



THE UNIVERSITY *of* EDINBURGH
**School of Physics
and Astronomy**

**Senior Honours Project
Exploring Compartmental Models to
Analyse the COVID-19 Pandemic**

Finn John Onori
March 2023

Abstract

Compartmental models and grid based simulations were used to explore the COVID-19 pandemic. Alternate scenarios were then predicted by adjusting the parameters of the compartmental models to explore methods of reducing infections. The results point towards a self-evident conclusion: A strict lockdown should be implemented as quickly as possible to minimise cases and deaths, this flattens the infection curve which ensures emergency services are not overwhelmed. However, lockdowns also increase the duration of a pandemic and cause immediate economic damage, therefore a lockdown should only be put in place if an outbreak is dangerous.

Declaration

I declare that this project and report is my own work.

Signature:

Supervisor: Dr. G. Ackland.

Date: 31/03/2023

10 Weeks

Contents

1	Introduction	2
1.1	Aims	2
1.2	Motivation	2
1.3	Estimating Cases with Limited Testing	3
1.4	SIR	3
1.4.1	Definition	3
1.4.2	Analysis	5
1.4.3	Numerical Solutions	8
1.5	SIRS	9
1.5.1	Definition	9
1.5.2	Analysis	9
1.5.3	Numerical solutions	14
1.6	COVIDGE	15
1.6.1	Definition	15
1.6.2	Analysis	16
1.6.3	Numerical Solutions	17
1.7	Grid based pandemics	18
2	Methods	18
2.1	Calculating Corrected Cases	18
2.2	Numerical integration	19
2.3	Adaptive integration	19
2.4	Data integration	19
2.5	Creating Vector fields	20
2.6	Calculating Coefficients	20
2.7	Grid simulations	21
3	Results & Discussion	22
3.1	Corrected Infection Curve	22
3.2	Grid Based Models	22
3.3	Adaptive Models	23
3.4	Data Models	23
3.5	Challenges and Further study	24
4	Conclusion	24
A	Appendices	26

1 Introduction

1.1 Aims

The beginning of the COVID-19 pandemic had limited testing which created a discrepancy between reported cases and deaths. Limited testing also made assessing the severity of the pandemic and the effectiveness of lockdown more difficult, even without the need to consider competing factors. To overcome these issues the COVID-19 pandemic in the UK was analysed with the SIR and SIRS models, along with a new model tailored to COVID-19 called COVIDGE. These models were then supplemented with grid based simulations and an analysis of the death to case ratio. The parameters of the models were then adjusted to achieve the goal of deducing how lockdowns can effect a pandemic, which can advise on how to limit the scale of an outbreak.

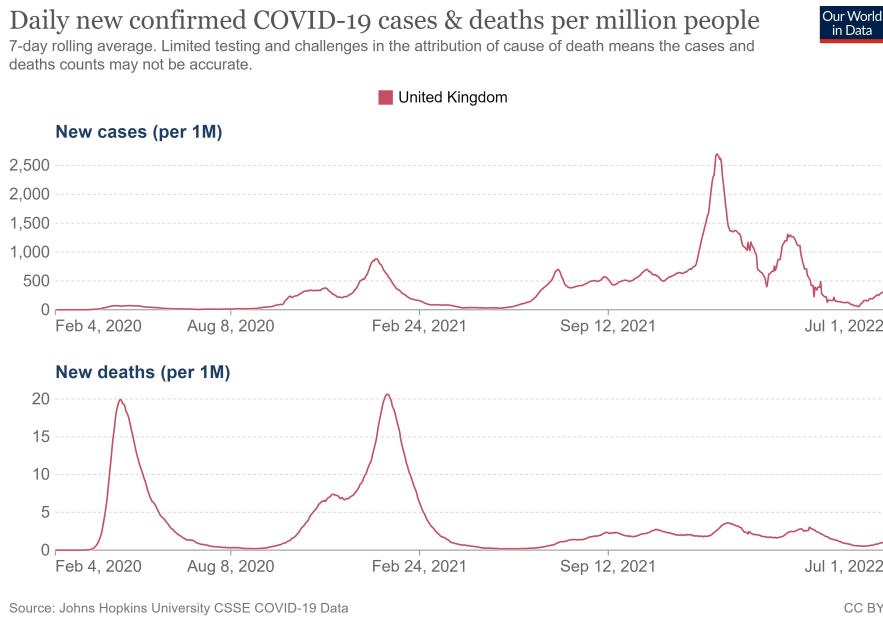


Figure 1: Cases and deaths during the COVID-19 pandemic in the UK, measured as cases per million people [11]. 2020 and 2021 give similar peaks in deaths, but divergent peaks in cases. This is possibly due to the limited testing available during the early stages of the pandemic.

1.2 Motivation

Global pandemics occur every few decades and can claim millions of lives, the ongoing COVID-19 pandemic has killed almost seven million people since December 2019 [1]. Vaccines and drug treatments mitigate outbreaks, however, safe treatments can take years to develop. In the meantime, compartmental models can advise on how to proceed to minimise cases and adjusting the parameters of the model allows for quantitative assessments of preventative measures. Studying these models can advise on how a lockdown can be most effectively implemented which could save lives for future outbreaks.

1.3 Estimating Cases with Limited Testing

Cases during a pandemic are difficult to quantify as they rely on either an entire population testing regularly and/or a method of self-reporting symptoms. On the other hand, deaths from COVID-19 are documented meaning they can be used to estimate the true number of cases during a period when widespread testing had yet to begin. If the average death to case ratio is calculated at a time after widespread testing began but before vaccination began, this ratio can be multiplied by the death curve to obtain an estimate for the true number of cases. With this in mind, compartmental models can now be explored.

1.4 SIR

1.4.1 Definition

A compartmental model is one where individuals are placed into one of several compartments. The compartments behave and interact differently with individuals moving between compartments under certain circumstances. This first model used here is SIR model [9], with three compartments named as such.



Figure 2: The transmission flow diagram for the SIR model where β represents the contact rate and γ represents the recovery rate. Once recovered an individual has immunity forever.

Initially, almost everyone is in S (susceptible) meaning they have not caught the infection and cannot spread it to others but can become infected. If exposed, susceptible individuals move into I (infected) meaning they can spread the illness to others in S . After a period of time, infected individuals move into R (recovered) meaning they can no longer catch or spread the infection as they have built up immunity.¹ Pandemics evolve differently depending to the illness in question, however, in general pandemics begin with an almost entirely susceptible population, whereupon they display a peak of infections, followed by secondary outbreaks, and finish in an endemic state where all compartments are fixed. Similarly, models also constantly change with the rate of movement between compartments dependant on the contact and recovery rates. The parallel to physical systems is quite striking in this sense as it's often easier to describe change instead of states and this can be done through the language of differential equations, in other words, deducing $\frac{dS}{dt}$, $\frac{dI}{dt}$, $\frac{dR}{dt}$. However, before a system of differential equations is defined for the SIR model consider the properties such a system must have. In all cases the compartments must satisfy $0 \leq S, I, R \leq N$. At $t = 0$ assume $R = 0$ and that $S \gg I$. Finally since the sum of all compartments equals the total population, the sum of the differential system must represent the total change in population. In the case where there are no births or

¹If the infection is deadly R is often generically denoted as "removed" to encapsulate both individuals who have recovered and individuals who have died. However, the models considered here will always denote R to be "recovered" as deaths are considered differently in future models.

deaths ² this sum is zero. The model can function with N set to any positive number, for ease of calculation it is set to one in all models.

$$S + I + R = N \quad (1)$$

$$N = \text{constant} \therefore \frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0 \quad (2)$$

With this, the differential equation for I can be defined. Assume that the number of infections after a given period of time is proportional to the number of susceptible individuals since that means there are more people available to infect.

$$\Delta I \propto S \quad (3)$$

Also, assume that it is proportional to the length of time considered since this gives more time for an infection to spread. All models considered here will use days as the unit of time.

$$\Delta I \propto S \Delta t \quad (4)$$

It is also defined to be proportional the probability of being infected, which is equivalent to the number of infected individuals divided by the total population.

$$\Delta I \propto \frac{I}{N} S \Delta t \quad (5)$$

A certain number of people who are going to recover during this period of time also needs to be subtracted where it is assumed that this is proportional to Δt and I . This is because more infections must result in more recoveries and a longer time-step gives more time for the infections to recover.

$$\Delta I \propto \left(\frac{I}{N} S - I \right) \Delta t \quad (6)$$

The recoveries and infections are independent, therefore, two proportionality constants are substituted: β which represents the contact rate and γ which represents the recovery rate. The equation is rearranged and an infinitesimal length of time is considered. This defines the following differential equation.

$$\frac{dI}{dt} = \beta \frac{IS}{N} - \gamma I \quad (7)$$

The first term represents the number of people becoming infected (S to I) and the second term represents the number of people recovering (I to R). Since the sum of all the differentials is considered to be zero for a constant population, the differential system is defined as follows.

²Which is true for the SIR model.

$$\frac{dS}{dt} = -\beta \frac{IS}{N}$$

$$\frac{dI}{dt} = \beta \frac{IS}{N} - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

1.4.2 Analysis

Solutions to such coupled systems are generally either impossible or incredibly difficult to find. However, analysis can still be performed without solutions. First, the following notation is introduced: Both β and γ have units of $[T]^{-1}$, therefore, $\frac{1}{\beta}$ equals the average time between transmissions of the virus and $\frac{1}{\gamma}$ equals the average time for an individual to recover. These coefficients together dictate whether I initially shrinks or grows with three possible cases. When $\gamma > \beta$, I shrinks since there are more recoveries than infections. Similar reasoning shows that I grows when $\beta > \gamma$, and that I is stable when $\beta = \gamma$. To illustrate this more compactly, a new value is often defined called the basic reproductive number R_0 .

$$R_0 = \frac{\beta}{\gamma} \tag{8}$$

Where $R_0 = 1$ corresponds to a stable pandemic, and anything above and below one corresponds to the pandemic growing or shrinking. Of course, this is assuming a fully susceptible population. To generalise to a partly recovered population the probability of an individual being susceptible is multiplied. This defines the effective reproductive number.

$$R_e(t) = R_0 \frac{S(t)}{N} \tag{9}$$

As the number of recoveries increases, R_e decreases until it is less than one. Once past this critical point I shrinks, S and R approach finite values, and the system becomes eternally stable. This is intuitively obvious with pandemics as they tend to fall into a stable endemic state, however, proving this rigorously and finding what the stable values for S and R are requires deep analysis of the system. To do this the forms of all three curves are deduced without analytical solutions.

The derivative of S is strictly negative, meaning it will continually decrease until I reaches zero. At this point the derivative equals zero meaning S will remain at a stable value. Similarly, the derivative for R is strictly positive meaning it will continually increase until I equals zero where it will also remain at stable value provided that I

eventually equals zero. Unlike $\frac{dS}{dt}$ and $\frac{dR}{dt}$, $\frac{dI}{dt}$ can be either negative or positive. However factoring out γI in $\frac{dI}{dt}$ and setting the derivative to zero, reveals there are only two possible cases where I is stationary.

$$\frac{dI}{dt} = \left(R_0 \frac{S}{N} - 1 \right) \gamma I \quad (10)$$

$$0 = \left(R_0 \frac{S}{N} - 1 \right) \gamma I \quad (11)$$

The first is when $I = 0$ which corresponds the fixed point of an entirely stable population. The second is when the condition $\frac{N}{R_0} = S$ is met. This corresponds to the infection peaking.

$$\frac{N}{R_0} = S \iff \frac{dI}{dt} = 0 \quad (12)$$

This suggests the derivative is strictly positive when condition 13 is met.

$$S > \frac{N}{R_0} \iff \frac{dI}{dt} > 0 \quad (13)$$

And strictly negative when condition 14 is met.

$$S < \frac{N}{R_0} \iff \frac{dI}{dt} < 0 \quad (14)$$

Since it's assumed that $S \gg I$ at $t = 0$, condition 13 will always be met and I will increase. However as S decreases, the rate of infections slows until condition 14 is met. After this, it's impossible I to increase or remain stable so it begins to shrink to zero. Therefore $\frac{dS}{dt}$ and $\frac{dR}{dt}$ approach zero and thus the compartments of S and R must always approach a stable value. This proves that $S(\infty) + R(\infty) = N$ and $I(\infty) = 0$. Computing these stable values requires an expression relating S to R and this can be done by diving the first SIR equation by the third SIR equation and integrating.

$$\frac{dS}{dR} = -\frac{R_0}{N} S \quad (15)$$

$$\int_{S(0)}^{S(t)} \frac{dS}{S} = \int_0^{R(t)} -\frac{R_0}{N} dR \quad (16)$$

$$\ln S(t) - \ln S(0) = -\frac{R_0}{N} R(t) \quad (17)$$

Rearranging gives the following expression, where the boundary condition of $R(0) = 0$ has been applied.

$$S(t) = S(0) \exp\left(-\frac{R_0}{N} R(t)\right) \quad (18)$$

Similarly, the system can also be solved for I in terms of S by dividing the first SIR equation by the second SIR equation (see appendix). Taking the limit as $t \rightarrow \infty$ gives expressions for $S(\infty)$ and $R(\infty)$ which are both of a finite value.

$$S(\infty) = S(0) \exp\left(-\frac{R_0}{N} R(\infty)\right) \quad (19)$$

$$S(\infty) = S(0) \exp\left(-\frac{R_0}{N} (N - S(\infty))\right) \quad (20)$$

$$S(\infty) = S(0) \exp(-R_0) \exp\left(\frac{R_0 S(\infty)}{N}\right) \quad (21)$$

$$S(0) \exp(-R_0) = S(\infty) \exp\left(-\frac{R_0 S(\infty)}{N}\right) \quad (22)$$

$$-\frac{R_0}{N} S(0) \exp(-R_0) = -\frac{R_0 S(\infty)}{N} \exp\left(-\frac{R_0 S(\infty)}{N}\right) \quad (23)$$

The solution for $S(\infty)$ in this equation is of the form for the Lambert-W function. Which is defined as the inverse of the function $f(x) = xe^x \therefore f^{-1}(x) = W(x)$. Where in this case only the range $N \geq x \geq 0$ is considered.

$$-\frac{R_0}{N} S(\infty) = W\left(-\frac{R_0}{N} S(0) \exp(-R_0)\right) \quad (24)$$

$$S(\infty) = -\frac{N}{R_0} W\left(-\frac{R_0}{N} S(0) \exp(-R_0)\right) \quad (25)$$

Evaluating the Lambert-W function can be done by substituting these values into a software package like scipy, and this was done for a continuum of R_0 values. This gives a plot of all possible stable states show below. For R_0 values less than one the system remains stable. As $R_0 \rightarrow \infty, S(\infty) \rightarrow 0$ however the returns are diminishing for larger R_0 values.

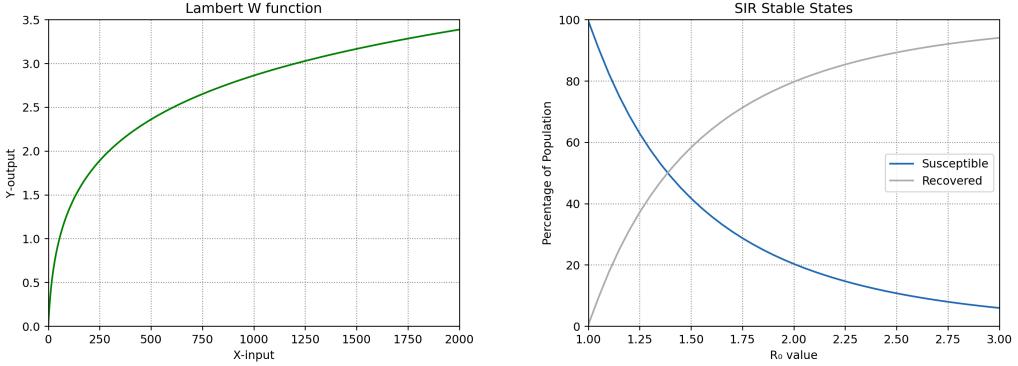


Figure 3: On the left the generic Lambert-W function is shown. On the right the possible stable states for varying R_0 are shown. In the SIR model, the final outcome of the system is dependant only on R_0 and the initial states of the system.

1.4.3 Numerical Solutions

While the above analysis is useful for proving properties, graphing the system still requires numerical integration. For these models two methods of numerical evaluation are considered. The first is the standard method where a computer is programmed to calculate a running total equivalent to expressing the integral in sigma notation. An arbitrary time step is used with smaller time steps giving more accurate results at the cost of being more expensive to compute. For this method, $dt = 0.01$ was used with a total time of 1000 days with $\beta = 0.18$ and $\gamma = 0.1$. The properties that were proved above can be seen visually, like the infection peaking and dying out while S and R approach stable states.

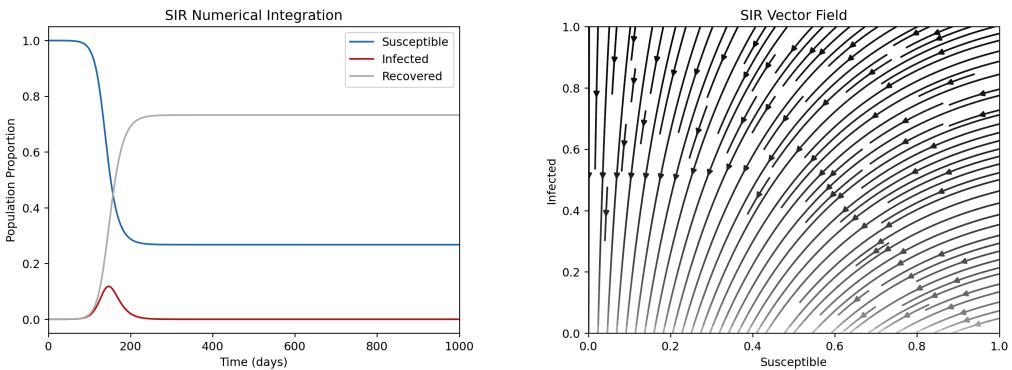


Figure 4: Two methods of numerical evaluation are shown here. On the left is the classical method, and on the right is the vector field method. The vector field plotted above omits the R axis because the magnitude of the R compartment can be inferred through the constant population

The second method uses vector field evaluation. Every possible state of system is defined by the variables S , I , and R , meaning the system is described a point in a 3D phase space. The compartments changing is analogous to the point moving in phase space where it must move in accordance to the coupled system. By taking the derivative

at each point and substituting in the coupled system, a vector field is defined that the point flows with. The vectors of ten thousand evenly spaced points were calculated, each axis having one hundred grid spacing each with $\beta = 0.3$ and $\gamma = 0.4$. It has been shown that point approaches stability by having the infected compartment shrink to zero. This is illustrated as the vector field always brings the points towards the I -axis no matter the starting condition, showing visually that the infection always dies out in the SIR model. What's more is that the vector field is not time dependant. The vector field can illustrate either the point reaching stability or flowing in motion forever. While traditional numerical integration is restricted with the specified temporal window, vector fields are restricted by the specified spatial window. Both can be used when appropriate.

1.5 SIRS

1.5.1 Definition

While the SIR model is powerful it is most accurate when infections give lasting immunity, however it is known that COVID-19 only gives immunity for several months after recovery [14]. When applying the SIR model to COVID-19 the implicit assumption is that the total number of infections is small compared to the total population. Compartmental models are created to be tailored to a specific illness so while the SIR model may be perfect for describing measles which gives lasting immunity, it's inaccurate for something like COVID-19. To account for this inaccuracy an immunity loss term ψR is introduced to the SIR model, added to $\frac{dS}{dt}$ and subtracted from $\frac{dR}{dt}$ to ensure a constant population. The immunity loss factor also has units of $[T]^{-1}$, therefore, $\frac{1}{\psi}$ equals the average immune period. Now people in R can move back into S at a rate proportional to the number of people recovered since a greater number of recoveries must result in a greater loss of immunity. This is called the SIRS model.

$$\frac{dS}{dt} = -\beta \frac{IS}{N} + \psi R$$

$$\frac{dI}{dt} = \beta \frac{IS}{N} - \gamma I$$

$$\frac{dR}{dt} = \gamma I - \psi R$$

1.5.2 Analysis

The extra term makes it easier to calculate fixed points which can now be done by setting all the differential equations in the system equal to zero, and solving for the three unknown values.

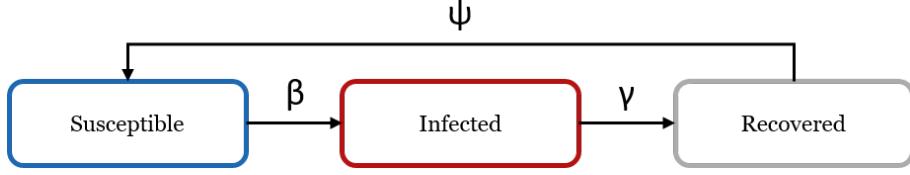


Figure 5: The transmission flow diagram for the SIRS model. β Represents the contact rate, γ represents the recovery rate, and ψ represents the immunity loss rate.

$$0 = -\beta \frac{IS}{N} + \psi R$$

$$0 = \beta \frac{IS}{N} - \gamma I$$

$$0 = \gamma I - \psi R$$

$$N = S + I + R$$

From inspection, the system is fixed when $S = N$, $I = 0$ and $R = 0$ which corresponds to a pre-pandemic population. However, finding endemic fixed points requires some algebraic manipulation of the above system which leads to the following relationships.

$$R = \frac{\gamma}{\psi} I \quad (26)$$

$$S = \frac{\gamma}{\beta} N \quad (27)$$

These expression can be substituted back into the fixed population equation to obtain a solution to I .

$$N = I + \frac{\gamma}{\psi} I + \frac{\gamma}{\beta} N \quad (28)$$

Which shows that at the endemic fixed point the values of S, I, R are dependant on the constants and the population. Unlike the SIR model, the endemic fixed point is independent of the initial conditions.

$$S = \frac{\gamma}{\beta} N$$

$$I = P_0 N$$

$$R = \frac{\gamma}{\psi} P_0 N$$

$$P_0 = \frac{1 - \frac{\gamma}{\beta}}{1 + \frac{\gamma}{\psi}}$$

These solutions give an infinite number of possible endemic states, however only a subset of these states are valid. The restriction $\gamma, \beta, \psi > 0$ is applied since negative coefficients imply backwards movement between compartments and vanishing coefficients implies no movement between compartments. With this restriction in place the nature of the fixed points can be deduced. Fixed points can be either stable or unstable, a stable fixed point indicates that a small perturbation results in the system returning to it's initial state, and an unstable fixed point indicates that a small perturbation results in the system accelerating away from it's initial state. When modelling a pandemic it's intuitively obvious that an entirely susceptible population represents a unstable fixed point and an endemic state represents a stable fixed point. However to rigorously prove this fact, the Jacobian matrix defined by the coupled system needs to be considered.

$$J = \begin{pmatrix} -\beta \frac{I}{N} & -\beta \frac{S}{N} & \psi \\ \beta \frac{I}{N} & \beta \frac{S}{N} - \gamma & 0 \\ 0 & \gamma & \psi \end{pmatrix} \quad (29)$$

Finding the eigenvalues of this matrix when evaluated at the fixed points will shed insight on the nature of the stable states. If at least one eigenvalue has real part that is positive then it implies the fixed point is unstable, otherwise the fixed point is stable. Substituting the fixed point of $S = N, I = 0, R = 0$ and calculating the eigenvalues results in the following expression.

$$\det |J - \lambda I| = 0 \quad (30)$$

$$\det \begin{vmatrix} -\lambda & -\gamma & \psi \\ 0 & \beta - \gamma - \lambda & 0 \\ 0 & \gamma & -\psi - \lambda \end{vmatrix} = 0 \quad (31)$$

$$-\lambda * \det \begin{vmatrix} \beta - \gamma - \lambda & 0 \\ \gamma & -\psi - \lambda \end{vmatrix} = 0 \quad (32)$$

$$-\lambda (\beta - \gamma - \lambda) (-\psi - \lambda) = 0 \quad (33)$$

$$\begin{aligned}\lambda &= -\psi \\ \lambda &= \beta - \gamma \\ \lambda &= 0\end{aligned}$$

The second eigenvalue is positive if $\beta > \gamma$, therefore proving that an entirely susceptible population is an unstable fixed point if this condition is met. Following the same procedure for an endemic state leads to the following expression.

$$J = \begin{pmatrix} -\beta P_0 & -\gamma & \psi \\ \beta P_0 & 0 & 0 \\ 0 & \gamma & -\psi \end{pmatrix} \quad (34)$$

$$\det \begin{vmatrix} -\beta P_0 - \lambda & -\gamma & \psi \\ \beta P_0 & -\lambda & 0 \\ 0 & \gamma & -\psi - \lambda \end{vmatrix} = 0 \quad (35)$$

$$(-\beta P_0 - \lambda) \begin{vmatrix} -\lambda & 0 \\ \gamma & -\psi - \lambda \end{vmatrix} + \gamma \begin{vmatrix} \beta P_0 & 0 \\ 0 & -\psi - \lambda \end{vmatrix} + \psi \begin{vmatrix} \beta P_0 & -\lambda \\ 0 & \gamma \end{vmatrix} = 0 \quad (36)$$

Which results in the below cubic equation.

$$\lambda^3 + (\beta P_0 + \psi) \lambda^2 + (\beta P_0 \psi + \beta P_0 \gamma) \lambda = 0 \quad (37)$$

First Eigenvalue: From inspection the first eigenvalue can be ignored because it equals zero which indicates neutral stability.

$$\lambda^2 + (\beta P_0 + \psi) \lambda + \beta P_0 \psi + \beta P_0 \gamma = 0 \quad (38)$$

Second Eigenvalue: Solving the remaining quadratic gives the form of the other two eigenvalues. If \pm is negative then the eigenvalue will also be negative since b is positive and the square root term results in either a positive or imaginary value.

$$\lambda = \frac{-b \pm \sqrt{b^2 - 4ac}}{2a}. \quad (39)$$

$$0 > -b - \sqrt{b^2 - 4ac} \quad (40)$$

Third Eigenvalue: When \pm is positive and the square root term leads to an imaginary value, the condition for a negative eigenvalue is as follows.

$$0 > -b \quad (41)$$

$$\beta P_0 + \psi > 0 \quad (42)$$

b, c , and P_0 are all positive therefore the condition will always hold and the eigenvalue will be negative. If the square root does not lead to an imaginary term, both sides will be positive and thus both sides can be squared while maintaining the inequality.

$$b^2 > b^2 - 4ac \quad (43)$$

$$0 > -4ac \quad (44)$$

$$0 > -4(\beta P_0 \psi + \beta P_0 \gamma) \quad (45)$$

Again, because all the terms in this expression are positive, the inequality is always true therefore the third eigenvalue is always negative. All three eigenvalues for the endemic fixed points are always negative, thus proving that the endemic state is a stable fixed point. While finding the stable endemic states is easier in the SIRS system, finding solutions in terms of the other unknowns can only be done in integral form. To find a solution to $I(t)$ in integral form the second SIRS equation is rearranged and integrated.

$$\int_{I(t_0)}^{I(t_f)} \frac{dI}{I} = \int_{t_0}^{t_f} \beta \frac{S(t)}{N} - \gamma dt \quad (46)$$

$$\ln \left(\frac{I(t_f)}{I(t_0)} \right) = -\gamma t_f + \gamma t_0 + \int_{t_0}^{t_f} \beta \frac{S(t)}{N} dt \quad (47)$$

$$I(t_f) = I(t_0) \exp \left(-\gamma t_f + \gamma t_0 + \int_{t_0}^{t_f} \beta \frac{S(t)}{N} dt \right) \quad (48)$$

An expression for R is found by rearranging the third SIRS equation into a form where an integrating factor can be used.

$$\frac{dR}{dt} + \psi R(t) = \gamma I(t) \quad (49)$$

$$I.F. = e^{\psi t} \quad (50)$$

$$e^{\psi t} \frac{dR}{dt} + e^{\psi t} \psi R = e^{\psi t} \gamma I \quad (51)$$

$$\frac{d}{dt} (e^{\psi t} R) = e^{\psi t} \gamma I \quad (52)$$

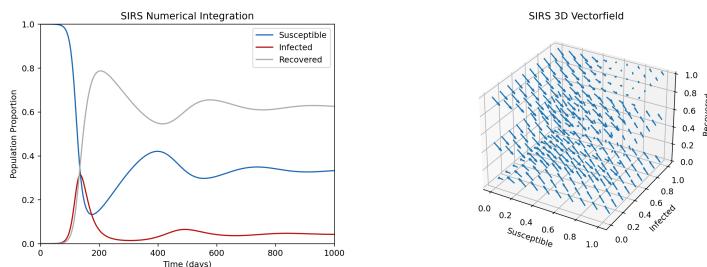
$$R(t_f)e^{\psi t_f} - R(t_0)e^{\psi t_0} = \int_{t_0}^{t_f} e^{\psi t} \gamma I(t) dt \quad (53)$$

$$R(t_f) = R(t_0)e^{\psi(t_0-t_f)} + \gamma e^{-\psi t_f} \int_0^{t_f} I(t)e^{\psi t} dt \quad (54)$$

A solution for S can be found with either an integration factor or by substituting the previous expressions into the constant population equation. However because these expressions are large, they are left in the appendix for the reader. These incomplete solutions can now be analysed, in equation 54 the integral term trends towards zero as a smaller $t_f - t_0 \rightarrow 0$ is considered, therefore, close to the initial time the function behaves as an inverse exponential. Furthermore, because the only way to add susceptible people into the system is for them to come from recovered individuals it can be said that S also behaves as an exponential close to initial time. What this implies is that the full solutions of these equations can be written as a sum of exponentials. While an exact solution to all three equations can be deduced by assuming the form of an exponential series [5], this is beyond the scope of this project.

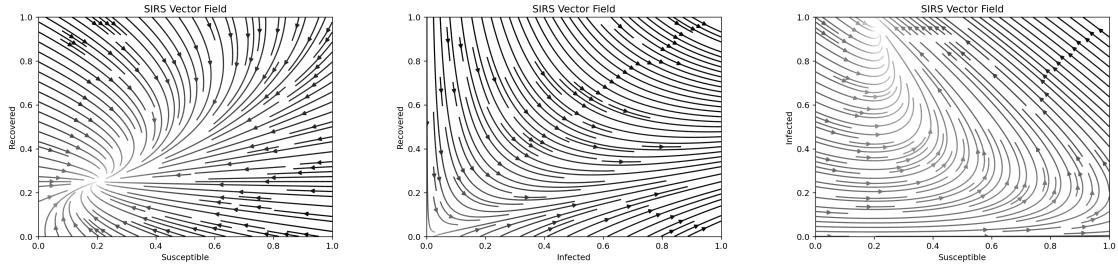
1.5.3 Numerical solutions

As stated before graphing the system still requires numerical integration. The values that were used in the classical numerical integration below were $\beta = 0.05$, $\gamma = 0.15$, and $\psi = 0.0035$. The time-step used was $dt = 0.01$ with a total time of 1000 days. These numerical solutions show visually that all compartments approach fixed values and that secondary outbreaks occur before settling into stability. This is a feature seen in real pandemics that was missing from the SIR model.



As before, each state can be associated with a point in 3D phase space, however, because the number of recovered individuals is not strictly increasing the susceptible-infected vector field gives less information. This means the phase space has to be visualised as either a 3D vector field or as 2D slices of the 3D vector field. All SIRS vector fields

have coefficients of $\beta = 0.05$, $\gamma = 0.01$, $\psi = 0.02$ and each 2D slice of the 3D space has a missing axis set to a value of 0.5. The 3D diagram vector has three hundred vectors with ten along S and I , and three along R . The 2D diagrams represent one thousand six hundred vectors with forty along each axis. Rather than trending towards to I -axis, vectors trend towards "sinks" in the phase space which shows visually that all points trend to a fixed endemic state that's represented as a point in the phase space.



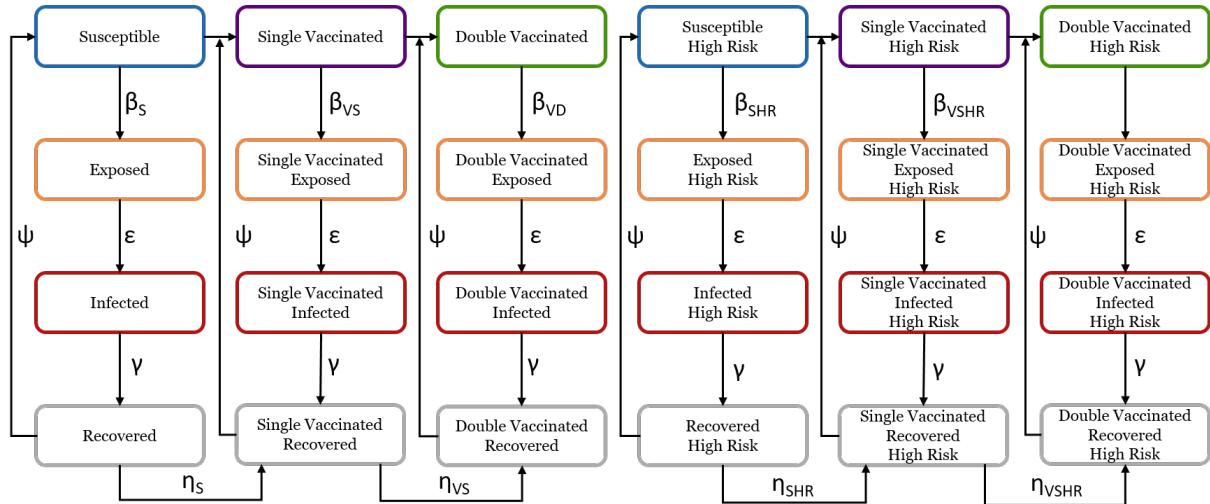
1.6 COVIDGE

1.6.1 Definition

SIRS is a good model for COVID-19, but no model is correct and all models can be improved. Below is a list of features and simplifying assumptions for COVID-19 that can be incorporated into a new larger model.

- All individuals are initially susceptible, except for the index case who is initially exposed.
- All exposed individuals to COVID-19 will have an incubation period where they do not display symptoms.
- Recovery from the infection results in a temporary period of immunity.
- People who are vaccinated (1st dose) are less likely become infected.
- People who are fully vaccinated (2nd dose) are even less likely to become infected.
- Only susceptible and recovered individuals are vaccinated.
- Only vaccinated individuals are fully vaccinated.
- A certain number of individuals are considered "high risk" meaning they are more likely to contract the infection and die.
- Births are proportional to the total population and are considered susceptible.
- Deaths are subtracted from each compartment and are proportional their respective compartment size.
- People that are in the Infected compartment have a higher chance of death, and only die of COVID-19.

To construct this model, which has been named COVIDGE, begin with the SIRS model. To incorporate an incubation period a new compartment E (exposed) is added, where new infections fall into exposed before moving into I at a rate ϵ . Exposed individuals are also considered to be contagious, therefore the term $\pm\beta \frac{IS}{N}$ is modified to $\pm\beta \frac{(E+I)S}{N}$. Exposed and infected terms are always added like this when a new contagious compartment has been created. Currently, this is a SEIRS model and it satisfies the first three conditions. Next a compartment called SV (single-vaccinated) is added and a vaccination term proportional S is subtracted from the susceptible compartment and added to the single-vaccinated compartment. Then a SEIRS loop is constructed for single-vaccinated individuals with the recovered compartment's vaccination rate proportional to and subtracted from R with it being added to the new SVR (single-vaccinated-recovered) compartment. A third SEIRS loop is added for DV fully-vaccinated individuals, with individuals being imported from the single-vaccinated loop in the same manner. Then the whole model is duplicated again, this time with each compartment being an equivalent system for "High-risk" individuals. After all of this, terms representing births are added to both susceptible compartments where they are proportional to the total population. Similarly, deaths are subtracted from each compartment with all compartments having their deaths proportional to themselves. Every category has an equal death rate, except for those in the infected category who have a higher death rate due to COVID-19. This results in a total of twenty four compartments, illustrated below. See the appendix for the full system of differential equations.



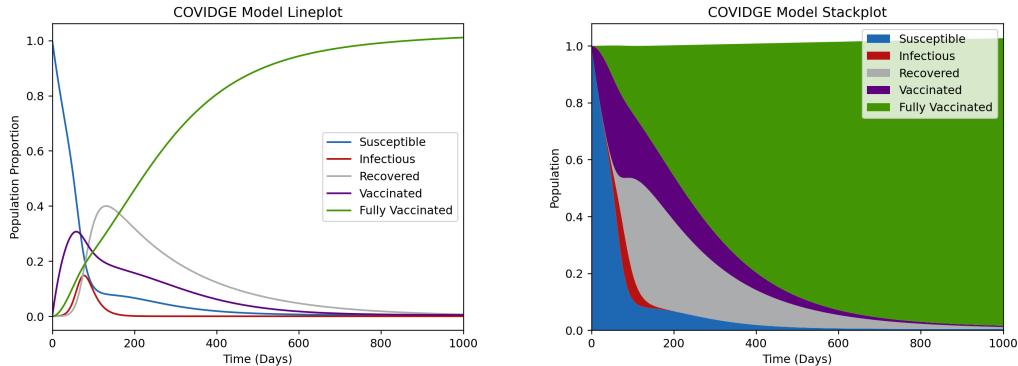
1.6.2 Analysis

While this model is far larger than any other model previously considered, the COVIDGE model is easier to understand when considered as six interacting SEIRS loops. It has been proven that a SEIRS system with a variable population will trend towards a stable fixed endemic state [10] and these states can be found by setting all derivatives to zero and solving for the unknowns as was done for the SIRS model.

$$\begin{aligned}
S &= \frac{\gamma}{\beta(1 + \frac{\gamma}{\varepsilon})} N \\
E &= \frac{\gamma}{\varepsilon} P_1 N \\
I &= P_1 N \\
R &= \frac{\gamma}{\psi} P_1 N \\
P_1 &= \left(\frac{1 - \frac{\gamma}{\beta(1 + \frac{\gamma}{\varepsilon})}}{1 + \frac{\gamma}{\varepsilon} + \frac{\gamma}{\psi}} \right)
\end{aligned}$$

It can therefore be argued that the nature of the COVIDGE model is to also approach a stable fixed point. The only difference being stability is constantly interrupt by births, deaths, and vaccinations. The vaccination rate causes S and R to shrink while SV and SVR grow. Once everyone have been vaccinated, the same happens for a second dose until the entire population has been moved into DV and DVR . After this the system is stuck in two SEIRS loops since the same occurs for the high risk portion of the model. The birthrate may add new susceptible people and deaths may subtract individuals from each compartment. But if both these rates are assumed to be negligible in size compared to the vaccination rate then S , SHR , SV and $SVHR$ will shrink close to zero. The stable fixed points of the DV and $DVHR$ loops can then be added together to find the endemic state of the whole model with the added caveat of the total population changing, thus requiring a non-constant N for the stability equations.

1.6.3 Numerical Solutions



Unfortunately, vector fields when plotted give little information for this model. The state of the COVIDGE model occupies a 24D phase space, therefore, while vectors fields are still effective abstractly, plotting any two of these dimensions gives very little information. However, classical numerical integration can still produce effective results. To make the plot clearer, all susceptible, infectious, recovered, single-vaccinated, and double-vaccinated compartments are added together. It can be seen that S and SV shrink to

zero while DV grows. Eventually, DV , DVE , DVI , and DVR will exist in a semi-stable state with new births and deaths causing the vaccinated population increase as it becomes impossible for susceptible and single vaccinated individuals to grow when the birthrate is lower than the vaccination rate. This indicates that in order to ensure a fully vaccinated population is maintained, the vaccination rate must be greater than the birth rate. The standard line plot is ideal for showing when infections peak, however, the plot can become cluttered justifying the provided stack plot. The coefficients used for the above numerical integration can be found in the appendix.

1.7 Grid based pandemics

While these numerical models are invaluable, they are based in calculus which means that they rely on the assumption that the compartments are continuous variables. This is not the case in reality where the population has to be an integer. To combat this a pandemic needs to be simulated in a way that is an analogue of reality, which can be done with a grid based simulation. In these simulations the population is represented as squares in a 2D grid with each grid square representing an individual. Each individual is coloured to fit into one of the compartments. The SIR grid then updates after each day with the following rules: If a susceptible grid square is adjacent to an infectious grid square then there is a probability the susceptible grid square will become infectious, if infected grid square has a probability of recovery on each day. This is similar to John Conway's game of life [7] except with probabilistic rules that can be modified to fit any desired model. This system has various advantages compared to numerical integration other than a discrete population. One of the values that is often measured is the speed of spread of a pandemic, this is impossible with numerical integration but easy in a grid based simulation. It reveals facts about herd immunity as recovered individuals can physically surround susceptible individuals, and a graphical simulation can tell a more visceral story of a pandemic which improves communication. Throughout this project, grid based simulations were used to confirm that the differentials systems that were defined followed a model that more closely resembled reality.

2 Methods

2.1 Calculating Corrected Cases

To estimate the true number of cases during a period of limited testing, the death to case ratio was calculated. This ratio is only accurate however if an appropriate time period is considered where testing was high and vaccination was low. The first case of COVID-19 in the UK was confirmed on 30 January 2020 [2], however, it wasn't until 18 May 2020 that everyone with symptoms was eligible for a COVID-19 test [4]. Furthermore, on 8 December 2020 the first clinically approved vaccine was administered [3]. Therefore between May and December the data most accurately reflects the true death to case ratio, cases documented before May are likely to be far lower than the true value. This ratio was computed by dividing the total number of cases by the total number of deaths on each day and then computing the mean, making sure to shift cases backwards in time by fourteen days to account for the time delay between infection and death. This ratio

was then multiplied by the number of deaths on each day to get an estimate of the true the number of cases and then this data was also shifted backwards in time by fourteen days to once again account for the time delay between infection and death.

2.2 Numerical integration

The numerically integrated graphs were generated with the numpy and matplotlib libraries. Object oriented programming was used to improve the modularity of the code as well as aiding in the management of the various coefficients. For the SIR model an object class called *SIR_MODEL()* was created, containing attributes corresponding to the total integration time, time-step, total population, the initial values for S and I , and the values of the coefficients γ and β . Numerical integration was then carried out in method called *Num_Int()* which defined lists with initial values for each compartment, a fixed loop of size dependant on total time and time-step then appends the values to the lists. Each iteration of the loop calculated the current value of the differential equation, and multiplied this value by the time-step to obtain the compartment's small perturbation. This value was then added to the compartment's current value and then appended to the appropriate list. These lists could then be plotted with the *plt.plot()* function. The same procedure was carried out for the other models, with the only difference being the differential equations that were integrated and compartments being displayed.

2.3 Adaptive integration

While constant coefficients can confirm a model's validity, it is generally not how pandemics play out. This is because governments respond to an illness with lockdowns if the number of infections is high which decreases the contact rate. To replicate this, adaptive models were created. These models were identical to the above numerical integration with a constant contact rate, however, if the number of infections reached a threshold the contact rate was decreased with an *if* statement inside the fixed loop. If the number of infections fell below the threshold then the contact rate was then reverted back to it's initial value. This simulated a government going in and out of lockdown as was seen in reality. In the COVIDGE model, the vaccination rate was set to zero below the threshold and set to a constant value permanently after the number of infections passed the threshold.

2.4 Data integration

Furthermore, there was an attempt to replicate the infection curve observed in the UK by feeding the models a time dependant contact rate based on reality. All other coefficients were assumed to be constant throughout³. The time dependant contact rate was obtained by using Our World in Data's estimated reproduction rate that was updated daily. All these values were then multiplied by the chosen γ to recover β . This was then imported into a list and the fixed loop responsible for the numerical integration called the next item in this list to obtain it's β value for that iteration which simulated a time dependant function. The same procedure was carried out for the SIRS and COVIDGE models with

³The vaccination rate was set to zero until December 8 and had a constant value afterwards

their respective differential equations. After this, the beta value was then multiplied by a variable called the *ContactFactor*, this allowed for the scaling of the contact rate which could represent a lockdown that was slightly more or less effective.

2.5 Creating Vector fields

To create vector fields in *matplotlib* the *np.meshgrid()* function was used to create a grid with arguments of the *np.linspace()* function to ensure even spacing. The components of the vectors at each point was then calculated by defining the differential equations in python and substituting the output values from the *np.meshgrid()* function in as unknowns. The grid and vectors could then be plotted with the *np.streamplot()* function. For the 3D vector field the *np.quiver()* function was used with a wider z-axis spacing to ensure clarity.

2.6 Calculating Coefficients

Before any of these models could be used to realistically simulate COVID-19, the coefficients seen in reality needed to be calculated. Simplifying assumptions sometimes had to be made, an example being that high risk individuals were assumed to make up about ten percent of the population. While these coefficients are based on fact, they are still estimates. Therefore it will be specified if the coefficients are modified in the model to give a more accurate result.

Birth Rate (α): This was calculated by measuring the average number of people born each day, and dividing it by the average population in 2020. This value was calculated to be $\alpha = 2.78363 \times 10^{-5}$ and this was constant for all time. [11]

Death Rate (μ): This was calculated by dividing the total number of new deaths by the average population in 2020. The value was calculated to be $\mu = 2.48321 \times 10^{-5}$ and was constant for all time. [11]

COVID Death Rate (μ_C): This was calculated by dividing the total number of deaths caused by COVID-19 by the total number of cases. The value was calculated to be $\mu = 8.95027 \times 10^{-4}$ and was constant for all time. [11]

Contact Rate (β): This was the only time dependant variable that was considered in the data models and was calculated from Our World in Data's estimated reproductive rate as described above. For the adaptive models, the average contact rate from before lockdown was calculated and defined as the high contact rate $\beta = 0.206$, while the average contact rate for the period during lockdown was defined as the low contact rate $\beta = 0.118$ with all other contact rates in the adaptive models being an interpolation between these two values. It is difficult to calculate how much more susceptible high risk individuals are, therefore it is assumed that the contact rate is doubled for high risk individuals. The first dose of the vaccine is said to be 81% effective, and the second dose is said to be 91% effective, therefore the base contact rate for the vaccinated and fully vaccinated compartments was multiplied by 0.19 and 0.09 respectively. [6] [11]

Latency Rate (ε): This coefficient is equal to the reciprocal of the average incubation period. This incubation period was found to be roughly six days therefore $\varepsilon = \frac{1}{6} = 0.167$ and was constant for all time. [12]

Recovery Rate (γ): The recovery rate is equal to the reciprocal of the recovery time. This time can vary from several days to months. However the mean recovery time was found to be fourteen days, therefore the recovery rate was defined as $\gamma = \frac{1}{14} = 0.0714$ and is constant for all time. [14]

Immunity Loss Rate (ψ): The immunity loss rate is equal to the reciprocal of the average immune period. It was discovered that antibodies are produced for up to seven months after infection, therefore the immunity loss factor was defined as $\psi = \frac{1}{210} = 0.00476$, which was constant for all time. [13]

Vaccination Rate (η): During the peak of the vaccination program, the UK managed to vaccinate roughly three hundred thousand people per day. Dividing this number by the total number of people in S and R gives an estimate for the vaccination rate. To simplify calculations, $S + R$ is approximated as the entire population, this gives a vaccination rate of roughly $\frac{1}{300}$ which is rounded to an order of magnitude approximation of $\frac{1}{100}$. High risk individuals have a vaccination rate of $\frac{1}{50}$ with the reasoning being the speed of vaccinations is doubled for high risk individuals. This is not constant for all time, the vaccination rate is set to zero until day 313 (December 8), whereupon it is set to these constant values. [8]

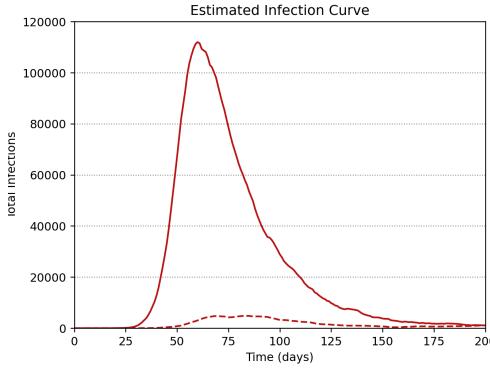
2.7 Grid simulations

To create the grid based simulations for the SIR model a function called `setup_grid_centre()` was defined, which created an arbitrarily sized square 2D numpy array. Each value in the array was set to the integer 1 (susceptible) except for the centre element which was set to 3 (infected), recovered squares were represented with 5. A new function was then written called `grid_frame_update()` which created a copy of the 2D array and iterated over each element in a 2D loop. Each element in this new array was updated with the previously defined rules in an *if* statement with the `random` package imported to create the probabilistic portions of the model. Once every element had been iterated over the updated array was returned. This function was used in a fixed loop where on each iteration the array was updated and counts of S , I , and R were appended to lists. After this loop had been completed the S , I , and R lists were plotted with `matplotlib`. Optionally, the array can be animated with the `imshow` function. The same procedure was then carried out with the SIRS and COVIDGE models, with the only difference being the applied rules.

3 Results & Discussion

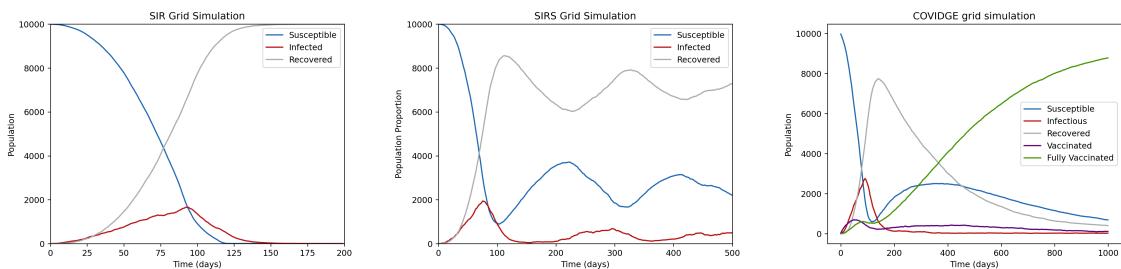
3.1 Corrected Infection Curve

When the case to death ratio for COVID-19 is multiplied by the total number of deaths the below infection plot is obtained.



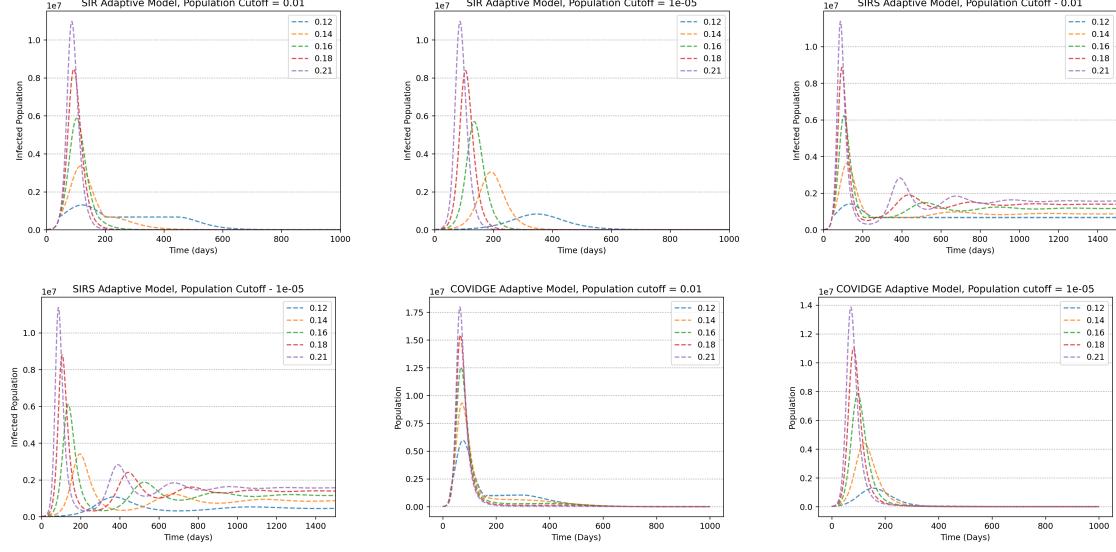
In 2021 infections reached a peak of sixty thousand people per day, this estimate for 2020 produced more than one hundred thousand cases for a similar number of deaths. This was contrary to what was predict, which was a similar peak for a similar number of deaths. This can be explained by how in 2020 COVID-19 was novel with almost nobody having immunity. By the time the second wave hit in 2021 there was a degree of herd immunity meaning that there were fewer cases overall. The cases in 2021 would then have been the people who where the most susceptible and thus had a higher chance of death. However, this can also be explain through inaccuracies in the data, such as deaths from COVID-19 being counted liberally or false positives when testing. Further investigation is required to take these factors into account to obtain a more accurate death to case ratio.

3.2 Grid Based Models



When the compartments are plotted from the grid based model the following plots are obtained. All plots show agreement with the numerically integrated graphs which justifies the definitions of the differential equations. Some noise does appear in the data, however, this can be easily explained through the probabilistic nature of the simulations. What matters is that the overall form of the grid based curves is the same as the numerically integrated curves.

3.3 Adaptive Models



The above plots have a high contact rate of 0.208, the values in the legend indicate the respective lowered contact rates. All adaptive models failed to replicate the true infection curve in the UK, but they still gave some key insights. All three models suggest that going into lockdown sooner causes there to be fewer infections overall. What's more, a strict lockdown extends the duration of a pandemic and lowers the overall peak of infections. This is what flattening the curve is and it is vital in ensuring that emergency services are not overwhelmed. In the SIRS model, it can also be seen that a stricter lockdown results in a lower point of stability, however, this is somewhat undone when lockdown is lifted. All of this suggests that lockdown should be as strict as possible and be implemented as soon as possible to minimise cases and deaths. However, lockdown is not an ideal solution as it guarantees economic damage. Also because lockdown extends the lifetime of a pandemic, it suggests that lockdown should only be put in place if the infection is dangerous.

3.4 Data Models

Please refer to the Appendix for graphs. By using real data, it can be estimated what would have happened if the same lockdowns were put in place only with slightly more or less effect. The SIRS models (as expected) more closely resemble the true infection curve because they account for lost immunity which creates a larger and more accurate peaks in 2022. However, what can be gathered overall from these results is that the models are incredibly sensitive. A contact rate that is ten percent greater, corresponding to $ContactFactor = 1.1$, causes more than a million infections. Conversely, a contact rate that is ten percent smaller, corresponding to $ContactFactor = 0.9$, causes fewer than ten thousand infections. What this suggests is that lockdowns should be gradually released as sudden change in contact rate can easily cause a second wave. The COVIDGE model was the least accurate when the same procedure was carried out as it always predicted a peak of over a million infections, with infections strangely dropping when the contact factor

was increased. The COIVDGE model provided more accurate results if the incubation period approached zero. Therefore, this suggests further investigation is required for the exposed compartment.

3.5 Challenges and Further study

One of the challenges that was encountered when completing this project was the creation of the large model. It was difficult to derive equations for the various models, especially when the model required a large set of differential equations. It increased the programming challenge greatly as solutions that were adequate for smaller models were impractical for large models. Often, the model had to be changed throughout the project when new studies were found to better fit the discovered evidence. If this were to be repeated I would ensure a firm understanding of the infection in question before constructing a large model to make debugging easier. I would also use a more accurate vaccination rate and modify the model to include booster vaccines. For further study I would suggest the creation of an even more detailed model which considered the variants of COVID-19. Many variants were identified over the pandemic and my exclusion of them in these models probably caused some inaccuracies. However, this would have resulted in an non linear growth in the number of compartments for each variant considered.

4 Conclusion

These models provide a clear insight into the nature of pandemics and advise on how to proceed without treatments. If a illness is confirmed to be deadly and highly infectious, then a strict lockdown should be implemented as quickly as possible to reduce the number of deaths. This will flatten the infection curve ensuring that emergency services are not overwhelmed. Once an effective vaccine has been created, then as many eligible people as possible should be given the vaccine to lower the number of infections that will be present in the endemic state. After this, lockdown can be gradually lifted to prevent a second wave. However, lockdowns cause immediate economic harm which may hinder a government's ability to develop an effective treatment. Therefore, lockdowns should only be implemented for an illness that is both infectious and deadly.

References

- [1] Who coronavirus (covid-19) dashboard.
- [2] Coronavirus: Two cases confirmed in uk, 2020.
- [3] Covid-19 vaccine: First person receives pfizer jab in uk, 2020.
- [4] Everyone in the united kingdom with symptoms now eligible for coronavirus tests, 2020.
- [5] L. Acedo, Gilberto González-Parra, and Abraham J. Arenas. An exact global solution for the classical sirs epidemic model. *Nonlinear Analysis: Real World Applications*, 11(3):1819–1825, 2010.
- [6] Centers for Disease Control and Prevention. Cdc covid-19 study shows mrna vaccines reduce risk of infection by 91 percent for fully vaccinated people, 2021.
- [7] Mathematical Games. The fantastic combinations of john conway’s new solitaire game “life” by martin gardner. *Scientific American*, 223:120–123, 1970.
- [8] Uk Government. Vaccinations inunited kingdom, 2023.
- [9] William Ogilvy Kermack, A. G. McKendrick, and Gilbert Thomas Walker. 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, 1927.
- [10] Guichen Lu and Zhengyi Lu. Global asymptotic stability for the seirs models with varying total population size. *Mathematical biosciences*, 296:17–25, 2018.
- [11] Edouard Mathieu, Hannah Ritchie, Lucas Rodés-Guirao, Cameron Appel, Charlie Giattino, Joe Hasell, Bobbie Macdonald, Saloni Dattani, Diana Beltekian, Esteban Ortiz-Ospina, and Max Roser. Coronavirus pandemic (covid-19). *Our World in Data*, 2020. <https://ourworldindata.org/coronavirus>.
- [12] J.A. Quesada, A. López-Pineda, V.F. Gil-Guillén, J.M. Arriero-Marín, F. Gutiérrez, and C. Carratalá-Munuera. Incubation period of covid-19: A systematic review and meta-analysis. *Revista Clínica Española (English Edition)*, 221(2):109–117, 2021.
- [13] Tyler J Ripperger, Jennifer L Uhrlaub, Makiko Watanabe, Rachel Wong, Yvonne Castaneda, Hannah A Pizzato, Mallory R Thompson, Christine Bradshaw, Craig C Weinkauf, Christian Bime, et al. Orthogonal sars-cov-2 serological assays enable surveillance of low-prevalence communities and reveal durable humoral immunity. *Immunity*, 53(5):925–933, 2020.
- [14] Irena Voinsky, Gabriele Baristaite, and David Gurwitz. Effects of age and sex on recovery from covid-19: Analysis of 5769 israeli patients. *Journal of Infection*, 81(2):e102–e103, 2020.

A Appendices

$$\frac{dS}{dI} = \frac{-1}{1 - \frac{N}{R_0 S}} \quad (55)$$

$$\frac{dI}{dS} = -1 + \frac{N}{R_0 S} \quad (56)$$

$$\int_{I(0)}^{I(t)} dI = \int_{S(0)}^{S(t)} -1 + \frac{N}{R_0 S} dS \quad (57)$$

$$I(t) - I(0) = -S(t) + \frac{\gamma N}{\beta} \ln S(t) + S(0) - \frac{N}{R_0 S} \ln S(0) \quad (58)$$

$$I(t) = S(0) + I(0) + \frac{N}{R_0} \ln S(t) - \frac{N}{R_0} \ln S(0) - S(t) \quad (59)$$

$$I(t) = N - \frac{N}{R_0} \ln \left(\frac{S(t)}{N - I(0)} \right) - S(t) \quad (60)$$

$$S(t_f) = S(t_0) + \exp \left(- \int_{t_0}^{t_f} \beta \frac{I(t)}{N} dt \right) \int_{t_0}^{t_f} \psi R(t) \exp \left(\int_{t_0}^{t_f} \beta \frac{I(t)}{N} dt \right) dt \quad (61)$$

Parameters for initial COVIDGE model	Value
Total Time	1000 days
Time-step	0.01 days
Low Risk Population	0.1
High Risk Population	0.9
Low Risk Initial Exposures	0.00005
High Risk Initial Exposures	0.00005
Birth Rate	2.78363e-5
Death Rate	2.48321e-5
COVID Death Rate	8.95027e-4
Contact Rate	0.2
Latency Rate	0.167
Recovery Rate	0.1
Immunity Loss Rate	0.00476
High Risk Vaccination Rate	0.02
Low Risk Vaccination Rate	0.01
High Risk Full Vaccination Rate	0.02
Low Risk Full Vaccination Rate	0.01

$$\begin{aligned}
\frac{dS}{dt} &= \alpha_L N + \psi R - \left(\beta_S \frac{C}{N} + \eta_S + \mu \right) S & \frac{dV_S}{dt} &= \psi R_{VS} - \left(\beta_{VS} \frac{C}{N} + \eta_{VS} + \mu \right) V_S + \eta_S S \\
\frac{dE}{dt} &= \beta_S \frac{CS}{N} - (\epsilon + \mu) E & \frac{dE_{VS}}{dt} &= \beta_{VS} \frac{CV_S}{N} - (\epsilon + \mu) E_{VS} \\
\frac{dI}{dt} &= \epsilon E - (\gamma + \mu_C) I & \frac{dI_{VS}}{dt} &= \epsilon E_{VS} - (\gamma + \mu_{CVS}) I_{VS} \\
\frac{dR}{dt} &= \gamma I - (\psi + \eta_S + \mu) R & \frac{dR_{VS}}{dt} &= \gamma I_{VS} - (\psi + \eta_{VS} + \mu) R_{VS} + \eta_S R \\
\\
\frac{dV_D}{dt} &= \psi R_{VD} - \left(\beta_{VD} \frac{C}{N} + \mu \right) V_D + \eta_{VS} V_S & \frac{dS_H}{dt} &= \alpha_H N + \psi R_H - \left(\beta_{SH} \frac{C}{N} + \eta_{SH} + \mu \right) S_H \\
\frac{dE_{VD}}{dt} &= \beta_{VD} \frac{CV_D}{N} - (\epsilon + \mu) E_{VD} & \frac{dE_H}{dt} &= \beta_{SH} \frac{CS_H}{N} - (\epsilon + \mu) E_H \\
\frac{dI_{VD}}{dt} &= \epsilon E_{VD} - (\gamma + \mu_{CVD}) I_{VD} & \frac{dI_H}{dt} &= \epsilon E_H - (\gamma + \mu_{CH}) I_H \\
\frac{dR_{VD}}{dt} &= \gamma I_{VD} - (\psi + \mu) R_{VD} + \eta_{VS} R_{VS} & \frac{dR_H}{dt} &= \gamma I_H - (\psi + \eta_{SH} + \mu) R_H \\
\\
\frac{dV_{SH}}{dt} &= \psi R_{VSH} - \left(\beta_{VSH} \frac{C}{N} + \eta_{VSH} + \mu \right) V_{SH} + \eta_{SH} S_H & \frac{dV_{DH}}{dt} &= \psi R_{VDH} - \left(\beta_{VDH} \frac{C}{N} + \mu \right) V_{DH} + \eta_{VS} V_S \\
\frac{dE_{VSH}}{dt} &= \beta_{VSH} \frac{CV_{SH}}{N} - (\epsilon + \mu) E_{VSH} & \frac{dE_{VDH}}{dt} &= \beta_{VDH} \frac{CV_D}{N} - (\epsilon + \mu) E_{VDH} \\
\frac{dI_{VSH}}{dt} &= \epsilon E_{VSH} - (\gamma + \mu_{CVSH}) I_{VSH} & \frac{dI_{VDH}}{dt} &= \epsilon E_{VDH} - (\gamma + \mu_{CVDH}) I_{VDH} \\
\frac{dR_{VSH}}{dt} &= \gamma I_{VSH} - (\psi + \eta_{VSH} + \mu) R_{VSH} + \eta_{SH} R_H & \frac{dR_{DH}}{dt} &= \gamma I_{DH} - (\psi + \mu) R_{DH} + \eta_{VS} R_{VSH}
\end{aligned}$$

