experiments – where exponential growth had the potential for similar catastrophic consequences. ❑

Q.12.48 Let's now briefly investigate what happens if we use more of the published data to fit the initial exponential growth. To do that, all you'll need to do is extend the residual r and residual squared r^2 columns in the **USA new infections** table and then run **Solver**

again, but before you do that you need to clear out the **SIR model table** as much as possible by deleting the entries for $R_i\ldots$ from $Step\ 2$ to the bottom of the table, but you should keep all the entries in the time t (d) column. Why? Well, for every step in the **Solver** algorithm, Excel recalculates the entire spreadsheet including the tens of thousands of formulas in the **SIR model table** that aren't even needed for finding k_u and N_u for the fit to the UG model. Once you've completed the LS fit using **Solver** you can then repopulate the **SIR model table** using the left-double-click copy method.
Note: When you're using **Solver**, you should close all other spreadsheets as their cells are also recalculated when **Solver** takes a step.
(a) Using the procedure described above, *sample* different ranges of data in the LS fit to the UG model. *Briefly summarize* what you discovered.
Hint: Don't forget to clear out the **SIR model table** before you run Excel's **Solver**!
(b) Using the procedure outlined above, try fitting the UG model to the USA data for the first 25 days. *Record* the value of $\mathcal{R}_0$ and *briefly summarize* what you discovered.
(c) *Record* your semi-log graph of graph of $R_i(t)$.

Before we move onto trying to model the USA data with social distancing, let's revisit what we discovered about the SIR model in **SECTION 12.3**.

Q.12.49 Using equations (12.27), (12.33), and your extended-time SIR spreadsheet with the LS fit to the day-19 data – add columns to the table you made for Q.12.46(c) for s_p, h_p, and s_∞.
(a) *Briefly summarize* what you discovered.
(b) *Briefly explain* how your new observations are consistent with the exponential dragon that occurs even when $\mathcal{R}_0$ is reduced to close to one.

About what you discovered: the dragon's tail

As you discovered in Q.12.49, the model fitted to the initial exponential growth is moderated if the mean infectious time τ_i is shorter, but the lower basic reproduction numbers that result ($\mathcal{R}_0 \lesssim 2$) don't save us from the exponential dragon. For an unrealistically low value of $\tau_i = 1$ d, the herd immunity threshold is reduced to just under $h_p \approx 0.21$ (21%) which sounds promising, but the exponential dragon still produces an unmanageable peak infection rate of three quarters of a million new infections per day (with $N = 3.3 \times 10^7$). However, shortening the dragon's exponential tail does save about 61% of the model population from being infected – if $\tau_i = 1$ d. Unfortunately, it seems more likely that τ_i is closer to a *week* or two for COVID-19 instead of a *day* or two. Hopefully, lowering k_i through social distancing and mask wearing will make the predictions of the SIR model more palatable. Let's see what we can discover … ❑

Fitting US data for early April 2020 – the butterfly effect

The preformatted spreadsheet BPM.Ch12_Butterfly_effect.xlsx contains data from the ECDC for April 2 through April 14, 2020, which appears to be *after* social distancing has taken effect in the US. In what follows, we're going to fit the SIR model first to data from April 2 through April 11

and then investigate the consequences of adding only *three more days* to the data used to make the fit. We'll then discover just how sensitive the SIR model is to the initial conditions used to fit the model …

Q.12.50 Open the preformatted spreadsheet BPM.Ch12_Butterfly_effect.xlsx. Note that there are two main tables – the **SIR model table** is for the FD implementation of the SIR model and the **USA new infections** table has the new infections data in the USA data from the ECDC for April 2 through April 14, 2020. The **Param$** column **J** for that table has places for a least-squares fit of the UG model to the USA data. Once again, we're using the symbol k_u for the UG infection rate constant and N_u for the UG model initial number infected to avoid confusion with the SIR model parameters k_i and N_0 (in **Param$** column **A**). t_d is the doubling time for the UG model that's calculated using equation (12.61). The chart to the right of the **USA new infections** table shows the prediction of UG model for the next 13 days (solid line) and the corresponding data published by the ECDC as a semi-log graph.
(a) Run Excel's **Solver** with a **Set Objective** of **J7**, the cell for the quality of fit Q; the **To:** radio button set to ⊙ **Min**; and **By Changing Variable Cells:** set to **J3,J5**, the cells for UG model parameters k_u and N_u. *Record* your fitted $R_i(t)$ graph for the UG model.
(b) Make a copy of the graph and change the vertical R_i-axis to a linear scale, i.e., uncheck the box for **Logarithmic scale** in the **Axis Options**. *Briefly describe* what new insights this new perspective provides about the predictions of the UG model.

Q.12.51 The **Param$** column **A** for the **SIR model table** has places for the SIR model parameters. I've already inputted $N = 3.3 \times 10^7$ (33 million) for the model population size, $\delta t = 0.1$ d for the timestep and $\tau_i = 16$ d for the mean infectious time. The recovery rate constant is calculated using $k_r = 1/\tau_i$. Fill in the blank cells in the rest of the **Param$** column using equations (12.60), (12.59) and (12.42). Then fill in the blank cells in the **SIR model table** with your SIR algorithm from Q.12.18(c), or the model answer BPM.Ch12_SIR_algorithm.pdf. The spreadsheet should automatically plot the new infection rate $R_i(t)$ predicted by the SIR model – one graph showing the first 14 days and the second showing the first 500 days.
(a) *Record* your $R_i(t)$ graph for the first 500 days.
(b) Change the formula for Q in the **Param$** column **J** to include one more day, i.e., change the formula for Q to **=SUM(Q3:Q13)**, then change the **data used in fit** series in all of the graphs to include the data point for April 12, 2020. Then clear out the **SIR model table** as much as possible by deleting the entries for R_i… from $Step$ 2 to the bottom of the table as we discussed in the preamble to Q.12.48. Then rerun the LS fit using **Solver** then repopulate the **SIR model table** using the left-double-click copy method. *Record* your new $R_i(t)$ graph for the first 500 days.
(c) Use the procedure outlined in part (b) to add the data point for April 13, 2020, then *record* your new $R_i(t)$ graph for the first 500 days.

(d) Use the procedure outlined in part (b) once more to add the data point for April 14, 2020, then *record* your new $R_i(t)$ graph for the first 500 days.
(e) *Briefly discuss* what you discovered about the sensitivity of the SIR model to the initial conditions of this fit to the first two weeks of April 2020.

About what you discovered: the butterfly effect

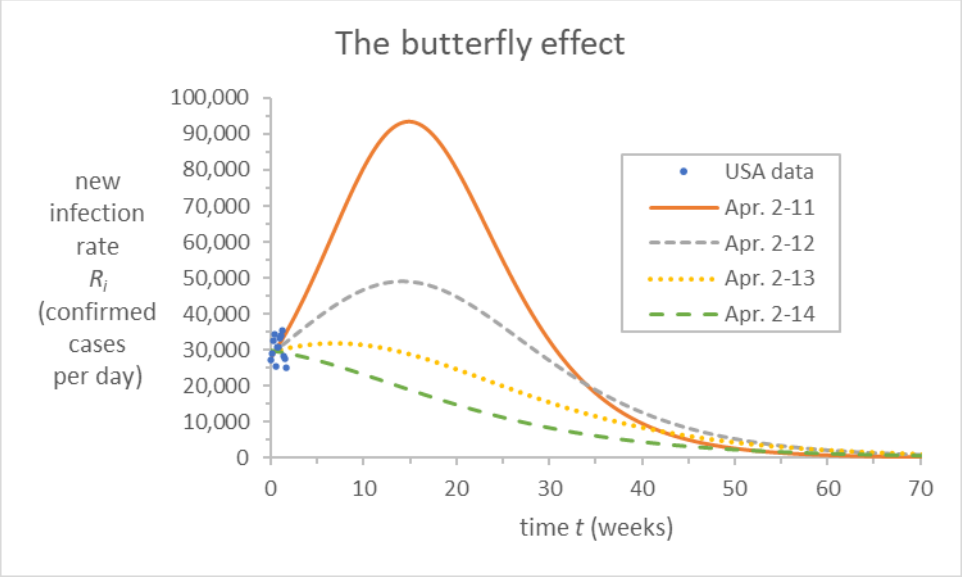


Fig.12.16 Excel chart showing the predictions of the SIR model (Fig.12.11) when fitted to USA new infection rate data in early April 2020. Solid circles show the data reported by the ECDC for April 2-14, 2020. The curves show the SIR model fitted to the time intervals indicated in the legend. As shown, the SIR model has a dramatic sensitivity to changes in the initial conditions used for the fits. It's an example of the **butterfly effect**.

Fig.12.16 summarizes your answers to Q.12.51(a)-(d) and shows the dramatic effect of adding just three days of published data to the fit of the SIR model. This is a straightforward example of the **butterfly effect** that spawned a whole new branch of computational modeling and physics, called **chaos theory**, or less ominously **nonlinear dynamics**. The idea behind the **butterfly effect** is that the equations predicting weather are so nonlinear that a butterfly flapping its wings in western Africa can eventually produce a category 5 hurricane that devastates southern Florida. Let's see what we can discover … ❑

12.5 Exponential decay

Modeling after the peak $(R_i \lesssim R_r)$

The fit to the USA data for April 2-14 in Fig.12.16 shows that the curve is essentially flat for the first few weeks. After I did this fit on April 15, it occurred to me that the approach we used in Section 12.4 is predicated on there being exponential growth at the beginning of the period we're trying to model. The optimistic thought I had was that maybe we can make a fit assuming that the

infection rate is decreasing. As a result, we'll need to change the procedure we used in **SECTION 12.4**, because the math is different.

Q.12.52 **(a)** If the number infectious is staying constant or decreasing, then we know from Q.12.25 that $R_i \leq R_r$. Using equations (12.8) and (12.16), *show that* this implies

$$k_i s_0 \leq k_r \tag{12.62}$$

where s_0 is the susceptible fraction at the beginning of the period after social distancing has taken effect, i.e., the value of the susceptible fraction s on April 3, 2020.
(b) By substituting equation (12.8) and equation (12.16) into equation (12.18), with $s = s_0$ *show that*

$$\delta N_i = -(k_r - k_i s_0) N_i \delta t \tag{12.63}$$

or

$$\delta N_i = -k_d N_i \delta t \tag{12.64}$$

where

$$k_d = k_r - k_i s_0 \tag{12.65}$$

is the initial **decay rate constant** for the number infectious, which is a positive quantity when N_i and $R_i = k_i N_i s$ (12.8) are decreasing.

Q.12.53 **CALCULUS QUESTION** **(a)** Using calculus, *show that* the analytical solution to FD equation (12.63) in the limit that $\delta t \to 0$ is an **exponential decay** of the form

$$N_i = N_0 e^{-k_d t} \tag{12.66}$$

where N_0 is the initial number infectious at time $t = 0$ for the social distancing period of the epidemic, i.e., $t = 0$ is the first time that k_d (or $\mathcal{R}_0$) has stabilized after social distancing has taken effect (with the susceptible fraction approximately constant at $s \approx s_0$). Your answer should use a format similar to the "Calculus can be useful" AWYD in **CHAPTER 3**.
Note: Equation (12.66) is mathematically equivalent to equation (2.16) for the exponential decay predicted in our model of drug elimination (**CHAPTER 2**).

Q.12.54 **(a)** By substituting the exponential decay equation (12.66) into equation (12.8), *show that* the analytical solution for the new infection rate $R_i(t)$ during the initial social-distancing period, assuming $s \approx s_0$, is an exponential decay of the form

$$R_i \approx k_i N_0 s_0 e^{-k_d t} \tag{12.67}$$

or

$$R_i \approx A_0 e^{-k_d t} \tag{12.68}$$

where

$$A_0 = k_i N_0 s_0 \tag{12.69}$$

(b) Exponential decay (ED) equation (12.68) includes an implicit assumption about how social distancing remains in place. *Briefly explain* what it is in words and using math.
(c) Using equation (12.66) and the definition of half-life (that $N_i = N_0/2$, when $t = t_{½}$) *show that*

$$t_{½} = \frac{\ln 2}{k_d} \tag{12.70}$$

which is the same as equation (4.22) that we first derived for drug elimination and radioactive decay in **CHAPTER 4**.

About what you discovered: exponential decay – the dragon's tail

A consequence of equation (12.68) is that after social distancing has taken effect, we can fit the first few weeks of data to an exponential decay of the same form that we used in **CHAPTERS 2**, **3**, **4**, **9** and **11**. The exponential decay predicted by equation (12.68) is much easier to fit than exponential growth. The equation is not as "stiff" as exponential growth – so long as the infection rate R_i is decreasing (on average). If social distancing is relaxed enough that R_i starts to increase again on average (by even a small percentage) then the butterfly can tickle the dragon's nose and our predictions become much more uncertain once again. As you'll discover, the USA data for April and early May are perilously close to the boundary between exponential decay and exponential growth. We'll return to this possibility in **SECTION 12.7** when we discuss the consequences of lifting social distancing measures prematurely. But before we do that, let's see what our SIR model predicts based on data for the first two weeks of April 2020.

As an aside, it's worth noting that while the approach taken above seems straightforward, it took a while for me to realize that it's important to allow for the possibility that $s_0 \approx 1$. This surprised me because as you'll discover, the fitted parameter s_0 is usually greater than $s_0 = 0.99$, which I would have thought would be close enough to $s_0 = 1$. But it appears that this situation is similar to what we discussed in the "misconceptions can be subtle" AWYD after Q.5.36 in **CHAPTER 5**. However, as you'll discover in Q.12.55, the calculated parameter s_0 is completely determined by the ED model parameters A_0 and k_d, so that including it in the model doesn't actually add an additional adjustable parameter. As we've discussed before, including only a minimum of adjustable parameters is important from a modeling perspective. ❑

Q.12.55 DISCUSSION QUESTION **(a)** By solving equation (12.65) for k_i, *show that* the infection rate constant for the SIR model can be calculated from a least-squares fit to the exponential decay equation (12.66) using

$$k_i = \frac{k_r - k_d}{s_0} \tag{12.71}$$

(b) Then, by combining equations (12.69) and (12.71), *show that* we can calculate the initial number infectious from the ED parameters A_0 and k_d using

$$N_0 = \frac{A_0}{k_r - k_d} \tag{12.72}$$

(c) Finally, using the definition of s (12.9) and the bookkeeping equation (12.15) with $N_r = 0$, *show that* we can then calculate the initial faction susceptible during the social distancing period using

$$s_0 = \frac{N - N_0}{N} \tag{12.73}$$

Q.12.56 Open the preformatted spreadsheet BPM.Ch12_Cloudy_with_dragons.xlsx. It has the same data that we first analyzed in Q.12.50, but now the **USA new infections** table has been extended to Memorial Day (May 25, 2020). The **Param$** column **J** for that table has places for the ED model parameters k_d, for the exponential decay rate constant and A_0 for the prefactor in the ED equation (12.68). $t_{½}$ is the half life for the ED model that's calculated using equation (12.70). The chart to the right of the **USA new infections** table shows the prediction of ED model for the next 40 days (solid line) and the corresponding data published by the ECDC as a semi-log graph. The parameter Q is calculated using equation (6.11) using **=SUM(Q3:Q14)** as the sum is of the r^2 values from April 3, 2020 to April 14, 2020, inclusive.

Note: I dropped the data point for April 2, 2020 because it seemed to be the last day in the transition period between the initial exponential growth and the period after social distancing had taken effect. **RESEARCH QUESTION** After you've completed Q.12.61, *investigate and report* on the validity of that assertion.

(a) Run Excel's **Solver** with a **Set Objective** of **J7**, the cell for the quality of fit Q; the **To:** radio button set to ⊙ **Min**; and **By Changing Variable Cells:** set to **J3,J5**, the cells for ED model parameters k_d and A_0. *Record* your fitted $R_i(t)$ graph for the ED model.

(b) Make a copy of the graph and change the vertical R_i-axis to a linear scale, i.e., uncheck the box for **Logarithmic scale** in the **Axis Options**. *Briefly describe* what new insights this new perspective provides about the predictions of the ED model (12.68).

(c) Add a linear trendline based on the **data used in fit** series to the linear-scale graph you just made. Then, extend the trendline out to day 52 using **Format Trendline… > Trendline Options > Forecast > Forward [41] periods.** (You'll also need to increase the width of the legend box to see all the series.) *Briefly comment* on the differences between the linear regression trendline and the ED model prediction based on the same **data used in fit**. Do you think the differences are significant? What can you conclude about the equivalency between the ED model and the linear trendline based on the **data used in fit**.

(d) Add another linear trendline to the linear-scale graph based on the **USA data** series. *Record* your graph and *briefly comment* on the differences between the linear regression trendline and the ED model prediction based on the **data used in fit**. Do you think the

differences are significant? What can you conclude about the equivalency between the ED model and the linear trendline fitted to all of the **USA data**.

(e) **CALCULUS DISCUSSION QUESTION** Using the exponential series (9.25) ($e^x \approx 1 + x + \cdots$) show that the ED model (12.68) can be approximated by the linear function

$$R_i \approx A_0 - A_0 k_d t \tag{12.74}$$

for $k_d t \ll 1$. Hence, if needed, we can use Excel's linear trendline and/or Excel's **slope** and **intercept** functions to estimate A_0 and k_d so long as $k_d t \ll 1$. I have not used this approximation, but it might prove useful for analyzing larger data sets rapidly in a full-blown programming environment like Python, R, MATLAB, Mathematica, SPSS etc.

Q.12.57 **DISCUSSION QUESTION** The **Param$** column **A** for the **SIR model table** has places for the SIR model parameters. I've already inputted $N = 3.3 \times 10^7$ (33 million) for the model population size, $\delta t = 0.1$ d for the timestep and $\tau_i = 16$ d for the mean infectious time. The recovery rate constant is calculated using $k_r = 1/\tau_i$. Fill in the blank cells in the rest of the **Param$** column using equations (12.72), (12.73), (12.71) and (12.42). Then fill in the blank cells in the **SIR model table** with your SIR algorithm from Q.12.18(c), or the model answer BPM.Ch12_SIR_algorithm.pdf. Then populate the **SIR model table** using the left-double-click copy method. The spreadsheet should automatically plot the new infection rate $R_i(t)$ predicted by the SIR model – one graph showing the first 52 days and the second graph showing the first 600 days after social distancing took effect.

Note: I know you've done this before, but it's a good way for us to remind ourselves about how the SIR model is implemented in the spreadsheet.

(a) *Record* your $R_i(t)$ graph for the first 52 days after social distancing took effect.

(b) *Briefly comment* on whether the SIR model does a better job than the ED model at predicting the USA data from day 12 (4/15/2020) onward.

(c) Change the mean infectious time to $\tau_i \in \{8, 4, 2, 1\}$ d. While you're doing that, pay attention to what happens to the prediction of the SIR model in the $R_i(t)$ graph for the first 52 days. Once again you can use **Undo** (Ctrl+Z) and **Redo** (Ctrl+Y) to cycle between the five values of τ_i. *Briefly summarize* what happens to the SIR prediction as you change τ_i.

Q.12.58 **DISCUSSION QUESTION** **(a)** With $\tau_i = 16$ d, add a linear trendline based on the **USA data** series to the graph for the first 52 days. (You'll also need to increase the width of the legend box to see all the series.) *Briefly comment* on the differences between the linear regression trendline and the SIR model prediction based on the **data used in fit**. Do you think the differences are significant? Which fit matches the USA data better? Based on this comparison how does the SIR model with $N = 3.3 \times 10^7$ compare with the ED model.

Note: As we discussed in **CHAPTER 6**, the low value of R^2 for the linear (LR) trendline doesn't mean the fit is bad – just that the slope is small compared with the scatter in the data.

(b) With $\tau_i = 16$ d, try changing the value of the model population size. $N = 3.3 \times 10^7$ corresponds to 1 in 10 of the total US population (3.3×10^8), then $N \in \{6.6 \times 10^7, 8.25 \times 10^7, 1.1 \times 10^8, 1.65 \times 10^8, \text{and } 3.3 \times 10^8\}$ that correspond to 1 in 5; 1 in 4; 1 in 3; 1 in 2; and 1 to 1, respectively. While you're doing that pay attention to how the SIR model curve changes and, in particular, pay attention to how it matches up with the linear trendline fitted to the data, recalling that our ED fit is to the first 12 data points. Once again, you can use **Undo** (Ctrl+Z) and **Redo** (Ctrl+Y) to cycle between the values of N that you chose. *Briefly summarize* what happens to the SIR prediction as you change N.
(c) *Record* your graph for the first 600 days with $\tau_i = 16$ d, and $N = 8.25 \times 10^7$ or ¼ of the total US population.
(d) *Comment* on the significance of the closeness of the predictions of the SIR model to the LR trendline fit to all the data in the graph of the first 52 days.
Note: The LR trendline is fit to all of the data after the fact, whereas the SIR model is a prediction based on only on data from the first two weeks of April 2020.
(e) *Briefly compare* your prediction in Q.12.58(c) with the last curve in the butterfly effect Fig.12.16. Are they qualitatively similar? Are they quantitatively similar?

About what you discovered: outlook based on early April

In Q.12.56 you discovered that when we fit the ED model to USA data for April 3 to April 14, 2020, it does an amazingly good job of predicting the future of the pandemic in the US for the next 41 days until Memorial Day. The closeness of the ED prediction to the linear (LR) trendline fit to *all* of the reported data from April 3 to May 25, 2020, allows us to make that conclusion because the LR trendline is a least-squares fit to all of the data and it matches the ED prediction throughout the entire social distancing period shown in the graph. The closeness of the ED model to the LR trendline for the first 20 days confirms that the ED model is working as advertised as a good way to fit the data during the April 3 to April 14, 2020 period. However, we should note that the ED model is not a complete epidemiological model, it's merely a convenient approximation to the SIR model that can be used to estimate two of the SIR models parameters.

Fig.12.17 shows my answer to Q.12.58(c). I changed the time units into weeks to better illustrate the timescale of the model predictions and I extended the linear trendline to intersect the time axis in panel (b). The closeness of the SIR model to the linear trendline shows that the SIR model successfully predicts what happened in the six weeks following the fit while social distancing was being maintained. With all the diversity of what's happening in different US states (most notably NY), it's quite amazing to me that the data for the country – as a whole – is still falling on a straight line.

In your answer to Q.12.57(b) you noted that the SIR predicts slightly lower values than the ED model and the actual USA data from day 12 (4/15/2020) onward when $N = 3.3 \times 10^7$. As the model population was increased, the SIR model matched the ED model and the USA data better. Reducing the mean infectious time from $\tau_i = 16$ d to $\tau_i = 8$ d made the SIR model slightly lower and further decreasing it to $\tau_i = 4$ d made the fit significantly worse.

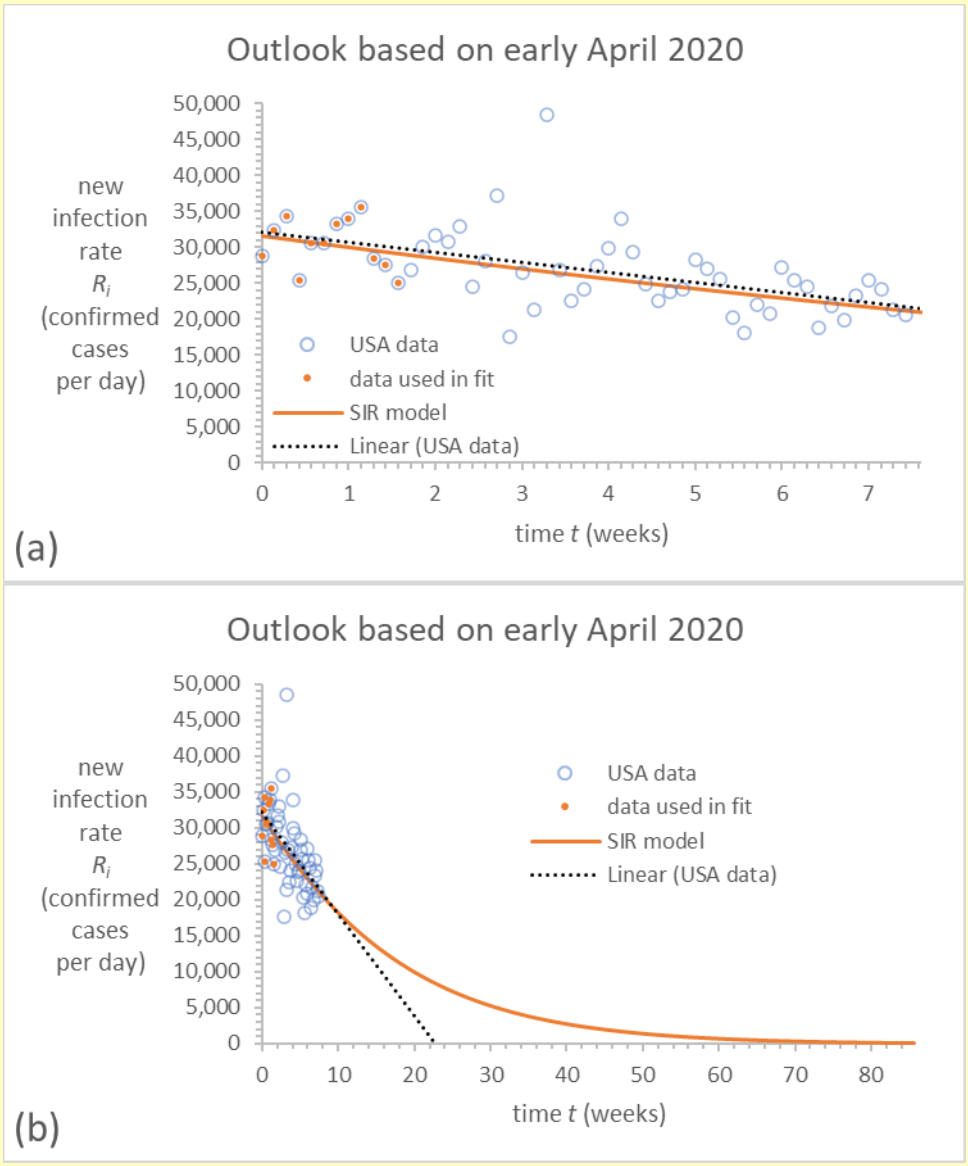


Fig.12.17 Excel charts showing the predictions of the SIR model (Fig.12.11) when fitted to USA new infection rate data from April 3 to April 14, 2020 inclusive (filled circles – data used in fit). The open circles show all the USA data reported by the ECDC from April 3 to May 25, 2020, 2020 (Memorial Day). The curve is the prediction of the SIR model fitted to the April 3 to April 14, 2020 data using the ED model with $N_0 = 569{,}000$ and $k_i = 0.0560\ \mathrm{d}^{-1}$, a model population size of $N = 8.25 \times 10^7$ and a mean infectious time of $\tau_i = 16$ d. The dotted line is a linear (LR) trendline fit to all the USA data from April 3 to May 25, 2020, (Memorial Day).

Fig.12.17 shows my answer to Q.12.58(c). I changed the time units into weeks to better illustrate the timescale of the model predictions and I extended the linear trendline to intersect the time axis in panel (b). The closeness of the SIR model to the linear trendline shows that the SIR model successfully predicts what happened in the six weeks following the fit while social distancing was being maintained. With all the diversity of what's happening in different US states (most notably

NY), it's quite amazing to me that the data for the country – as a whole – is still falling on a straight line.

In your answer to Q.12.57(b) you noted that the SIR predicts slightly lower values than the ED model and the actual USA data from day 12 (4/15/2020) onward when $N = 3.3 \times 10^7$. As the model population was increased, the SIR model matched the ED model and the USA data better. Reducing the mean infectious time from $\tau_i = 16$ d to $\tau_i = 8$ d made the SIR model slightly lower and further decreasing it to $\tau_i = 4$ d made the fit significantly worse.

In Q.12.58, you also discovered that exponential decay is much easier to fit to real data than exponential growth. The general shape of the predictions of the model – once fitted using the ED model – is relatively robust with respect to changes in the two remaining parameters with the shape of the curves staying the same and with no dramatic changes in qualitative behavior like the butterfly effect shown in Fig.12.16. As you discovered in Q.12.18(e), the ED model does a better job of fitting the USA data than the UG model but the shapes of the two curves are similar.

As shown in Fig.12.17(b) the fitted SIR model makes a rather depressing prediction for how the infection rate declines if all the parameters are unaffected by seasonal variations, changes in social distancing or testing, or any medical breakthroughs etc. Unfortunately (from a modeling perspective), we'll have to wait another 50 days to see if the model's predicted differences from a linear decline are correct (assuming the model parameters k_i etc. stay the same). ❑

Q.12.59 **DISCUSSION QUESTION** **(a)** With the model population set to $N = 8.25 \times 10^7$ and $\tau_i = 16$ d, change the formula for Q in the **Param$** column **J** to sample different ranges of data to get an idea of how the choice affects the predictions of the model, i.e., change the formula for Q from **=SUM(Q3:Q14)**, then change the **data used in fit** series in all of the graphs to include the data that you selected to fit. E.g. you can fit the ED model to days 0-18 using **=SUM(Q3:Q21)**. Then clear out the **SIR model table** as much as possible by deleting the entries for $R_i\ldots$ from $Step\ 2$ to the bottom of the table as we discussed in the preamble to Q.12.48. Then rerun the LS fit using **Solver**. Then repopulate the **SIR model table** using the left-double-click copy method. Try changing N and τ_i to reasonable values to see how that affects the SIR model. *Briefly discuss* what you discovered about fitting the SIR model to the initial conditions using the exponential decay (ED) model.
Reminder: When you're using **Solver**, you can save time by closing all other spreadsheets as their cells are also recalculated when **Solver** takes a step.
(b) With the model population set to $N = 8.25 \times 10^7$ and $\tau_i = 16$ d, change the formula for Q in the **Param$** column **J** to include all the data in the **USA new infections** table, i.e., change the formula for Q to **=SUM(Q3:Q55)**, then delete the **data used in fit** series in all of the graphs as we're fitting all the **USA data**. Then clear out the **SIR model table** as much as possible by deleting the entries for $R_i\ldots$ from $Step\ 2$ to the bottom of the table as we discussed in the preamble to Q.12.48. Then rerun the LS fit using **Solver** then repopulate the **SIR model table** using the left-double-click copy method. Add a linear trendline to the

600-day graph and **Forecast** it forward until it intersects the time axis. Set $\tau_i = 16$ d, change the chart title to something appropriate and *record* your new $R_i(t)$ graph with both the SIR model and the LR trendline for the first 600 days after social distancing took effect and *compare* your new graph with Fig.12.17(b).

(c) Change the mean infectious time to $\tau_i = 8$ d and the model population size to $N = 1.65 \times 10^8$. *Compare* your new graph with Fig.12.17(b) and to your answer for Q.12.59(b).

About what you discovered: fit to US data from April 3 to May 25, 2020

Your answers to Q.12.58(b) and Q.12.58(c) are both very similar to Fig.12.17(b). Indicating once again that the fit to the SIR model doesn't depend very strongly on the value chosen for τ_i or N if the ED fit is used and the other parameter is adjusted to compensate. Personally, I prefer the fit in Q.12.59(c) because the fitted model parameters seem more reasonable. The model parameter $\tau_i = 8$ d matches the value reported for the SIR model fitted to Chinese data in a recent *Science* article by Maier and Brockmann [2020] and the value of $N_0 = 275500$, seems like a reasonable ballpark estimate for the number infectious in the US on April 3, 2020. The model population size $N = 1.65 \times 10^8$ corresponds to ½ of the total US population indicating that half of those infected are symptomatic and tested. Interestingly, the value of $\mathcal{R}_0 = 6.2$ reported by Maier and Brockmann for China compares favorably with the value of $\mathcal{R}_0 = 5.8$ that we reported in Table 12.1. ❑

Q.12.60 **DISCUSSION QUESTION** In equation (12.73) we assumed that $N_r = 0$. Let's investigate the consequences of that assumption by sampling reasonable starting values for the number recovered on April 3, 2020. Save a fresh copy of your spreadsheet for Q.12.59(c) and change model by adjusting formula for the initial susceptible fraction to $s_0 = N_{s_0}/N$ where N_{s_0} is the value of N_s in $step\ 0$ of the SIR model. Then sample reasonable values of N_{r_0}, then try some unreasonably large values.

(a) *Briefly report* on what you discovered about the effect on the fitted SIR model of changing N_{r_0} to reasonable nonzero values on April 3, 2020.

(b) *Briefly explain* why the values of k_i and $\mathcal{R}_0$ automatically adjust when you change N_{r_0}.

(c) How big does N_{r_0} have to be to make a visual difference to the SIR model? *Briefly comment* on whether that's a reasonable value for the US on April 3, 2020.

(d) With $N_{r_0} = 0$, change the timestep in the SIR model from $\delta t = 0.1$ d to $\delta t = 1$ d. *Briefly describe* the effect on the fitted SIR model.

LS fit to the SIR model

As you discovered in Q.12.60(d), changing the timestep to $\delta t = 1$ d has an effect on the fitted SIR model that's barely noticeable. As a result, I think it's reasonable for us to consider using a timestep of $\delta t = 1$ d after social distancing has taken effect on April 3, 2020. The advantage of doing so is that the SIR timestep then matches up with the data reported by the ECDC. That in turn allows us to use Excel's **Solver** to do a least-squares fit of the full SIR model to the ECDC data in a straightforward manner.

Q.12.61 DISCUSSION QUESTION Open the spreadsheet BPM.Ch12_LS_fit_to_SIR.xlsx. It has the same ECDC data that we've been analyzing in the column headed **USA (1/d)**, but it's now located in the same table as the SIR model. The residuals r column should be calculated using equation (4.12), i.e., the first entry in cell **K4** should end up being **=J4-E4**. The r^2 column should be calculated by squaring the residuals, and the **quality of fit** Q should be calculated using equation (6.11), which should end up being **=SUM(L4:L55)**.

(a) Make sure that $\tau_i = 16$ d then run Excel's **Solver** with a **Set Objective** of **A19**, the cell for the quality of fit Q; the **To:** radio button set to ⊙ **Min**; and **By Changing Variable Cells:** set to **A3**, the cell for the model population size. Make a table to record τ_i, N and Q and then run **Solver** with $\tau_i \in \{16, 8, 4, 2\}$ d. *Record* your results in the form of a table.

(b) *Briefly comment* on the validity of the fitted values of N that you obtained.

(c) Set $N = 3.3 \times 10^8$ and then run Excel's **Solver** with a **Set Objective** of **A19**, the cell for the quality of fit Q; the **To:** radio button set to ⊙ **Min**; and **By Changing Variable Cells:** set to **A7**, the cell for the mean infectious time. Make a table to record N, τ_i and Q then run **Solver** with $N \in \{3.3 \times 10^8, 1.65 \times 10^8, 1.1 \times 10^8\}$. *Record* your results in the form of a table.

(d) *Briefly comment* on the validity of the fitted values of N that you obtained.

(e) Now use **Solver** to find the "best-fit" values of both N and τ_i simultaneously. You'll need to change **By Changing Variable Cells:** to **A3,A$7**. Run **Solver** to find the "best-fit" values of N and τ_i. *Briefly discuss* your results and their significance. Try various starting points to determine the uniqueness of your "best-fit" parameters.

Note: If you get an error while running **Solver**, try a different starting point. Recall the "puddles in the parking lot" that we talked about in Chapter 6. Errors can occur when a puddle drains into a zero-value drain.

(f) Now use **Solver** to find the "best-fit" values of N, τ_i and k_i simultaneously. You'll need to change **By Changing Variable Cells:** to **A3,A$7,$A$15**. Run **Solver** to find the "best-fit" values of N, τ_i and k_i. *Briefly discuss* your results and their significance. Try various starting points to determine the uniqueness of your "best-fit" parameters.

(g) Finally, use **Solver** to find the "best-fit" values of N, τ_i, N_0 and k_i simultaneously. You'll need to change **By Changing Variable Cells:** to **A3,A$7,$A$11,$A$15**. Run **Solver** to find the "best-fit" values of N, τ_i, N_0 and k_i. *Briefly discuss* your results and their significance. Try various starting points to determine the uniqueness of your "best-fit" parameters.

About what you discovered: USA data underspecifies SIR parameters

In questions Q.12.57 and Q.12.58 we discovered that we could fit the SIR model equally well with $(\tau_i, N) = (16\text{ d}, 8.25 \times 10^7)$ or $(\tau_i, N) = (8\text{ d}, 1.65 \times 10^8)$, i.e., that changing one of (τ_i, N) could be compensated for by changing the other accordingly. In questions Q.12.61(a) and Q.12.61(c) we discovered that selecting a value of one of (τ_i, N) allowed us to find the least-squares "best-fit" value of the other parameter. Because of those fits, it's tempting to conclude that the best-fit value of the model population is $N \approx 3.3 \times 10^8$ and that the best-fit value of the mean infectious time is $\tau_i \approx 8$ d. Indeed, they do seem like reasonable values, but as you already

discovered, the improvement in the fit is only minimal as you saw in the fit to the first 52 days and by noting that the quality of fit Q doesn't change much.

What you discovered in parts (e), (f) and (g) of Q.12.61 is that the USA data **underspecifies** the SIR model parameters. Alternatively, we can say that the SIR model **overspecifies** the USA data from April 3 to May 25. The easiest way to see what that means is to realize that the ED model can fit the data almost as well with only two adjustable parameters. The SIR model has four adjustable parameters (5 if you count N_{r_0}). Hence, it's simply not possible to use the USA data from April 3 to May 25 to accurately determine the "best-fit" values of all those parameters. The USA data simply don't have enough "structure" to them as they are basically a straight line with **random noise**. That's why you got crazy values for the parameters in parts (f) and (g). You should also have noticed that Q hardly changed at all during the fit, which means that the parameters are not well-determined by the data that we're fitting to the model.

This type of situation is much more common than you might think. In my research into modeling ion channel permeation (e.g. [Nelson 2011]), I frequently ran into the issue of published data being fitted to models with too many adjustable parameters. ❑

Q.12.62 **RESEARCH QUESTION** Model data from a US state or another country during the time of social distancing, e.g. the tail of the $R_i(t)$ curve in New York State.

Modeling the death rate

The SIR model doesn't explicitly model the death of infected individuals. However, it seems reasonable to assume that (at least initially) a fixed fraction m_r of people who become infectious will eventually die of the disease and that on average they die t_m days after their infection was confirmed and reported. Hence, we'll assume that the **mortality rate** R_m is related to the **infection rate** R_i by

$$R_m(t) = m_r R_i(t - t_m) \tag{12.75}$$

where m_r is the apparent **mortality ratio** (a **scaling factor**) and t_m is the **mortality delay time** (a **time shift**).

We're now going to find the best-fit values of m_r using Excel's **Solver** and find the best-fit value of t_m using a **Progress table** – like we did in **CHAPTER 6** for O_2 binding to myoglobin. There are automatic methods for finding t_m, but the **progress table** method is very straightforward. *Open* the preformatted spreadsheet BPM.Ch12_Infection_and_death.xlsx to see how it works. It has the same ECDC data up to Memorial Day 2020 that we've been analyzing. It also includes the confirmed **mortality rate** data (confirmed deaths per day) reported by the ECDC in the column headed ***R*m (1/d)**. The column headed **e (1/d)** is the value expected using equation (12.75) with $t_m = 4$ d. *Click* in cell **G13** and then in the **Formula bar** (**CHAPTER 1**) to see how equation (12.75) $R_m = m_r R_i$ is implemented using the value of R_i from 4 days earlier than the current row. The residuals r column is calculated using equation (4.12), and the first entry in cell **H13** is **=F13-G13**.

The r^2 column is calculated by squaring the residuals. The **quality of fit** Q is calculated using equation (6.11), i.e., **=SUM(I13:I49)**, as we're going to fit equation (12.75) to the period between March 7, 2020 and April 12, 2020 inclusive – when the death rate was changing most rapidly.

Q.12.63 **DISCUSSION QUESTION** **(a)** The initial value of the mortality ratio is $m_r = 0.03$, which corresponds to 3% of people reported infected with COVID-19 dying from the disease. *Adjust* m_r by hand to see how it affects the **scaled infection rate** series in the **Correlation between infection and death** graph. By eyeballing the graph and monitoring the value of Q, find the best-fit value of m_r to the nearest 0.01. Then *run* Excel's **Solver** with a **Set Objective** of **A6**, the cell for the quality of fit Q; the **To:** radio button set to ⊙ **Min**; and **By Changing Variable Cells:** set to **A3**, the cell for the mortality ratio m_r. *Record* the best-fit values of the mortality ratio m_r and the quantity of fit Q in the **Progress table** using **Paste Values**. Notice that the value of Q is automatically plotted in the **Finding the smallest Q with a progress table** graph. *Record* your **Correlation between infection and death** graph for $t_m = 4$ d.
(b) Then change the formula for the expected value of R_m in cell **G13** to **=A3*E8**, which corresponds to equation (12.75) with $t_m = 5$ d, then repopulate the **e (1/d)** column using the left-double-click copy method. Then rerun Excel's **Solver** to find the least-squares fit value of m_r for $t_m = 5$ d and *record* the best-fit values of the mortality ratio m_r and the quantity of fit Q in the **Progress table**. Finally, repeat that same procedure for $t_m = 6$ d, $t_m = 7$ d, $t_m = 8$ d and $t_m = 9$ d. Add a series using small filled circles for the four smallest Q values and add a quadratic trendline to show minimum of Q. *Record* your progress table and *record* the Q versus t_m graph.
(c) Change the formulas in the **e (1/d)** column back to the formula for the best-fit value of t_m, rerun **Solver** and then *record* your best-fit **Correlation between infection and death** graph, together with the best-fit parameters m_r and t_m.
(d) *Briefly comment* on the quality of the observed correlation.
(e) *Briefly comment* on the values of the fitted parameters and how they relate what you've learned about COVID-19 from other sources.

Q.12.64 **(a)** Extend the **Correlation between infection and death** graph to plot all the data out to Memorial Day (day 89). *Briefly comment* on how well the correlation equation (12.75) does in predicting the mortality rate from the infection rate for the next 43 days.
(b) Make a copy of the correlation graph and change the vertical R_m-axis to a **Logarithmic scale**. *Record* your semi-log graph for the mortality rate R_m as a function of time.
Note: The warning that you get from Excel is caused by the reported value of zero deaths on March 20, 2020. Click the **[OK]** button but note that the zero-value data point for R_m is not plotted in the semi-log graph.
(c) *Briefly describe* what new insights this new perspective provides about the correlation and the nature of both the new infection rate and the death rate.

Q.12.65 STATISTICS QUESTION *Test* whether your best-fit results from Q.12.63 and Q.12.64 are consistent with the hypothesis that they are correlated.
Note: If you've taken a statistics class, you should use what you learned to design your answer.

About what you discovered: correlation between infection and death

Fig.12.18 shows my answer to Q.12.63(b). I changed the name of the polynomial trendline to something more descriptive and I used the **Forecast** feature to extend the quadratic fit a day on either side of the four days fitted. The fitted curve illustrates how the minimum in Q versus t_m is a quadratic (**CHAPTER 6**). Another feature of Fig.12.18 that you should note is that there is a large proportional decrease between the values of Q for $t_m = 5$ d and $t_m = 6$ d and between $t_m = 8$ d and $t_m = 7$ d. This can be contrasted with the miniscule differences in Q that you noticed when fitting the overspecified SIR model to the USA data in Q.12.61. If the changes in Q are relatively small, then the parameters are not well determined. The large changes in Q shown in Fig.12.18 indicate that our estimate of 6 d $\leq t_m \leq$ 7 d is well determined for the period of the fit – March 7 to April 12, 2020.

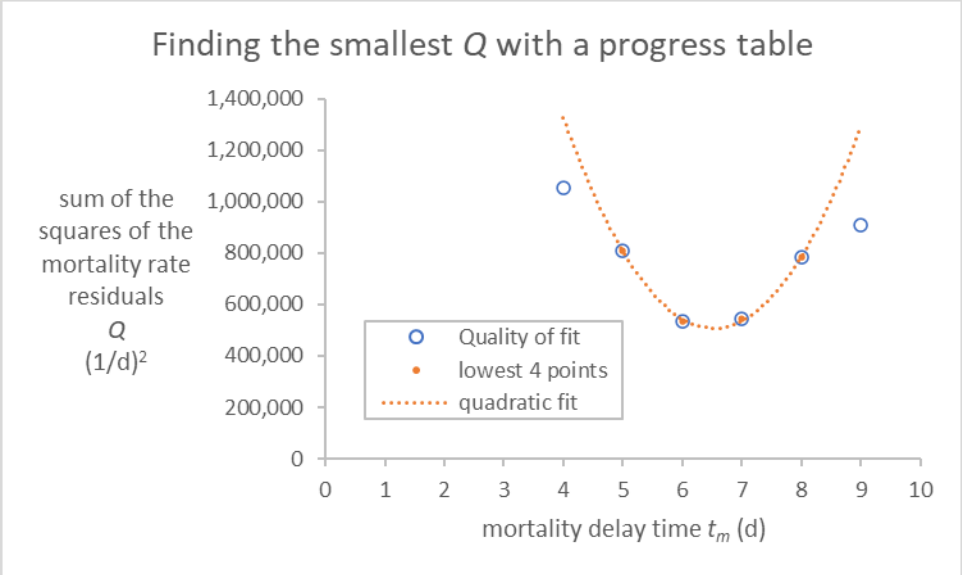


Fig.12.18 Excel chart showing data from the progress table you made in Q.12.63(b). The four lowest points have been fit to a **Polynomial Order 2** (a quadratic) showing that the minimum in Q lies between 6 and 7 days, indicating that the best-fit integer value of $t_m = 6$ d and the corresponding best-fit value of $m_r = 0.061$.

Data analysis

It's important when you're analyzing data to be mindful of how it's collected and what it actually means. When I first did the analysis for Q.12.63, I was surprised by the fitted value of $t_m = 6$ d, as I had heard that it usually took from two weeks to two months for someone to die from COVID-19. The first thing we should do when interpreting data is to make sure that we're clear about what the data actually represent. Our data for new infections (confirmed cases per day) doesn't represent when people are first infected. It represents when their first test for COVID-19 came

back positive and was officially reported. During the initial period that you analyzed in Q.12.63, the official report may have occurred a week or more after their sample was taken, which in turn could have been some time after they were actually infected. In addition, during the initial part of the outbreak, only people who were already exhibiting severe symptoms were usually tested, and then often only after they'd been hospitalized. Hence, it's not surprising that many of the fitted parameters changed later on.

Fig.12.19 shows your answer to Q.12.64(b). The apparent correlation between the reported death rate R_m (USA deaths) and the prediction of equation (12.75) (**scaled infection rate** based on R_i) seems quite remarkable. However, we should note that there's a lot of scatter in both series, particularly the death rate. In addition, there are 4 R_m data points at days 75, 82, 82 and 89 that appear to be substantially lower than the prediction of equation (12.75). Despite the differences, I was quite surprised by the closeness of the correlation. There are a lot of assumptions about the reported data that have been called into question, so my expectation was that there would be clear qualitative differences between the infection rate data and the death rate data. More on this topic in **SECTION 12.6**.

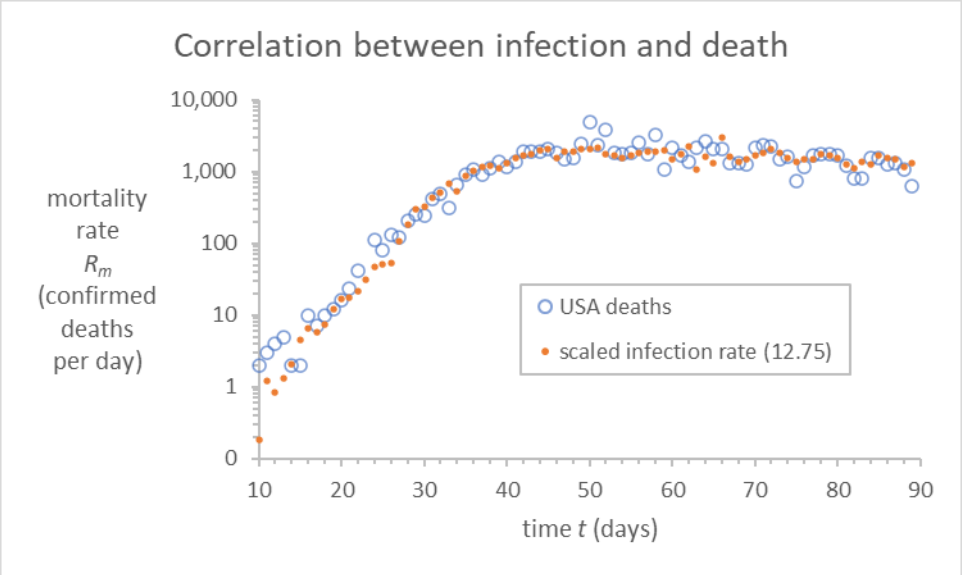


Fig.12.19 Excel chart showing the reported death rate in the USA from March 7 to May 25, 2020, (Memorial Day). The scaled infection rate series was calculated from the reported confirmed new cases per day R_i using equation (12.75) using the best-fit parameters you found in Q.12.63, $m_r = 0.061$ and $t_m = 6$ d. Data source ECDC.

Fig.12.20 shows **empirical fits** (they are exponentials) motivated by the shape of the infection rate and death rate data for the US from February 27 to May 25, 2020 shown in Fig.12.19. If I had started writing this **CHAPTER 12** on May 25, 2020, I probably would have started with this graph as motivation. It's worth noting that we've already explained the functional form of these empirical fits with the **UG** and **ED models**, which are special cases of the **SIR model**. Finally, it's interesting to note that there are only 9 days (empty open circles) between the exponential growth and exponential decay curves shown in Fig.12.20.

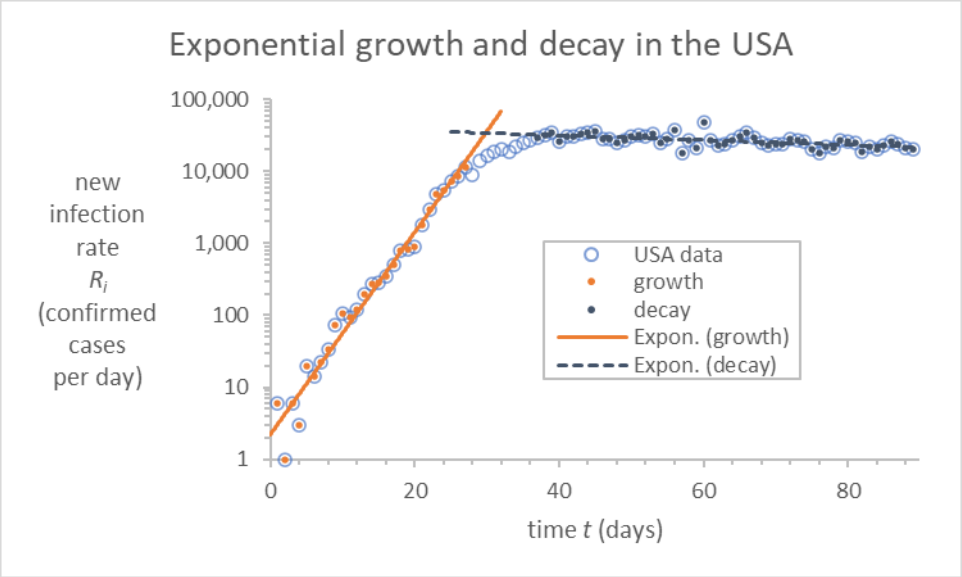


Fig.12.20 Excel chart showing a semi-log plot of the initial stages of the COVID-19 outbreak in the United States. The open circles show the new infection rate data, reported as confirmed cases per day by the ECDC. The fitted lines show a linear regression fit to the log of the raw data (using Excel's exponential trendline). The solid line shows the fit before social distancing from February 27 until March 24, 2020, and the dashed line shows the fit from April 3 until May 25, 2020 showing the effect of social distancing.

❑

Q.12.66 **RESEARCH QUESTION** The correlation in Fig.12.19 and the exponential fits in Fig.12.20 suggest a simple way to analyze the data and to investigate how many people in the U.S. could have been spared COVID-19 if social distancing was implemented earlier and the ED model decay constant remained the same. Using a simple empirical model, *investigate* and *report* how implementing social distancing earlier could have saved lives.

About what you discovered: estimated lives lost caused by one week of inaction

Fig.12.21 shows my answer to Q.12.66. It utilizes a very simple fit to the USA data using the UG model up to March 24, 2020, using a function of the form

$$R_i = B_0 e^{k_g t} \tag{12.76}$$

The USA data from April 3, 2020 onward are modeled using the ED model using equation (12.68) and the transitional data are modeled using an equation of the same form as equation (12.76), but with a different prefactor and rate constant. The basic idea behind the projection is that earlier implementation of social distancing can be modeled by a **time shift** of $\Delta t = 7$ d in the starting point of the ED model and the transitional curves, but that the slope of the exponential decay doesn't change significantly because social distancing and mask wearing etc. were implemented in the same manner. The lower piecewise continuous projection was made using that assumption. The fact that the slopes of the upper and lower curves are the same in the semi-log plot in panel (a) of Fig.12.21 is a direct consequence of that assumption. The time shift can be confirmed by

noting that the beginning of the transitional line connecting the UG and ED lines is indeed shifted backward 7 days and that the intersection of the projected ED model (dashed line) with the UG model also appears to be seven days earlier than the intersection of the LS fitted UG and ED models.

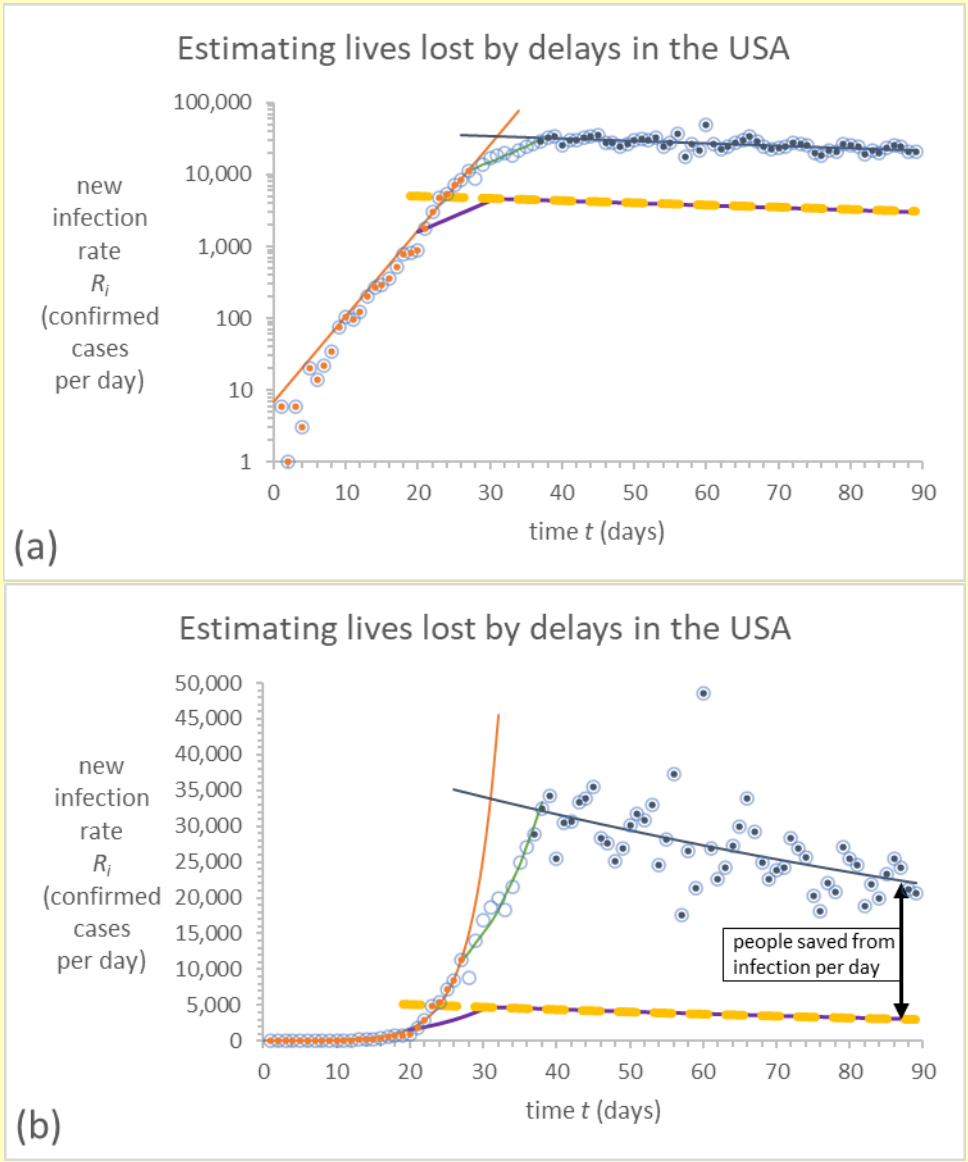


Fig.12.21 Excel charts showing a semi-log plot of the initial stages of the COVID-19 outbreak in the United States. The open circles show the USA data, reported as confirmed cases per day by the ECDC. The fitted lines show LS fits to exponential functions of the form of equations (12.76) and (12.68). The dashed line shows the change in the prediction, assuming that social distancing occurred 7 days earlier. (a) Semi-log graph. (b) Linear-scale graph of the same data and projections. The area between the solid purple line and the USA data indicate lives lost by a 7-day delay in implementing social distancing.

Table 12.2 shows data from estimates shown in Fig.12.21. The first row is the data reported by the ECDC . Dividing the number of reported deaths by the number of infections yields the **crude mortality ratio** of $m_c = 0.0595$. The number of deaths in the empirical fit was calculated by

multiplying the number of infections by the crude mortality ratio. As shown in Table 12.2, the empirical fit matches the ECDC numbers to within 0.11%.

Table 12.2 Data from the ECDC and model estimates for cumulative infections and deaths in the US from February 27 to May 25, 2020

	infections	deaths
ECDC	1,643,185	97,720
empirical fit	1,645,000	97,830
7 days earlier	261,000	15,530
saved	1,384,000	82,300

The "7 days earlier" row shows the cumulative predictions for the same period (February 27 to May 25, 2020) if social distancing had been implemented just 7 days earlier, and the "saved" row shows the predicted reductions in the cumulative totals of about 84%. It's important to note that the effects of the delay are ongoing. For example, the prediction shown in Fig.12.21 is that the predicted daily infection rate on May 23, 2020 (arrow in figure) would be reduced by about 19,000 infections per day if social distancing measures were implemented 7 days earlier in March 2020. That corresponds to about 1000 lives that would have been saved on that day according to the projection. That's an ongoing illustration of the importance of acting quickly during the initial exponential growth phase of the outbreak. It's an important **public health policy** lesson. ❑

Q.12.67 **RESEARCH QUESTION** Use the full SIR model to investigate how many US infections and lives could have been saved if social distancing was implemented earlier. *Report* your findings including the total number of infections and deaths until the outbreak dies out, assuming the model parameters remain unchanged.

Q.12.68 **DISCUSSION QUESTION** **(a)** During US state re-openings in early to mid-May 2020 some politicians made claims that the infection rate in their region was staying the same or going up because of increased testing. If their assertions are correct, and more mild or asymptomatic cases are being detected, *briefly describe* your prediction for what should happen to the reported mortality ratio m_r.

(b) *Fact check* those political claims using the data in your spreadsheet to investigate if there has been any significant change in the national mortality ratio during the last four weeks of data up to Memorial Day (May 25, 2020). *Briefly report* your conclusions including graph(s).

Hint: A straightforward way to do that might be to calculate the daily (or weekly average) mortality ratio. Can you devise a more sophisticated test?

(c) Calculate and *record* the average value of m_r for the last week of data in BPM.Ch12_Infection_and_death.xlsx.

(d) *Briefly discuss* what other factors might affect the mortality ratio over time, e.g. more effective treatments, widespread randomized testing, or any medical breakthroughs etc.
(e) On March 6, 2020 the World Health Organization reported the **crude mortality ratio** (the number of reported deaths divided by the reported cases) for COVID-19 as $m_c = 3 - 4\%$ [WHO 2020]. This number is comparable with, but not identical to, the mortality ratio m_r in equation (12.75). *Briefly compare* the WHO value of m_c with the values of m_r you've calculated from the ECDC data for the US.
(f) Using the ECDC data, calculate the crude mortality ratio for the period from February 27 to May 25, 2020 and *briefly discuss* factors that might be responsible for it being significantly greater than the $3 - 4\%$ reported by the WHO [2020].

About what you discovered: the mortality ratio is decreasing

As you discovered in Q.12.68(f), the US crude mortality ratio for the period from February 27 to May 25, 2020 is $m_c = 0.0595 \approx 0.06$. That's significantly greater than the $m_c = 0.03 - 0.04$ reported by the WHO [WHO 2020]. Lack of adequate testing can explain some of the difference. However, people of color have been (as of late May 2020) disproportionately represented in the US death toll. The US mortality ratio is currently (mid May 2020) double the low end of the range reported by the WHO.

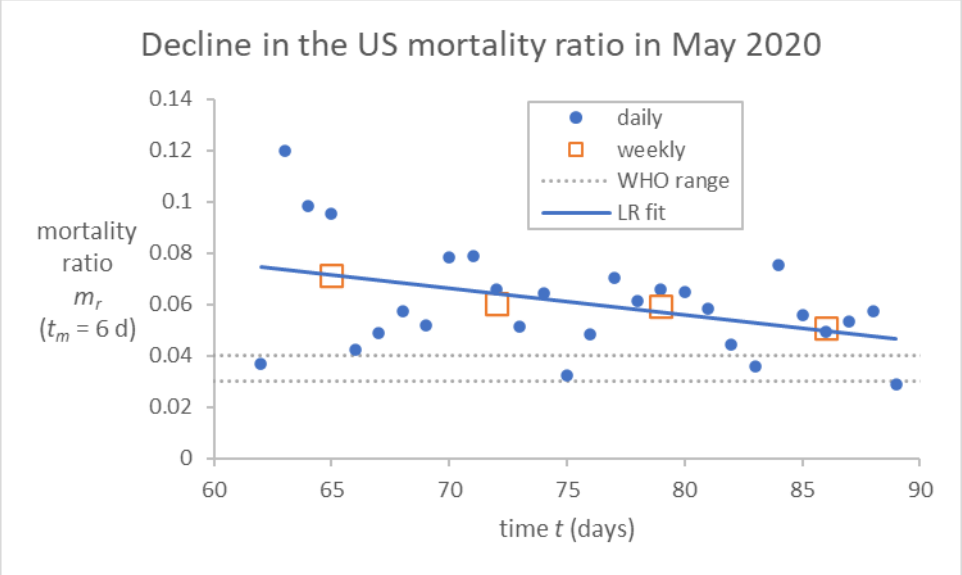


Fig.12.22 Excel chart showing the mortality ratio m_r calculated using equation (12.75) for the four weeks leading up to Memorial Day (May 25, 2020). The filled circles are the daily values and the open squares show the corresponding weekly-average values. The dotted horizontal lines show the range reported by the WHO on March 6, 2020.

Fig.12.22 shows my graphical answer to Q.12.68(b). It shows the mortality ratio m_r calculated using a mortality delay time of $t_m = 6$ d. The figure shows a steady decline in the mortality ratio during the month of May 2020. This observation actually lends credence to the idea that more mild or asymptomatic cases are being detected because of increased testing on the national level – assuming that the **intrinsic mortality ratio** (probability of an infected person eventually dying

from COVID-19) is a constant. However, there may be other contributing factors to the decline in m_r. One is that the proportion of high-risk groups being infected is declining and that the proportion of lower-risk groups is increasing, e.g., proportionally less people over 65 are getting infected and more under 30s are getting infected. Another possibility is that therapeutics and/or better treatment protocols are helping to reduce the number of deaths. Then there are the reported inconsistencies between states' criteria for reporting cases and deaths… The decline in the mortality ratio during May 2020 also makes projections for the death toll even more uncertain. ❑

Q.12.69 **RESEARCH QUESTION** *Investigate and report* on the changes in the mortality ratio and the crude mortality ratio in the data reported by the ECDC and/or from other sources for the US, individual states or other regions/countries.

Q.12.70 **RESEARCH QUESTION** Some people have argued that the mortality rate R_m is a more reliable measure of the spread of the novel SARS-CoV-2 coronavirus than the infection rate because of inconsistencies in testing by state and over time. Using that idea, *develop and report* the results of fitting the SIR model to R_m to the social distancing period in the US.
Note: There are also problems with the mortality rate data because of unreported COVID-19 deaths, which also vary by state.

About what you discovered: disclaimer – the purpose of simple models

Because of the seriousness of this topic, I think it's important to be super clear that the models we've been developing in this **CHAPTER 12** are not state-of-the-art epidemiological models. The SIR model that we've been studying has been around for almost a century and there are many more sophisticated models that professional epidemiologists use for informing public health policy. The real purpose of this chapter is the same as for all the others in this book – to highlight a scientific approach using simple models to provide insights into how the real world works. As I mentioned before, people aren't molecules! They don't wander around randomly and have random encounters with others in the population. They can follow instructions for social distancing, mask wearing and good hygiene – but they can also ignore them. The models we've been developing

can be improved in many ways, but I would caution anyone considering using models with too many adjustable parameters … Recall from **CHAPTER 6** the quote attributed to John von Neumann "With four parameters I can fit an elephant, and with five I can make him wiggle his trunk." [Mayer *et al.* 2010]. Finding an equation that merely summarizes existing data is *not* our goal – nor is it to predict exactly what will happen in the future. The purpose of our introductory modeling approach is to discover if a simple model can *explain* something about what's happening out in the real world and hopefully provide new insights.

The advantage of simple models like the SIR model is that they are – well – simple. That simplicity is a modeling virtue because it means that we can completely understand the whole model and its

implications. No mysterious **fudge factors** are allowed to make it fit real data better. We're not trying to predict tomorrow's weather; we're trying to understand why clouds form in layers.[1] ❑

12.6 Modeling the transition to social distancing

Lives lost because people didn't wear masks

The ultimate goal for this **SECTION 12.6** is to estimate how many lives were lost in the US up to Memorial Day because people didn't wear masks etc. However, before we do that, we'll need to investigate modeling the transition from the initial exponential growth to the initial period of social distancing in the US. One way to do that is to allow for a change in the infection rate constant k_i as time progresses in the SIR model [Hilborn 2020].

From our research so far, we know that the SIR model can explain the exponential growth at the beginning of the outbreak and that it can also model the gradual decay in the infection rate during the period of social distancing from April 3 to Memorial Day (May 25, 2020). In **SECTION 12.5** we made the change to social distancing and mask wearing by starting a fresh version of the SIR model with a different infection rate constant, but that meant that we had to fit a different value of N_0 to make the model match the starting point of the data. An alternate method would be to simply change the k_i "on the fly" to model the switch to social distancing. We can do that in our spreadsheet by making k_i a variable and adding a column for it in the **SIR model table**. Since k_i is no longer a *constant* parameter, let's call it the **infection rate coefficient**. Let's start by finding a good value of k_i for the initial exponential growth period if the timestep is $\delta t = 1$ d.

Finding $k_i = k_1$ when $\delta t = 1$ d

Open the preformatted spreadsheet BPM.Ch12_Step_change.xlsx. The **Param$** column **A** now includes two values for the infection rate coefficient. k_1 is the value of k_i during the initial exponential growth period (epoch ①) and k_2 is the value of k_i during the period of social distancing (decay) (epoch ②). **Param$** column **A** also includes a parameter for the **transition time** t_{12} between epochs ① and ②. However, before we investigate making the transition, we need to make sure that we have a good fit to the initial exponential growth in epoch ①. Let's start by using the same method we used in Q.12.43 and Q.12.44.

> **Q.12.71 DISCUSSION QUESTION** **(a)** In spreadsheet BPM.Ch12_Step_change.xlsx *run* Excel's **Solver** with a **Set Objective** of **P7**, the cell for the quality of fit Q for the first 25 days in the **USA new infections** table; the **To:** radio button set to ⊙ **Min**; and **By Changing Variable Cells:** set to **P3,P5**, the cells for UG model parameters k_u and N_u. *Record and comment on* your LS fitted $R_i(t)$ graph for the UG model (12.54) for the first 40 days.

[1] Hmm… that sounds like an interesting project that could be tackled by adapting our marble game model of the atmosphere in **CHAPTER 9** to the "adiabatic atmosphere" and combining it with our marble game model of water evaporation and condensation, also from **CHAPTER 9**.

(b) As you noted in part (a), the LS fit to the UG model during the first 25 days is quite good. By inspecting cells **A11**, **F4** and **G4**, *write out* the algorithm instructions for k_1, k_i^{new} and R_i^{new}, to set out how the algorithm differs from Q.12.59(c).
(c) *Briefly comment* on the correspondence between the SIR model and the USA data for the $R_i(t)$ data for the first 25 days of the outbreak and *briefly explain* why the formula for k_1, equation (12.60) does such a poor job of matching $k_i = k_1$ to the initial growth in the SIR model.
Hint: Compare the SIR timestep in the current spreadsheet with the one we used in Q.12.44.

About what you discovered: the discrete-time SIR model comes to the rescue

As you discovered in Q.12.71(c), a timestep of $\delta t = 1$ d is way too big for our FD implementation of the SIR model. However, Appendix 12.A outlines a way to account for the errors caused by the timestep being too big ($\delta t = 1$ d) during the initial exponential growth period. It involves replacing k_u with a **growth rate parameter** g given by equation (12.A.1). We can then calculate k_1 using equation (12.60) but with k_u replaced with $g/\delta t$ using equation (12.A.8), so that the infection rate constant during the initial exponential growth period can be calculated using

$$k_1 = \frac{g}{\delta t} + k_r = (2^{1/t_d} - 1) + k_r = 2^{1/t_d} + k_r - 1 \qquad (12.77)$$

with $\delta t = 1$ d.
Note: An alternative would be to use the continuous-time formulation with $\delta t = 0.01$ d. While that's awkward to do in Excel, it's fairly straightforward to do in a programming language like Python. ❑

Q.12.72 **DISCUSSION QUESTION** **(a)** *Change* the formula for k_1 in the **Param$** column **A** to match equation (12.77) using the instruction

$$k_1 = 2\text{^}(1/t_d) + k_r - 1 \qquad (12.78)$$

then *record and comment on* your $R_i(t)$ graph for the new SIR model during the first 40 days.
(b) *Compare* the values of $k_i = k_1$ calculated with equations (12.60) and (12.78).
Hint: Don't forget to use what you learned from the "talking numbers" AWYD in **CHAPTER 2**. You might find the BPM.Ch02_Talking_numbers.xlsx preformatted spreadsheet useful.
(c) *Briefly discuss* which value of k_1 (from equation (12.60) or (12.78)) should be used to find the value of $\mathcal{R}_0$. I.e., which one is more representative of the underlying process that the model represents? Then *change* the formula for $\mathcal{R}_0$ accordingly.
Hint: The underlying process that the model is based upon is a **continuous-time Poisson process**.

About what you discovered: correcting $\mathcal{R}_0$ in the discrete-time SIR model

As you discovered in Q.12.72, the more representative value of infection rate coefficient is $k_i = k_1 = 0.447\ \text{d}^{-1}$ calculated using (12.60). That's because it doesn't depend on the value of δt. Hence, the formula for the basic reproduction number in the spreadsheet should be

$$\mathcal{R}_0 = (k_u + k_r)\tau_i \tag{12.79}$$

which uses equation (12.60) for k_i because it better represents the underlying **continuous-time process** ($\delta t \to 0$) that the SIR model is based upon.
Note: Using the value from (12.78) is a work around that accounts for the timestep of $\delta t = 1$ d being too big during the exponential growth during epoch ①. ❑

A step change in k_i

Using the value for k_1 (for $\delta t = 1$ d) from Q.12.72, we can now investigate how changing k_i affects the model. The spreadsheet includes a value of $k_2 = 0.1178\ \text{d}^{-1}$ in the **Param$** column **A**. That value of $k_2 = 0.1178\ \text{d}^{-1}$ is taken from our fit in Q.12.59(c) to the USA data from April 3 to May 25, 2020 with $N = 8.25 \times 10^7$ and $\tau_i = 8$ d. Let's start by investigating what the model predicts, if we simply switch from $k_i = k_1$ to $k_i = k_2$ to model the transition from initial exponential growth (epoch ①) to the decay after social distancing took effect (epoch ②).

As we saw in Q.12.71(b), the spreadsheet you've been working on has a column for k_i because it's now a variable in the simulation. The spreadsheet also has a column for a "transition function" F_{12} used to change k_i. **Param$** column **A** also includes a parameter for the **transition time** t_{12} between epochs ① and ②. Using k_1 and F_{12} we can calculate k_i using

$$k_i^{\text{new}} = k_1 + F_{12}^{\text{new}} * \Delta k_{12} \tag{12.80}$$

where $\Delta k_{12} = (k_2 - k_1)$ is the change in k_i at the transition time, and F_{12} is the **transition function**, between epoch ① and epoch ②. It's a step change or **step function** given by

$$F_{12}^{\text{new}} = \text{IF}(t^{\text{new}} < t_{12}, 0, 1) \tag{12.81}$$

which means that $F_{12} = 0$ when $t^{\text{new}} < t_{12}$ and $F_{12} = 1$ when $t^{\text{new}} \geq t_{12}$. The net effect of equations (12.80) and (12.81) is that $k_i = k_1$ when $t < t_{12}$ and $k_i = k_2$ when $t \geq t_{12}$. Equation (12.80) can then be written as

$$k_i^{\text{new}} = k_1 + F_{12}^{\text{new}} * (k_2 - k_1) \tag{12.82}$$

to eliminate Δk_{12} from the spreadsheet.

Using the combination of equations (12.81) and (12.82) might seem overly complicated, but as you'll discover after Q.12.73, the advantage is that we can make changes to how k_i transitions from k_1 to k_2 by simply changing the transition function F_{12}.

Q.12.73 **DISCUSSION QUESTION** **(a)** Fill in the column for F_{12} using equation (12.81) and the initial guess for the transition time of $t_{12} = 30$ d. Then fill in the column for k_i using equation (12.82). Then adjust the value of t_{12} by hand to the nearest day that makes the SIR model curve visually match the period of social distancing as well as possible. *Record* your semi-log graph of $R_i(t)$ for the new SIR model during the first 100 days and *briefly comment* on the fitted model.
(b) Use Excel's **Solver** to find the best-fit value of t_{12} (change the **Set Objective** to **A21**, the cell for the quality of fit Q; the **To:** radio button set to ⊙ **Min**; and **By Changing Variable Cells:** set to **A19**, the cells for the transition time t_{12}). *Briefly comment* on why the fitted curve doesn't change from the value you found by hand in part (a) with $t_{12} = 35$ d
(c) Before reading ahead, *briefly explain* why the value of R_i in epoch ① must reach such a high value in order to make the SIR value of R_i match the USA data during epoch ②.
(d) **CHALLENGE QUESTION** Before reading ahead, see if you can come up with a way to make the transition fit the data better.

About what you discovered: $R_i(t)$ is a rate

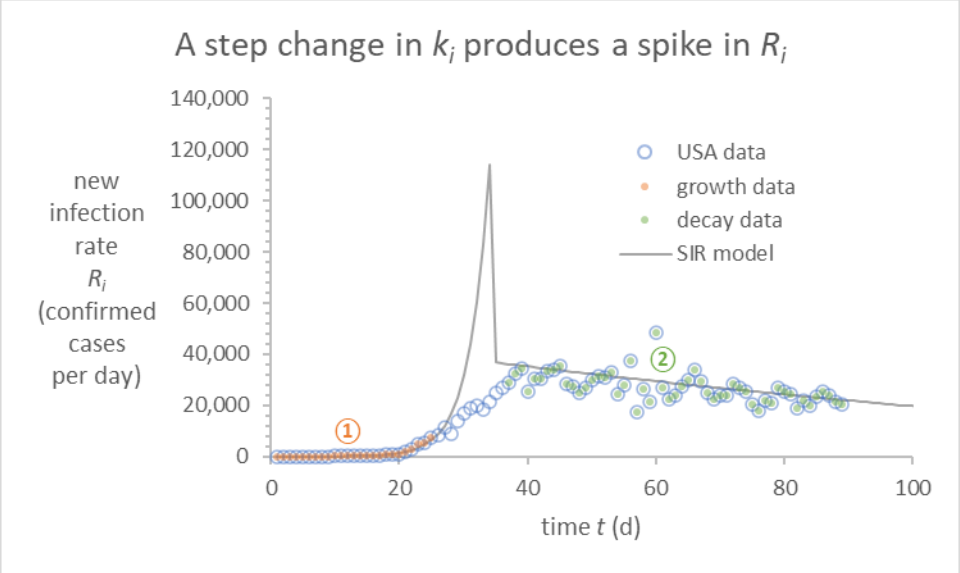


Fig.12.23 Excel chart showing the fitted SIR model with a step change in the infection rate coefficient from from $k_i = k_1 = 0.505$ d^{-1} to $k_i = k_2 = 0.118$ d^{-1}. k_1 is calculated using equation (12.78) for the initial epoch ① of exponential growth (orange dots) and k_2 is your value from Q.12.59(c) for the epoch ② of social distancing (green dots). The only adjustable parameter in the fit is the transition time $t_{12} = 35$ d between k_1 and k_2. The other parameters in the model are $N = 8.25 \times 10^7$, $\delta t = 1$ d, $\tau_i = 8$ d, and $N_0 = 5.541$ calculated using equation (12.59). As shown, the fit produces a **transition spike** (grey line) that doesn't match the reported transition data. Data source ECDC [2020].

One of the things that you should have noticed in Q.12.73 is that the infection rate $R_i(t)$ makes a dramatic step change downward when you make a step change in the infection rate coefficient (see Fig.12.23). That's because the infection rate is given by equation (12.8), i.e., $R_i = k_i N_i s$.

When we change k_i, the values of N_i and s don't change. Hence, as you discovered in Q.12.73, a step change in k_i must necessarily produce a similar step change in R_i. The result is that if we want the model to match the fitted ED model during epoch ②, then R_i must overshoot the reported USA data before the step change occurs producing the **transition spike** shown in Fig.12.23. That apparent inconsistency between the model and the USA data was the reason why we didn't initially try to use the SIR model with a variable k_i to model USA data from Feb. 26 through May 25, 2020. However, after many misstarts and failed attempts, on June 23, 2020 I finally realized that there's a simple way to modify the step change in k_i – that can be justified by a simple common-sense argument, and that can make the transition match up with the USA data by only adding only one more adjustable parameter. Let's see what we can discover.

Note: We're assuming that the mean infectious time τ_i doesn't change after the transition, which implies that the fraction of infectious people that self-isolate doesn't change. Clearly if testing and contact tracing in the US were more widespread, and isolation protocols were enforced, then k_r would increase in epoch ② and k_r would then need to be interpreted as the **removal rate constant** of infectious people from the model population due to isolation following contact tracing. ❑

The US is a union of many states and individuals

Maybe you figured this out in Q.12.73(d), but it took me more than a week to realize that the transition model needs to explicitly account for the fact that not all states, communities or individuals took up social distancing etc. at exactly the same time or to the same extent. That was step one. Step two was to realize we could implement that idea in Excel by adding a single additional parameter that accounts for the statistical spread in the times at which individual people began practicing social distancing etc. It's an idea that's so ubiquitous that we've already talked about how it relates to the marble game in **CHAPTER 8**. You probably learned about it in high school – it's the **normal** (or **Gaussian**) **distribution**. The implementation that we'll use has two parameters: t_{12} is the **mean transition time** and σ_{12} "sigma-1-2" is the **standard deviation** of the distribution of transition times. As we discovered in **CHAPTER 8**, the normal distribution can be implemented in Excel using the **NORM.DIST** function as follows

$$F_{12}^{\text{new}} = \text{NORM. DIST}(t^{\text{new}}, t_{12}, \sigma_{12}, \text{TRUE}) \tag{12.83}$$

The Excel function **NORM.DIST(x, mean, standard_dev, cumulative)** used in equation (12.83) matches up with our application as follows: F_{12}^{new} is the value of the **cumulative normal distribution** for the current time t^{new}; **x** = t^{new} is the time in the current row of spreadsheet; **mean** = t_{12} is the mean transition time; **standard_dev** = σ_{12} is the standard deviation of the distribution of transition times; and **cumulative** = **TRUE** means that the function returns the cumulative distribution function. If **cumulative** = **FALSE**, the function returns the probability density function p_{12} (the normal "bell" curve – see **CHAPTER 8** and Probability Density Functions from Histograms [Nelson 2015]). We want the cumulative distribution function because we want our

function to go from $F_{12} = 0$ to $F_{12} = 1$, which is exactly what the cumulative normal distribution does.

Q.12.74 **DISCUSSION QUESTION** **(a)** Add the parameter σ_{12} [=] d to the **Param$** column **A** of your spreadsheet and enter a number of days for the standard deviation that you think might be a reasonable initial guess. Change the formula for F_{12} to instruction (12.83), then *copy* the formulas for the residuals r and the square of the residuals r^2 from day 37 up to day 1 using the left-click-drag copy method. Then rerun **Solver** to find the best-fit value of t_{12}. Then try a range of values for σ_{12} to get a feel for how its value affects the fitted function after you run **Solver**. You should try $\sigma_{12} \in \{1, 4, 7, 14, 21\}$ d. *Briefly summarize* what you discovered.

(b) Run Excel's **Solver** again but first set **By Changing Variable Cells:** to the cells for both t_{12} and σ_{12} so that **Solver** simultaneously finds the best-fit values of both t_{12} and σ_{12}. *Record* your linear-scale graph of $R_i(t)$ for the new SIR model during the first 100 days and *briefly comment* on the fitted model.

(c) Make a copy of your linear scale chart of $R_i(t)$ and add a series for $k_i(t)$, the infection rate coefficient as a function of time (column **F**) on the secondary axis (right-hand) axis. *Record* your linear-scale graph including $k_i(t)$ during the first 100 days and *briefly comment* on the infection rate coefficient and how it changes with time. Don't forget to save your spreadsheet for this question, we'll be needing it again later.

About what you discovered: visualizing the transition to social distancing

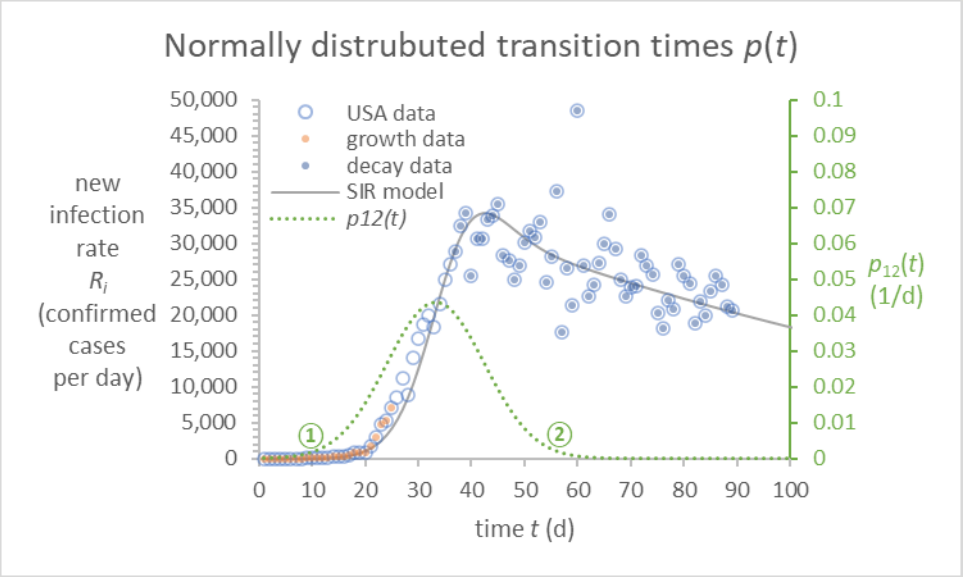


Fig.12.24 Excel chart showing the SIR model (solid line) fitted to the USA data (open circles). The infection rate constant of $k_1 = 0.505$ d^{-1} for epoch ① was obtained by fitting the UG model to the first 25 days (orange dots). The infection rate constant of $k_2 = 0.118$ d^{-1} for epoch ② was obtained by fitting the SIR model from April 3 to May 25 (gray dots). The transition from epochs ① → ② is modeled using a Gaussian (normal) distribution (12.83) with mean $t_{12} = 33.3$ d and standard deviation $\sigma_{12} = 9.19$ d. $p_{12}(t)$ (dotted line) is the corresponding Gaussian probability density function (12.84). Data source ECDC [2020].

Fig.12.24 shows your answer to Q.12.74(b) with an additional dotted-line series for $p_{12}(t)$, the probability density of the normal (Gaussian) distribution shown on the secondary (right-hand) axis, it's generated using the instruction

$$p_{12}^{\text{new}} = \text{NORM. DIST}(t^{\text{new}}, t_{12}, \sigma_{12}, \text{FALSE}) \tag{12.84}$$

The dotted line series $p_{12}(t)$ represents the distribution of times in the model that people transition to social distancing etc. and hence change the infection rate coefficient from $k_i = k_1$ to $k_i = k_2$. As such, it's a useful graphical representation of the transition from exponential growth to gradual decay. A notable feature of the $p_{12}(t)$ graph is that the mean of the distribution (also the peak) occurs on day 33 (March 30), which falls near the middle of the linear growth period (empty open circles) between the fitted epochs ① and ②.

The fitted SIR model in Fig.12.24 has a rounded peak before the steady decay during social distancing. That rounded peak is produced the combination of many transition spikes (Fig.12.23), which are spread out according to the ensemble average dotted line that represents the distribution $p_{12}(t)$ of times at which individuals adopted social distancing/lockdown.

Another feature of Fig.12.24 is that the fitted model underpredicts the USA data during the transition time and during the last 5 days of the 25 days (orange dots) used to fit the exponential growth period. That's caused in the model by people transitioning to social distancing etc. during those 5 days, as can be seen by the non-zero value of $p_{12}(t)$ during that time. One way to compensate for that is to restrict the exponential growth fit to the first 10 days. We'll investigate that approach next and see what we can discover… ❑

Open BPM.Ch12_NORM.DIST.xlsx, it's a preformatted spreadsheet based on your answer to Q.12.74 and it also contains a graph formatted like Fig.12.24. As you can see in cell **O4**, $p_{12}(t)$ is calculated using equation (12.84). The parameters in **Param$** column **A** are from the LS fit for t_{12} and σ_{12} that you obtained in Q.12.74(b).

Q.12.75 **DISCUSSION QUESTION** At the far right under the two **Exponential growth in the USA** charts, the spreadsheet has an **LS fit parameters table** for you to record the parameters for Q.12.74(b) and your answers to parts (b) and (c) of this question. The row above the table contains links to the cells containing the parameters N_0, $\mathcal{R}_0$, k_1, k_2, t_{12}, σ_{12}, and Q. You'll need the table for part (d). *Record* the current values of the fitted parameters (your answer to Q.12.74(b)) using **Copy** and **Paste Values** from cells **AA32:AG32** into the first row (**AA35:AG35**) of the **LS fit parameters table**.

(a) After confirming that you understand how spreadsheet BPM.Ch12_NORM.DIST.xlsx works, run Excel's **Solver** with a **Set Objective** of **Q7**, the cell for the quality of fit Q for the first 10 days in the **USA new infections** table; the **To:** radio button set to ⊙ **Min**; and **By Changing Variable Cells:** set to **Q3,Q5**, the cells for UG model parameters k_u and N_u.

Record and comment on your LS fitted $R_i(t)$ graph for the UG model (12.54) for the first 40 days.

(b) Use Excel's **Solver** to find the best-fit value of t_{12} (change the **Set Objective** to **A23**, the cell for the quality of fit Q; the **To:** radio button set to ⊙ **Min**; and **By Changing Variable Cells:** set to **A19**, the cells for the transition time t_{12}). *Briefly comment* on why the fitted curve doesn't match the USA data as well as in Q.12.74. Don't forget to fill out the row for Q.12.75(b) in the **LS fit parameters table** using **Copy** and **Paste Values** from cells **AA32:AF32**

(c) Rerun Excel's **Solver** to find the best-fit values of both t_{12} and σ_{12} simultaneously. *Record* your linear scale graph of $R_i(t)$ and $k_i(t)$ for the new SIR model during the first 100 days and *briefly comment* on the fitted model for both $R_i(t)$ and $k_i(t)$.

(d) *Record* your table of N_0, $\mathcal{R}_0$, k_1, k_2, t_{12}, σ_{12}, and Q values for Q.12.74(b) and parts (b) and (c) of this question.

Using least squares to find k_1 directly

In this subsection we're going to use least squares to find the discrete-time k_1 directly instead of using the UG model fit. Hence, we can't use equation (12.61) to find the doubling time t_d or equation (12.79) to find the basic reproduction number $\mathcal{R}_0$.

Q.12.76 **(a)** Using the mathematical identity $2^x = e^{x \ln 2}$, *solve* equation (12.78) for t_d to *show that* we can calculate the doubling time t_d from the fitted discrete-time k_1 using

$$t_d = \frac{\ln 2}{\ln(k_1 - k_r + 1)} \tag{12.85}$$

(b) By substituting equation (12.A.2) into equation (12.79), *show that* we can then estimate the continuous time $\mathcal{R}_0$ using

$$\mathcal{R}_0 = \left(\frac{\ln 2}{t_d} + k_r\right)\tau_i \tag{12.86}$$

where t_d is given by equation (12.85).

Q.12.77 **DISCUSSION QUESTION** Open and inspect spreadsheet BPM.Ch12_Gaussian.xlsx. You should notice that the **USA new infections** table has been removed because we won't be doing a fit to the UG model to find k_u, N_u and t_d. You should confirm that parameters t_d and $\mathcal{R}_0$ are calculated using equations (12.85) and (12.86). The spreadsheet includes an **LS fit parameters table** that already includes the parameters for your answers to Q.12.74(b), Q.12.75(b) and Q.12.75(c). Once again, the row above the table contains links to the cells containing the parameters N_0, $\mathcal{R}_0$, k_1, k_2, t_{12}, σ_{12}, and Q. You should fill the table as you go for part (c).

(a) Run Excel's **Solver** to find the best-fit values of t_{12}, σ_{12} and k_1 simultaneously. Then *record* your linear scale graph of $R_i(t)$ and $p_{12}(t)$ for the new SIR model during the first

100 days and *briefly comment* on the fitted model for $R_i(t)$, $k_i(t)$ and $p_{12}(t)$. Don't forget to fill out the row for Q.12.75(b) in the **LS fit parameters table** using **Copy** and **Paste Values** from cells **R1:X1**.

(b) Rerun Excel's **Solver** to find the best-fit values of t_{12}, σ_{12}, k_1 and N_0 simultaneously. Then *make and record* a semi-log graph of $R_i(t)$ with a linear-scale graph of $k_i(t)$ for the new SIR model during the first 100 days and *briefly comment* on the validity of the fitted parameters you obtained.

Hint: You can **Copy** and **Paste** and then modify the linear-scale graph of $R_i(t)$ and $k_i(t)$.

Note: If the value of N_0 does not change significantly, try a starting value of $N_0 \in \{1, 0.1, 0.01\}$ and record the fitted parameters with the smallest Q. You may have to run **Solver** multiple times.

Warning: Depending on the speed of your computer, this could take a while – at least a couple of minutes.

(c) *Record* your updated table of N_0, $\mathcal{R}_0$, k_1, k_2, t_{12}, σ_{12}, and Q values including your values for parts (a) and (b) of this question.

Q.12.78 DISCUSSION QUESTION **(a)** Set the value of the initial number infectious to $N_0 = 5$, and the values of k_1, k_2, t_{12} and σ_{12} to the values you found in Q.12.74(b), then run Excel's **Solver** to find the best-fit values of k_1, k_2, t_{12} and σ_{12} simultaneously. *Record* a linear-scale graph of $R_i(t)$ and $p_{12}(t)$ for the SIR model during the first 100 days and *record* the fitted parameters you obtained with $N_0 = 5$, $N = 8.25 \times 10^7$ and $\tau_i = 8$ d in the **LS fit parameters table**.

Hint: You can **Copy** and **Paste Values** from cells **R1:X1**.

(b) *Record* a linear-scale graph of $R_i(t)$ and $k_i(t)$ for the new SIR model during the first 100 days *Briefly discuss* the validity of the parameters you found in part (a) and *comment* on what you learned from both the $k_i(t)$ and $p_{12}(t)$ curves.

(c) Sample different staring points for the parameters k_1, k_2, t_{12} and σ_{12} to discover if the fit you found in part (a) is unique. You can save your parameters in the **LS fit parameters table**. *Briefly discuss* any fits that you found and comment on what you discovered. Use any format for your answer that you think works best. Don't forget to save your best-fit spreadsheet for this question, we'll be needing it later.

(d) In part (c) of this question, the initial number infected was set to the value $N_0 = 5$ that's approximately the value you calculated using equation (12.59) for the UG model when fitted to the first 25 days. *Investigate and briefly report* on what happens if we set $N_0 = 2$ (the value obtained from the UG model fitted to the first 10 days).

(e) Change the LS fit to include N_0 as a parameter and find the LS "best-fit" values of the five parameters k_1, k_2, t_{12}, σ_{12} and N_0 (this may take a while). By inspecting the "best-fit" semi-log graph, *briefly explain* why the fitted N_0 value is pushed to such low values.

Hint: What part of the USA data does the fit seem to match particularly well?

Note: If the value of N_0 does not change significantly, try a starting value of $N_0 \in \{1, 0.1, 0.01\}$ and record the values with the smallest Q. You may have to run **Solver** multiple times.

Warning: Depending on the speed of your computer, this could take a while – at least a couple of minutes.

(f) Based on what you discovered in Q.12.75, Q.12.77 and Q.12.78, *report* your "best" meaningful values of the model parameters, with an indication of their uncertainty.

About what you discovered: don't use too many parameters in a least-squares fit

In Q.12.61 we discovered that it's not wise to blindly use a least-squares (LS) fit for all the adjustable parameters of a model with more than two adjustable parameters. Adding extra parameters to the LS fit will always make the fit better (lower Q), but you should always do a **sanity check** on the parameters that you obtain. The strategy I recommend (and that Q.12.75 and Q.12.77 follow) is to start with the minimum number of free parameters in your LS fit. If possible, use straight-forward, easy-to-explain-and-understand methods to estimate as many of the model parameters as possible first. Then add additional parameters to the LS fit as sparingly as possible. Making sure that the fitted values make sense at every step. Remember, our goal here is *not* to make the orange line go through all the data as accurately as possible – it's to gain insights into what's happening in the real system by fitting a simplified model to observed data. For example, in Q.12.78(e) I found $N_0 = 0.020$, $\mathcal{R}_0 = 9.1$, $k_1 = 1.9\ \mathrm{d}^{-1}$, $k_2 = 0.12\ \mathrm{d}^{-1}$, $t_{12} = 10$ d, $\sigma_{12} = 17$ d using the LS fit method. Even though this is the "best-fit" that I found (smallest $Q = 1{,}164{,}753{,}993$), none of the parameters make physical sense! They're clearly bogus and provide no insights into what's happening in the real system – except to indicate that the model is not 100% representative of the real system or the reported data – which is something that we already know! … people aren't molecules.

I think you could make an argument for using the fit in Fig.12.24 in preference to the any of the fits that you obtained in Q.12.75, Q.12.77 or Q.12.78. Not because it fits the data best – but because we have more confidence that the fitted parameters are meaningful. You could also make an argument for the fit in Q.12.75(c) because the procedure is the same as for Fig.12.24 (Q.12.67(b)). My advice is to use the difference between the parameter values in Q.12.74(b) and Q.12.75(c) as an indication of the uncertainty in the fitted parameters.

Like you, I discovered the fit in Q.12.78(a) after first going through the procedure outlined in Q.12.75 and Q.12.77. Considering what we learned in Q.12.75 and Q.12.77, we can now have more confidence in the fit shown in Fig.12.25. The parameter values seem to be reasonable. The peak in the $p_{12}(t)$ curve (at $t = t_{12} \approx 27$ d) occurs near the middle of the linear transition period of the linear-scale $R_i(t)$ curve (from $t \approx 20$ d to $t \approx 40$ d). The value of $\sigma_{12} \approx 12.3$ d seems rather long. It predicts that the two-standard-deviation range (95%) of $p_{12}(t)$ goes from day 2 through day 52. As you saw from the $k_i(t)$ curve, the resulting infection rate coefficient $k_i(t)$ stayed near its initial value for about 10 days, which is consistent with what you discovered in Q.12.75(c) using the UG model.

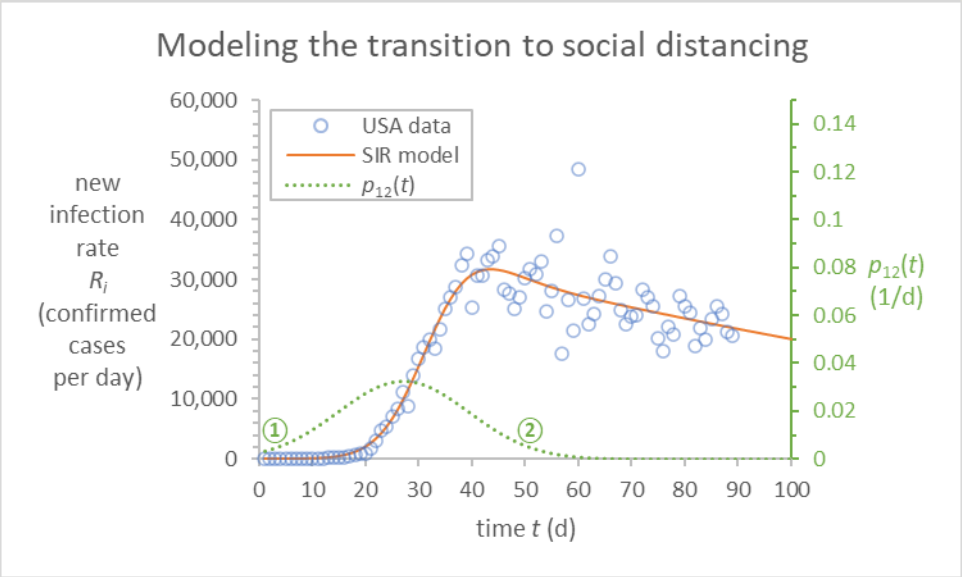


Fig.12.25 Excel chart showing the fitted SIR model (solid line) to the USA data (open circles). SIR model parameters $k_1 = 0.60$ d^{-1}, $k_2 = 0.12$ d^{-1}, $t_{12} = 27$ d and $\sigma_{12} = 12.3$ d were fit simultaneously using the least squares (LS) method. The remaining SIR model parameters were set to $N = 8.25 \times 10^7$, $\delta t = 1$ d, $\tau_i = 8$ d and $N_0 = 5$. The transition from $k_1 \rightarrow k_2$ is modeled using a Gaussian (normal) distribution with mean t_{12} and standard deviation σ_{12}. The dotted line shows $p_{12}(t)$, the probability density function (12.84) of the Gaussian transition function $F_{12}(t)$ (12.83). Circled numbers indicate epochs ① and ② of the pandemic. Data source ECDC [2020].

As you discovered in Q.12.77(b) and Q.12.78(e) it doesn't make sense to allow N_0 to be a LS fit parameter because the resulting fit pushes N_0 and t_{12} to unreasonably low values, and k_1, $\mathcal{R}_0$ and σ_{12} to unreasonably high values caused by the fit matching the data near day 20 better. As we discovered, deciding on a choice of fit can be more of an art than a science. ❑

Now that we have a fit of the SIR model to the USA data for the whole pandemic up to Memorial Day, let's see what we can discover…

Lives lost by delay in the US – revisited

Q.12.79 DISCUSSION QUESTION **(a)** By changing the mean transition time from the value you found in Q.12.74(c) to 7 days earlier, use your spreadsheet to *estimate* how many lives could have been saved by Memorial Day (May 25) if social distancing etc. had been implement just 7 days earlier.

Hint: You can do that by first calculating the number of infections saved and then use the observed crude mortality ratio $m_c = 0.0595$ on May 25, 2020 to predict the number of lives saved.

(b) By changing the mean transition time from the value you found in Q.12.78(c) to 7 days earlier, use your spreadsheet to *estimate* how many lives could have been saved by Memorial Day if social distancing etc. had been implement just 7 days earlier.

(c) *Briefly discuss* how your answers to parts (a) and (b) compare with the values in Table 12.2 for the empirical fit in Fig.12.21.

If you can do it there, you can do it anywhere …

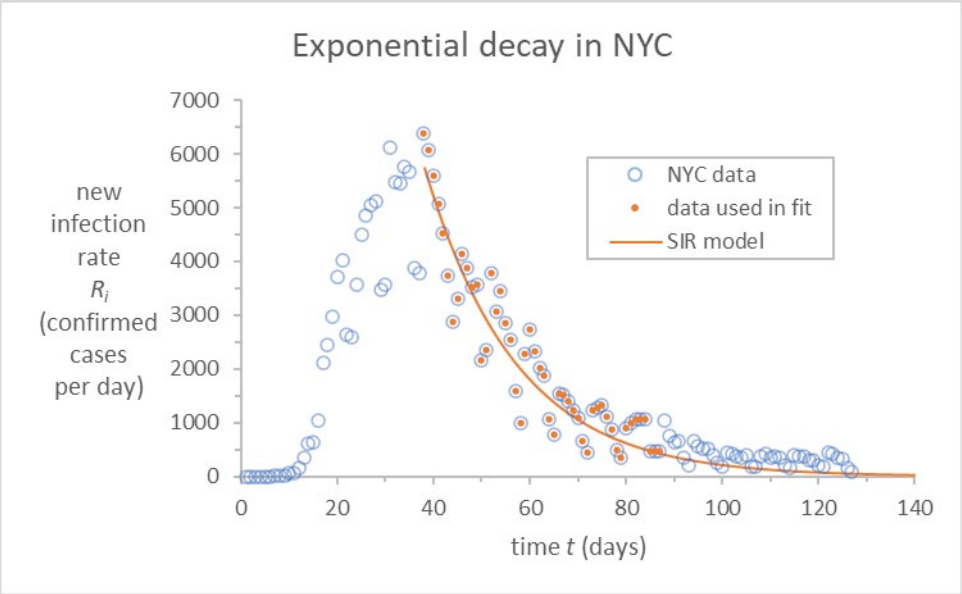


Fig.12.26 Excel chart showing infection rate data for New York City (NYC data – open circles) reported by NYC OpenData from February 29 to July 4, 2020. The solid line shows the prediction of the SIR model when fitted to the April 6 to May 25 (Memorial Day), 2020 data (data used in fit – orange dots) using the ED model – see Q.12.80.

New York, New York – In late March 2020, the big apple was sickening from the inside out. Hospitals were reaching capacity and the infection rate was fast approaching 5,000 cases per day – see Fig.12.26. New York City (NYC) is the biggest city in the US with the highest population density making it an ideal breeding ground for the highly contagious SARS-CoV-2 virus. NYC was the epicenter of the initial COVID-19 outbreak in the US. The initial picture wasn't pretty. It was up to New York to do something, and they did. In this subsection, we'll investigate how the city that never sleeps was different from the US as a whole and then discover what would have happened, if the rest of the United States had decided to do it New York's way.

Q.12.80 DISCUSSION QUESTION Open the preformatted spreadsheet BPM.Ch12_NYC.xlsx. It contains the NYC data shown in Fig.12.26. The form of the spreadsheet is based on the one you used for Q.12.57. The **NYC data** table contains the infection rate R_i, hospitalization rate R_H and the death rate R_m data for NYC from March 29 through July 4, 2020. After confirming that you understand how the spreadsheet works, *run* Excel's **Solver** with a **Set Objective** of **J7**, the cell for the quality of fit Q for April 6 through May 25, 2020 in the **NYC data** table; the **To:** radio button set to ⊙ **Min**; and **By Changing Variable Cells:** set to **J3,J5**, the cells for ED model parameters k_d and A_0.

(a) *Record* the value of k_i you obtained for NYC during social distancing.

(b) *Record and comment on* your linear-scale $R_i(t)$ graph for the SIR model for the 105 days after April 6, 2020.

Q.12.81 DISCUSSION QUESTION **(a)** Make a copy of the spreadsheet you saved for Q.12.74(c), then modify your spreadsheet to add a series to the $R_i(t)$ graph to show how the USA $R_i(t)$ would have changed if everyone behaved like New Yorkers, i.e., change k_2 to the value $k_i = 0.07838\ \text{d}^{-1}$ you found for NYC in Q.12.80. *Record* your graph.
(b) Make a copy of the spreadsheet you saved for Q.12.78(c), then modify your spreadsheet to add a series to the $R_i(t)$ graph to show how the USA $R_i(t)$ would have changed if everyone behaved like New Yorkers, i.e., change k_2 to the value $k_i = 0.07838\ \text{d}^{-1}$ you found for NYC in Q.12.80. *Record* your graph.
(c) Use your results for parts (a) and (b) to *estimate* how many lives could have been saved from infection and death if everyone in the US did it NYC's way.
Hint: You can do that by first calculating the number of infections saved and then use the observed crude mortality ratio $m_c = 0.0595$ on May 25, 2020 to predict the number of lives saved. Don't forget to include the uncertainty of your estimate.
(d) *Compare* the values of k_2 for NYC with the k_2 for the whole of the US during social distancing.
Hint: Don't forget to use what you learned from the "talking numbers" AWYD in **CHAPTER 2**. You might find the BPM.Ch02_Talking_numbers.xlsx preformatted spreadsheet useful.
(e) *Briefly explain* why the USA model appears linear (on a linear-scale graph) during social distancing whereas the graph with the NYC k_2 looks like an exponential decay.
(f) Assume that the US population consists of two groups of people, (i) those that wear masks, socially distance and obey stay-at-home orders – and (ii) those that don't. If we assume that everyone in NYC is in group (i) and followed the public health guidelines to the letter, what fraction of the whole US population would need to be in group (ii) and completely ignore (not follow) those public health guidelines to account for the increase in k_2 for the US as a whole compared with NYC?
Hint: You can use $k_2 = 0.07838\ \text{d}^{-1}$ for group (i) and $k_2 = 0.5207\ \text{d}^{-1}$ for group (ii), which means that those in group (ii) infect others at the same rate as during the beginning of the initial outbreak.
Note: The value of $k_2 = 0.5207\ \text{d}^{-1}$ for group (ii) is the estimated continuous-time infection rate coefficient k_i during the initial outbreak before social distancing, calculated from the discrete-time k_1 using equations (12.85), (12.61) and (12.60).

About what you discovered: if you can do it there, you can do it anywhere …

Fig.12.27 shows my answer to Q.12.81(a) with an added arrow indicating the number of people that could have been saved from infection per day if the whole of the US had behaved like NYC wearing masks and following public health guidelines etc. Panel (a) is a semi-log plot and the linear appearance of both model curves after about day 40 (April 6) indicates the predicted exponential decay in the infection rates. The linear-scale plot in panel (b) clearly shows the more

rapid exponential decay if everyone wore masks etc. The reason that the USA SIR model still appears linear in panel (b) is because the half-life calculated using equations (12.70) and (12.65) is $t_{½} \approx 100$ d, whereas the masks etc. curve has a half-life of $t_{½} \approx 15$ d. The large value of the USA half-life compared with the timescale of the graph makes the exponential decay appear linear (see Fig.9.5). Whereas the much smaller value of the NYC half-life compared with the timescale of the graph explains why the full shape of the exponential decay is apparent.

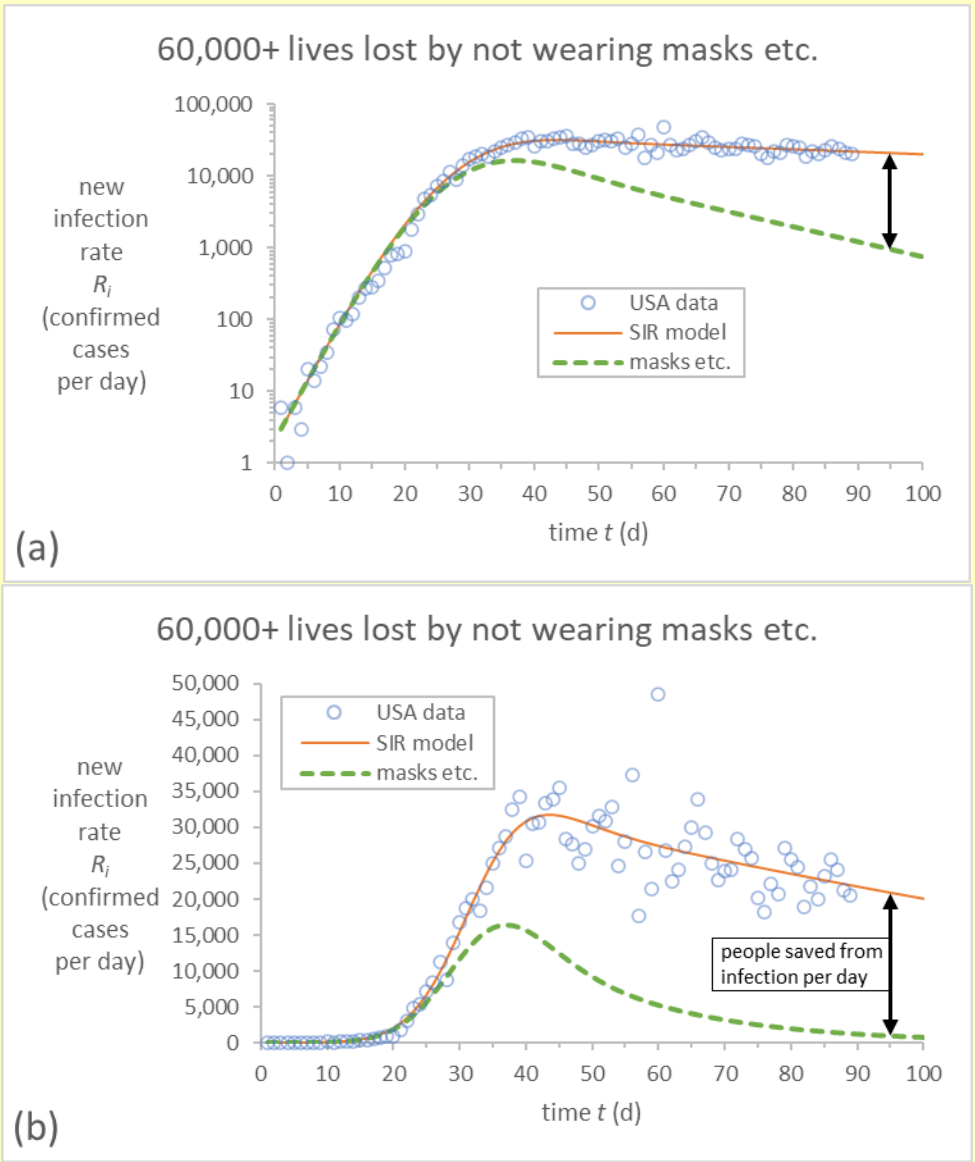


Fig.12.27 Excel chart showing the predictions of the SIR model (solid line) with a Gaussian transition function. The model parameters $k_1 = 0.603$ d^{-1}, $k_2 = 0.120$ d^{-1}, $t_{12} = 27.0$ d, and $\sigma_{12} = 12.3$ d were obtained by least-squares fit to all the USA data from February 27 to May 25, 2020 inclusive (open circles) with $N = 8.25 \times 10^7$, $\delta t = 1$ d, $\tau_i = 8$ d. The dashed line shows the prediction of the same model if the entire US had followed NYC's lead with masks and social distancing etc., resulting in an infection rate constant of $k_2 = 0.0784$ d^{-1}. **(a)** Semi-log graph illustrating the increased decay rate if everyone wore masks etc. **(b)** The same prediction on a linear-scale plot – clearly showing the non-linear shape of the predicted decrease. The estimate of 60,000+ lives lost by Memorial Day is based on the observed crude mortality ratio of $m_c = 0.0595$. Data source ECDC [2020].

The number of people saved from infection is the area between the two curves in panel (b). By comparing the estimates from Q.12.81(a) and (b) I came up with an estimate of $64{,}000 \pm 5{,}000$ lives saved is the whole of the US had followed NYC's lead with mask wearing etc. during the initial period of social distancing up to Memorial Day. As you discovered in Q.12.81(f), the loss of those lives can be explained by just 9% of the US population refusing to follow social distancing guidelines and wear masks etc. ❑

Q.12.82 **RESEARCH QUESTION** **(a)** The preformatted spreadsheet BPM.Ch12_NYC.xlsx contains the infection rate R_i, hospitalization rate R_H and the mortality (death) rate R_m data for NYC from March 29 through July 4, 2020. There are many things that you can discover by analyzing that data (and similar data from other states, countries, or regions). Using that data what can you discover about the time between the report of infection and hospitalization; hospitalization and death; the chance of getting out of hospital alive; the mortality ratio; and other ratios such as the hospitalization ratio. I was surprised by some of the things you can figure out just from the raw data.
Note: The values you'll obtain relate to the initial outbreak in NYC. Since then, the US medical profession has become much better at treating patients with severe COVID-19.
(b) You could also investigate using a Gaussian transition function to fit the NYC data or data from other states, countries, or regions.
Hint: For NYC, you might need to assume that the infection rate was under-reported during the peak from about day 20 to day 40.

12.7 Cloudy with a chance of dragons

Lifting social distancing – the butterfly and the dragon

In this section we'll talk about the consequences of reducing social distancing prematurely. When I first planned this section, the approach used was theoretical. Unfortunately, as of early September 2020, we now have published data that can be used to validate the approach – we'll call this period of the pandemic in the US the **summer surge**.

As you might recall, there was considerable political pressure placed on local leaders at the end of spring (i.e., in the weeks preceding and following Memorial Day – May 25, 2020) to open up their economies, to lift stay-at-home recommendations/orders and to allow activities inconsistent with maintaining social distancing. All the while, mask wearing had been politicized and was not universally mandated or even encouraged.

Let's start our analysis with data reported by the ECDC up to July 4, 2020, that represent the beginning of the summer surge. *Open and inspect* spreadsheet BPM.Ch12_Summer_dragon.xlsx. It's an extension of the BPM.Ch12_Gaussian.xlsx spreadsheet that you analyzed in the previous section but with $N = 6.6 \times 10^7$ (20% of the actual US population). There are three new parameters in the **Param$** column to model the third epoch (period) of the COVID-19 pandemic

in the US caused by lifting social distancing measures prematurely. The new parameter k_3 [=] d^{-1} is the infection rate constant in epoch ③, t_{23} is the mean transition time between epoch ② and epoch ③, and σ_{23} is the standard deviation of the transition times between epochs ② and ③. The spreadsheet also includes a new column for $F_{23}(t)$ and a new column for $p_{23}(t)$. F_{12} and F_{23} represent the transition functions between epochs, ① and ②, and epochs ② and ③ respectively, and p_{12} and p_{23} represent the probability densities of the corresponding normal (Gaussian) distributions. F_{12} and p_{12} are given by equations (12.83) and (12.84) and F_{23} and p_{23} are given by

$$F_{23}^{\text{new}} = \text{NORM. DIST}(t^{\text{new}}, t_{23}, \sigma_{23}, \text{TRUE}) \tag{12.87}$$

and

$$p_{23}^{\text{new}} = \text{NORM. DIST}(t^{\text{new}}, t_{23}, \sigma_{23}, \text{FALSE}) \tag{12.88}$$

The infection rate coefficient k_i is now given by

$$k_i^{\text{new}} = k_1 + F_{12}^{\text{new}} * (k_2 - k_1) + F_{23}^{\text{new}} * (k_3 - k_2) \tag{12.89}$$

Q.12.83 **DISCUSSION QUESTION** In spreadsheet BPM.Ch12_Summer_dragon.xlsx, *complete* the SIR model table by entering equations (12.87) and (12.88) in the columns for F_{23} and p_{23} respectively. Then *confirm* that k_i is given by equation (12.89).

(a) Then *adjust* the values of the parameters k_3, t_{23}, and σ_{23} *by hand* to make the SIR model match the beginning of the summer surge approximately. See if you can determine the best-fit values of k_3 to the nearest 2 significant figures and t_{23} and σ_{23} to the nearest day. *Record* your "by hand" estimates in the **LS fit parameters table** using **Copy** and **Paste Values** from cells **T1:AB1**. Then *record* them in your Word doc answer.

(b) Now use **Solver** to find the least-squares best-fit values of k_3, t_{23}, and σ_{23} simultaneously and *record* you graph of $R_i(t)$ together with the graph of $k_i(t)$ and record the best-fit values in the **LS fit parameters table**.

(c) Finally, use **Solver** to find the least-squares best-fit values of all of k_1, k_2, t_{12}, σ_{12}, k_3, t_{23}, and σ_{23} simultaneously and *record* your graph of $R_i(t)$ together with the graphs of $p_{12}(t)$ and $p_{23}(t)$, and record the best-fit values of k_3, t_{23}, and σ_{23} in the **LS fit parameters table**.

(d) *Record* the **LS fit parameters table** of your answers to parts (a), (b) and (c).

(e) *Quantitatively discuss* the significance of your fitted parameters.

About what you discovered: America unmasked – the exponential dragon returns

As you discovered in Q.12.83, the beginning of the summer surge can be modeled by a change in the infection rate coefficient from $k_i = k_2 = 0.120\ \mathrm{d}^{-1}$ to $k_i = k_3 = 0.179\ \mathrm{d}^{-1}$ with a mean transition time of $t_{23} = 113$ d and standard deviation $\sigma_{23} = 7.2$ d. Fig.12.28 shows my answer to Q.12.83(c) with some additional series (not asked for) indicating Memorial Day and July 4th. As you discovered, an increase of about 50% in the infection rate coefficient can account for the rather dramatic change in qualitative behavior of $R_i(t)$ from gradual exponential decay back to

rapid exponential growth. If we follow the procedure of Q.12.81(f) we can an estimate that only 12% of people abandoning social distancing can account for the emergence of the summer dragon.

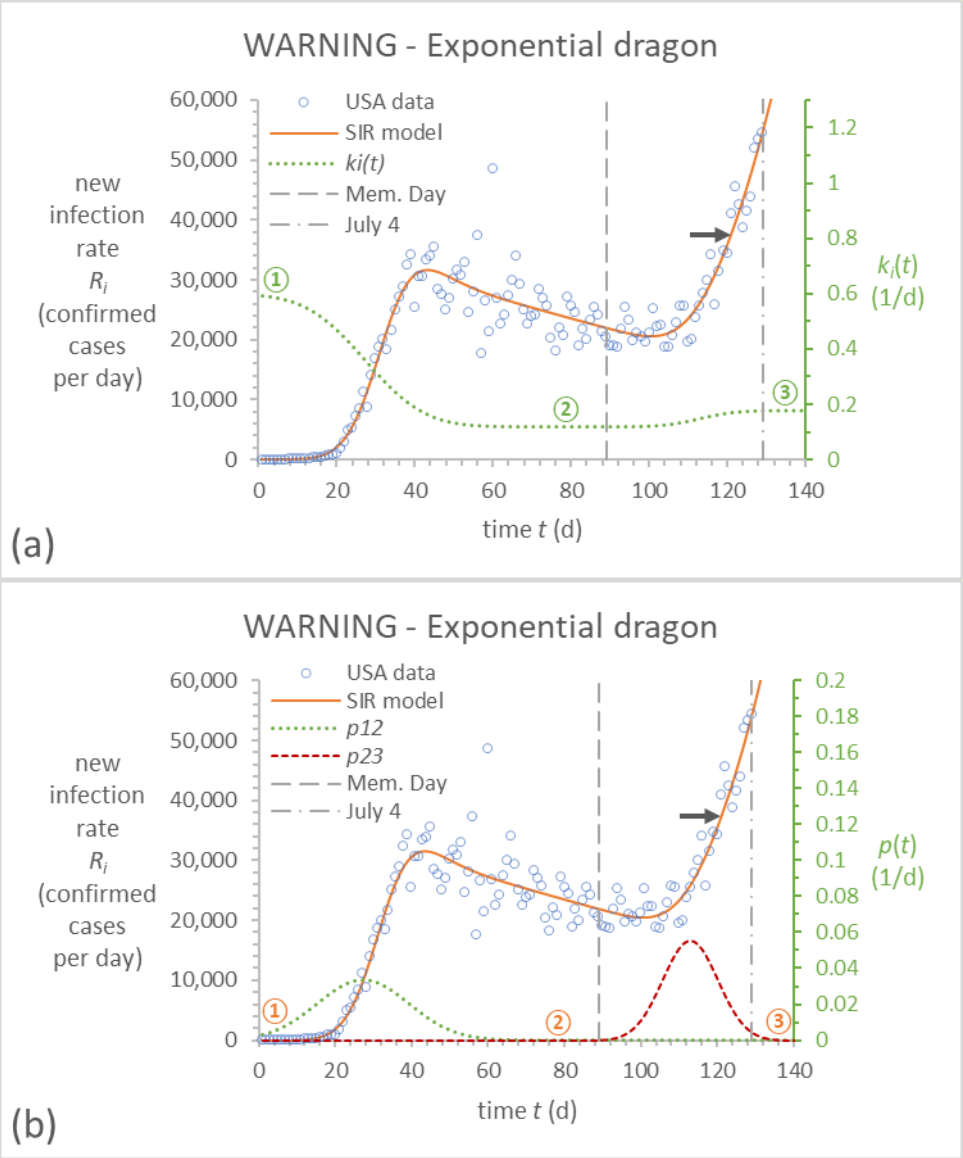


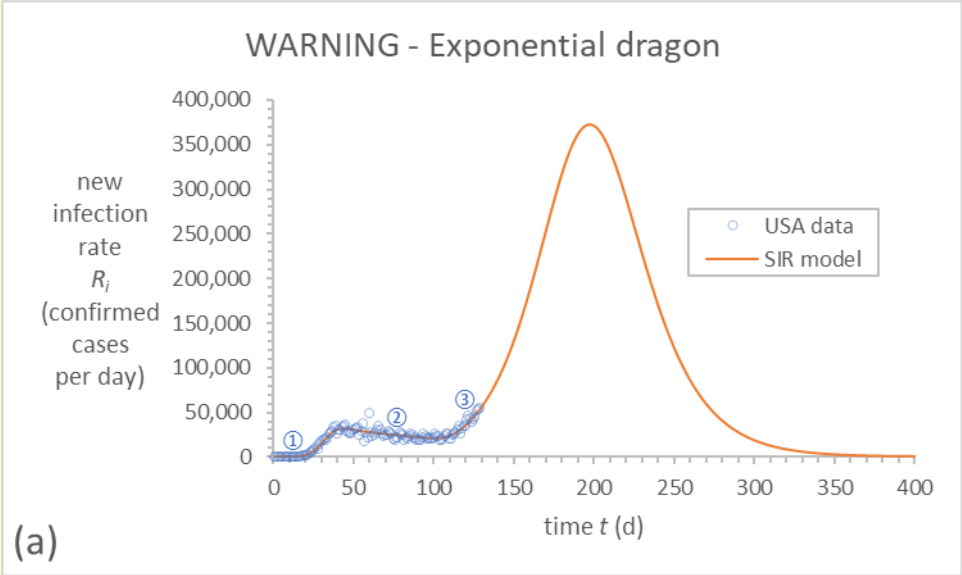
Fig.12.28 (a) & (b) Excel charts showing the predictions of the SIR model (solid orange line) when fitted to USA data reported as confirmed cases per day by the ECDC (blue open circles) for three epochs – ① the initial exponential growth, the period ② of social distancing, and ③ the relaxation of social distancing following Memorial Day. The vertical dashed lines indicate Memorial Day (May 25, 2020 – dashed line) and July 4th (dash-dot line). The arrow points to the nose of the exponential dragon caused by premature relaxation of social distancing etc. Panel **(a)** also includes the infection rate coefficient $k_i(t)$ on the secondary vertical axis. Panel **(b)** shows the transition time distributions p_{12} and p_{23} for the transition times t_{12} and t_{23}.

Fig.12.28(a) shows the infection rate coefficient as a function of time $k_i(t)$ on the secondary axis (right). As shown, only a relatively small change in $k_i(t)$ accounts for the rather dramatic change in the infection rate following Memorial Day. Fig.12.28(b) shows the corresponding graphs of the

probability densities – p_{12} for the transition time t_{12} and p_{23} or the transition time t_{23} from epoch ② to epoch ③. The graph of $p_{23}(t)$ is particularly interesting because it highlights a feature of the fitted model that's not immediately obvious in the $R_i(t)$ graph – namely that the mean transition time is well after Memorial Day and that the transition is basically complete by the 4th of July weekend. Hence, if reports in the popular press are correct that changes in behavior over Memorial Day weekend really were the cause of the summer dragon then the delay between cause and average effect is $(113\text{ d}) - (89\text{ d}) = 24\text{ d}$ or over three weeks! Unfortunately, further investigation of this fascinating topic is beyond the scope of this chapter. However, one thing that you should recall is that the SIR model doesn't include a box (**exposed**) to represent those recently infected who are not yet infectious. Hence, our SIR model doesn't explicitly include any incubation period. As we've mentioned before, the jumps from box $s \to i$ are not required to occur instantaneously. The **SEIR model**, where the E stands for exposed, is the simplest model that accounts for that effect. ❑

Q.12.84 **DISCUSSION QUESTION** Copy your $R_i(t)$ graph and then extend it to show the full predicted summer dragon. Then *record* your model predictions on:
(a) a linear-scale graph; and
(b) a semi-log graph.
(c) Then *briefly comment* on what you discovered.
(d) **RESEARCH QUESTION** *Investigate and report* on how your results depend on N and τ_i.

About what you discovered: here be dragons!



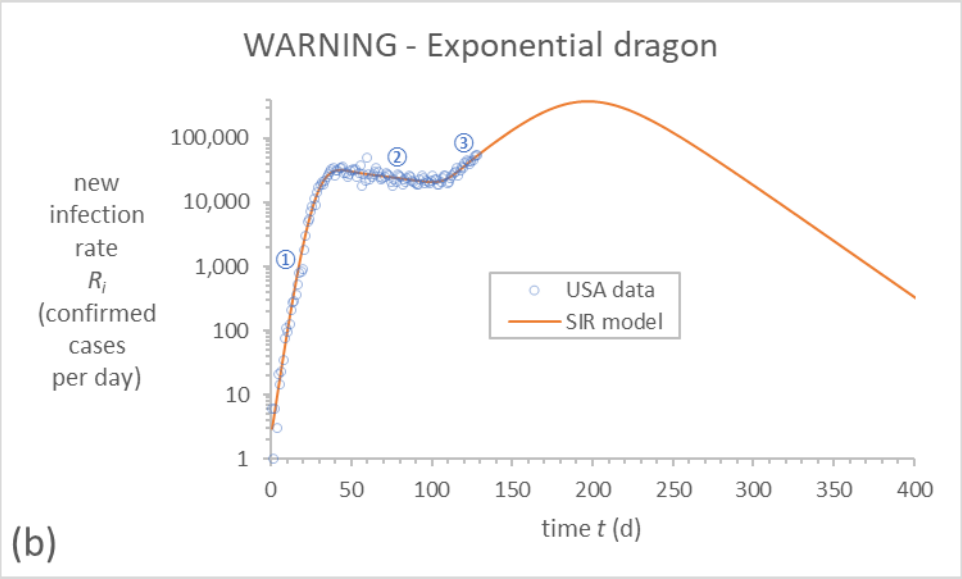


Fig.12.29 Excel chart showing the predictions of the SIR model (solid orange line) when fitted to USA data reported as confirmed cases per day by the ECDC (open blue circles) for three epochs – ① the initial exponential growth, ② the period of social distancing, and ③ the relaxation of social distancing following Memorial Day. **(a)** Linear-scale plot showing the complete exponential dragon. **(b)** Semi-log graph illustrating the dragon's exponential head and accentuating its long exponential tail, *cf.* Fig.12.15.
Note: This estimate based on 20% of the US population ($N = 6.6 \times 10^7$) being included in the model and it assumes that the model parameters stop changing after July 4, 2020, which was not true.
Also note: The inverted vee (Λ) shape of the dragon's head in the semi-log graph in Fig.12.29(b) that we first noted in Fig.12.15. The peak value is not well-determined. It can range from about $R_i = 200{,}000$ d^{-1} to about $R_i = 1{,}000{,}000$ d^{-1}, simply by changing the size N of the model population (see Q.12.47).

❑

The summer surge and the butterfly

Thankfully, people in the US didn't let the summer dragon continue to grow unabated. Social distancing mandates were reinstated in various states and the net result was that the exponential dragon was suppressed before the long-term predictions of Fig.12.29 came reality. In this subsection, we'll analyze what actually happened and analyze the response using our fitted model. **Spoiler alert:** I was quite surprised by what the analysis revealed about the nature of the response.

Open and inspect spreadsheet BPM.Ch12_Summer_surge.xlsx. It's an extension of the BPM.Ch12_Summer_dragon.xlsx spreadsheet that you analyzed in Q.12.83 and Q.12.84. I added three new parameters in the **Param$** column to model the fourth epoch of the COVID-19 pandemic in the US caused by reimposing social distancing measures and more responsible behavior by younger people. Parameter k_4 [=] d^{-1} is the infection rate constant in epoch ④, t_{34} is the mean transition time between epoch ③ and epoch ④, and σ_{34} is the standard deviation of the transition times between epochs ③ and ④. The spreadsheet also includes two new columns: F_{34} represents the transition function between epochs ③ and ④, and p_{34} represents the probability density of the corresponding normal (Gaussian) distribution. F_{12}, p_{12}, F_{23} and p_{23} are given by are given by equations (12.83), (12.84), (12.87) and (12.88). F_{34} and p_{34} are given by

$$F_{34}^{\text{new}} = \text{NORM. DIST}(t^{\text{new}}, t_{34}, \sigma_{34}, \text{TRUE}) \tag{12.90}$$

and

$$p_{34}^{\text{new}} = \text{NORM. DIST}(t^{\text{new}}, t_{34}, \sigma_{34}, \text{FALSE}) \tag{12.91}$$

The infection rate coefficient k_i is now given by

$$k_i^{\text{new}} = k_1 + F_{12}^{\text{new}} * (k_2 - k_1) + F_{23}^{\text{new}} * (k_3 - k_2) + F_{34}^{\text{new}} * (k_4 - k_3) \tag{12.92}$$

Q.12.85 **DISCUSSION QUESTION** In spreadsheet BPM.Ch12_Summer_surge.xlsx, *complete* the SIR model table by entering equations (12.90), (12.92) and (12.91) in the columns for F_{34}, k_i and p_{34} respectively.

(a) Then *adjust* the values of the parameters k_4, t_{34}, and σ_{34} *by hand* to make the SIR model match the downslope of the summer surge approximately. See if you can determine the best-fit values of k_4 to the nearest 2 significant figures and t_{34} and σ_{34} to the nearest day. *Record* your "by hand" estimates in the **LS fit parameters table** using **Copy** and **Paste Values** from cells **V1:AC1**.

Note: In part (c) you'll be asked to record your **LS fit parameters table** for parts (a) through (c) as a single table in your Word doc answer.

(b) Now use **Solver** to find the least-squares best-fit values of k_4, t_{34}, and σ_{34} simultaneously and *record* the best-fit values in your **LS fit parameters table**.

(c) Finally, use **Solver** to find the least-squares best-fit values of all of k_3, t_{23}, σ_{23}, k_4, t_{34}, and σ_{34} and record the best-fit values of k_3, t_{23}, and σ_{23} in your **LS fit parameters table**. *Record* your **LS fit parameters table** to answer parts (a) – (c) simultaneously.

(d) *Record* your graph of $R_i(t)$ together with the graph of $k_i(t)$.

(e) *Record* your graph of $R_i(t)$ together with the graphs of $p_{12}(t)$ and $p_{23}(t)$.

(f) *Quantitatively discuss* the significance of your fitted parameters. Pay particular attention to k_4 and how it compares with k_2.

About what you discovered: The summer surge unmasked

As you discovered in Q.12.85, the summer surge can be explained by a small increase in the infection rate coefficient k_i centered on June 17th followed by a small decrease centered on July 20th (Fig.12.30). Interestingly, the mean time for the increase is just over three weeks (23 days) after Memorial Day and the mean time for the decrease is 16 days after July 4th. As you can see in Fig.12.30(a) that means that the fourth of July holiday weekend occurred approximately in the middle of epoch ③. As shown in Fig.12.30(a), the SIR model infection rate coefficient k_i stayed approximately constant in the weeks preceding and following July 4th. This description is quite different from comments in the popular press that stated that the Memorial Day and July 4th holiday weekends were the main causes of the summer surge.

Another thing that you should have noticed and commented on was that the infection rate coefficient in epoch ④, $k_4 = 0.121\ \text{d}^{-1}$ is almost the same as $k_2 = 0.123\ \text{d}^{-1}$, actually 2% higher. That surprised me. The slope of the decrease in epoch ④ is clearly steeper than the slope

in epoch ②. Hence, my naïve expectation was that k_4 would significantly less than k_2, which would have indicated that Americans were finally implementing social distancing and mask wearing etc. better than they did during epoch ② – but I was mistaken! The fitted model isn't consistent with that interpretation as the infection rate constant k_4 for epoch ④ is approximately the same as k_2 for epoch ②, which indicates that the effectiveness of social distancing/mask wearing etc. were essentially the same during epochs ② and ④ on average across the US taken as a whole.

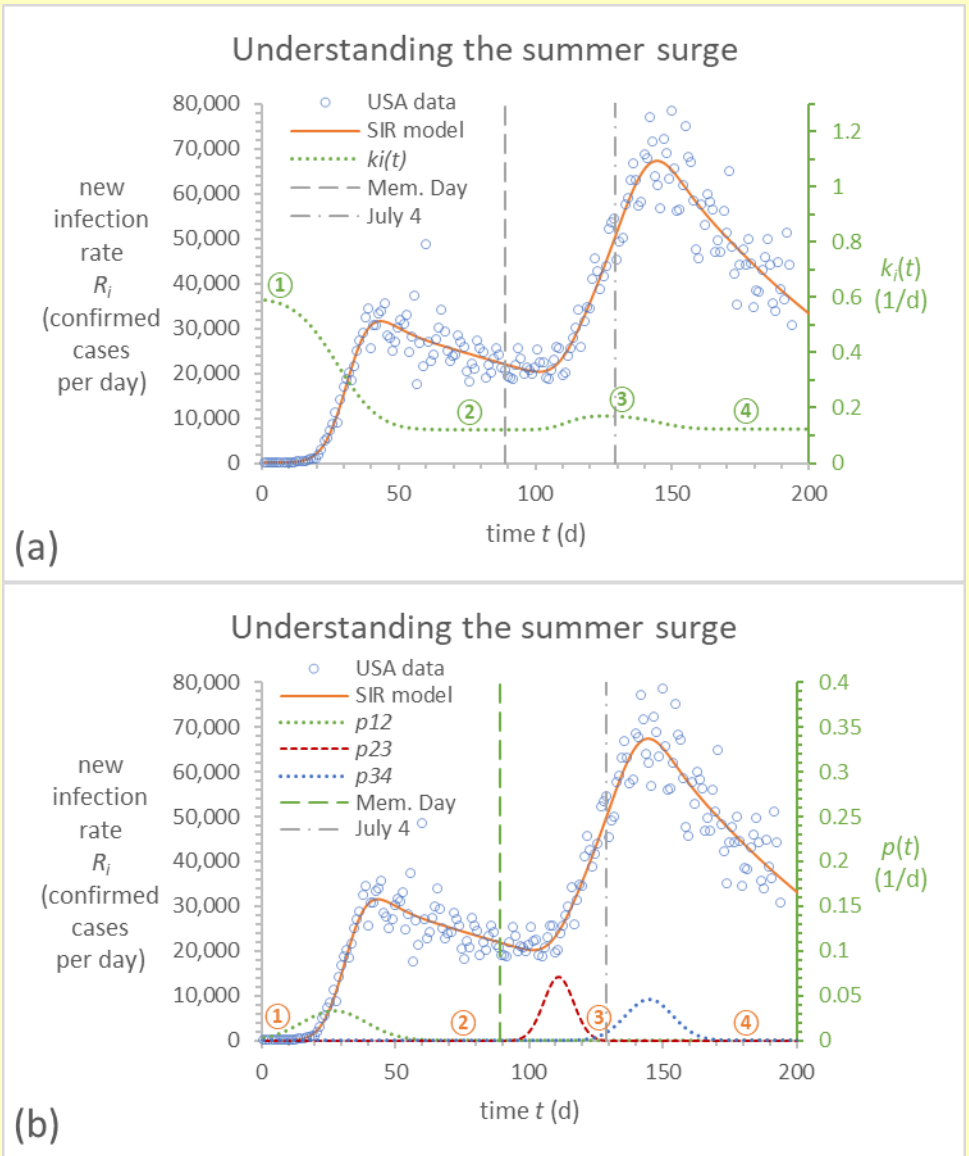


Fig.12.30 Excel chart showing the predictions of the SIR model (solid orange line) when fitted to USA data reported as confirmed cases per day by the ECDC (blue circles) up to Labor Day (September 7, 2020) for four epochs of the pandemic (circled numbers) – ① the initial exponential growth, ② the epoch of social distancing, ③ the relaxation of social distancing following Memorial Day, and ④ the return to social distancing following July 4th. The vertical dashed lines indicate Memorial Day and July 4th. The graph also includes the infection rate coefficient $k_i(t)$ (green dotted line) on the secondary vertical axis. Data source ECDC [2020].

❑

Q.12.86 **DISCUSSION QUESTION** Copy your $R_i(t)$ graph and then extend it to show the full predicted summer dragon. Then *record* your model predictions on:
(a) a linear-scale graph; and
(b) a semi-log graph.
(c) Then *briefly comment* on what you discovered.
(d) **RESEARCH QUESTION** *Investigate and report* on how your results depend on N and τ_i.

12.8 Model population size and the fall dragon

Model population size

In this section we're going to investigate how model population size N affects the SIR model with variable k_i that we've been developing. On January 19, 2021, the CDC released a report estimating that only 1 in 4.6 (95% UI 4.0 – 5.4) of total COVID-19 infections were reported in the period from February–December 2020 (18,19). Rounding up to one significant figure, that means only about 1 in 5 (or 20%) of actual COVID-19 infections appear in the reported data that we've been analyzing. Comparing the model predictions with reported data is central to our modeling exercise. Hence, let's start by making our estimate of the model population size match up with the CDC estimate. The simplest way to do that is to make the model population size be $q \approx 20\%$ of the actual US population, where q is defined as

$$q \equiv \frac{N}{N^\star} \tag{12.93}$$

where N is the model population size and $N^\star = 3.3 \times 10^8$ is the estimated actual population of the United States. Hence, the model population size can be calculated as $N = qN^\star$, so that when $q = 20\%$, then $N = 6.6 \times 10^7$.

The fall dragon

Open and inspect spreadsheet BPM.Ch12_Fall_dragon.xlsx. It's an extension of the BPM.Ch12_Summer_surge.xlsx spreadsheet that you analyzed in Q.12.85 and Q.12.86. It now extends to Thanksgiving Day – November 26, 2020. It now includes the parameter q as a calculated parameter using equation (12.93) and I added three new parameters (k_5, t_{45}, σ_{45}) in the **Param$** column to model the fifth epoch of the COVID-19 pandemic in the US caused by loosening of social distancing measures and continued opposition to mask wearing in the lead up to the 2020 US Presidential elections.

On December 14, 2020, the ECDC discontinued providing daily data. Hence, the spreadsheet contains daily data from a different source – Our World in Data https://ourworldindata.org/coronavirus/country/united-states [OWID 2022a]. They report data in spreadsheet form from Johns Hopkins University. Those data are slightly different from the ECDC data we've used previously. Hence, I redid the fit in spreadsheet BPM.Ch12_Fall_dragon.xlsx.

The spreadsheet also includes new columns for F_{45}, s and p_{45}. I've included instructions for s and p_{45}., you'll compete the column for F_{45} in Q.12.87(b). In part (d) of Q.12.87 we'll investigate how changing the model population size affects the model. As we'll discover, the size of the model population – as indicated by q – is a key parameter affecting the model's predictions after Thanksgiving Day (November 26, 2020). The susceptible fraction $s \equiv N_s/N$ (12.9) is inversely proportional to N, and as we'll discover, it provides key insights into how N (or q) affects the model. That's why I added the column for s in the **SIR model table** and I added an entry for s_{Thx}, the value of s on Thanksgiving Day, in the **LS fit parameters table**. I also added columns for $s_{p,5}$ and Δs, which we'll discuss in Q.12.90.

Q.12.87 **DISCUSSION QUESTION** **(a)** Using equation (12.9) *write out* an instruction for s, and by generalizing equations (12.90), (12.92) and (12.91) *write out* algorithm instructions for F_{45}, k_i, and p_{45}.
(b) In spreadsheet BPM.Ch12_Fall_dragon.xlsx, *confirm* that the equations for k_i, s and p_{45} are implemented correctly then *complete* the **SIR model table** by entering your instruction for F_{45}. Then *adjust* the values of the parameters k_5, t_{45}, and σ_{45} *by hand* to make the SIR model match the nose of the fall dragon. By monitoring the value of Q, determine the best-fit values of: k_5 to the nearest 2 significant figures; and the best-fit values of t_{45} and σ_{45} to the nearest day. *Record* your "by hand" estimates in the **LS fit parameters table** using **Copy** and **Paste Values** from cells **Y1:AG1**.
Note: In part (f) you'll be asked to record your **LS fit parameters table** for parts (b) through (f) as a single table in your Word doc answer.
(c) Now use **Solver** to *find* the least-squares best-fit values of k_5, t_{45}, and σ_{45} simultaneously and *record* the best-fit values in your **LS fit parameters table**.
(d) *Change* value of the model population to $N = 1.32 \times 10^8$ ($q = 40\%$ of the actual US population) then use **Solver** to *find* the least-squares best-fit values of all of k_1, k_2, $t_{12}, \sigma_{12}, k_3, t_{23}, \sigma_{23}$, $k_4, t_{34}, \sigma_{34}, k_5, t_{45}$, and σ_{45} and *record* the best-fit values in your **LS it parameters table**. Don't forget to *save* this spreadsheet, you'll need it later.
(e) *Change* value of the model population back to $N = 6.6 \times 10^7$ ($q = 20\%$ of the actual US population) then use **Solver** to find the least-squares best-fit values of all of k_1, k_2, $t_{12}, \sigma_{12}, k_3, t_{23}, \sigma_{23}, k_4, t_{34}, \sigma_{34}, k_5, t_{45}$, and σ_{45} and *record* the best-fit values in your **LS fit parameters table**. Don't forget to *save* this spreadsheet, you'll need it later.
Note: Coming back to $q = 20\%$ tests the convergence of the LS fit.
(f) *Change* value of the model population to $N = 3.3 \times 10^7$ ($q = 10\%$ of the actual US population) then use **Solver** to find the least-squares best-fit values of all of k_1, k_2, $t_{12}, \sigma_{12}, k_3, t_{23}, \sigma_{23}$, $k_4, t_{34}, \sigma_{34}, k_5, t_{45}$, and σ_{45} and *record* the best-fit values in your **LS fit parameters table**. Don't forget to *save* this spreadsheet, you'll need it later. *Record* the **LS fit parameters table** of your answers to parts (b) – (f) in your Word doc answer. (You can copy and "paste as picture" into Word.)

Q.12.88 DISCUSSION QUESTION **(a)** Using your spreadsheet answer for Q.12.87(e) with $q = 20\%$, *record* your graph of $R_i(t)$ together with the graph of $k_i(t)$ up to day $t = 400$ d for $q = 20\%$ ($N = 6.6 \times 10^7$).
(b) Also *record* your semi-log graph of $R_i(t)$ together with the graphs of $p_{12}(t)$ through $p_{45}(t)$ up to day $t = 400$ d for $q = 20\%$ ($N = 6.6 \times 10^7$).
(c) Using your spreadsheet answers to Q.12.87(d)-(f), *briefly summarize* the visible effect of changing the percentage q of people in the model population on the fitted model in the period up to Thanksgiving Day, then
(d) *Briefly summarize* the effect of changing q on the predictions of the model *after* November 26, 2020.
(e) *Briefly compare* the values of k_5 for the different values of q and discuss what you can conclude.

About what you discovered: the fall dragon and population size

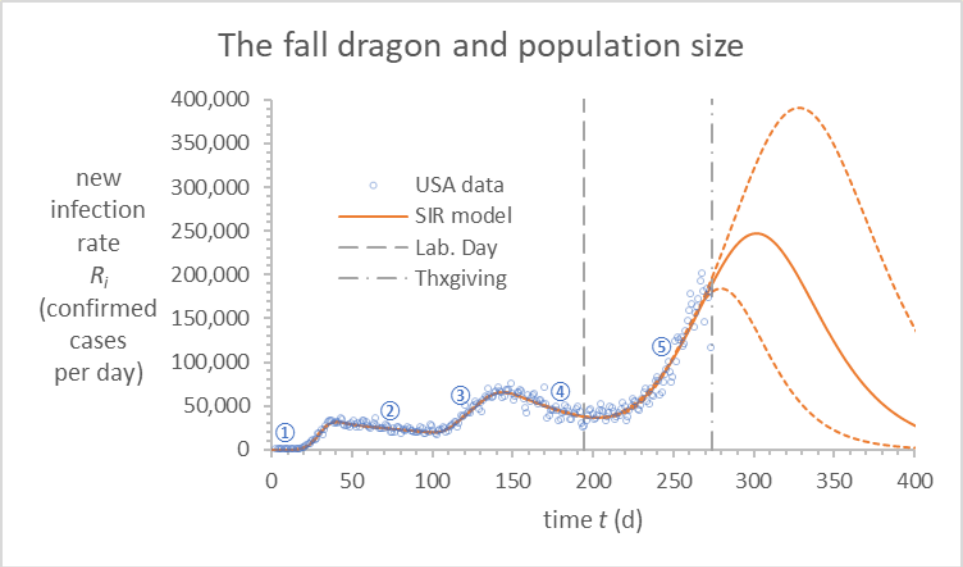


Fig.12.31 Excel chart showing the predictions of the SIR model when fitted to five different epochs – ① the initial exponential growth, ② the period of social distancing, ③ the relaxation of social distancing following Memorial Day, ④ the return to social distancing following July 4th, and ⑤ the fall surge following Labor Day (September 7, 2020). The blue open circles show the USA data reported as confirmed cases per day by OWID up to Thanksgiving (November 26, 2020). The solid orange line represents a model population of $q = 20\%$ of the actual US population. The orange dashed lines represent the fitted model predictions for model populations of $q = 10\%$ (lower) and $q = 40\%$ (higher) of the actual US population.

Fig.12.31 graphically summarizes your answers to Q.12.87(d)-(f) and Q.12.88 (you were not expected to reproduce Fig.12.31). It shows the predictions of the fitted SIR model for the fall exponential dragon for different model population sizes corresponding to $q = 10\%$, 20%, and 40% of the actual US population ($N = 3.3 \times 10^7$, 6.6×10^7, and 1.32×10^8 respectively). As you discussed in Q.12.88(c), changing the model population size has no visible effect on the fitted model up to Thanksgiving Day even though the fitted infection rate constants ($k_1 - k_5$) are

different for the three fitted models (Fig.12.31). However, the model predictions for the fall exponential dragon almost immediately diverge depending on the size of the model population.

As you discovered in Q.12.88(e) the fitted value of $k_5 = 0.23\ \mathrm{d}^{-1}$ for $q = 10\%$ is clearly higher than the other two fits. Because its peak occurs soon after Thanksgiving, $q = 10\%$ is just about the smallest model population size that's consistent with the data up to November 26, 2020 (Fig.12.31). We'll analyze data after Thanksgiving in the next section. However, before we do that, there's an interesting question posted by the fits shown in Fig.12.31 – why do the fits all match up to Thanksgiving, but then diverge almost immediately? It's as if the population size doesn't seem to matter up to Thanksgiving, but then suddenly it does! As a scientific modeler you should ask yourself – why is that? We'll discuss that important question in Q.12.90 below. As a **CHALLENGE QUESTION**, see if you can provide an explanation using the tabulated data you recorded for Q.12.87(b)-(f). ❑

Q.12.89 DISCUSSION QUESTION **(a)** For your fitted model in Q.12.87(e) with $q = 20\%$, *compare* the values of k_5 for the fall dragon with the value of k_3 for summer dragon.
Hint: Don't forget to use what you learned from the "talking numbers" AWYD in **CHAPTER 2**. You might find the BPM.Ch02_Talking_numbers.xlsx preformatted spreadsheet useful.
(b) *Briefly discuss* the significance of your comparison in part (a), focusing on the percent difference between k_3 and k_5.
(c) *Compare* the value of k_4 with the value of k_2 for $q = 20\%$.
(d) *Briefly discuss* the significance of your comparison in part (c).

About what you discovered: stricter and more relaxed social distancing

As you discovered in Q.12.89(a)&(b), the fits with a model population of $q = 20\%$ of the actual US population have an infection rate constant for the fall dragon (k_5 in epoch ⑤) that's within $\pm 5\%$ of the corresponding value for the summer dragon (k_3 in epoch ③). In Q.12.89(c)&(d) you discovered that the fits with $q = 20\%$ have an infection rate constant for k_4 in epoch ④ that's within about $\pm 2\%$ of the corresponding value for k_2 in epoch ②. That suggests that the behavior of the US population – after the initial outbreak (with $q \approx 20\%$) – can be separated into two classes **stricter social distancing** and **relaxed social distancing**. Epochs ② and ④ correspond to stricter social distancing with $k_2 \approx k_4 = 0.122 \pm 0.001\ \mathrm{d}^{-1}$ and epochs ③ and ⑤ correspond to more relaxed social distancing with $k_3 \approx k_5 = 0.178 \pm 0.004\ \mathrm{d}^{-1}$. Hence, the inception of both the summer and fall surges can be explained by a modest 30% increase in the infection rate coefficient k_i. Personally, I found this conclusion to be quite remarkable given the diversity of public health responses in individual states that make up the Union. This is a good example of the insights that can be gained from simple models. ❑

Why does model population size matter after Thanksgiving but not before?

We're now going to investigate an important question raised by the fits in Fig.12.31. Why do the fits match each other before Thanksgiving, but then diverge almost immediately? As we noted

above, it's as if the population size doesn't matter up to Thanksgiving, but then suddenly … it does! Whenever a simple model does something apparently unexpected, it's always worthwhile trying to figure out why. The insights provided are usually worth the effort. Let's see what we can discover …

Q.12.90 DISCUSSION QUESTION Using your spreadsheet answers to Q.12.87(d)(e)&(f),
(a) *Tabulate* the values of $q, s_{\text{Thx}}, k_4, k_5$, $s_{p,5} = k_r/k_5$ (12.27) and the quantity $\Delta s = s_{\text{Thx}} - s_{p,5}$.
Hint: You can copy (as values) the **LS fit parameters table** and then delete the columns that you don't want. You can then copy the table into word.
(b) *Calculate* the average and range of the values of k_5 for the models with $q = 20\%$ and 40% and *compare* them with k_5 for $q = 10\%$.
(c) Using the values of Δs for the three values of q *briefly explain* why the predicted peak for $q = 10\%$ occurs so soon after Thanksgiving and why the predicted peaks for $q = 20\%$ and $q = 40\%$ occur at successively later times.
Note: The s_p gives the value of s at the peak in $N_i(t)$, which soon occurs after the peak in $R_i(t)$ – see Fig. 12.12(b).

About what you discovered: population size matters because …

During epoch ⑤, the fitted the fitted values of the infection rate constant are $k_5 = 0.23$, 0.18 and $0.17\ \text{d}^{-1}$ for models with $q = 10\%$, 20%, and 40%, respectively. The two infection rate constants for $q = 20\%$ and 40% are approximately the same with an average of $k_5 = 0.174 \pm 0.008$. Hence, the large difference between $q = 20\%$ and 40% in Fig.12.31 can't be explained by the modest difference in the infection rate constants.

Susceptible fraction left at Thanksgiving

The third peak in the pandemic predicted in Fig.12.31 is the first peak in the fitted model that corresponds to the exponential dragon predicted by the SIR model. The N_i peak is predicted to occur when $s = k_r/k_5 = s_{p,5}$ but the fitted susceptible fractions at Thanksgiving s_{Thx} get larger as q is increased, meaning that there are more susceptible people left at Thanksgiving, so it takes longer to reach the peak in the fall dragon. The susceptible fractions remaining at Thanksgiving are $s_{\text{Thx}} = 0.607$, 0.803 and 0.902 for model population sizes of $q = 10\%$, 20% and 40%, respectively. The corresponding values of the predicted peak values are $s_{p,5} = 0.542$, 0.684 and 0.752, respectively, indicating that the predicted peak in $N_i(t)$ gets further away from the value of the susceptible fraction at Thanksgiving s_{Thx} (as measured by the quantity $\Delta s = s_{\text{Thx}} - s_{p,5} = 0.065$, 0.12 and 0.15, respectively). Recall that the susceptible fraction s must *always* decrease in the SIR model because once an individual is infected, they're permanently removed from the susceptible box. Hence, for $q = 10\%$, s only needs to decrease by $\Delta s = 0.065$ (from 0.607 to 0.542) for the model to reach the $N_i(t)$ peak in the fall dragon. For the model with $q = 20\%$, the susceptible fraction needs to decrease by $\Delta s = 0.12$ for the model to reach the $N_i(t)$ peak in the fall dragon. For $q = 40\%$ the susceptible fraction needs to decrease by $\Delta s = 0.15$. In addition,

for larger values of q, more infections need to be reported for s to decrease by the same amount. ❑

Model validation

Q.12.91 DISCUSSION QUESTION Using your spreadsheet from Q.12.87(f), change value of the model population to $N = 7.16 \times 10^7$ ($q = 21.7\%$ of the actual US population, which corresponds to the estimate in the CDC report dated January 19, 2021 [CDC 2021a]) then use **Solver** to find the least-squares best-fit values of all of k_1, k_2, $t_{12}, \sigma_{12}, k_3, t_{23}, \sigma_{23}, k_4, t_{34}, \sigma_{34}, k_5, t_{45}$, and σ_{45} and *record* the best-fit values in your **LS fit parameters table**. Don't forget to *save* this spreadsheet, you'll need it later.
(a) *Record* your graph of $R_i(t)$ together with the graph of $k_i(t)$ up to day $t = 400$ d.
(b) *Record* your semi-log graph of $R_i(t)$ together with the graphs of $p_{12}(t)$ through $p_{45}(t)$.

Open and inspect spreadsheet BPM.Ch12_Model_validation.xlsx. It's an extension of the BPM.Ch12_Fall_dragon.xlsx spreadsheet that you analyzed in Q.12.91. In addition to the data up to Thanksgiving Day (November 26, 2020), it also includes additional USA data up to February 14, 2021, that have not yet been plotted. Our plan is to test the predictions of the SIR model for the fall dragon from Thanksgiving through the holiday period up to February 14, 2021. The solid orange line in the spreadsheet chart shows the predictions of the SIR model fitted up to Thanksgiving Day (November 26, 2020) with $N = 7.16 \times 10^7$ or $q = 21.7\%$. It's important to note that it's the same fit that you made in Q.12.91 – you should check that your model parameters match those in the preformatted spreadsheet.
Note: In the preformatted spreadsheet, I used the Excel **Freeze Panes** option to freeze **Row 1**, **Row 2**, and **Column A** of the spreadsheet – see **View** > **Freeze Panes** or look up **Freeze Panes** in Excel's **Help**.

Q.12.92 DISCUSSION QUESTION In the preformatted spreadsheet, use **Select Data…** to plot the unfitted data from November 27, 2020, up to February 14, 2021. You can do that by **Editing** the **unfitted data** series and *changing* the end point of the **Series X values** from **D278** to **D357** and *changing* the end point of the **Series Y values** from **P278** to **P357**. You should now see the unfitted data up to February 14, 2021, plotted as grey diamonds. *Briefly discuss* what you can conclude from the graph, i.e., how well does the SIR model predict the unfitted data from November 27, 2020, up to February 14, 2021?

Because the unfitted data you just plotted show large fluctuations over the 2020-2021 holiday season, the preformatted spreadsheet also includes a **<7-day>** column in column **S** of the spreadsheet, it contains a moving 7-day average of the OWID data. You should *inspect* cell **S7** in the **Formula bar** and make sure that you understand how the formula for the **centered moving average** [NIST 2021] works. It's a 7-day average that's *centered* on the current day. This can be contrasted with Excel's build-in **Moving Average** trendline (with **Period** [**7**]), which is an average of the seven days leading up to and including the current day.

Q.12.93 **DISCUSSION QUESTION** **(a)** In your spreadsheet from Q.12.92, use **Select Data…** to plot the 7-day average from March 1, 2020, up to February 14, 2021. You can do that by **Edit**ing the **7-day ave.** series by *changing* the end point of the **Series X values** from **D8** to **D354** and *changing* the end point of the **Series Y values** from **R8** to **R354**. *Record* your graph.
(b) *Briefly discuss* what you can conclude from the new graph. I.e., is it easier to compare the SIR model with the 7-day average of the unfitted data?
(c) Select the **unfitted data** series in your graph and **Add Trendline…** and in the **Trendline Options** *select* Excel's build-in **Moving Average** trendline (with **Period** [**7**]). In order to see it properly, *change* the series **Dash type** to **Solid** and the **Width** to **0.75 pt** and the color to red. *Briefly discuss* what you can conclude about the difference between our centered 7-day average and Excel's moving 7-day average.

About what you discovered: centered 7-day average and model validation

As you discovered, the data for the 2020-2021 holiday season show large fluctuations. The centered 7-day average smooths out the data making them easier to visually compare with our model predictions. The advantage of the *centered* moving average over Excel's built-in **Moving Average** trendline (with **Period** [**7**]) is that it doesn't introduce a systematic 3-day time-shift in the average (you may have seen graphs of this same type widely reported in the popular press). The only catch with the centered average is that the last three days of data are averages over 6, 5 and 4 days, respectively, instead of 7 days – if you only want to plot the true 7-day average (and we do), you should omit any points that are not averaged over the full 7 days.

The reason for averaging over 7 days is that there are variations in testing and reporting that generally depend on the day of the week, e.g., Friday's data are usually larger than average, and Saturday and Sunday's data are usually lower than average. The centered 7-day average smooths out those **systematic** daily **variations**.

As you discovered, the SIR model does a good job of *predicting* the general shape of the $R_i(t)$ curve after Thanksgiving through the holiday season and up to February 14, 2021. In your discussion it's important to note that the fit only uses data up to Thanksgiving so that the comparison really is a test of what the model predicts. We'll come back to this discussion after we've added vaccinations to the model. ❑

12.9 Modeling vaccination

In late December 2020, the FDA approved COVID-19 vaccines for use in the United States (emergency use authorization). Fig.12.32 shows a simple model of how **vaccination** can be added to the SIR model, resulting in the susceptible-infected-recovered-vaccinated (SIRV) model.[2] The

[2] Before vaccinations started in the United States, I developed an even simpler SIR-V model that included vaccinations, but it was based on susceptible people being the only ones that were vaccinated. See https://arxiv.org/abs/2104.08856v1. That assumption didn't match what actually happened in the US.

new feature is box v for **fully vaccinated** individuals. The arrows entering box v indicate the rates at which individuals are effectively vaccinated. Once "**fully vaccinated**," people are assumed to be permanently immune to COVID-19 in the SIRV model of Fig. 12.33. The three rates leading to box v are labeled $R_{v,s}$, $R_{v,i}$, and $R_{v,r}$ where the subscript v indicates vaccination and the subscripts s, i, and r indicate the originating box. These three vaccination rates are related to the to the total rate of vaccination R_v in the *model population* by

$$R_v = R_{v,s} + R_{v,i} + R_{v,r} \tag{12.94}$$

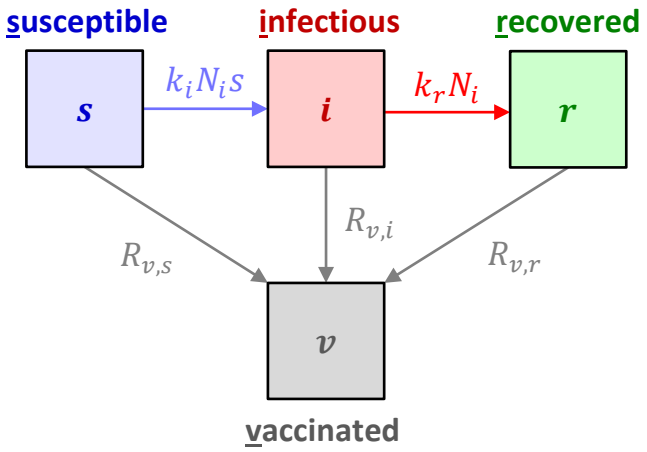


Fig.12.32 FD diagram of a simple modification of the SIR model that accounts for vaccinations – the SIRV model. The four boxes represent the four parts of the model population that can be affected by the disease. Box s represents the portion of the population that's susceptible to the disease. Box i represents the portion of the population that's infectious. Box r represents the portion of the population that has recovered from the infection (or died). Box v represented the portion of the population that's been fully vaccinated.

The bookkeeping equation for the SIRV model is

$$N = N_s + N_i + N_r + N_v \tag{12.95}$$

where the subscripts once again spell out the letters of the model.

The number of vaccinated individuals in the model population is calculated from the "**number fully vaccinated**" $N_v^\star$ reported by OWID [2022a][2022b] using

$$N_v^{\text{new}} = qN_v^{\star\text{new}} \tag{12.96}$$

which assumes that vaccinations are 100% effective in fully vaccinated individuals – something that's not universally true for vaccinations but gives us a best-case scenario. The FD instruction for the vaccination rate in the model population is

$$R_v^{\text{new}} = \left(N_v^{\text{new}} - N_v^{\text{old}}\right)/\delta t \tag{12.97}$$

The rate of vaccination of susceptible individuals in the model population can be calculated using

$$R_{v,s}^{\text{new}} = N_s^{\text{old}} * R_v^{\text{new}} / \left(N_s^{\text{old}} + N_i^{\text{old}} + N_r^{\text{old}}\right) \tag{12.98}$$

similarly

$$R_{v,i}^{\text{new}} = N_i^{\text{old}} * R_v^{\text{new}} / \left(N_s^{\text{old}} + N_i^{\text{old}} + N_r^{\text{old}}\right) \tag{12.99}$$

and

$$R_{v,r}^{\text{new}} = N_r^{\text{old}} * R_v^{\text{new}} / \left(N_s^{\text{old}} + N_i^{\text{old}} + N_r^{\text{old}}\right) \tag{12.100}$$

Equations (12.98), (12.99), and (12.100) assume that individuals in each of the three boxes s, i, and r are equally likely to be vaccinated. In the SIRV model, the numbers in boxes, i and r can be calculated using

$$N_i{}^{\text{new}} = N_i{}^{\text{old}} + \left(R_i^{\text{new}} - R_r^{\text{new}} - R_{v,i}^{\text{new}}\right) * \delta t \tag{12.101}$$

$$N_r^{\text{new}} = N_r^{\text{old}} + \left(R_r^{\text{new}} - R_{v,r}^{\text{new}}\right) * \delta t \tag{12.102}$$

Q.12.94 **(a)** Combining equations (12.101), (12.99) and the bookkeeping equation (12.95) (noting that $N_s^{\text{old}} + N_i^{\text{old}} + N_r^{\text{old}} = N - N_v^{\text{old}}$), *show that*

$$N_i{}^{\text{new}} = N_i{}^{\text{old}} + \left(R_i^{\text{new}} - R_r^{\text{new}} - N_i^{\text{old}} * R_v^{\text{new}} / \left(N - N_v^{\text{old}}\right)\right) * \delta t \tag{12.103}$$

(b) By combining equations (12.102) and (12.100), *show that*

$$N_r^{\text{new}} = N_r^{\text{old}} + \left(R_r^{\text{new}} - N_r^{\text{old}} * R_v^{\text{new}} / \left(N - N_v^{\text{old}}\right)\right) * \delta t \tag{12.104}$$

(c) Using the bookkeeping equation (12.95), *show that* we can find N_s^{new} using

$$N_s^{\text{new}} = N - N_i{}^{\text{new}} - N_r^{\text{new}} - N_v^{\text{new}} \tag{12.105}$$

Note: When comparing the model variables with the published data, it's important to recall that all vaccinations are reported, but only about one-in-five infections were reported.
Also Note: People are considered fully vaccinated 2 weeks after their second dose of the Pfizer-BioNTech or Moderna COVID-19 vaccines, or 2 weeks after the single-dose Johnson & Johnson's Janssen COVID-19 vaccine [CDC 2021]. Just like the other jumps in the SIR models, this extended process is approximated by a single jump transition of variable duration. As a result, students should once again be reminded that we're only trying to understand the basics of epidemiology with our SIRV model.

Testing the SIRV model

Open and inspect spreadsheet BPM.Ch12_Vaccinations.xlsx. It's an extension of the BPM.Ch12_Model_validation.xlsx spreadsheet that you analyzed in Q.12.92 and Q.12.93. It contains additional columns for R_v, N_v, and $N_v^\star$. The data for $N_v^\star$ are taken directly from those reported by OWID [2022a].

Q.12.95 **DISCUSSION QUESTION** In spreadsheet BPM.Ch12_Vaccinations.xlsx, R_v is calculated using instruction (12.97), N_i is calculated using instruction (12.103), N_r is calculated using instruction (12.104), N_s is calculated using instruction (12.105) but N_v is calculated using $N_v^{\text{new}} = 0$ to make the spreadsheet prediction initially match the SIR model with no vaccination. You should *confirm* that the spreadsheet prediction for $R_i(t)$ matches your answer to Q.12.93(a) made with the original SIR model, then *change* cell **P3** to use instruction (12.96) and then copy it down to the bottom of the spreadsheet using the left-double-click method to change the solid-orange-line prediction from the SIR model to that for the SIRV model with the number vaccinated calculated using instruction (12.96).

(a) *Record* your graph, and

(b) *Briefly discuss* whether the resulting SIRV model prediction better matches the reported data than the SIR model.

Hint: After you make the change, you can use **Undo** (Ctrl+Z) and **Redo** (Ctrl+Y) to switch between the SIR and SIRV models – look at the graphs as they change to get a visual idea of the comparison.

About what you discovered: SIRV model validation

Fig.12.33(a) and Fig.12.33(b) show the SIRV model fitted to USA data up to Thanksgiving Day (November 26, 2020) with a model population of $q = 21.7\%$ that's based on the CDC estimate [CDC 2021a]. The combination of the two graphs correspond to your answer to Q.12.95. Fig.12.33(a) includes the infection rate coefficient $k_i(t)$ that was included in your answer, but I have added circled numbers in green (not asked for) to indicate the epochs of the fitted model. Fig.12.33(a) shows only the data used in the fit whereas Fig.12.33(b) includes the unfitted that you had in your answer to Q.12.95. The purpose for showing the two graphs together is to visually summarize what we did in our modeling. It's important to take the time to design graph(s) that summarize your research as clearly and succinctly as possible. A casual reader of your research will always look at the figures even if they don't read the text all the way through. Hence, designing stand-alone graphs and writing good captions is an important part of scientific writing.

As discussed above, Fig.12.33(a) visually highlights that the fit only uses data up to Thanksgiving Day. It further highlights that the infection rate coefficient remains constant at the same value $k_i = k_5 = 0.18\ \text{d}^{-1}$ that started the fall dragon – throughout the entire 2020/2021 holiday period and beyond. Comparing Fig.12.33(a) and Fig.12.33(b), it's clear that we've tested the predictions of the model using the unfitted data (grey diamonds) that were *not* used in the fit. As you discovered in Q.12.93, the centered 7-day moving average of the USA data makes for an easier comparison of the USA data with the model predictions.

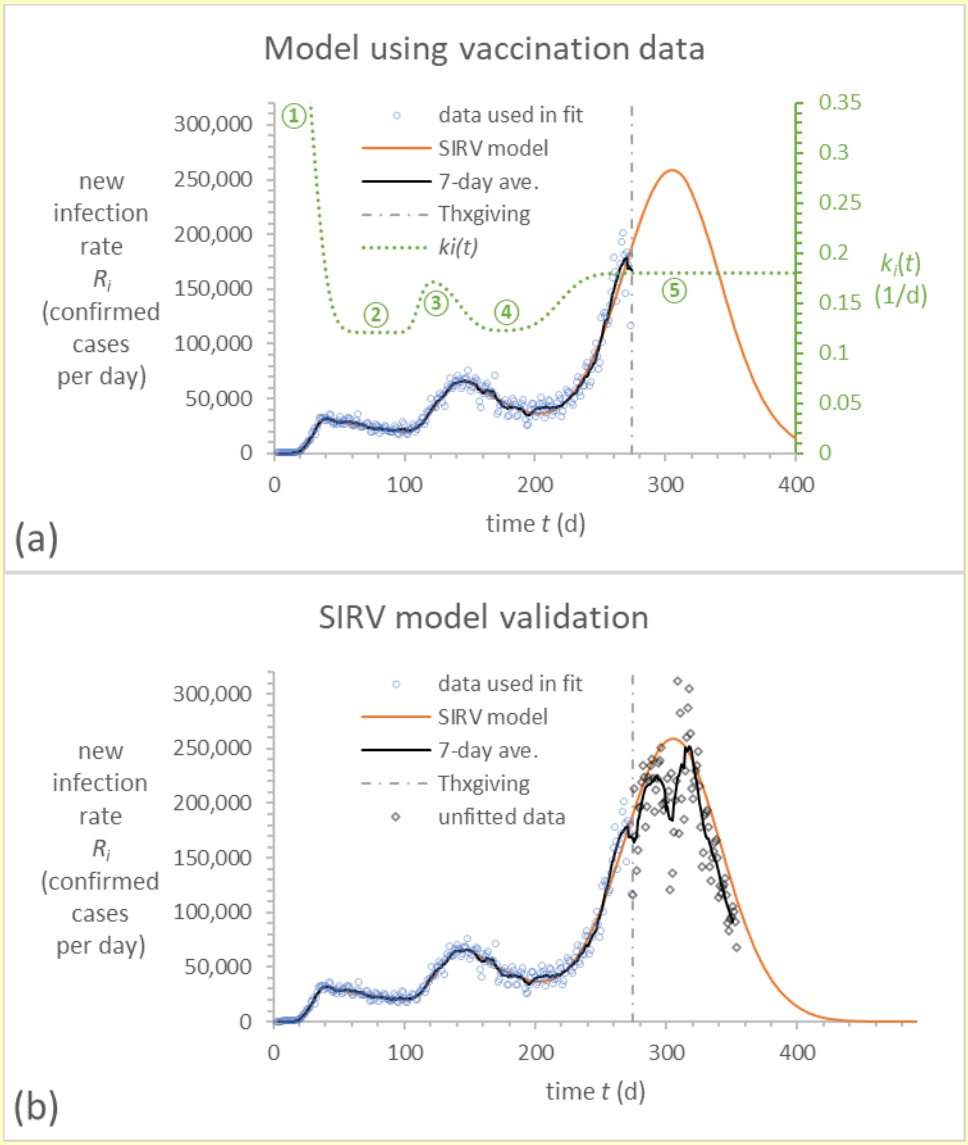


Fig.12.33 Excel charts showing US data and the predictions of the SIRV model. The blue circles show USA data reported as confirmed cases per day up to Thanksgiving Day (November 26, 2020). The jagged black line shows the centered 7-day moving average of the USA data. The solid orange line shows the predictions of the SIRV model assuming that the model population is $q = 21.7\%$ of the actual population [CDC 2021a]. Chart **(a)** shows the infection rate coefficient $k_i(t)$ as a function of time on the secondary vertical axis. Circled numbers indicate the epochs of the pandemic. Chart **(b)** shows additional USA data (grey diamonds) up to February 14, 2021, that were *not* used in the fit and the corresponding 7-day average (jagged black line). These unfitted data validate the predictions of the SIRV model with a constant infection rate coefficient of $k_5 = 0.18\ \text{d}^{-1}$ in epoch ⑤ of the pandemic. Day 400 corresponds to April 1, 2021. Data source OWID [2022a].

❑

In Q.12.95 we tested the predictions of the SIRV model for the 2020/2021 holiday period based on data only up to Thanksgiving 2020. We're now going to redo the fit to the SIRV model using all the USA data up to February 14, 2021. Let's see what we can discover …

Q.12.96 **DISCUSSION QUESTION** *Extend* the **data used in fit** series to include all the data up to February 14, 2021 (**Row 357**). Then remove the **unfitted data** series. You should then extend the r and r^2 columns down to row **357**. Check the formula for Q in cell **A45** and make sure that it calculates the sum of all the r^2 values up to February 14, 2021.

(a) Now use **Solver** to find the least-squares best-fit values of all of k_1, k_2, t_{12}, σ_{12}, k_3, t_{23}, σ_{23}, k_4, t_{34}, σ_{34}, k_5, t_{45}, σ_{45}, and the model population size N and *record* your best-fit graph.

(b) *Briefly discuss* and *compare* the best-fit value of q with the CDC estimated value of $q = 21.7\%$.

Hint: Don't forget to use what you learned from the "talking numbers" AWYD in **CHAPTER 2**. You might find the BPM.Ch02_Talking_numbers.xlsx preformatted spreadsheet useful.

(c) *Compare* the new best-fit value of k_5 with the value you obtained with $q = 21.7\%$.

(d) Using your current fit, estimate the size of the peak in $R_i(t)$ if no social distancing measures had been implemented. *Record* the height of the uncontrolled $R_i(t)$ peak and *compare* it to the height of the $R_i(t)$ peak in your fitted model in part (a).

Hint: You can do that by changing the instruction for the infection rate coefficient to $k_i^{\text{new}} = k_1$ in your spreadsheet.

About what you discovered: the peak we flattened

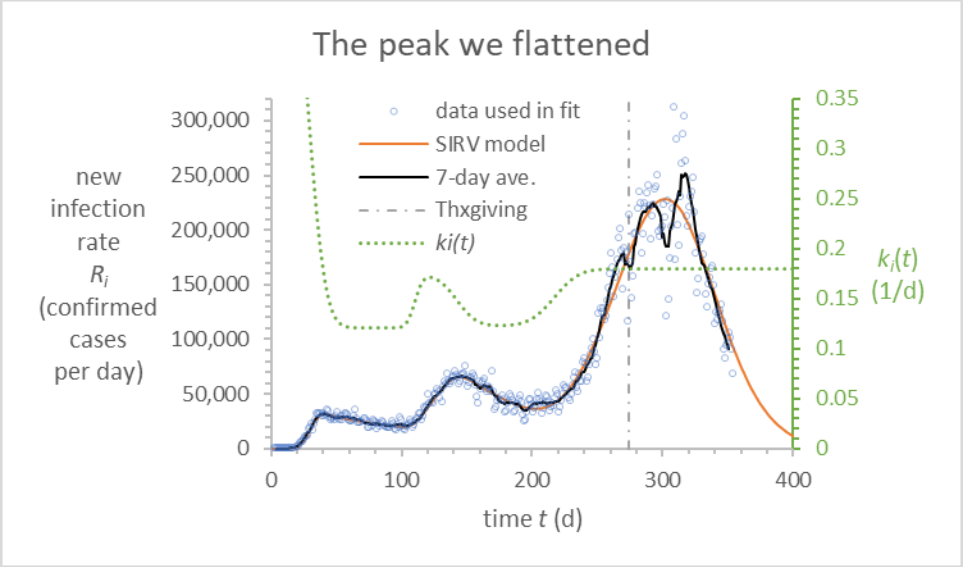


Fig.12.34 Excel chart showing US data and the predictions of the SIRV model. The blue circles show USA data reported as confirmed cases per day up to February 14, 2021. The jagged black line shows the centered 7-day moving average of the USA data. The solid orange line shows the SIRV model with a fitted model population of $q = 20.1\%$ of the actual population. Data source OWID [2022a].

Fig.12.34 shows your answer to Q.12.96(a). The general character of the fit is unchanged from Fig.13.34, but because we have now made the model population size an adjustable parameter and refitted to all the data including the 2020/2021 holiday period, the fitted model matches the

reported data more closely during the holiday period without changing the goodness of fit up to Thanksgiving Day. The value of the fitted model population, $q = 20.1\%$, is only 7% less than the CDC estimate of $q = 21.7\%$ and the value of k_5 is essentially unchanged (decreasing by just 0.01%).

While the three model peaks in Fig.12.33 have a somewhat similar appearance, it's important to note that the third peak in Fig.12.33 is qualitatively different from the first two peaks. The first peak is caused by a transition from uncontrolled spread ① to the first period of stricter social distancing (epoch ②) that prevented the exponential dragon peak in epoch ①. The second peak is similarly caused by a transition from relaxed social distancing (epoch ③) to a second period ④ of stricter social distancing that prevented the exponential dragon peak in epoch ③. In contrast, the third peak during the middle of epoch ⑤ of Fig.12.33 is simply the **exponential dragon** (Fig.12.12(b)) that's intrinsic to the SIR model with a *constant* infection rate coefficient throughout the peak. Thus, the success of the model in predicting the qualitative behavior of the spread of COVID-19 during the holiday period and the first month and a half of 2021 is a significant validation of the basic SIR model and it's SIRV variant.

At the beginning of the pandemic in the US, there was a lot of public discussion about **flattening the curve** (Fig.12.02 and Fig.12.10). It's important to note that the extended period of relaxed social distancing during epoch ⑤ really is the peak (exponential dragon) that we were trying to flatten. Hence, the correspondence between the SIRV model and the USA data during the third peak confirms what you predicted in Q.12.20(a) about flattening the curve in the SIR model. As you discovered in Q.12.96(d) the model peak in Fig.12.34 is actually about *30-times* lower than predicted by the same model ($R_i \approx 7.2 \times 10^6$ 1/d) if no social distancing measures had been taken. ❑

Open and inspect spreadsheet BPM.Ch12_Alpha.xlsx. It's an extension of the BPM.Ch12_Vaccinations.xlsx spreadsheet that you analyzed in Q.12.95. It now extends to May 31, 2021. I added three new parameters in the **Param$** column to model the sixth epoch of the COVID-19 pandemic in the US caused by further loosening of social distancing measures and renewed opposition to mask wearing. The spreadsheet includes new columns for F_{56} and p_{56}. I've included instructions for p_{56}. You'll compete the column for F_{56} in Q.12.97(b).

Q.12.97 DISCUSSION QUESTION **(a)** By generalizing equations (12.90), (12.92) and (12.91) *write out* algorithm instructions for F_{56}, k_i and p_{56}.
(b) In spreadsheet BPM.Ch12_Alpha.xlsx *confirm* that the equations for k_i, and p_{56} are implemented correctly then *complete* the **SIRV model table** by entering your instruction for F_{56}. Then *adjust* the values of the parameters k_6, t_{56}, and σ_{56} *by hand* to make the SIRV model match the exponential dragon for epoch ⑥. By monitoring the value of Q, determine the best-fit values of: k_6 to the nearest 2 significant figures; and the best-fit values of t_{56} and σ_{56} to the nearest day. *Record* your "by hand" estimates for k_6, t_{56}, and σ_{56} in the **LS fit parameters table** using **Copy** and **Paste Values** from cells **AE1:AM1**.

Note: In part (d) you'll be asked to record your **LS fit parameters table** for parts (b) through (d) as a single table in your Word.docx answer.

(c) Now use **Solver** to find the least-squares best-fit values of all of k_1, k_2, t_{12}, σ_{12}, k_3, t_{23}, σ_{23}, k_4, t_{34}, σ_{34}, k_5, t_{45}, σ_{45}, k_6, t_{56}, and σ_{56} (don't change the value of N or q) and *record* the best-fit values in your **LS fit parameters table**.

(d) Now use **Solver** to find the least-squares best-fit values of all of k_1, k_2, t_{12}, σ_{12}, k_3, t_{23}, σ_{23}, k_4, t_{34}, σ_{34}, k_5, t_{45}, σ_{45}, k_6, t_{56}, σ_{56}, and the model population size N. Don't forget to *save* this spreadsheet, you'll need it later. *Record* the **LS fit parameters table** of your answers to parts (b) – (d) in your Word doc answer. (You can copy and "paste as picture" into Word.)

(e) *Record* your graph of $R_i(t)$ together with the graph of $k_i(t)$ up to day $t = 500$ d.

(f) *Briefly discuss* what you can conclude from your fit.

About what you discovered: modeling the alpha variant

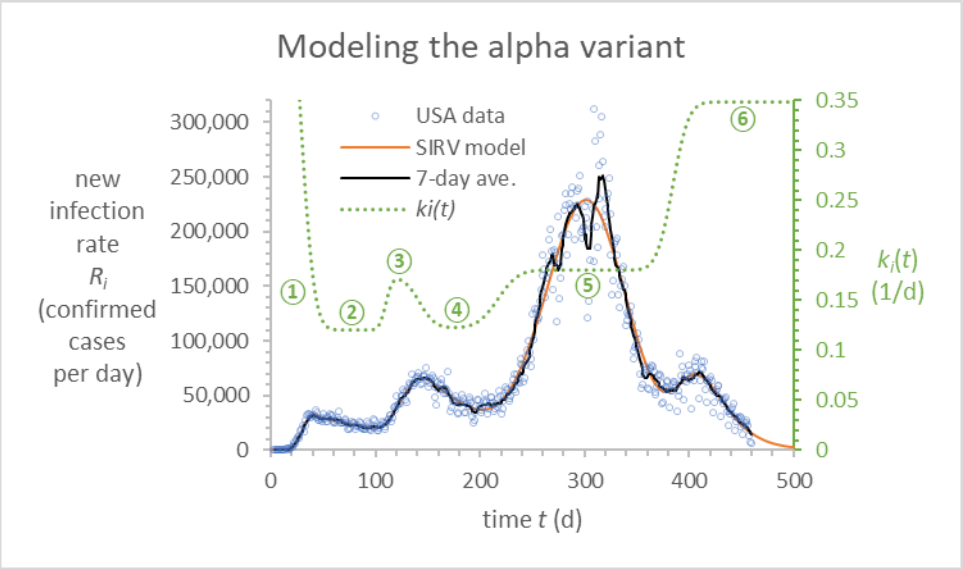


Fig.12.35 Excel chart showing USA data and the predictions of the SIRV model. The blue circles show USA data reported as confirmed cases per day up to May 31, 2021. The jagged black line shows the centered 7-day moving average of the USA data. The solid orange line shows the predictions of the SIRV model with a fitted model population of $q = 19.8\%$ of the actual population. The chart also shows the infection rate coefficient $k_i(t)$ as a function of time on the secondary vertical axis. Circled numbers indicate the epochs of the pandemic. Data source OWID [2022a].

Fig.12.35 shows your answer to Q.12.97(e). The SIRV model does an excellent job of modeling the pandemic up to May 31, 2021. It predicts that the pandemic was nearly over by May 31, 2021 (day 460). The fourth peak around day 406 (April 7, 2021), corresponds to an exponential dragon with an infection rate constant of $k_i = k_6 = 0.349$ 1/d. Hence, the herd immunity threshold for epoch ⑥ is $h_p = h_6 = 64\%$. The model population's immunity has increased to $h = 74.1\%$ by May 31, 2021, and the model predicts that pandemic is nearly over in the US – assuming that the infection rate constant stays constant at $k_i = k_6 = 0.349$ 1/d and that immunity is permanent.

The fact that the fit shown in Fig.12.35 has essentially the same value of $q \approx 20\%$ as the fit in Fig.12.34, provides strong support for the SIRV model and the hypothesis that q is approximately constant (at least up to May 31, 2021). The fitted value of $k_6 = 0.349\ \mathrm{d}^{-1}$, is nearly double k_3 and k_5 reflecting a significant further reduction in social distancing during epoch ⑥, although the infection rate constant is just over half of what it was during the uncontrolled spread in epoch ① with $k_1 = 0.60\ \mathrm{d}^{-1}$ at the beginning of the pandemic. The fact that the fourth peak in the pandemic is modeled as an exponential dragon with a single constant $k_i = k_6$ is a further significant validation of the SIRV model. ❑

12.10 Failure of the SIRV model – breakthrough infections and delta

The success of the SIRV model in explaining the fourth smaller peak in the pandemic (Fig.12.35) with a constant $k_i = k_6$ and a fitted value of $q \approx 20\%$ (the same as the rest of the pandemic), is a significant additional validation of the SIRV model. However, key predictions of the SIRV model have yet to be tested – particularly those that relate to the end of the pandemic. As we discovered (Fig.12.35), the SIRV model of the alpha variant with a final infection rate coefficient of $k_i = k_6 = 0.349\ \mathrm{d}^{-1}$ predicted that the pandemic was nearly over. However, as everyone in the US discovered, that prediction turned out to be incorrect for reasons that are now common knowledge (as of mid-February 2022).

The delta variant

Open and inspect spreadsheet BPM.Ch12_Delta_dragon.xlsx. It's an extension of the BPM.Ch12_Alpha.xlsx spreadsheet that you analyzed in Q.12.97. It now extends to August 12, 2021. I added three new parameters in the **Param$** column to model the seventh epoch of the COVID-19 pandemic in the US caused by further loosening of social distancing measures and the appearance of the delta variant of the SARS-CoV-2 virus. The spreadsheet includes new columns for F_{67} and p_{67}. I've included instructions for p_{67}. You'll compete the column for F_{67} in Q.12.98(b).

Q.12.98 **DISCUSSION QUESTION** **(a)** By generalizing equations (12.90), (12.92) and (12.91) *write out* algorithm instructions for F_{67}, k_i and p_{67}.
(b) In spreadsheet BPM.Ch12_Delta_dragon.xlsx *confirm* that the equations for k_i, and p_{67} are implemented correctly then *complete* the **SIRV model table** by entering your instruction for F_{67}. Then *adjust* the values of the parameters k_7, t_{67}, and σ_{67} *by hand* to make the SIRV model match the beginning of the exponential dragon for epoch ⑦. By monitoring the value of Q, determine the best-fit values of: k_7 to the nearest 2 significant figures; and the best-fit values of t_{67} and σ_{67} to the nearest day. *Record* your "by hand" estimates for k_7, t_{67}, and σ_{67} in the **LS fit parameters table** using **Copy** and **Paste Values** from cells **AG1:AP1**.
Note: In part (d) you'll be asked to record your **LS fit parameters table** for parts (b) through (d) as a single table in your Word.docx answer.

(c) Now use **Solver** to find the least-squares best-fit values of all of k_1, k_2, t_{12}, σ_{12}, k_3, t_{23}, σ_{23}, k_4, t_{34}, σ_{34}, k_5, t_{45}, σ_{45}, k_6, t_{56}, σ_{56}, k_7, t_{67}, and σ_{67} (don't change the value of N or q) and *record* the best-fit values in your **LS fit parameters table**.
(d) Finally, use **Solver** to find the least-squares best-fit values of all of k_1, k_2, t_{12}, σ_{12}, k_3, t_{23}, σ_{23}, k_4, t_{34}, σ_{34}, k_5, t_{45}, σ_{45}, k_6, t_{56}, σ_{56}, k_7, t_{67}, σ_{67}, and the model population size N. Don't forget to *save* this spreadsheet, you'll need it later. *Record* the **LS fit parameters table** of your answers to parts (b) – (d) in your Word doc answer. (You can copy and "paste as picture" into Word.)
(e) *Record* your graph of $R_i(t)$ together with the graph of $k_i(t)$ up to day $t = 600$ d.
(f) **DISCUSSION QUESTION** *Briefly discuss* what you can conclude from your fit.

As mentioned above, the seventh epoch of the pandemic coincides with the appearance of the delta variant in the US. During epoch ⑦, delta rapidly took over as the dominant variant and by August 9, 2021, delta accounted for more than 97% of the SARS-CoV-2 sequences in the US [OWID 2022c].

Q.12.99 **DISCUSSION QUESTION** **(a)** *Compare* your fitted value of k_7 with the fitted value of k_6, and
(b) *Briefly discuss* what you can conclude about the infectiousness of the delta variant compared with the alpha variant assuming that the level of social distancing was unchanged during epochs ⑥ and ⑦, that the fitted value of k_7 accurately represents the delta variant, and that the mean infectious time τ_i is the same for the delta variant.

About what you discovered: modeling the delta dragon

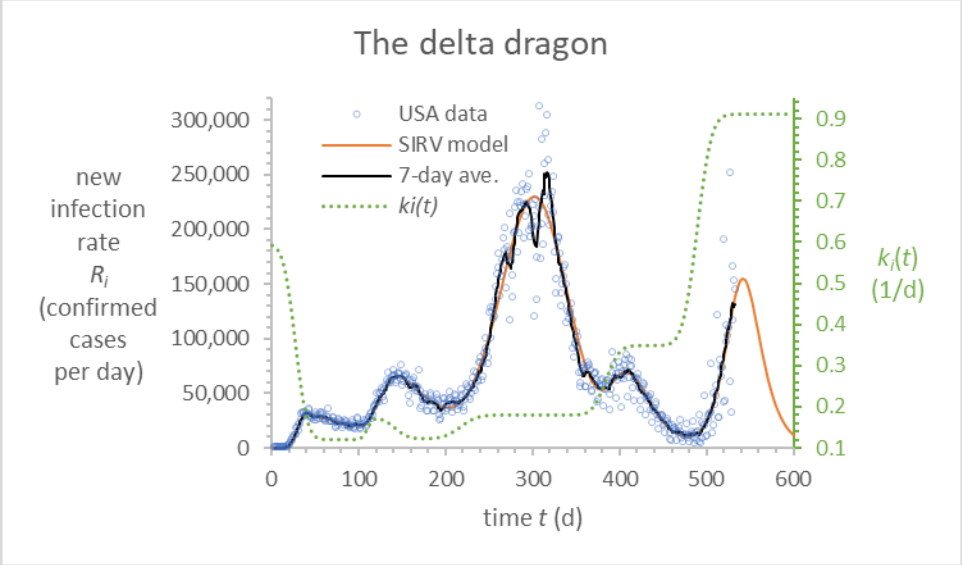


Fig.12.36 Excel chart showing USA data and the predictions of the SIRV model. The blue circles show USA data reported as confirmed cases per day up to August 12, 2021. The jagged black line shows the centered 7-day moving average of the USA data. The solid orange line shows the predictions of the SIRV model with a fitted model population of $q = 19.8\%$ of the actual population. The chart also shows the infection rate

coefficient $k_i(t)$ as a function of time on the secondary vertical axis. Day 600 corresponds to October 18, 2021. Data source OWID [2022a].

Fig.12.36 shows your answer to Q.12.98(e). As you discovered, the SIRV model can successfully explain the pandemic up to August 12, 2021. It predicts that the delta dragon should reach its peak at around day 541 (August 20, 2021). That peak corresponds to an exponential dragon with an infection rate constant of $k_i = k_7 = 0.913\ 1/\text{d}$. Hence, the predicted herd immunity threshold for epoch ⑦ is $h_p = h_7 = 86\%$. The model population's immunity has increased to $h = 82.4\%$ by August 12, 2021, and the model predicts that infection rate should soon begin to come down quite rapidly – assuming that the infection rate constant stays constant at $k_i = k_7 = 0.913\ 1/\text{d}$ and that immunity is permanent etc.

The fact that the fit shown in Fig.12.36 has essentially the same value of $q \approx 20\%$ as the fit in Fig.12.34 and Fig.12.35, provides strong support for the SIRV model and the hypothesis that q is approximately constant (at least up to August 12, 2021).

As shown in Fig.12.36, the fitted value of $k_7 = 0.913\ \text{d}^{-1}$, is substantially higher than the value at any other time during the pandemic. As you discussed in Q.12.99, The fitted infection rate constant for the delta variant ($k_i = k_7 = 0.913\ \text{d}^{-1}$) is ~2.6 times higher than the previous variants of the virus during epoch ⑥, which, if the level of social distancing is the same, would imply that the basic reproduction number for the delta variant could be as high as $\mathcal{R}_0 \approx 11$ in the absence of any social distancing measures. However, it's not clear that this interpretation is realistic because it fails to account for breakthrough infections – see below. ❑

Failure of the SIRV model

Open and inspect spreadsheet BPM.Ch12_Failure_of_SIRV.xlsx. It's an extension of the BPM.Ch12_Delta_dragon.xlsx spreadsheet that you analyzed in Q.12.98. In addition to the data up to August 12, 2021, it also includes additional USA data up to October 18, 2021, that have not yet been plotted. Our plan is to test the predictions of the SIRV model for the delta dragon. The solid orange line in the spreadsheet chart shows the predictions of the SIR model fitted up to August 12, 2021. It's important to note that it's the same fit that you made in Q.12.98 – you should check that your model parameters match those in the preformatted spreadsheet.

Q.12.100 DISCUSSION QUESTION (a) In the preformatted spreadsheet, use **Select Data…** to plot the unfitted data from August 13, 2021, up to October 18, 2021. You can do that by **Edit**ing the **unfitted data** series and *changing* the end point of the **Series X values** from **D538** to **D603** and *changing* the end point of the **Series Y values** from **T538** to **T603**. You should now see the unfitted data up to October 18, 2021, plotted as grey diamonds. Then use **Select Data…** to extend the 7-day average from August 13, 2021 up to October 18, 2021. You can do that by **Edit**ing the **7-day ave.** series by *changing* the end point of the **Series X values** from **D536** to **D603** and *changing* the end point of the **Series Y values** from **X536** to **X603**. *Record* your graph.

(b) *Briefly discuss* what you can conclude from the graph, i.e., how well does the SIRV model predict the unfitted data from August 13, 2021, up to October 18, 2021? Can you come up with an explanation for what you see in the graph?
Hint: Are there any basic assumptions of the SIRV model that turned out to be incorrect for the delta variant?

In Q.12.100 we tested the predictions of the SIRV model up to October 18, 2021, based on data only up to August 12, 2021. The prediction was not particularly accurate. We're now going to try redoing the fit to the SIRV model using all the USA data up to October 18, 2021, to see if the model does any better if we include the new data in the fit. Let's see what we can discover …

Q.12.101 **DISCUSSION QUESTION** *Extend* the **USA data** series to include all the data up to October 18, 2021 (**row 603**). Then remove the **unfitted data** series and the **Aug. 12, 2021** series. You should then extend the r and r^2 columns down to **row 603**. Check the formula for Q in cell **A57** and make sure that it calculates the sum of all the r^2 values up to October 18, 2021.
(a) Use **Solver** to find the least-squares best-fit values of k_7, t_{67}, and σ_{67} for the data up to October 18, 2021. *Record* your graph of $R_i(t)$ together with the graph of $k_i(t)$ up to day $t = 600$ d and *record* your "best fit" estimates for k_7, t_{67}, and σ_{67} in the **LS fit parameters table** using **Copy** and **Paste Values** from cells **AG1:AP1**.
Note: In part (d) you'll be asked to record your **LS fit parameters table** for parts (a) through (c) as a single table in your Word.docx answer.
(b) Now use **Solver** to find the least-squares best-fit values of all of k_1, k_2, t_{12}, σ_{12}, k_3, t_{23}, σ_{23}, k_4, t_{34}, σ_{34}, k_5, t_{45}, σ_{45}, k_6, t_{56}, σ_{56}, k_7, t_{67}, and σ_{67} (don't change the value of N or q) and *record* the best-fit values in your **LS fit parameters table**.
(c) Finally, use **Solver** to find the least-squares best-fit values of all of k_1, k_2, $t_{12}, \sigma_{12}, k_3, t_{23}, \sigma_{23}$, k_4, t_{34}, σ_{34}, k_5, t_{45}, σ_{45}, k_6, t_{56}, σ_{56}, k_7, t_{67}, σ_{67} and the model population size N. *Record* the **LS fit parameters table** of your answers to parts (a) – (c) in your Word doc answer. (You can copy and "paste as picture" into Word.)
(d) *Record* your graph from part (c) of $R_i(t)$ together with the graph of $k_i(t)$ up to day $t = 600$ d.
(e) *Briefly discuss* what happened to the fit when you fitted k_7, t_{67}, and σ_{67} in part (a), and how that fit changed as you redid the fit in parts (b) and (c).
(f) **DISCUSSION QUESTION** *Briefly discuss* what you can conclude from your fits.

About what you discovered: failure of the SIRV model

Fig.12.37(a) shows your answer to Q.12.100(a). As you discovered, the SIRV model prediction successfully predicts that peak will occur soon after August 12, 2021. It also successfully predicts the approximate height of the peak, but the actual values almost immediately diverge from the predicted values. The predicted peak is too narrow, too symmetrical, and occurs too soon. These differences might be explained, in part, by **breakthrough infections** that were reported to occur

during August, September and October 2021, when recovered or vaccinated people were infected with the delta variant – a phenomenon that's not part of the SIRV model of Fig.12.32.

Breakthrough infections

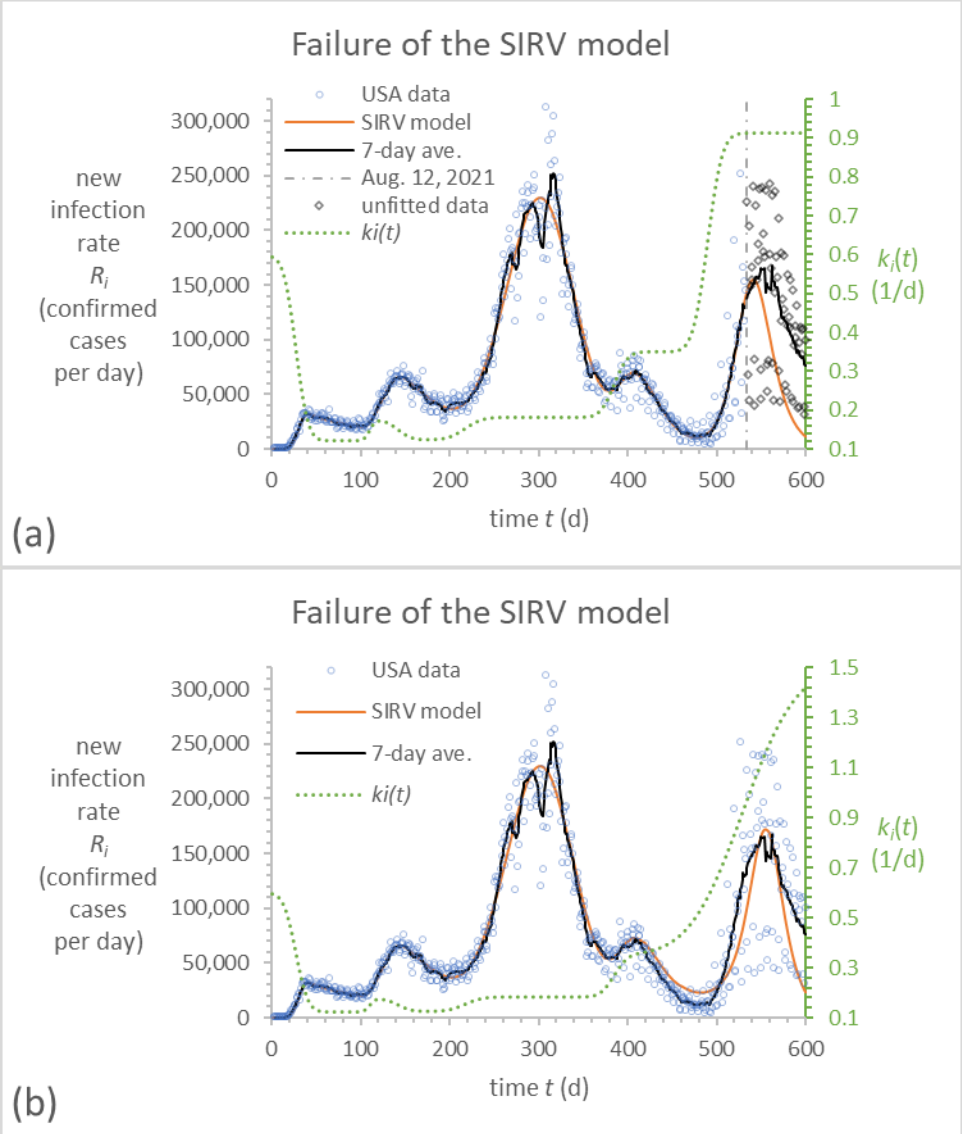


Fig.12.37 Excel charts showing USA data and the predictions of the SIRV model with a fitted model population of $q = 19.8\%$ of the actual population. The jagged black line shows the centered 7-day moving average of the USA data. The infection rate coefficient $k_i(t)$ is shown as a function of time on the secondary vertical axis. **(a)** The blue circles show data up to August 12, 2021, that were used for the fit and the grey diamonds show additional data up to October 18, 2021, that were *not* used in the fit. **(b)** A refit of the SIRV model to all the data up to October 18, 2021, allowing only k_7, t_{67}, and σ_{67} to be adjusted in the LS fit. Day 600 corresponds to October 18, 2021. Data source OWID [2022a].

Fig.12.37(b) shows your answer to Q.12.101(a). The fit to k_7, t_{67}, and σ_{67} in part (a) makes the SIRV model fit the delta peak better. It centers the peak at approximately the correct time. The peak is wider, but it's still narrower than the observed peak and the predicted delta peak is still

too symmetrical. The fit prior to the delta peak is now compromised as the dip between the fourth and fifth peaks is now not deep enough. A simple explanation for all of that is provided by the immune fraction h and the herd immunity threshold h_p. For the fit in Fig.12.37(a) $h_p = 86.3\%$. For the fit in Fig.12.37(b) $h_p = 91.7\%$. The increase in h_p in the refitted model reflects an increased infection rate constant for delta, from $k_7 = 0.910\ \mathrm{d}^{-1}$ to $k_7 = 1.50\ \mathrm{d}^{-1}$. Increasing k_7 is the only way that the fitted SIRV model can increase the width and the height of the delta peak to account for the extra previously unpredicted breakthrough infections, but the cost is that the fit to the fourth peak and the transition to the fifth peak are now compromised. Our conclusion is that the SIRV model simply cannot model the entire pandemic – if we want to include the delta peak up to October 18, 2021.

As you discovered in Q.12.101(b), adding k_1, k_2, t_{12}, σ_{12}, k_3, t_{23}, σ_{23}, k_4, t_{34}, σ_{34}, k_5, t_{45}, σ_{45}, k_6, t_{56}, σ_{56} makes the fit to the delta peak only slightly better at the expense of the quality of the fit to the fourth peak. Adding N to the fitted parameters increases the fitted model population to $q \approx 23\%$. This further improves the fit to the delta peak by increasing its width, but the fit to the third peak is degraded making the fitted third model peak too wide. The improvement to the delta peak is explained by there being more susceptible people left in the model population so that there can be more infections during the delta peak. This supports our conclusion that the SIRV model cannot account for the delta peak shown in Fig.12.37. Unfortunately, further development of the model to account for breakthrough infections is beyond the scope of this chapter.

Problems with the fitted k_i for delta

In addition to the problems noted above for $R_i(t)$, there are also problems with the value of k_7 in the fits. In the fit of Fig.12.37(a), $k_7 = 0.91\ \mathrm{d}^{-1}$ for the delta variant, which is 53% higher than the fitted value of $k_1 = 0.60\ \mathrm{d}^{-1}$ for the original alpha variant with no social distancing or mask wearing etc. Hence, that high number for k_7 should raise a concern about whether the SIRV model (with no breakthrough infections) is still applicable. Either that or the delta variant really is 50% more transmissible than the original alpha variant.

The fitted value for $k_7 = 1.5\ \mathrm{d}^{-1}$ for the delta variant in Fig.12.37(b), is 150% higher than $k_1 = 0.60\ \mathrm{d}^{-1}$, which seems implausibly high. That conclusion is also supported by the ever-increasing shape if $k_i(t)$ during the delta peak in Fig.12.37(b), which seems improbable within the SIRV model, but does support the idea of breakthrough infections caused by the new delta variant becoming more and more common at that time.

Convergence problems with Solver

When I was first working on the fits for Fig.12.37, I tried to short-cut our usual procedure … I attempted to fit all of our usual model parameters (except N) for the extra data. That didn't work. Excel's **Solver** failed to find a solution. The error message from **Solver** (2021) was "**Solver encountered an error value in the Objective Cell or a Constraint cell.**" with an additional explanation of "One of the cells in the worksheet became an error value when Solver tried certain values for the Variable Cells." In this case, **Solver** tried to make σ_{56} a negative value and that gave an error

for F_{56} as negative values for σ_{56} in **NORM.DIST()** are not allowed and return **#NUM!** (this error occurred even though I had checked **[✓] Make Unconstrained Variables Non-Negative**). As mentioned previously, you should recall the "puddles in the parking lot" that we talked about in **CHAPTER 9**. Errors can occur when a puddle drains into a zero-value drain. The solution is to try different starting points for solver or to use a more systematic approach like we did in Q.12.101. ❑

Q.12.102 **RESEARCH QUESTION** *Investigate and compare* the **SEIR model** with the **SIR model**.
Note: The SEIR model is discussed in the "America unmasked – the exponential dragon returns" AWYD after Q.12.83.

Conclusion – about what you discovered

Congratulations! If you made it here, then you've successfully learned how to apply our FD method from **CHAPTER 3** to simple epidemiological models of COVID-19 in the United States. As we discovered, these models can do a surprisingly good job of modeling the daily infection rate $R_i(t)$. Along the way, we gained a different perspective on kinetic models and rate constants by applying them to the behavior of people. While people don't jiggle around like molecules in solution, they do have interactions with others at a rate that can be successfully modeled using the FD techniques we first developed in **CHAPTER 3**.

We started with the simplest-possible **unlimited growth** (**UG**) **model**. It predicted unconstrained exponential growth because the infection rate $R_i = k_i N_i$ was directly proportional to the number already infectious N_i. It's another example of **proportional change** (**CHAPTER 3**). While this model isn't realistic in the long run, we were able use least-squares fits to show that it successfully predicted the initial exponential growth of reported COVID-19 cases in the US during the first 19 days of the outbreak in the US (epoch ①).

We then modified the infection rate to be $R_i = k_i N_i s$, where $s = N_s/N$ is the fraction of people that an infectious person interacts with that are still susceptible – because they haven't been infected yet. The resulting **finite population** (**FP**) **model** accounts for the finite size of the model population and leads to classic **logistic growth** and can be used to show the effect of social distancing by changing the infection rate constant k_i.

We discovered that adding recovery to the FP model leads directly to the **susceptible-infected-recovered model** (**SIR model**). The infection rate $R_i = k_i N_i s$ is the same as the FP model and recovery is modeled as a simple first-order elimination process with rate $R_r = k_r N_i$ that's analogous to first-order drug elimination (**CHAPTER 4**). As we discovered, adding recovery makes the resulting SIR model much more realistic. We spent the rest of the chapter investigating the predictions of the SIR model and comparing them with published data for the United States.

The SIR model is the origin of the epidemiological parameter $\mathcal{R}_0$. For $\mathcal{R}_0 > 1$, the SIR model always predicts that the infection rate curve, $R_i(t)$ will have a characteristic peaked shape – the **exponential dragon**. A simple algebraic analysis allowed us to show that the SIR model predicts that the fraction susceptible s_p at the peak in N_i is given by

$$s_p = \frac{k_r}{k_i} = \frac{1}{\mathcal{R}_0} \tag{12.27}$$

where $\mathcal{R}_0 \equiv k_i \tau_i = k_i / k_r$ is the **basic reproduction number** and $\tau_i = 1/k_r$ is the **mean infectious time**. We also discovered that "herd immunity" is reached when the fraction immune $h = 1 - s$ reaches the **herd immunity threshold**

$$h_p = 1 - s_p = 1 - \frac{1}{\mathcal{R}_0} \tag{12.33}$$

In an optional calculus section, we were able to show that the **final fraction susceptible** s_∞ is predicted by

$$\mathcal{R}_0(1 - s_\infty) + \ln s_\infty \approx 0 \tag{12.47}$$

Equation (12.47) is an implicit equation that predicts the fraction of susceptible people s_∞ that aren't infected at the end of the pandemic ($t \to \infty$) assuming that the infection rate coefficient k_i is constant throughout the epidemic. It provides support for Espe's claim in the introduction – that not all people need be infected in a pandemic because s_∞ is not zero for finite values of $\mathcal{R}_0$.

The initial public health response to the pandemic in the US was to recommend/mandate social distancing. Various cities, counties and states implemented lockdowns or "safer-at-home" measures. In a short while, the public learned that mask wearing was also an effective weapon in fighting the spread of the virus. In section 12.5, we discovered that we could model the initial period of stricter social distancing (epoch ②) by changing the infection rate constant k_i. Later, we discovered that we could make k_i a variable **infection rate coefficient**, so that the change from the initial exponential growth to the period of exponential decay following the peak in the spring surge could be modeled using a **Gaussian transition function** that could be implemented in Excel using the **NORM.DIST** function. We subsequently confirmed that later changes between stricter and more relaxed social distancing could also be modeled with Gaussian transition functions between epochs.

Detailed analysis of the initial period of stricter social distancing (epoch ②) led us to discover a simple method for determining the decay rate constant $k_d = k_r - k_i s$, which allowed us to characterize the exponential decay with a **half-life** $t_{½}$. Similar analysis allowed us to characterize periods of exponential growth with a growth rate constant, k_g or k_u, and a **doubling time** t_d. We were also able to discover a correlation between the death rate with the infection rate using a correlation function that used a **scaling factor** m_r and a **time shift** t_m. Using those correlations,

we were able to estimate that 60,000+ lives were lost because the rest of the US failed to follow NYC's lead in the time leading up to Memorial Day (May 25, 2020). In **APPENDIX 12.A**, we discovered a way to account for some of the discrete-time errors caused by the timestep being too big ($\delta t = 1$ d) during the initial exponential growth period.

Even though the approach uses only introductory methods, the modeling approach is remarkably successful in modeling the spread of COVID-19 in the US. Because of its simplicity, the model also provides surprising insights into the spread of the virus. Notably, after the initial exponential outbreak (epoch ①) the behavior of the US population up to February 14, 2021, can be separated into two categories – **stricter social distancing** and **relaxed social distancing**. Epochs ② and ④ of the model in Fig.12.33(a) correspond to stricter social distancing with $k_2 \approx k_4 = 0.122 \pm 0.001$ d^{-1} and epochs ③ and ⑤ of the model correspond to more relaxed social distancing with $k_3 \approx k_5 = 0.176 \pm 0.006$ d^{-1}. Hence, the inception of both the summer and fall surges can be explained by a relatively modest 30% increase in the infection rate coefficient k_i.

We were able to model vaccinations in the US by adding a fourth box v to the model. The form of the resulting SIRV model (Fig.12.32) was chosen to match the vaccination program in the United States. COVID-19 tests were not a prerequisite for vaccination. Hence, the status of individuals receiving vaccinations is not included in the data. As a result, the SIRV model assumes that vaccinations were administered to anyone in the population that was asymptomatic at the time. That assumption is reflected in equation (12.100) and the corresponding equations for $R_{v,i}^{\text{new}}$, and $R_{v,r}^{\text{new}}$, so that the rate of vaccination of individuals in each of boxes s, i, and r is directly proportional to the numbers currently in each respective box. This assumption overestimates the vaccination rate of people in box i (because symptomatic individuals were not supposed to be vaccinated) and underestimates vaccinations of individuals in boxes s and r. The model does not consider partially vaccinated individuals. Recall, $N_v^{\star\text{new}}$ is the reported number of *fully vaccinated* individuals.

It was a bold assertion that the under-reporting of positive cases can be accounted for by a single parameter $q \equiv N/N^{\star}$, where N is the model population size and $N^{\star} \approx 3.3 \times 10^8$ is the estimated actual population of the United States. The use of a single q from the beginning of the pandemic through May 31, 2021, cannot be supported by direct measurement of actual infections – those data are simply not available. The best estimate I was able to find was published by the CDC (2021b), but their estimates have changed over time. From a modeling perspective, the assumption that q is a constant throughout the pandemic can only be justified *a posteriori* as it was in Fig.12.35 because the model was consistent with the published cases-per-day data up to May 31, 2021.

The simplest way to interpret q is that it's the percentage of actual infections that appear in the reported data. Using that as a measure of what's happening in the actual population assumes that those outside of the model population – spread COVID-19, are infected by COVID-19, recover from COVID-19, and are vaccinated – in a similar manner to those in the model population. This

implies that individuals in the model population are mixed in with the rest of the actual population and that the rate of reported cases is proportional to the rate of actual cases.

While the first three model peaks in Fig.12.33 have a somewhat similar appearance, it's important to note that the third peak in Fig.12.33 is qualitatively different from the first two peaks. The first peak is caused by a transition from uncontrolled spread ① to the first period of stricter social distancing (epoch ②) that prevented the exponential dragon peak in epoch ①. The second peak is similarly caused by a transition from relaxed social distancing (epoch ③) to a second period ④ of stricter social distancing that prevented the exponential dragon peak in epoch ③. In contrast, the third peak during the middle of epoch ⑤ of Fig.12.33 is simply the **exponential dragon** (Fig.12.12(b)) that's intrinsic to the SIR model with a *constant* infection rate coefficient throughout the peak. Thus, the success of the model in predicting the qualitative behavior of the spread of COVID-19 during the holiday period and the first month and a half of 2021 is a significant validation of the basic SIR model and it's SIRV variant.

The fourth peak in the fitted SIRV model in epoch ⑥ is also the exponential dragon that's intrinsic to the SIRV model with a constant infection rate coefficient $k_i = k_6 = 0.349\ \mathrm{d}^{-1}$ that represents a further relaxation of social distancing measures in early March 2021. The fact that the fit shown in Fig.12.35 has essentially the same value of q as the fit in Fig.12.33 and Fig.12.34, provides strong support for the SIRV model and the hypothesis that q is approximately constant (at least up to the beginning of the delta epoch ⑦). The fitted value of $k_6 = 0.349\ \mathrm{d}^{-1}$, is about double $k_3 \approx k_5 = 0.18\ \mathrm{d}^{-1}$ reflecting a significant further reduction in social distancing during epoch ⑥, although the infection rate constant is just over double what it was during the uncontrolled spread in epoch ① with $k_1 = 0.60\ \mathrm{d}^{-1}$ at the beginning of the pandemic.

The fifth peak in the pandemic corresponded to the emergence of the delta variant of the SARS-CoV-2 virus. The SIRV model predicted that the delta dragon during epoch ⑦ would be a narrow peak that quickly decayed down to low infection rates because the virus would simply run out of people to infect (Fig.12.36). That was the prediction made in an article written at the beginning of the delta peak [Nelson 2021]. However, with the benefit of hindsight, we discovered in this **WEB EDITION** of **CHAPTER 12** that the SIRV model failed to correctly predict the rate of infection during the delta surge (Fig.12.37) because of **breakthrough infections** that occurred during and after August 2021, when recovered or vaccinated people were infected with the delta variant. These breakthrough infections are not part of the SIRV model of Fig.12.32. The net effect was that more infections occurred than were possible according to the SIRV model where immunity (of any kind) was assumed to be permanent. Hence, we concluded that the SIRV model could not be used to model the pandemic after May 31, 2021.

For me, this **CHAPTER 12** started out with a question – could the methods we've developed based on the marble game be successfully applied to modeling the spread of COVID-19? The answer was much better than I had hoped. This **CHAPTER 12** now serves as a capstone to the molecular modeling approach presented in this book. It illustrates how the approach and methods first

developed with the marble game can be extended from the molecular realm to viruses and the world of human behavior. As I worked on this unexpected chapter, I was repeatedly surprised by how relevant nearly all the ideas we've developed in this book are to epidemiology. As we discovered, people aren't molecules … but sometimes they behave like them.

12.A Appendix – The discrete-time SIR model

Penn-CHIME

This appendix talks about a model that I came across in early April 2020 that posed a modeling puzzle for me that took a few days to solve. Strictly speaking, this section isn't needed to follow the flow of most of the chapter, but I think you might find it interesting – I know I did.

The Penn-CHIME model was developed by Penn Medicine's Predictive Healthcare Team to help hospitals and public health officials with hospital capacity planning. The Penn-CHIME model is similar to the FD SIR model that we developed in this chapter. Fig.12.A shows a comparison between the Penn-CHIME model and our FD SIR model. As you can see, they do match, but it took me a while to figure out how to make that happen. Let's see what *you* can discover …

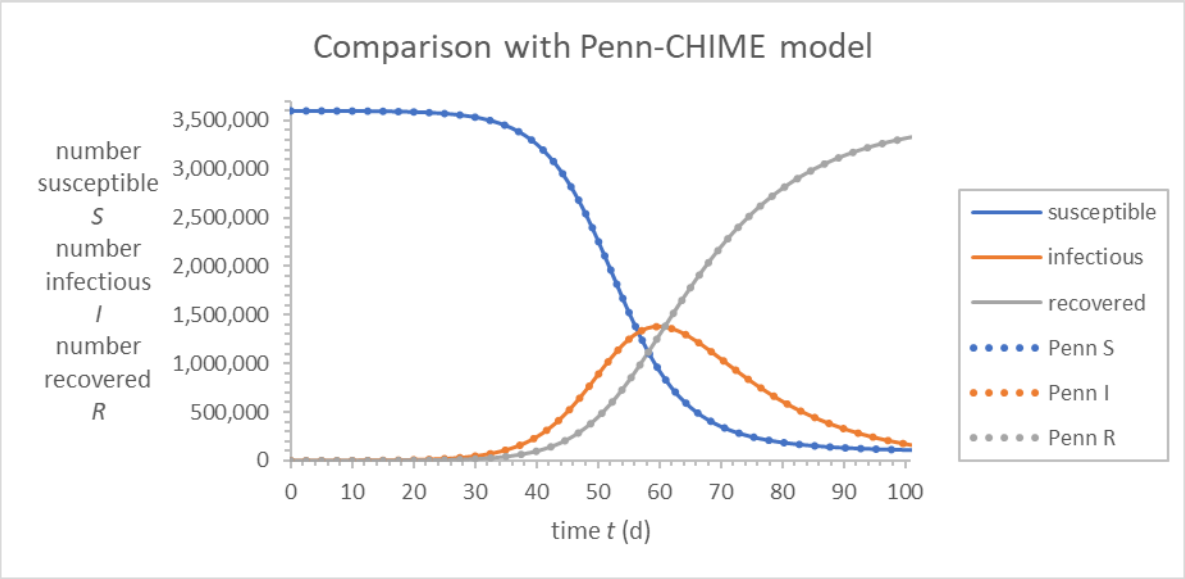


Fig.12.A Excel chart showing the predictions of the Penn-CHIME discrete-time SIR model and the corresponding spreadsheet SIR model developed in this chapter. Solid lines are our SIR model and dotted lines are the corresponding Penn-CHIME model. The parameters for both models are $N = 3{,}600{,}000$, $\delta t = 1$ d, $\tau_i = 14$ d, $t_d = 4$ d, $N_0 = 267$ and $k_i = 0.261$ d^{-1}.

In my initial comparison between our FD SIR model and the Penn-CHIME model, I could not make the two models match exactly. There was always a small-but-significant difference between them. As a modeler, that made me very frustrated. The same models should make the same predictions! The only equation that seemed to be different in the Penn-CHIME model is equation (12.A.1), which relates their initial **growth rate parameter** g to the doubling time t_d for the initial exponential growth

$$g = 2^{1/t_d} - 1 \tag{12.A.1}$$

This equation confused me when I first saw it, because it doesn't match our equation (12.7) for the doubling time, which can be rearranged as

$$k_u = \frac{\ln 2}{t_d} \tag{12.A.2}$$

There's no way that equation (12.A.1) for g can be rearranged to give equation (12.A.2) for k_u. Believe me, I tried – repeatedly – to make it happen, but no joy!

Okay, this might be another example of me being a bit slow, but it didn't occur to me that the Penn-CHIME model wasn't the same as our SIR model. The Jones [2007] paper that I referenced before, used basically the same notation as the Penn-CHIME model and the Jones SIR model is – as far as I can tell – mathematically equivalent to our SIR model. However, I failed to notice a key difference – that maybe you'll notice … The Penn-CHIME model (when translated into our algorithm notation) includes the following instruction for updating the number infectious

$$N_i^{\text{new}} = N_i^{\text{old}} + \beta * N_i^{\text{old}} * N_s^{\text{old}} - \gamma * N_i^{\text{old}} \tag{12.A.3}$$

Q.12.A.1 **DISCUSSION QUESTION** By mathematically comparing equation (12.A.3) with our equivalent equation (12.21) (with equations (12.12), (12.20) substituted in), *briefly explain* what needs to be true for our FD SIR model to be mathematically equivalent to the Penn-CHIME model.
Hint: Your answer should be two very simple equations relating the Penn-CHIME model parameters β and γ to the model parameters included in your algorithm for Q.12.18(c).

About what you discovered: discrete-time *vs* continuous-time models

As you discovered in Q.12.A.1, Penn-CHIME equation (12.A.3) is the same as our FD SIR model if

$$\beta = \frac{k_i}{N}\delta t \tag{12.A.4}$$

and

$$\gamma = k_r \delta t \tag{12.A.5}$$

Using equation (12.A.4) is mathematically correct, but in this book, we've been careful since **CHAPTER 2** to make sure that all our rate constants, e.g., $k_{\text{something}}$, don't depend on the size N of the system. For example, the jump rate constant k in the original marble game doesn't depend on the total number of marbles $N = N_1 + N_2$ in the game. Similarly, the association and dissociation rate constants k_a and k_d in our blood plasma oxygenation model didn't depend on the number of oxygen molecules, and our drug elimination rate constant k_e didn't depend on the number of drug molecules. The same is true for all of the marble game's myriad derivatives in

CHAPTERS 2-11 and the infection and recovery rate constants k_i and k_r in our UG, FP and SIR models. Unlike β in equation (12.A.4) they don't depend on the model population size N.

One aspect of Penn-CHIME equation (12.A.3) that you might not have realized – I didn't see it either – is that the **discrete-time** approach used in equation (12.A.3) implicitly assumes that the timestep is exactly

$$\delta t = 1 \text{ d} \tag{12.A.6}$$

Using a timestep of $\delta t = 1$ day makes sense for the Penn-CHIME model, because the data reported by government agencies are usually aggregated as daily counts, e.g., "new confirmed cases per day" as shown in Fig.12.07 etc.

However, unlike the **discrete-time** Penn-CHIME model, the approach taken in this book is a **continuous-time** approach. The FD methodology we first developed in **CHAPTER 3** is explicitly aimed at treating time as a continuous variable. As we've discovered over and over in our FD models, the timestep δt is a **freely adjustable parameter** that must be made sufficiently small – to ensure that our FD model doesn't depend on our choice for δt. In contrast, the Penn-CHIME model only works with $\delta t = 1$ d, i.e., equation (12.A.1) is only true if the timestep is exactly $\delta t = 1$ d. Let's see what we can discover … ❑

Okay, so now that we've discovered what the difference is between our continuous-time FD model and the discrete-time Penn-CHIME model, let's see if we can discover why equation (12.A.1) is different from our equation (12.A.2) and if the two equations can be made equivalent.

Q.12.A.2 DISCUSSION QUESTION At the beginning of the outbreak, the number susceptible $N_s \approx N$ and the fraction susceptible $s \approx 1$ and the SIR model can be approximated by the UG model. Hence, the change δN_i in the number infectious can be written as

$$\delta N_i = k_u N_i \delta t \tag{12.A.7}$$

which is the same as equation (12.49) with $k_g = k_u$ given by equation (12.57). Let's define the **dimensionless growth parameter** as

$$g \equiv k_u \delta t \tag{12.A.8}$$

and the timestep as $\delta t = 1$ d (12.A.6).

(a) By substituting equation (12.A.8) into equation (12.A.7) and then substituting the result into the **FD update equation** (3.31) for N_i, *show that* the ensemble average number infectious on day 1 according to the SIR model is

$$I_1 = (1 + g) I_0 \tag{12.A.9}$$

where I_0 is the number infectious (N_i) on day 0 of the model and I_1 is the number infectious on day 1, i.e., $N_i^{\text{old}} = I_0$ and $N_i^{\text{new}} = I_1$;
(b) then *show that* number infectious on day 2 is

$$I_2 = (1+g)I_1 = (1+g)^2 I_0 \tag{12.A.10}$$

and on day 3

$$I_3 = (1+g)I_2 = (1+g)^3 I_0 \tag{12.A.11}$$

Noting the pattern in equations (12.A.10) and (12.A.11), I think it's easy to see that the general formula for day t is

$$I_t = (1+g)^t I_0 \tag{12.A.12}$$

Q.12.A.3 **MATH QUESTION** Formally **prove** equation (12.A.12) **by induction**.

Q.12.A.4 When we reach the doubling time $t = t_d$, the number infectious has doubled so that

$$I_{t_d} = 2I_0 \tag{12.A.13}$$

(a) By substituting $t = t_d$ into equation (12.A.12), and then equating the result with equation (12.A.13) *show that*

$$I_{t_d} = (1+g)^{t_d} I_0 = 2I_0 \tag{12.A.14}$$

so that

$$(1+g)^{t_d} = 2 \tag{12.A.15}$$

(b) By rearranging equation (12.A.15), *show that*

$$g = 2^{1/t_d} - 1 \tag{12.A.1}$$

which is the equation we were trying to derive.
Hint: For exponents we know that $(a^x)^{1/x} = a$.

Now that we understand how equation (12.A.1) fits into the discrete-time SIR model, let's see if we can use the same approach for our continuous-time FD model. In our FD approach, the timestep δt is a **free parameter** that should be made as small as necessary to make the solution independent of the size of the timestep δt (**CHAPTER 3**). The implication is that the growth parameter g – as defined by equation (12.A.8) – is a **computed parameter** (not a constant) in our continuous time FD model. The question you should now be asking is – can we use the same approach we followed in Q.12.A.2 – Q.12.A.4 to derive UG equation (12.A.2)? If we can, then we've resolved the puzzle of how the discrete-time SIR model relates to our continuous-time SIR model. Let's see what we can discover …

Q.12.A.5 **DISCUSSION QUESTION** **(a)** Using FD equation (12.A.7) the definition of g (12.A.8) and the **FD update equation** (3.31) for N_i *show that* the ensemble average number infectious after step 1 is according to the continuous-time SIR model is

$$I_1 = (1 + g)I_0 \tag{12.A.9}$$

which is the same equation (12.A.9) that we derived in Q.12.A.2, but now I_1 means the number infectious after step 1 rather than on day 1.
(b) then *show that* number infectious after step 2 is

$$I_2 = (1 + g)^2 I_0 \tag{12.A.10}$$

and that after step n

$$I_n = (1 + g)^n I_0 \tag{12.A.16}$$

Q.12.A.6 **DISCUSSION QUESTION** When we reach the doubling time $t = t_d$, the number infectious has doubled so that

$$I_{t_d} = 2I_0 \tag{12.A.13}$$

(a) By substituting $n = n_d$ into equation (12.A.16), where n_d is the number of steps required to reach the doubling time t_d, which in turn is given by

$$t_d = n_d \delta t \tag{12.A.17}$$

Then equating that result with equation (12.A.13), *show that*

$$I_{n_d} = (1 + g)^{n_d} I_0 = 2I_0 \tag{12.A.18}$$

so that

$$(1 + g)^{n_d} = 2 \tag{12.A.19}$$

(b) By rearranging equation (12.A.19), *show that*

$$g = 2^{1/n_d} - 1 \tag{12.A.20}$$

which is *not* what we were trying to show! … but it does look like equation (12.A.1).

As you noticed, equation (12.A.20) is of the same form as equation (12.A.1), but with the doubling time t_d replaced with n_d, the number of steps required to reach t_d. However, want we really want to show is that equation (12.A.20) is equivalent to UG equation (12.A.2). In order to do that, we'll need to resort to a math trick that's similar to one that we used in **CHAPTER 9** and **CHAPTER 11**. If you like a mathematical **CHALLENGE**, see if you can get from equation (12.A.20) to equation (12.A.2) on your own. If you get stuck, the following questions will provide you with an outline of how to get there.

Q.12.A.7 Using the mathematical identity $2^x = e^{x \ln 2}$, *show that* equation (12.A.20) can be rearranged to give

$$1 + g = e^{(1/n_d) \ln 2} \tag{12.A.21}$$

so that taking the natural log of both sides yields

$$\ln(1 + g) = \frac{1}{n_d} \ln 2 \tag{12.A.22}$$

Q.12.A.8 **DISCUSSION QUESTION** **(a)** Using the **logarithmic series**

$$\ln(1 + x) = x - \frac{x^2}{2} + \frac{x^3}{3} - \frac{x^4}{4} + \cdots \tag{12.A.23}$$

with $x = g$, *show that*

$$\ln(1 + g) \approx g \tag{12.A.24}$$

for $g \ll 1$.

(b) Hence, by substituting equations (12.A.8), (12.A.24) and (12.A.17) into equation (12.A.22) *show that* equation (12.A.22) becomes

$$k_u = \frac{\ln 2}{t_d} \tag{12.A.2}$$

which is equivalent to our UG model equation (12.7) or (12.A.2) when $g = k_u \delta t \ll 1$, which is the same limit as when $\delta t \to 0$, which in turn is the limit in which our FD model becomes independent of the timestep δt (**CHAPTER 3**).

Note: The criterion that $k_u \delta t \ll 1$ explains why we can use a larger δt values when k_u is small – because it's the product $k_u \delta t$ that has to be small for the continuous-time approximation implied by equation (12.A.2) to be valid.

About what you discovered: our FD SIR model is the continuous-time equivalent of the discrete-time Penn-CHIME model

Phew! That took a while, but the result is that we now know precisely how our continuous-time SIR model relates to the discrete-time SIR model used in Penn-CHIME. Even though this mathematical detour took us a while, and the scenery was rather dry and mathematical, it's important that we look back and recognize the overall importance of what we discovered. Namely that there is another closely related way of implementing the SIR model that gives almost the same results, especially when the growth rate constant k_u (or k_g) is small ($k_u \ll 1\ \mathrm{d}^{-1}$) or the decay rate constant is small $k_d \ll 1\ \mathrm{d}^{-1}$.

As I discovered in late June 2020, discrete-time equation (12.A.1) also turns out to be useful if we want to model the entire course of the outbreak using a timestep of $\delta t = 1$ d, which is too big for our continuous-time analysis during the initial exponential growth period. See the beginning of **SECTION 12.6**. Return to Section 12.6. ❑

Summary: COVID-19 and epidemiology

Key epidemiological concepts

Unlimited growth model

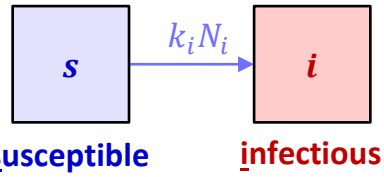


Fig.12.03 FD diagram of a two-box epidemiological model. The two boxes in this **unlimited growth** (**UG**) **model** represent the two parts of the model population. Box s represents people that are susceptible to the disease. Box i represents people that are infectious. (Repeated from main text).

- In the simplest possible **unlimited growth** (**UG**) **model**, the model population is split into two categories (boxes) **susceptible** and **infectious**.
- N_i is the **number infectious** and k_i is the **infection rate constant**
- The **infection rate** R_i [=] d^{-1} is given by

$$R_i = k_i N_i \tag{12.1}$$

- In an optional calculus question, we showed that the analytical solution for R_i according to the UG model is

$$R_i = k_i N_0 e^{k_i t} \quad \text{or} \quad R_i = k_u N_u e^{k_u t} \tag{12.6)(12.56}$$

- The model's predictions for R_i can be directly compared with official data reported as confirmed new cases per day
- Later we changed the notation from k_i and N_0 to k_u and N_u when we applied the **unlimited growth model** to later epochs of the pandemic in the US
- Because the model predicts exponential growth (12.6), a plot of $R_i(t)$ should appear linear on semi-log graph – see Fig.12.05 and Fig.12.08
- The unlimited growth model is characterized by a doubling time

$$t_d = \frac{\ln 2}{k_i} \quad \text{or} \quad t_d = \frac{\ln 2}{k_u} \tag{12.7)(12.61}$$

Finite population model

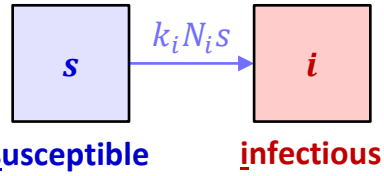


Fig.12.09 FD diagram of a two-box epidemiological model exhibiting limited growth. The two boxes in this **finite population** (**FP**) **model** represent the two parts of the model population that can be affected by the disease. Box s represents the portion susceptible to the disease. Box i represents the portion infectious. Lowercase s is the fraction of the model population that are still susceptible to infection. (Repeated from main text).

- The UG model assumes every person that an infectious individual encounters is still susceptible. However, as the infection spreads, it becomes more likely that the infectious person will encounter others that have been infected (box i) rather than those that haven't been infected (box s). The **finite population** (**FP**) **model** accounts for that by changing the **infection rate** R_i to be

$$R_i = k_i N_i s \tag{12.8}$$

- s [=] 1 is the **susceptible fraction** (note the lowercase "s") of the model population *defined* by

$$s \equiv \frac{N_s}{N} \tag{12.9}$$

- N_s is the **number susceptible** and N (with no subscript) is the total number of people in the **model population**, where

$$N = N_s + N_i \tag{12.10}$$

- The FP model is the simplest model that shows how social distancing can flatten the $R_i(t)$ curve (Fig.12.10)

The SIR model

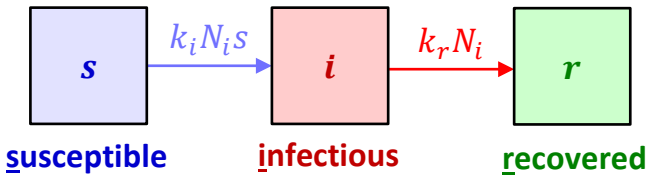


Fig.12.11 FD diagram of the SIR epidemiological model. The three boxes represent the three parts of the model population that can be affected by the disease. Box s represents the portion that's susceptible to the disease. Box i represents the portion infectious. Box r represents the portion that's recovered from the infection (or died). Sometimes this box is labeled removed – as in removed from consideration. (Repeated from main text).

- The **SIR model** extends the FP model by adding a third box r for those who have **recovered**.
- k_r [=] d^{-1} is the **recovery rate constant** for jumps from box $i \to r$
- In the SIR model, recovery is assumed to be a Poisson process so that the average time an individual is infectious – the **mean infectious time** – is given by

$$\tau_i = \frac{1}{k_r} \tag{12.17}$$

- In the SIR model, the **basic reproduction number** $\mathcal{R}_0$ tells us the intensity of the outbreak

$$\mathcal{R}_0 \equiv k_i \tau_i \tag{12.42}$$

  a value of $\mathcal{R}_0 \leq 1$ means that the disease will die out on its own and an $\mathcal{R}_0 > 1$ means the disease will spread exponentially before it starts to subside.
- **Herd immunity** occurs when the number of people who've been removed from the susceptible portion reaches the **herd immunity threshold** h_p given by

$$h_p = 1 - s_p = 1 - \frac{1}{\mathcal{R}_0} \tag{12.33}$$

  assuming that k_i and k_r (and hence $\mathcal{R}_0$) are fixed and where individuals are removed from being susceptible by either becoming infected or by effective vaccination.
- The SIR model implicitly predicts (12.47) the **final fraction susceptible** s_∞ if the model parameters k_i and k_r remain constant.
- During a short period of time, when the susceptible fraction s is approximately constant $s \approx s_0$, the full SIR model can be approximated by either **exponential growth** (12.6)(12.56) or an **exponential decay**

$$R_i \approx A_0 e^{-k_d t} \tag{12.68}$$

  that can be characterized by a **half-life**

$$t_{½} = \frac{\ln 2}{k_d} \tag{12.70}$$

  where $k_d = k_r - k_i s_0$ (12.65).

Model population size *N*

- The **model population size** N is the portion of the actual population $N^\star$ that's included in the model.
- In discussing the size of the model population, it's convenient to define

$$q \equiv \frac{N}{N^\star} \tag{12.93}$$

which is the fraction of the US population included in the model population (fraction of cases per day that are reported).

- In January 2021 the CDC estimated that 1 in 4.6 total COVID–19 infections were reported (or $q = 21.7\%$) [CDC 2021].

Making k_i a variable

- Changes in social distancing and mask wearing can be accounted for by making k_i a variable. For example, if there are 4 distinct epochs in the model, then the infection rate coefficient k_i is

$$k_i^{\text{new}} = k_1 + F_{12}^{\text{new}} * (k_2 - k_1) + F_{23}^{\text{new}} * (k_3 - k_2) + F_{34}^{\text{new}} * (k_4 - k_3) \tag{12.92}$$

where k_1, k_2, k_3, and k_4 are the infections rate constants in the four epochs and the "F"s are **cumulative normal distributions**, or Gaussian transition functions between the indicated epochs, which for example are given by

$$F_{12}^{\text{new}} = \text{NORM. DIST}(t^{\text{new}}, t_{12}, \sigma_{12}, \text{TRUE}) \tag{12.83}$$

where t_{12} is the transition time between epochs ① and ②. σ_{12} is its standard deviation.

- The transition functions can be visualized using the corresponding probability density functions, e.g.

$$p_{12}^{\text{new}} = \text{NORM. DIST}(t^{\text{new}}, t_{12}, \sigma_{12}, \text{FALSE}) \tag{12.84}$$

Modeling vaccination

- Vaccination can be added to the SIR model FD diagram by adding a box for **fully vaccinated** individuals (Fig.12.32). The three rates leading to box v are labeled $R_{v,s}$, $R_{v,i}$, and $R_{v,r}$ where the subscript v indicates vaccination and the subscripts s, i, and r indicate the originating box.

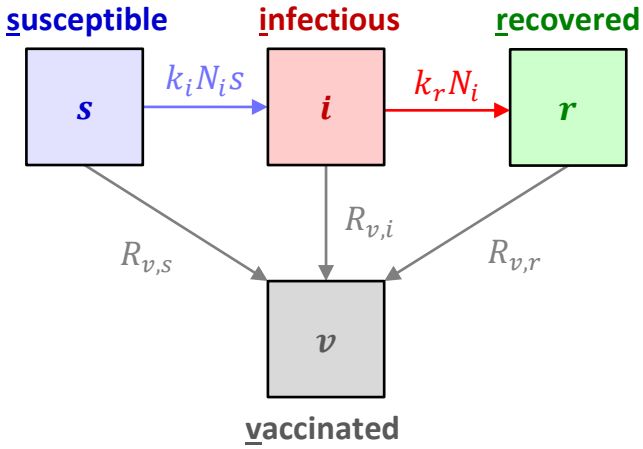


Fig.12.32 FD diagram of a simple modification of the SIR model that accounts for vaccinations – the SIRV model. The four boxes represent the four parts of the model population that can be affected by the disease. Box s represents the portion of the population that's susceptible to the disease. Box i represents the portion of the population that's infectious. Box r represents the portion of the population that has recovered from the infection (or died). Box v represented the portion of the population that's been fully vaccinated. (Repeated from main text).

- The OWID data includes a column for $N_v^\star$ the "**number fully vaccinated**." The number of vaccinated individuals in the model population is calculated using

$$N_v^{\text{new}} = qN_v^{\star\text{new}} \tag{12.96}$$

and the vaccination rate in the model population is

$$R_v^{\text{new}} = \left(N_v^{\text{new}} - N_v^{\text{old}}\right)/\delta t \tag{12.97}$$

The rate of vaccination of susceptible individuals in the model population can be calculated using

$$R_{v,s}^{\text{new}} = N_s^{\text{old}} * R_v^{\text{new}}/\left(N_s^{\text{old}} + N_i^{\text{old}} + N_r^{\text{old}}\right) \tag{12.98}$$

and similarly, for $R_{v,i}^{\text{new}}$, and $R_{v,r}^{\text{new}}$, which assumes that individuals in each of the three boxes s, i, and r are equally likely to be vaccinated.

In the SIRV model, the numbers in boxes, i and r can be calculated using

$$N_i{}^{\text{new}} = N_i{}^{\text{old}} + \left(R_i^{\text{new}} - R_r^{\text{new}} - N_i^{\text{old}} * R_v^{\text{new}}/\left(N - N_v^{\text{old}}\right)\right) * \delta t \tag{12.103}$$

$$N_r^{\text{new}} = N_r^{\text{old}} + \left(R_r^{\text{new}} - N_r^{\text{old}} * R_v^{\text{new}}/\left(N - N_v^{\text{old}}\right)\right) * \delta t \tag{12.104}$$

and

$$N_s^{\text{new}} = N - N_i{}^{\text{new}} - N_r^{\text{new}} - N_v^{\text{new}} \tag{12.105}$$

Note: When comparing the model variables with the published data, it's important to recall that all vaccinations are reported, but only about one-in-five infections are reported.

Corrections for discrete-time errors

- If the SIR model is fitted to daily infection rate data R_i using a timestep of $\delta t = 1$ d, then the fitted model parameters need to be corrected to account for systematic errors during the initial exponential growth. The doubling time can be calculated using

$$t_d = \frac{\ln 2}{\ln(k_1 - k_r + 1)} \tag{12.85}$$

and the basic reproduction number can be calculated using

$$\mathcal{R}_0 = \left(\frac{\ln 2}{t_d} + k_r\right)\tau_i \tag{12.86}$$

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