Examples of Mathematical Models from the Covid-19 Pandemic of 2020

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1 Overview

The overwhelming global media coverage of the Covid-19 pandemic has provided many useful examples of mathematical modeling related to the community college mathematics curriculum. This report reviews some areas where real-life events may be connected to our classes, as well as suggests some problems or projects for students to explore.

2 College Algebra

2.1 Exponentila Decay and the Stability of Virus on Various Surfaces

Covid-19, like most viruses, follow the law of exponential decay when measured from various surfaces as well as from aerosols (van Doremalen et al., 2020), although the rate of decay varies depending on the surface.

Problem 2.1. *The median half-life for Covid-19 in aerosols is 1.2 hours. For stainless steel and plastic, the half life estimate is 5.6 hours and 6.8 hours, respectively. Suppose a patient releases aerosols with virus level of* 10^5 $TCID_{50}/mL$ *into the encapsulated air as well as on the stainless steel and plastic surfaces. How long does it take for the virus level to drop below* 10 $TCID_{50}/mL$*, the level of detection?*

Problem 2.2. *Based on the data reported in (van Doremalen et al., 2020), shown in Figure 1, use linear regression to create a model that predicts* $\log(titer)$ *from time. Then convert this model to an exponential model. What does your model predict about the half life of CoV-19 on plastic surfaces?*

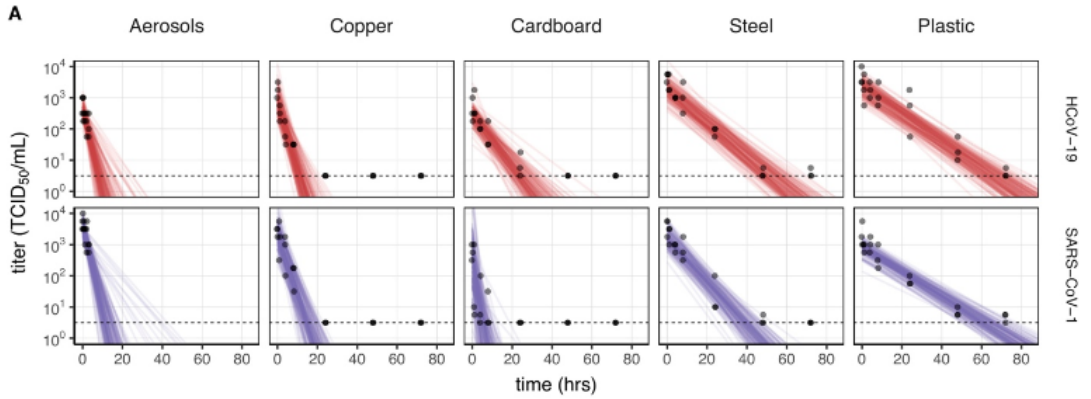


Figure 1: Decay of Covid-19

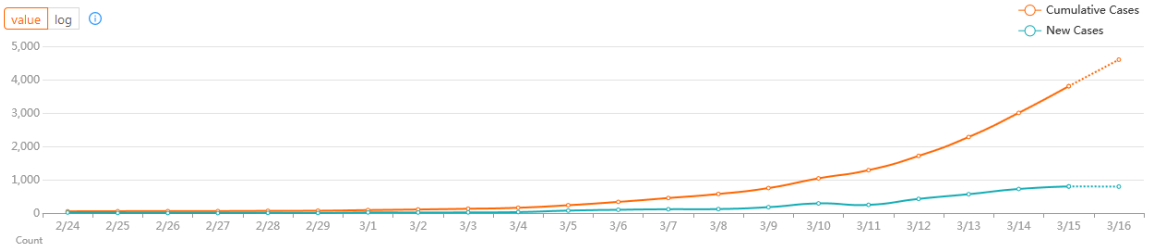


Figure 2: Covid-19 Reported Cases in the U.S. until March 16, 2020

2.2 Sequence and Series

The daily new reported cases and accumuldated cases (not considering recovery) are examples of the relationship between sequence and series.

Problem 2.3. *The New and Cumulative cases reported in the U.S. are shown in Figure 2. Assume that the sequence is geometric and* $a_1 = 18$. *Estimate when the Cumulative cases will reach 10,000.*

3 Differential Equations

3.1 Logistic Growth

In many countries where the pandemic took place, the growth of the number of infected patients exhibits the classical logistic growth model, which results from the followin first order ODE:

$$\frac{dy}{dx} = ry(1 - \frac{y}{C}) \tag{1}$$

subject to the boundary value $y(0) = P_0$.

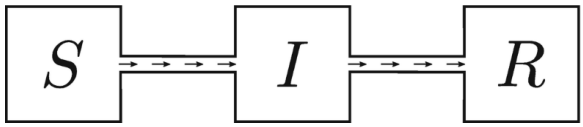


Figure 3: Flow chart for the S-I-R model

Problem 3.1. *Solve the separable differential equation for logistic growth using the initial value.*

3.2 System of First Order ODEs

A landmark model used in infectious diseases is the S-I-R model was proposed shortly after the Spanish flu pandemic of 1918 (Kermack and McKendrick, 1927). The three letters were named after Susceptible, Infected, and Resistant, the categories within the population. In epidemiology, the strategy of dividing the population into disjoint categories is also called "compartmental model", as illustrate by Figure 3:

The system of ordinary differentiation is non-linear and has two parameters [1]

$$\begin{aligned} \frac{dS}{dt} &= -\beta SI \\ \frac{dI}{dt} &= \beta SI - \gamma I \\ \frac{dR}{dt} &= \gamma I \end{aligned} \tag{2}$$

The parameter β controls the rate that the susceptible population gets infected when they are mixed the infected. γ controls the rate which the infected recover from the disease. When I is small, and $\beta S - \gamma > 0$, the second equation $\frac{dI}{dt} = (\beta S - \gamma)I$ describes near exponential growth in I, with growth rate of $\beta S - \gamma$. As the value of S is gradually depleted to the point when $\beta S - \gamma = 0$, the number of Infected people reaches the inflection point.

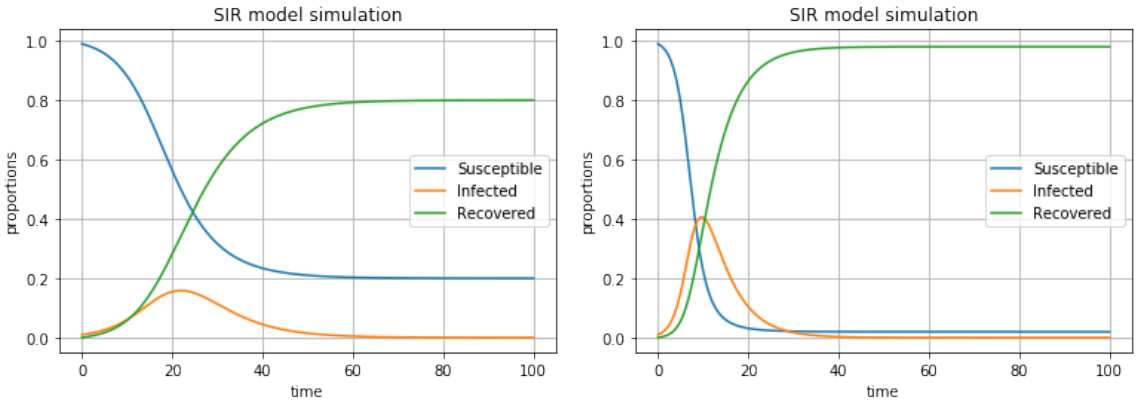
Problem 3.2. *Use theorems in Calculus to prove that when $S + I + R = N$ for some fixed N, it follows that $\lim_{t\to\infty} I(t) = 0$, and $\lim_{t\to\infty} S(t) = S_\infty$ for some $0 \leq S_\infty \leq N$.*

The value of S_∞ can be determined by dividing the equations for dS/dt over dR/dt:

$$\frac{dS}{dR} = -\frac{\beta}{\gamma} S \tag{3}$$

Problem 3.3. *Use Equation 3, and the property that as $t \to \infty$, $I = (N - S - R) \to 0$ to identify an equation for S_∞, the limiting value of $S(t)$.*

[1] The model presented here is slightly simplified compared to what is presented in the epidemiology literature for the ease of analysis.



(a) $\beta = 0.4, \gamma = 0.2$ (b) $\beta = 0.8, \gamma = 0.2$

Figure 4: Sample Solutions to the SIR Model

If we let $N = S+I+R$, then we can also defined the famed "reproductive number" R_0, defined as:

$$R_0 = \frac{\beta N}{\gamma} \tag{4}$$

In epidemiology, R_0 has the interpretation of the number of secondary infection as the result of contacting with an infected case. When $R_0 > 1$, this is equivalent to $\beta N - \gamma > 0$. In such circumstances, $\frac{dI}{dt} > 0$, and an epidemic is under way.

For example, by using the initial values $(S(0), I(0), R(0)) = (0.99, 0.01, 0)$, the S, I an R solution curves is shown for two sets of parameter values in Figure 4. Here we can interpret the lower β value as strategies encouraging "social distancing", lending credence to the claim by public health officials that social distancing can help us "flatten the curve".

The non-linear system in Equation 2 can also be visualized as a direction field. For example, Figure 5 displays the direction field and the solution curve with the initial condition $(S_0, I_0, R_0) = (0.99, 0.01, 0)$ and the parameters $\beta = 0.20, \gamma = 0.05$.

Equation 2 satisfies $\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0$. This suggests that we can remove R from the dynamic system and reduce the degree of freedom to 2. This amounts to studying the projection of Figure 5 on the S-I plane. Hence we can study the phase portrait of the system $(S(t), I(t))$, as shown in Figure 6.

From Figure 6 we can see that the system generally has sinks at $(S_\infty, 0)$, i.e. the equilibrium occurs when $I \to 0$. At this critical point, the system has Jacobian:

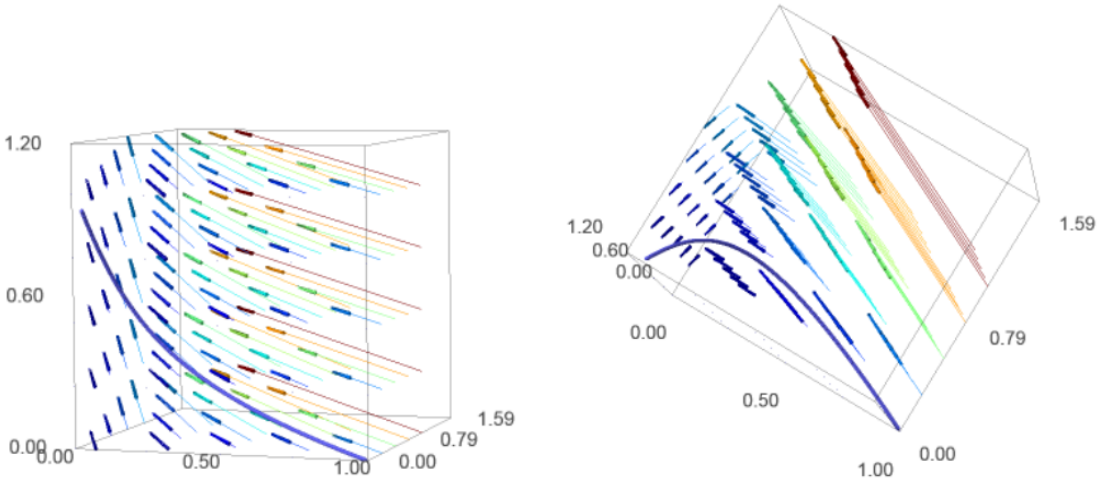


Figure 5: One solution and the direction field for the SIR model

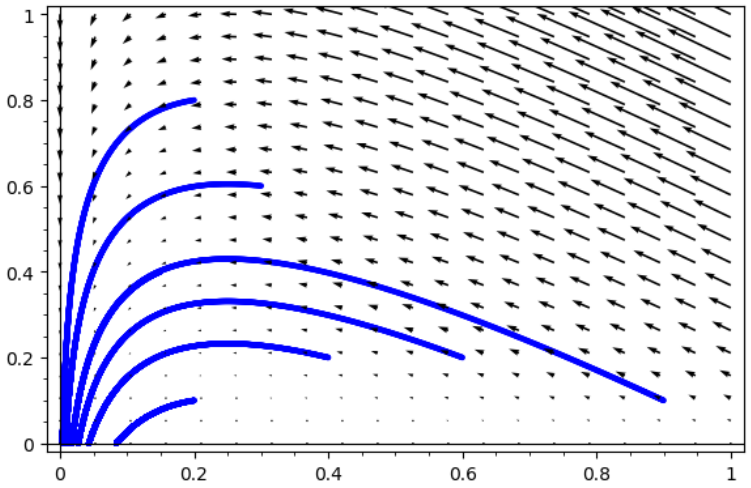


Figure 6: Phase portrait and slope field for $(S(t), I(t))$, based on parameters $\beta = 0.20, \gamma = 0.05$ and the initial values: (0.9, 0.1, 0), (0.4, 0.2, 0.4), (0.6, 0.2, 0.2), (0.2, 0.1, 0.7), (0.2,0.8,0), and (0.3, 0.6, 0.1). The initial values be non-negative and must satisfy $S(0) + I(0) + R(0) = 1$.

$$
\begin{aligned}
J(S_\infty, 0) &= \begin{pmatrix} \frac{d}{dS}(-\beta SI) & \frac{d}{dI}(-\beta SI) \\ \frac{d}{dS}(\beta SI - \gamma I) & \frac{d}{dI}(\beta SI - \gamma I) \end{pmatrix}_{S=S_\infty, I=0} \\
&= \begin{pmatrix} -I\beta & -S\beta \\ I\beta & S\beta - \gamma \end{pmatrix}_{S=S_\infty, I=0} \\
&= \begin{pmatrix} 0 & S_\infty \\ 0 & \beta S_\infty - \gamma \end{pmatrix}
\end{aligned} \tag{5}
$$

which also shows that $(S_\infty, 0)$ is a sink since the non-zero eigenvalue of the Jacobian satisfies $\beta S_\infty - \gamma < 0$.

We can also observe that when I reaches the maximum, i.e. $dI/dt = 0$, there is $\beta SI - \gamma I = 0$. Although this is not a critical point, solving for S gives us:

$$
S = \frac{\gamma}{\beta} \tag{6}
$$

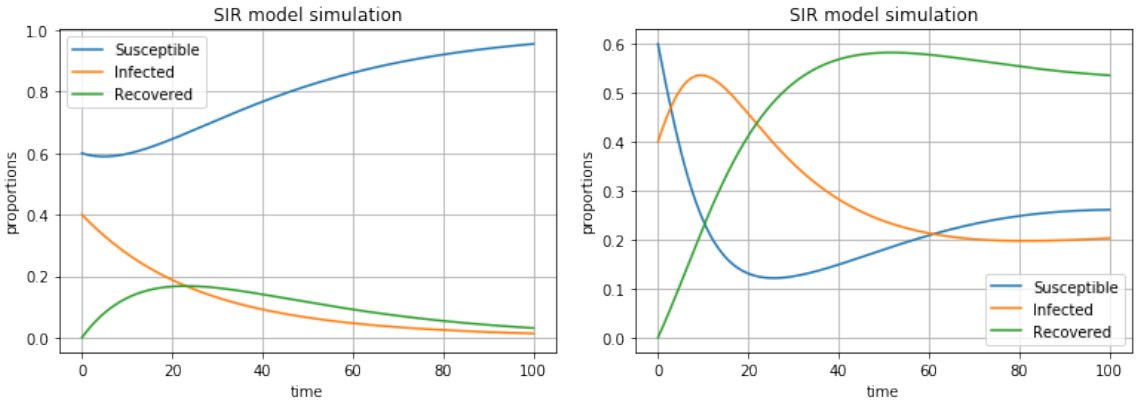
This can be useful for analytically solving for the maximum of Infected cases, as described in (Brauer, Castillo-Chavez, and Feng, 2019).

Problem 3.4. *Modify the model given in Equation 2 so that it captures mortality, i.e. the fact that some of the infected patients will die from the disease. Does it change the shape of the Infected curve?*

Problem 3.5. *Equation 2 assumes that the whole population will eventually develop immunity to the disease (also known as "herd immunity"). In other words, patients who recovered will not be re-infected. What happens if the virus behaves like the flu, mutates (Tang et al., 2020) after people have developed immunity, and some of the patients become susceptible again after recovery? Confirmed cases of re-infection by Covid-19 have also been reported around the world (Iwasaki, 2020). Can "herd immunity" protect the population if both virus and people are evolving?*

Solution. *We can add a term to dR/dt to capture the assumption that part of the recovered population may become susceptible again due to the mutation of the virus. We also make the assumption that the rate in which the recoverd lost their immunity is represented by a new parameter $\alpha \in (0, 1)$, the rate in which the infected will recover from the disease.*

$$
\begin{aligned}
\frac{dS}{dt} &= -\beta SI + \alpha R \\
\frac{dI}{dt} &= \beta SI - \gamma I \\
\frac{dR}{dt} &= \gamma I - \alpha R
\end{aligned} \tag{7}
$$



(a) $\alpha = 0.05, \beta = 0.02, \gamma = 0.05$ (b) $\alpha = 0.02, \beta = 0.20, \gamma = 0.05$

Figure 7: Sample solutions to the SIR Model with mutation
$S_0 = 0.60, I_0 = 0.40, R_0 = 0$

The S,I and R solution curves are shown in Figure 7 for two different sets of parameters based on the same initial condition $S_0 = 0.60, I_0 = 0.40, R_0 = 0$.

Since Equation 7 still satisfies $\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0$, *we can eliminate R as before, and rewrite Equation7 as:*

$$\begin{aligned} \frac{dS}{dt} &= -\beta SI + \alpha(1 - S - I) \\ \frac{dI}{dt} &= \beta SI - \gamma I \end{aligned} \tag{8}$$

System 8 resembles the non-linear predator-prey model, also known as the Lotka-Volterra Equations (Vitanov, Dimitrova, and Ausloos, 2010). The phase portrait of this system is shown in Figure 8. There are two critical points for this system: one is $(1, 0)$, *the other is:*

$$\begin{aligned} S &= \frac{\gamma}{\beta} \\ I &= \frac{\alpha(\beta - \gamma)}{(\alpha + \gamma)\beta} \end{aligned} \tag{9}$$

Based on the phaes portrait, this second critical point appears to be stable. To confirm this, we can linearize the system at the critical value by computing the Jacobian matrix:

$$J = \begin{pmatrix} -I\beta - \alpha & -S\beta - \alpha \\ I\beta & S\beta - \gamma \end{pmatrix} \tag{10}$$

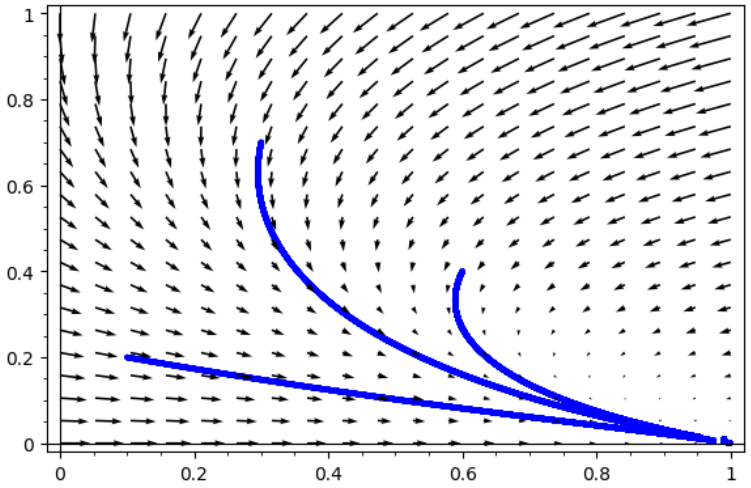


Figure 8: Phase portrait and slope field for System 8.
$\alpha = 0.05, \beta = 0.02, \gamma = 0.05$

Evaluting the Jacobian matrix at the critical point $(1, 0)$ *yields:*

$$\begin{pmatrix} -\alpha & -\alpha - \beta \\ 0 & \beta - \gamma \end{pmatrix} \tag{11}$$

This upper triangule matrix has eigenvalues $\lambda_1 = -\alpha$, *and* $\lambda_2 = \beta - \gamma$. *Since we assume that* $\alpha > 0$, *then if* $\beta > \gamma$, *the two real eigenvalues have opposite signs, and* $(1, 0)$ *is a saddle point, which is unstable. When* $\beta < \gamma$ *(i.e. the infection rate is very low compared to the recovery rate), then* λ_1 *and* λ_2 *have the same sign, and* $(1, 0)$ *becomes a a nodal sink, as shown in Figure 8. This stable solution represents the scenario that the virus gradually disappears from the population, i.e. "herd immunity" worked wonders!*

On the other hand, evaluting the Jacobian matrix at the critical point (9) yields:

$$\begin{pmatrix} -\alpha - \frac{(\alpha\beta - \alpha\gamma)}{\alpha+\gamma} & -\alpha - \gamma \\ \frac{(\alpha\beta - \alpha\gamma)}{\alpha+\gamma} & 0 \end{pmatrix} \tag{12}$$

The characteristic polynomial for this matrix is:

$$\lambda^2 + \frac{\alpha(\alpha + \beta)}{\alpha + \gamma}\lambda + \alpha(\beta - \gamma) \tag{13}$$

Since $\frac{\alpha(\alpha+\beta)}{\alpha+\gamma} > 0$, *such a system will have an attractor at the critical point (9), when Equation 13 has a pair of complex solutions that are conjugates of each other. This happens when the following condition is met:*

$$\left[\frac{\alpha(\alpha + \beta)}{\alpha + \gamma}\right]^2 - 4\alpha(\beta - \gamma) < 0 \tag{14}$$

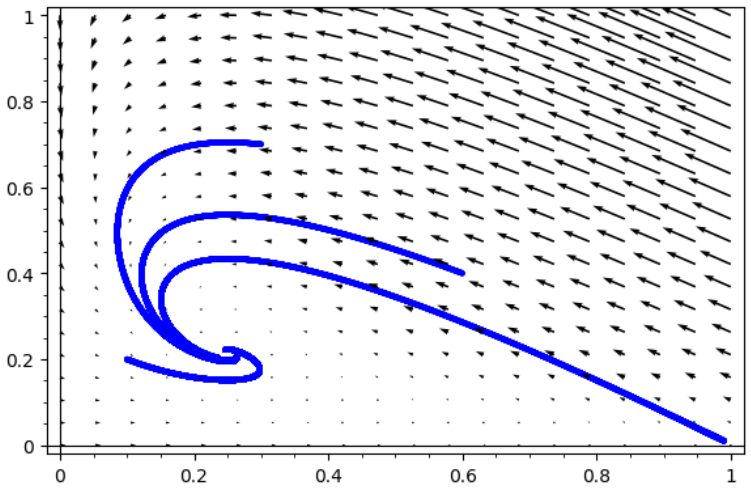


Figure 9: Phase portrait and slope field for System 8.
$\alpha = 0.02, \beta = 0.2, \gamma = 0.05$

A phase portrait with $\alpha = 0.05, \beta = 0.02, \gamma = 0.05$ *is shown in Figure 9. In this scenario, the percentages of susceptible, infected, and recovered reach an equilibrium: as* $t \to \infty$, $(S, I, R) \to (0.246, 0.222, 0.532)$. *So the inequality (14) leads to the consequence that a certain percentage of the population will always be infected, which is unfortunate for the advocates of "herd immunity".*

Problem 3.6. *How can the basic SIR model be modified to account for the introduction of vaccine? Imagine that a large proportion of the population is vaccinated, i.e. moving them from the initial value* $S(0)$ *to* $R(0)$. *Does this affect the stable solution?*

4 Probability and Statistics

4.1 False Positive and False Negatives in the Covid-19 Tests

Conditional probability, based on the notation $P(A|B)$, is an important concept in statistics. In medicine, $P(\text{Test} = -|\text{Infected} = no)$ is also known as "specificity" of a test, while $P(\text{Test} = +|\text{Infected} = yes)$ is referred to as "sensitivity". For example, in a recent paper proposing a new nucleic acid test (Li et al., 2020), testing sensitivity was 88.66% and specificity was 90.63%, indicating a false positive rate of about 11% and false negative rate of 9%.

In comparison, another diagnostic tool – the chest CT has a higher sensitivity: 97% (580/601), and lower specificity: 25% (105/413) according to recent research on Covid-19 (Ai et al., 2020). However, in the same study, only 601 out of 1014 patients (59%) had positive RT-PCR results, the standard test that is performed on the throat swab samples.

This low sensitivity is consistent with the estimate that the RT-PCR testing may have a false negative rate as high as 30-50%. This has led to the author's recommendation that the chest CT as the primary screening tool if the goal was to catch as many infected patients as possible.

The low sentivity of RT-PCR testing is often related to the low level of the virus in the upper respiratory system, as well as the RNA virus is rather unstable and can break down in the sample.

Problem 4.1. *Assume that a patient infected with Covid-19 received did a series of RT-PCR test and the sensitivity of the test is 60%. All the tests were performed independently. Find the probability that the patient tested negative once before testing positive a second time.*

Problem 4.2. *Due to the shortage of test kits, 3 independent samples taken from 3 different patients were combined to create a single sample. This strategy was also adopted in many countries to accelerate testing of entire populations (Lohse et al., 2020). If the combined sample tests negative, then each person in the group will be called back for individual testing. One test was performed on this combined sample. Find the probability that the combined sample will test positive.*

Problem 4.3. *How likely are the so-called "asymptomatic carriers" (Bai et al., 2020)? (i.e. people who don't show symptoms but are capable of spreading the virus, as desribed in) Assume someone who is infected is taking the Chest CT and receiving an RT-PCR test in short succession. Find the probability that this person receives negative results in both tests.*

4.2 Bayes Rule

Bayes rule allows one to answer the question: "if someone tested positive for Covid-19, how likely is this person infected?" by computing the more useful conditional probability $P(\text{Infected} = yes|\text{Test} = +)$ based on the following equation:

$$\begin{aligned} &P(I = yes|T = +) \\ &= \frac{P(I = yes, T = +)}{P(T = +)} \\ &= \frac{P(T = +|I = yes) \cdot P(I = yes)}{P(T = +|I = yes) \cdot P(I = yes) + P(T = +|I = no) \cdot P(I = no)} \end{aligned} \tag{15}$$

Computing such probabilities helps public health officials determine how widely available the tests should be, since a low probability $P(I = yes|T = +)$ implies perhaps not everyone should get tested, unless they should some flu-like symptoms.

For example, assuming that PCR test has specificity of 90%, i.e. $P(T = -|I = no) = 0.7$, sensitivity of 70%, i.e. $P(T = +|I = yes) = 0.9$, and the prior probability

$P(I = yes) = 0.4$, we can calculate the posterior probability $P(I = yes|T = +)$ as follows:

$$\begin{aligned} P(I = yes|T = +) &= \frac{P(I = yes, T = +)}{P(T = +)} \\ &= \frac{P(T = +|I = yes) \cdot P(I = yes)}{P(T = +|I = yes) \cdot P(I = yes) + P(T = +|I = no) \cdot P(I = no)} \\ &= \frac{0.7 \cdot 0.4}{0.7 \cdot 0.4 + (1 - 0.9) \cdot 0.6} \\ &= 0.824 \end{aligned} \tag{16}$$

Problem 4.4. *Assume that in our local area, 1% people are infected. Use Bayes rule to compute the probability that someone is infected after receiving a positive test result from RT-PCR. You can use a sentivity of 60% and specificity of 90%.*

Problem 4.5. *Elon Musk attended a party and was tested for COVID afterwards 4 times. Two tests were positive and two were negative. Assuming that 40% of the guests at this party ended up getting infected. How likely was Musk infected, given his mixed test results?*

Solution.

$$\begin{aligned} &P(I = yes|\{T_i = t_i\}) \\ &= \frac{P(I = yes, \{T_i = t_i\})}{P(\{T_i = t_i\})} \\ &= \frac{P(\{T_i = t_i\}|I = yes) \cdot P(I = yes)}{P(\{T_i = t_i\}|I = yes) \cdot P(I = yes) + P(\{T_i = t_i\}|I = no) \cdot P(I = no)} \\ &= \frac{\prod_{i=1}^{4} P(T_i = t_i|I = yes) \cdot P(I = yes)}{\prod_{i=1}^{4} P(T_i = t_i|I = yes) \cdot P(I = yes) + \prod_{i=1}^{4} P(T_i = t_i|I = no) \cdot P(I = no)} \\ &= \frac{0.3^2 \cdot 0.7^2 \cdot \ 0.4}{0.3^2 \cdot 0.7^2 \cdot \ 0.4 + 0.9^2 \cdot 0.1^2 \cdot \ 0.6} \\ &= 0.784 \end{aligned} \tag{17}$$

Here we assume that the test results were $\{t_1 = -, t_2 = +, t_3 = -, t_4 = +\}$, and we assume that the tests were conditionally independent when the underlying infection condition is known. If, however, these test results were from someone from the general public, where the infection rate is at 2%. Then the posterior probability becomes:

$$\begin{aligned} &P(I = yes|\{T_i = t_i\}) \\ &= \frac{0.3^2 \cdot 0.7^2 \cdot \ 0.02}{0.3^2 \cdot 0.7^2 \cdot \ 0.02 + 0.9^2 \cdot 0.1^2 \cdot \ 0.98} \\ &= 0.100 \end{aligned} \tag{18}$$

Problem 4.6. *Similar to the previous problem, now assume that this person is also showing flu-like symptoms. Modify the Bayes formula to identify which probabilities need to determined in order to compute* $P(Infected = yes | Test = +, Symptoms = +)$.

Problem 4.7. *Use Bayes formula and the relevant parameters in 4.1 to calculate the probability that someone is infected, given that this person tests positive on both RT-PCR and chest CT. Assume that 1% of the population is infected.*

Problem 4.8. *Supposed a number of* k *samples were pooled before the PCR test, how does the specificity and sensitivity of the PCR test change with regard to* k*?*

4.3 Hypothesis Testing

The most anticipated hypothesis tests during the time of the pandemic were the ones coming from the vaccine trials. This is a good opportunity to review the Type I and Type II error, as well as the issues of designing a trial. In the press releases about vaccine trials, generally the following figure was reported:

$$\text{Vaccine Efficacy}(VE) = 1 - \frac{\text{Infection rate in the vaccine group}}{\text{Infection rate in the placebo group}} \tag{19}$$

For example, in Phase-3 of the Pfizer trial, 43,661 were randomly assigned to the vaccine group and control group with the same probability. 8 cases of Covid-19 were found in the vaccine group, and 162 were found in the control group, resulting in an efficacy value of 95%. Generally, vaccines need to reach 50% efficacy in order to be reviewed for approval.

Problem 4.9. *What are the Type I and Type II errors in the vaccine trial, respectively? Which one is more serious in your opinion?*

Problem 4.10. *The sample size of the trial is calculated based on both the signficance level* (α) *and the power of the test* ($1-\beta$)*. Assume that in the general population 2% of the people are infected, and vaccine is expected to reduce the infection rate to 1%. About how many subjects must be included in the trial so that the power of the test is at least 90%, and the significance level is set to 5%?*

Problem 4.11. *Based on the same test of one proportion as the previous problem, but assume that the trial is double-blind, and the trial is stopped when the number of infections reaches a certain level. Based on the same assumptions as the previous problem, use randomization to determine the number of infections needed in order to reach the desired* α *and* β*.*

Problem 4.12. *(Programming required) In the Pfizer trial, it was decided that 43,500 subjects need to be recruited from around the world, much higher than the sample size found above. This was due to the fact a different hypothesis test is used instead of the*

simple test of one proportion. In Pfizer's trial, the null hypothesis $H_0 : VE = 0.60$ was used. Use randomization simulations to find the sample size required for the test, if the vaccine was expected to achieve $VE = 0.70$, and the power of the test needs to be at least 90%.

5 Discrete Mathematics

An alternative to differential equations is to use recurrence relations that are defined over discrete sequences. Here we make the following assumptions:

- The virus spreads in discrete moments.
- A carrier of the virus has the same chance of recovery at any moment in time
- A carrier does not immediately become infectious.
- If a carrier does not recover, then in the next moment, s/he will pass the virus to a fixed number of persons.

Hence we defined a second-order recurrence relation:

$$a_n = (R_0 + 1)(1 - \gamma) \cdot a_{n-2} + (1 - \gamma) \cdot a_{n-1} \tag{20}$$

Here R_0 value is the average number of person a Covid-19 patient infects, and γ is the same recovery rate as in Section 3.2. Based on the estimates in (Kucharski et al., 2020), we can use $R_0 \approx 2.7$, and $\gamma = 0.8$.

Problem 5.1. *Solve the recurrence relation in Equation 20 by using the initial values $a_0 = a_1 = 1$.*

Problem 5.2. *Prove that your formula works correctly for all n by using mathematical induction.*

6 Linear Algebra

Based on the same recurrence relation as in Equation 20, define the vector $\vec{F}_n$ as follows:

$$\vec{F}_n = \begin{pmatrix} a_n \\ a_{n+1} \end{pmatrix} \tag{21}$$

Problem 6.1. *Rewrite the recurrence relation in 20 in matrix form so that we have:*

$$\vec{F}_{n+1} = A\vec{F}_n \tag{22}$$

Then diagonalize $A = PDP^{-1}$ to obtain a formula for $\vec{F}_n$.

Problem 6.2. *Assume γ is given. Find the range of R_0 so that $\vec{F}_n$ converges.*

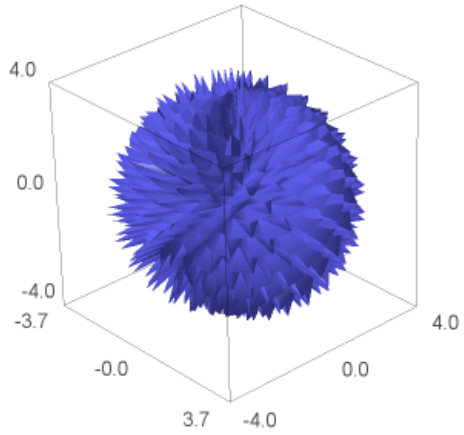


Figure 10: The graph of the surface described by Equation 23

7 Surfaces and Solids in Three Dimensions

The spiky appearance of the Covid-19 virus can be approximated by the following equation in spherical coordinates:

$$\rho = 3 + \sin(20 \cdot (\phi + \theta)) \tag{23}$$

A 3d plot of this surface is shown in Figure 10.

Problem 7.1. *Find the volume and surface area of the region shown in Figure 10*

References

Ai, Tao, Zhenlu Yang, Hongyan Hou, Chenao Zhan, Chong Chen, Wenzhi Lv, Qian Tao, Ziyong Sun, and Liming Xia. 2020. Correlation of chest ct and rt-pcr testing in coronavirus disease 2019 (covid-19) in china: A report of 1014 cases. *Radiology*, page 200642.

Bai, Yan, Lingsheng Yao, Tao Wei, Fei Tian, Dong-Yan Jin, Lijuan Chen, and Meiyun Wang. 2020. Presumed asymptomatic carrier transmission of covid-19. *JAMA*.

Brauer, Fred, Carlos Castillo-Chavez, and Zhilan Feng. 2019. *Mathematical models in epidemiology*. Springer.

Iwasaki, Akiko. 2020. What reinfections mean for covid-19. *The Lancet Infectious Diseases*.

Kermack, William Ogilvy and Anderson G McKendrick. 1927. A contribution to the mathematical theory of epidemics. *Proceedings of the royal society of london. Series A, Containing papers of a mathematical and physical character*, 115(772):700–721.

Kucharski, Adam J, Timothy W Russell, Charlie Diamond, Yang Liu, John Edmunds, Sebastian Funk, Rosalind M Eggo, Fiona Sun, Mark Jit, James D Munday, et al. 2020. Early dynamics of transmission and control of covid-19: a mathematical modelling study. *The Lancet Infectious Diseases*.

Li, Zhengtu, Yongxiang Yi, Xiaomei Luo, Nian Xiong, Yang Liu, Shaoqiang Li, Ruilin Sun, Yanqun Wang, Bicheng Hu, Wei Chen, et al. 2020. Development and clinical application of a rapid igm-igg combined antibody test for sars-cov-2 infection diagnosis. *Journal of Medical Virology*.

Lohse, Stefan, Thorsten Pfuhl, Barbara Berkó-Göttel, Jürgen Rissland, Tobias Geißler, Barbara Gärtner, Sören L Becker, Sophie Schneitler, and Sigrun Smola. 2020. Pooling of samples for testing for sars-cov-2 in asymptomatic people. *The Lancet Infectious Diseases*.

Tang, Xiaolu, Changcheng Wu, Xiang Li, Yuhe Song, Xinmin Yao, Xinkai Wu, Yuange Duan, Hong Zhang, Yirong Wang, Zhaohui Qian, et al. 2020. On the origin and continuing evolution of sars-cov-2. *National Science Review*.

van Doremalen, Neeltje, Trenton Bushmaker, Dylan Morris, Myndi Holbrook, Amandine Gamble, Brandi Williamson, Azaibi Tamin, Jennifer Harcourt, Natalie Thornburg, Susan Gerber, et al. 2020. Aerosol and surface stability of hcov-19 (sars-cov-2) compared to sars-cov-1. *medRxiv*.

Vitanov, Nikolay K, Zlatinka I Dimitrova, and Marcel Ausloos. 2010. Verhulst–lotka–volterra (vlv) model of ideological struggle. *Physica A: Statistical Mechanics and its Applications*, 389(21):4970–4980.