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The mSIR model for the spread of infectious diseases

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dsEA.py **dsEC19.py** **(Covid-19)**

MODELLING THE SPREAD OF A DISEASE

Many human diseases are contagious: you "catch" them from someone who is already infected. Contagious diseases are of many kinds. Smallpox, polio, plague, and Ebola are severe and even fatal, while the common cold and the childhood illnesses of measles, mumps, and rubella are usually relatively mild. Moreover, you can catch a cold over and over again, but you get measles only once. A disease like measles is said to "confer immunity" on someone who recovers from it. Some diseases have the potential to affect large

segments of a population; they are called epidemics and epidemiology is the scientific study of these diseases.

Mathematical modelling can provide insights to the spread of diseases that would be impossible otherwise. A mathematical model helps us understand the way a contagious disease spreads through a population and predict what fraction will fall ill, require hospitalization, die, and when. Modelling can be an important tool during an infectious disease outbreak to help understand the dynamics of the disease and the potential impact any interventions might have on its spread. This modelling can be done to run experiments in order to better understand the dynamics of an infectious disease before an outbreak occurs. This could provide vital information to improve the response to an outbreak if it does occur.

The importance of models such as the SIR model is not the matching of model predictions with real data for a disease outbreak but the trends that occur in the population dynamics predicted by the models. It is possible to run simulation experiments to study the trends in the population dynamics for many scenarios to gain valuable insights to the progress and control of a disease outbreak. This indicates that predictions using more complex models may not be more reliable compared to using simpler models.

COMPARTMENTAL EQUATION BASED MODELS

Compartmental equation-based models such as the SIR, SIRS, SIRD, and SEIR models are the most popular and well-known types of models used in infectious disease modelling. This paper examines a modified model called the mSIR model which incorporates many features a number of SIR type models.

There are a number of important assumptions when running compartmental equation-based models and this may place serve restrictions on the performance of a model to match real data of the spread of a disease. The population in a compartmental model is assumed to be homogeneous and mixing within and between compartments is also assumed to be homogeneous where all individuals within a compartment had the same probability of moving to another.

It is well known that these assumptions are not true to life. For example, contact rates often vary between age groups, but the models have been shown to be robust, predictive and give rough but reasonable predictions for many populations. It is a difficult task to find a models parameter values and initial conditions that give good agreement between experimental simulations and real population values.

The mSIR model divides the population into five compartments: Susceptible ***S***, Exposed ***E***, Infected ***I***, Removed ***R*** and dead ***D***. When a few infected individuals are introduced into a susceptible population, individuals become exposed to the disease and it leads to the growth of the active infected population. The infected individuals are eventually removed from the infected population to recover (gain immunity from the disease) or become susceptible again or die. The total living population at time t is

$$N(t) = S(t) + E(t) + I(t) - D(t)$$

This mSIR model is based upon as a set of five ordinary differential equations plus initial conditions and the time evolution of the populations determined by the values for the input parameters which specify the equations.

Model populations (compartments)

Susceptible ***S***: individuals that are able to catch the disease when they contact an infected individual.

Exposed ***E***: People who are infected but not yet infectious (incubation period.

Infected ***I***: individuals that can spread the disease to susceptible individuals. The time they spend in the infected compartment is the infectious period, after which they enter the removed compartment.

Removed ***R***: individuals in the removed compartment are those that have recovered and are immune. Others who were infectious die or become susceptible again.
Dead ***D***: individuals who have died as a result of the infection.

The input parameters are not necessarily constants as they may change during the course of an epidemic. The time unit is days.

Susceptible population dynamics $dS(t)/dt$

Susceptible people become exposed when they come into contact with an infectious individual. The **transmission rate *a*** is used to calculate the rate at which susceptible individuals become infected. The transition from the susceptible ***S*** to the exposed ***E*** compartment is modelled as a process dependent on the interaction between susceptible and infected individuals.

Each susceptible individual is assumed to have a certain average number of contacts per unit of time (contact rate c) and there is a probability that a contact between a susceptible person and an infected person results in the transmission of the disease (transmission probability per contact p).

The overall transmission rate a is the product of the contact rate c and the transmission probability per contact p

transmission rate $a = c\,p$ [day^{-1}]

The transmission rate a is the per-capita rate at which a susceptible person contracts the infection from any random infected person they encounter in a homogeneously mixing population.

The instantaneous probability or rate at which a specific susceptible individual becomes infected at time t is called the **force of infection** ***f***. It is defined as

$$f = \frac{a\,I}{N}$$

The more infected people in the population, the higher the likelihood of a susceptible person becoming infected

Infected people recover from the disease but become susceptible again at a rate s.

The governing equation for $dS(t)/dt$ is thus given by

$$\frac{dS(t)}{dt} = -\left(a(t)\,\frac{I(t)}{N(t)} \right) S(t) + s(t)\,R(t)$$

The first term of this equation signifies that the number of susceptible individuals decreases at a rate proportional to the product of the number of susceptible people $S(t)$ and the number of infected people $I(t)$ modulated by the transmission rate $a(t)$. The second term signifies that the rate at which people who become infected again is proportional to the removed population $R(t)$.

The disease can breakout to new communities resulting in an increase in the susceptible population by $S_B(t)$. This can be modelled by the equation

$$S(t) = S(t) + S_B(t)$$

Exposed population dynamics $dE(t)/dt$

After a delay (the incubation period), exposed individuals become infectious. This transition occurs at a rate e [1/day], which is the inverse of the average incubation period T_e [day].

$$e = 1/T_e$$

For example, if the average incubation period for a disease is $T_e = 5$ days, then $e = 1/5$ day^{-1}, meaning 20% of the exposed individuals will become infectious each day.

The governing equation for $dE(t)/dt$ is

$$\frac{dE(t)}{dt} = +\left(a(t)\,\frac{I(t)}{N(t)} \right) S(t) - e(t)\,E(t)$$

Infectious population dynamics $dI(t)/dt$

Infectious individuals removed at a rate b, the inverse of the average infectious period T_b

removal rate $b = 1/T_b$ [day^{-1}])

Infectious individuals die at the rate d

death rate d [day^{-1}]

For example, for a disease with an average infectious period of T_b = 10 days, b =1/10, meaning 10% of the infectious population will be removed each day.

The governing equation for $dI(t)/dt$ is

$$\frac{dI(t)}{dt} = +e(t)E(t) - b(t)I(t) - d(t)I(t)$$

The disease can be enhanced by the introduction new infected people into a community of susceptible people. This results in an increase in the infectious population by $I_B(t)$. This can be modelled by the equation

$$I(t) = I(t) + I_B(t)$$

Removal (Recovered) population dynamics $dR(t)/dt$

The governing equation is

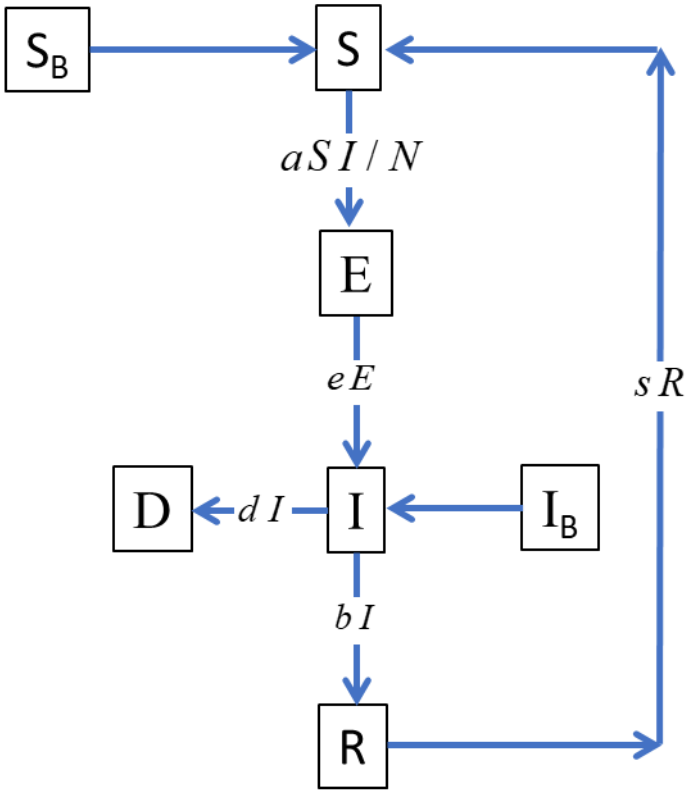
$$\frac{dR(t)}{dt} = +b(t)I(t) - s(t)R(t)$$

Dead population dynamics $dD(t)/dt$

The governing equation is

$$\frac{dD(t)}{dt} = +d\,I(t)$$

The flow diagram below shows the population compartments and the transitions between compartments.



Fig, 1. Flow diagram of the population interactions. S_B and I_B are new populations that occur in a breakout of the infection to new population centres.

The complete set of ODEs for the population dynamics for the time evolution of a contagious infection

$$\frac{dS(t)}{dt} = -\left(a(t)\,\frac{I(t)}{N(t)} \right) S(t) + s(t)\,R(t) \tag{1.1}$$

$$S(t) = S(t) + S_B(t)$$

$$\frac{dE(t)}{dt} = +\left(a(t)\,\frac{I(t)}{N(t)} \right) S(t) - e(t)\,E(t) \tag{1.2}$$

(1.3) $$\frac{dI(t)}{dt} = +e(t)E(t) - b(t)I(t) - d(t)I(t)$$

$$I(t) = I(t) + I_B(t)$$

(1.4) $$\frac{dR(t)}{dt} = +b(t)I(t) - s(t)R(t)$$

(1.5) $$\frac{dD(t)}{dt} = d(t)I(t)$$

Key Metric: Basic reproduction number

We will make an approximation to find the basic reproduction rate R_0 using the simpler SIR model. The basic reproduction number R_0 is the average number of new infections caused by a single infected individual in a fully susceptible population and is given by equation (2)

$$R_0 = \begin{pmatrix} \text{transmission} \\ \text{coefficient} \\ [1/\text{time}] \end{pmatrix} \times \begin{pmatrix} \text{average duration} \\ \text{of infection} \\ [\text{time}] \end{pmatrix}$$

(2)

$$R_0 = \frac{a}{b}$$

R_0 provides a threshold condition for the stability of the disease-free equilibrium point for most models. The basic reproduction number R_0 is a key parameter in epidemiology. R_0 tells us about the initial rate of spread of the disease. For a for simple homogeneous autonomous

models R_0 is fixed over all time. If $R_0 > 1$, there will be an epidemic, and if $R_0 < 1$, the introduced

- The disease-free equilibrium point is locally asymptotically stable when $R_0 < 1$ and the disease dies out. An infected person will recover without being able to replace themselves by new infections. An epidemic wanes in the SIR framework when the susceptible fraction of the population is gradually depleted, achieving 'herd immunity', so that on average a single infected person can only infect less a single susceptible person.
- The disease-free equilibrium point is unstable when $R_0 > 1$ and the disease establishes itself in the population or an epidemic occurs.

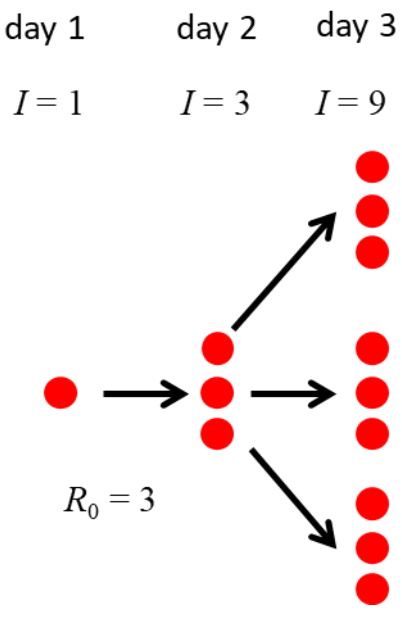
The initial phase of the epidemic with $R_0 = 3 > 1$. At the start, the growth of the number of infected individuals is approximately exponential. Time unit: days	

Fig. 2. Basic reproduction number R_0.

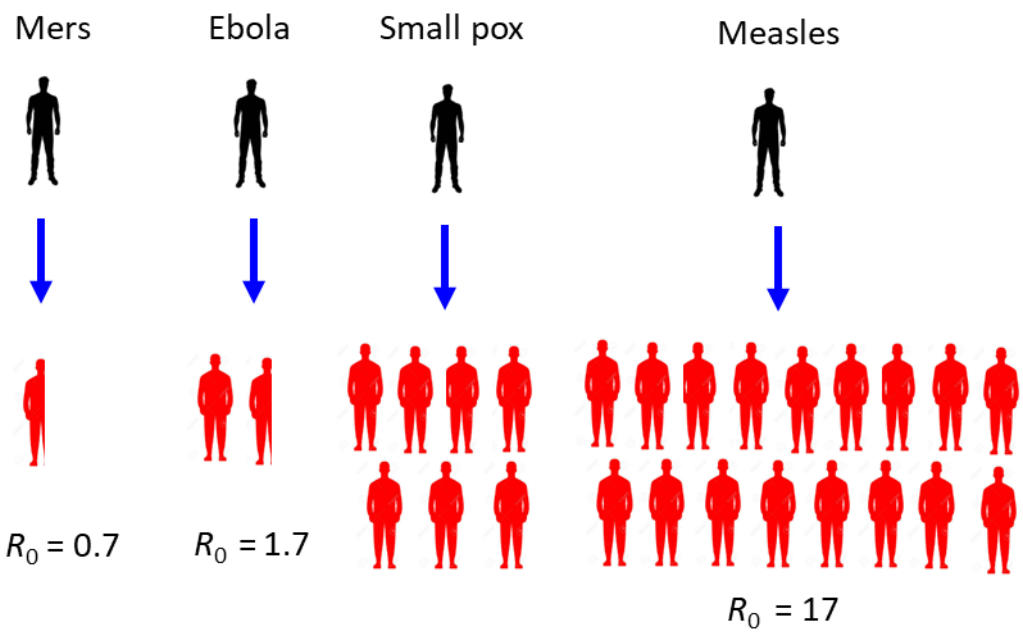


Fig. 3. Basic reproduction number.

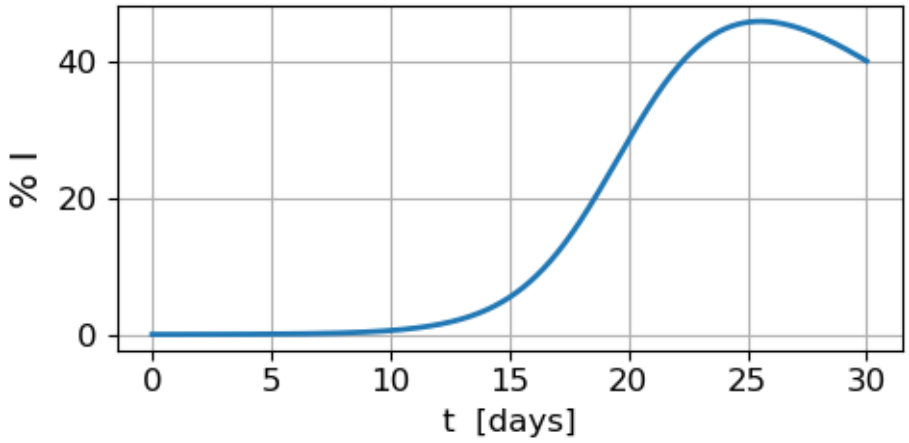


Fig. 4. At the start of an epidemic $N_o = 10\ 000$, there is a rapid increase in the number of infected people.

$c = 2$, $p = 0.95$, $T_e = 5$, $T_b = 10$, $T_b = 10.00$, $R_0 = 19.00$.

Within two week (day 10 to day 14), the daily infection numbers increase from ~50 to ~4500.

For the case in which $s = 0$, the susceptible population always decreases with time $S(t) < S_0$.

Time rate of change of infections

$$\frac{dI(t)}{dt} = \left(a\,S(t)/N - b\right)I(t) < \left(a\,S_0/N - b\right)I(t)$$

If the infection population decreases, then

$$\left(a\,S_0/N - b\right) < 0 \quad \left(a\,S_0/bN - 1\right) < 0 \quad \left(\frac{a}{b}\right)\left(\frac{S_0}{N}\right) < 1 \quad S_0 \approx N$$

$$R_0 < 1$$

Hence, if the infection population increases to give an epidemic, then

$$R_0 > 1$$

The effective reproductive number R_e is the number of secondary infections that one infected person would produce through the entire duration of the infectious period. Typically, but not always, R_e is the product of R_0 and the proportion of the population that is susceptible. R_e describes whether the infectious population increases or not. It increases when $R_e > 1$, and decreases when $R_e < 1$. When $R_e = 1$ the disease is at equilibrium. R_e change over time as $S(t)$ and $N(t)$ change.

$$R_e(t) = \frac{a}{b}\frac{S(t)}{N(t)} = R_0\frac{S(t)}{N(t)}$$

When $R_0 > 1$ then many individuals will become infected. Eventually, this susceptible population will become small enough that it can no

longer sustain growth in the infected population (assuming infected population is initially growing). At this point, $I(t)$ will peak, and thereafter will dwindle. The threshold value of the susceptible population S_T is the value of S at which the peak infection I_{peak} occurs. At the peak when $I(t) = I_{peak}$ then $dI/dt = 0$. Then from equation 1,

$$S_T = \frac{b\,N}{a}$$

The threshold susceptible population S_T can be found numerically from the infected population I(t)

```
ST = S[I==max(I)]
```

The time at which the peak infection occurs is calculated by the Code

```
Tpeak = t[I==max(I)]
```

PYTHON CODE

Since the mSIR model uses time varying parameters, the set of ODEs given by equation 1 are solved using the Euler Method.

Model input parameters

Time span: number of time steps nT, simulation time tS.

Initial conditions

$S[0] = S_o$ $E[0]) = E_o$ $I[0] = I_o$ $R[0] = R_o$ $D[0] = D_o$

Contact rate [day^{-1}] c

Transmission probability p

Rate $R \rightarrow S$ [day^{-1}] s

Incubation period T_e [day]

Infection period T_b [day]

Death rate d [day^{-1}]

Computations

Transmission rate [day^{-1}] $a = c\,p$

Rate $S \to E$ $e = 1/T_e$ [day^{-1}]

Rate $E \to I$ $b = 1/T_b$ [day$_{-1}$]

Basic reproduction number $R_0 = a/b$

Populations $S[t]$ $E[t]$ $I[t]$ $R[t]$ $D[t]$

Basic reproduction number $R_0 = a/b$

Effective reproduction number $R_e = R_0\,S[t]/N[t]$

Threshold susceptible population $S_T = b\,N_o/a$

Time at peak infection T_{peak}

Infection load (area under t vs I plot) L

The disease-free state corresponds to: $S = N$, $I = 0$, $R = 0$.

The infection load L (area under t vs I plot) is used as a measure of the severity of the infection over the course of the infection.

SIMULATIONS

We can use simulation experiments to answer question like:

If infected individuals are introduced into a susceptible population what might be the consequences?

How many people will be infected?

How quickly will it spread - what is the time course of the disease?

Is there going to be an epidemic?

What control measures can be implemented?

How can vaccination against the disease help prevent an epidemic?

Take the population of a small town with a susceptible population S = 10 000 An infected individual comes into town and the disease spreads. The mSIR model can be used to investigate the dynamical changes in population. The predictions of the model are very realistic. However, the model is in general not sophisticated enough to match the data for real occurrence of epidemics.

SIMULATION 1 NO EPIDEMIC $R_0 < 1$

We will first consider the case when the basic reproduction number is less than one, $R_0 = 0.96 < 1$ in which case there will be no epidemic.

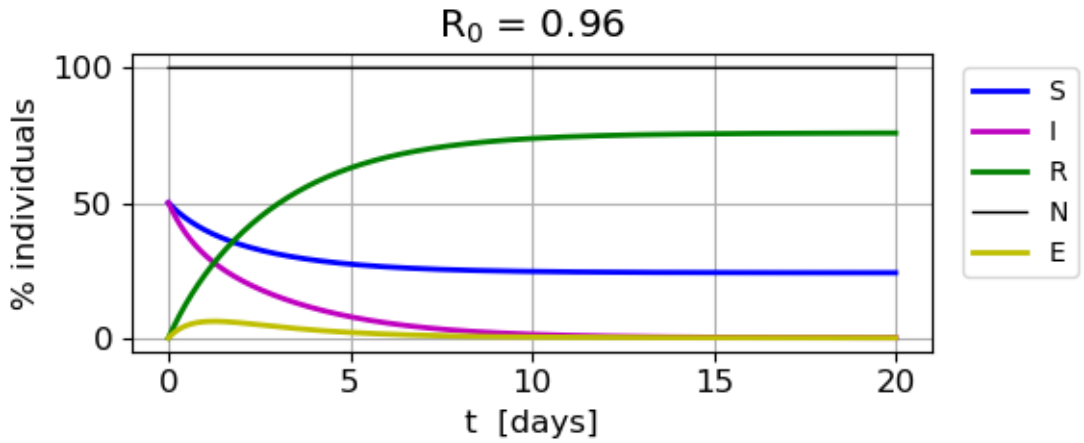


Fig. S1.1. Population dynamics for $R_0 = 0.96 < 1$.

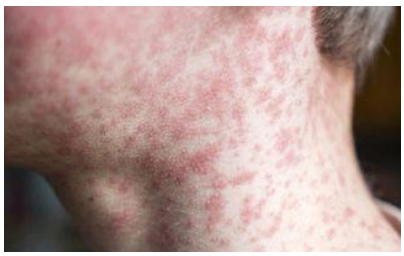
p = 0.72 c = 0.80 a = 0.58 Te = 1.00 e = 1.00
Tb = 1.00 b = 1.00
Initial populations
So = 50.0 Eo = 0.0 Io = 50.0 Ro = 0.0 Do = 0.0
Final populations
Sf = 24.1 Ef = 0.0 If = 0.0 **Rf = 75.9** Df = 0.0

Both the susceptible S and infected populations I decrease monotonically to their steady-state values

$$t \to \infty \quad S_f \to 24 \quad I_f \to 0 \quad R_f \to 76$$

76% of the initial susceptible population become infected and all of them recover and are immune to the disease. So, for $R_0 < 1$ there is no epidemic.

SIMULATION 2 MEASLES EPIDEMIC $R_0 = 19.0 > 1$



We can simulate a measles epidemic, but remember it is the trends in the population dynamics that is important and one should not try and relate the mSIR predictions to real case numbers.

Consider a small community with a population of 10 000 with one infected person. On contact with an infected person, the probability of catching measles is very high, $p = 0.95$. Assume that the rate of contact between a susceptible person and an infected person is $c = 2$ per day. Typically, the recovery time from measles is around 10 days, and the incubation period about 5 days. Assume that no person dies from the infection. The simulation uses scaled population units, so that populations are expressed as percentages. A population of 10 000 is equal to a 100 scaled population.

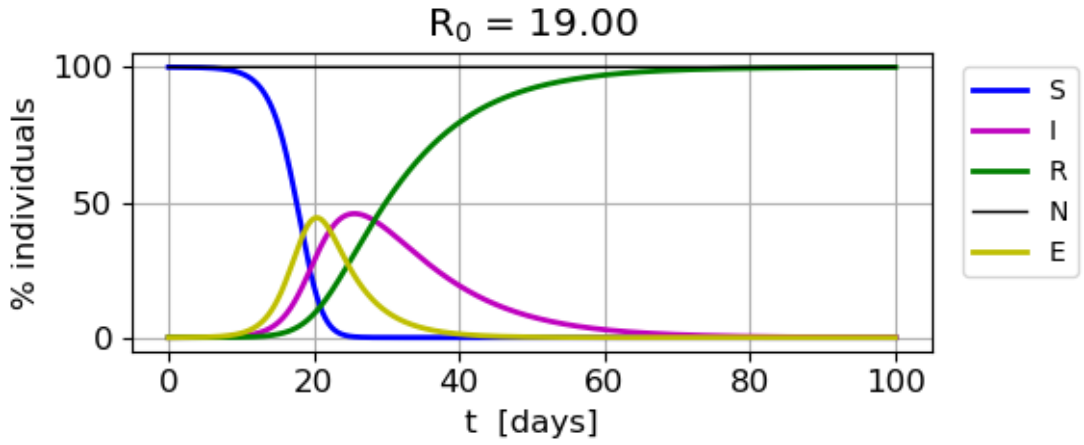


Fig. 2.1. Population dynamics for $R_0 = 19$.

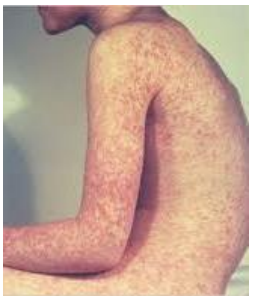
p = 0.95 c = 2.00 a = 1.90 Te = 5.00 e = 0.20
Tb = 10.00 b = 0.10 d = 0.00 s = 0.00
R0 = 19.00
Initial populations
So = 99.99 Eo = 0.00 **Io = 0.01** Ro = 0.00 Df = 0.00
Final populations
Sf = 0.0 Ef = 0.0 If = 0.1 Rf = 99.9 Df = 0.0
Max Populations
Smax = 100.0 Emax = 44.3 **Imax = 45.8** Rmax = 99.9
ST = 0.3 **tST = 25.6 days**
Infection load: L = 999

The infected numbers increase rapidly with the peak infection at 46% after 26 days. All people in the community were infected during the epidemic.

When $R_0 > 1$ then many individuals will become infected. The susceptible population $S(t)$ can only decrease in size. Eventually, this susceptible population will become small enough that it can no longer sustain growth in the infected population (assuming infected population is initially growing). At this point, $I(t)$ will peak, and thereafter will dwindle.

SIMULATION 3

Preventative measures: masks, hand washing, social distancing



Measles is a highly contagious disease caused by a virus. It spreads easily when an infected person breathes, coughs or sneezes. It can cause severe disease, complications, and even death. Measles can affect anyone but is most common in children. Measles infects the respiratory tract and then spreads throughout the body. Symptoms include a high fever, cough, runny nose and a rash all over the body.

Wearing a mask, washing hands and social distancing are three crucial steps in preventing the spread of measles, especially if you have symptoms or have been exposed and are not immune. People with suspected or confirmed measles should wear a mask and practice social distancing when seeking medical care and isolate at home, avoiding public places like work or school, until they are no longer contagious or deemed safe by a healthcare professional. Masks are also recommended for healthcare workers providing care for suspected measles patients to minimize the risk of infection, particularly those who are not immune.

Simulation 2, the probability of catching the disease was $p = 0.95$. Wearing of a mask with social distancing and washing hands will reduce the probability of being infection.

$$p = \left(\frac{\text{probability of disease transmision}}{\text{contact}} \right)$$

We can ask, what changes will result in the population dynamics if the probability is reduced to $p = 0.45$.

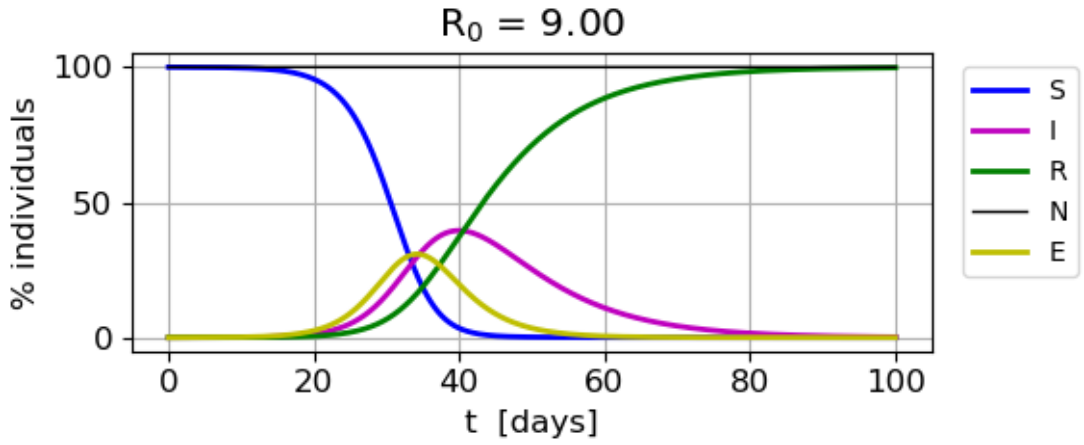


Fig. 3.1. Population dynamics $p = 0.45$, $R_0 = 9$.

p = 0.45 c = 2.00 a = 0.90
Te = 5.00 e = 0.20 Tb = 10.00 b = 0.10
Initial populations
So = 99.99 Eo = 0.00 Io = 0.01 Ro = 0.00 Do = 0.00
Final populations
Sf = 0.0 Ef = 0.0 If = 0.2 Rf = 99.8 Df = 0.0
Max Populations
Smax = 100.0 Emax = 30.9 **Imax = 39.6** Rmax = 99.8 Dmax = 0.0
Peak: ST = 3.5 tST = **39.9 days**
Infection load: L = 998

The peak infected population was reduced from 46% to 40% and the peak occurred later after 40 days rather than 26 days.

We see that preventative measures help and reduce the peak infection number and delays the spread of the disease. By delaying the peak in infections gives more time to implement preventative measures. To be an effective strategy it would require a very large percentage of the community to be wearing marks, washing hands and practicing social distancing. If there were very extensive preventative measures then it would reduce the probability further. Consider the case $p = 0.20$.

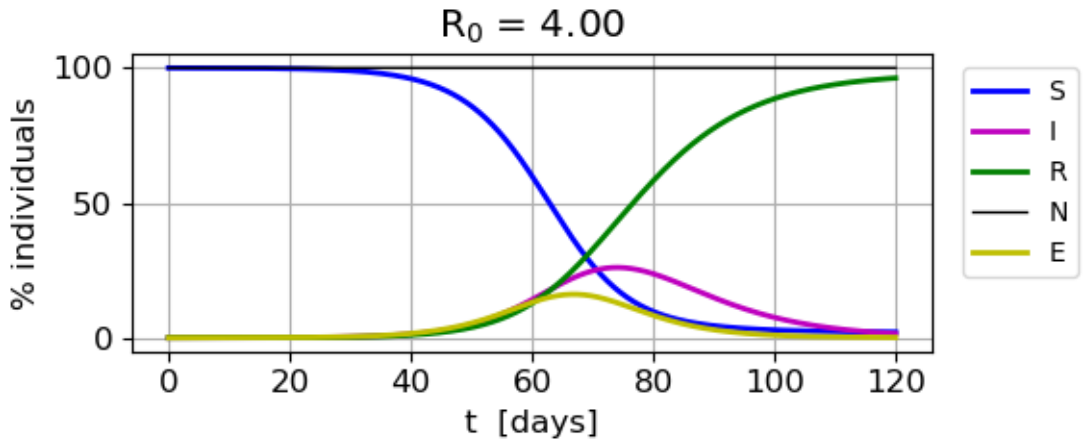


Fig. S3.2. Population dynamics $p = 0.20$ $R_0 = 4$.

p = 0.20 c = 2.00 a = 0.40
Te = 5.00 e = 0.20 Tb = 10.00 b = 0.10
R0 = 4.00
Initial populations
So = 99.99 Eo = 0.00 Io = 0.01 Ro = 0.00 Do = 0.00
Final populations
Sf = 2.1 Ef = 0.1 If = 1.5 Rf = 96.2 Df = 0.0
Max Populations
Smax = 100.0 Emax = 16.1 Imax = **26.1** Rmax = 96.2
Peak: ST = 17.8 tST = **74.0 days**
Infection load: **L = 962**

The peak infected population is now 26% and occurs at day 75. About 2% of the susceptible population were not affected by the disease. The infection load has dropped to 962 from 999.

It is unlikely that implementing the policy of only wearing masks, washing hands, and social distancing would stop an epidemic. Other measures would need to be implemented as well.

SIMULATION 4

Preventative measures – limiting contacts (lockdowns)

Limiting the number of contacts between an infected person and a susceptible person can help reduce the severity of an epidemic. Governments can implement policies that quarantine people to prevent their movements. Melbourne (Australia) had the longest "shut-down" of any major global city. In China there were drastic lockdowns across the country which was brutally enforced by the "white guards". Simulations experiments can be done to look at the dynamics of quarantining by adjusting the parameter *c* for the number of contacts between a susceptible person and an infected person.

The dynamics of the disease can be shown in a phase portrait. This plot helps visualize the relationship between the infected population and the susceptible population when one of the input model parameters is changed as shown in figure 4.1.

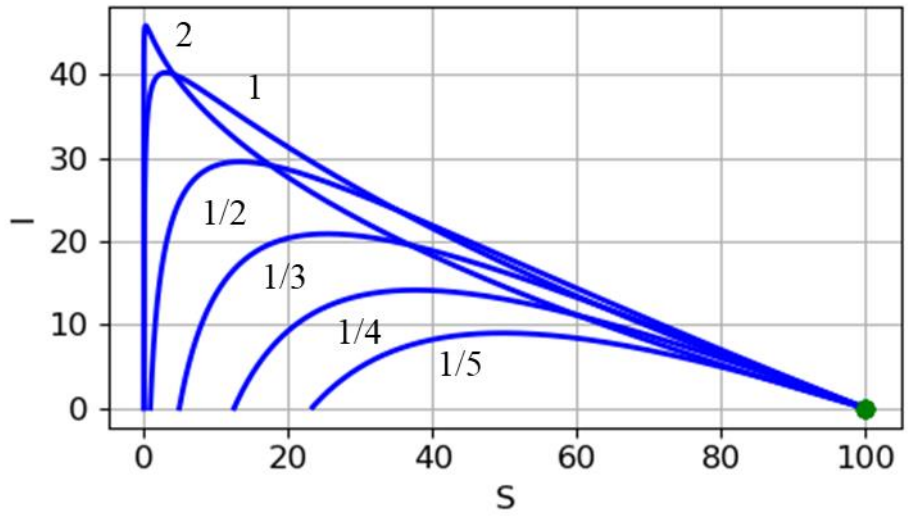


Fig. 4.1. Phase portrait ($p = 0.95$) for varying $S \rightleftarrows I$ contacts given by the variable c.

$c = 2$	2 contacts in 1 day
$c = 1$	1 contact in 1 day
$c = 1/2$	1 contact in 2 days
$c = 1/3$	1 contact in 3 days
$c = 1/4$	1 contact in 4 days
$c = 1/5$	1 contact in 5 days

Table 1 shows a summary of the model parameters. The population is 10 000 and this corresponds to a scaled population of 100. So I_{peak} and R_{max} populations shown are percentages. Assume that 2% of the infected population require hospitalization. Therefore, we can estimate the number of hospital beds required during the epidemic (BEDS) for different isolation measures.

Table 1. Contacts between infected and susceptible people.

c	2	1	1/2	1/3	1/4	1/5
R_0	19.0	9.5	4.75	3.17	2.37	1.90
I_{peak}	46	40	30	20	14	9
R_{max}	100	100	99	95	88	77
t_{ST} day	26	39	64	72	127	172
S_T	0.3	3	13	25	38	50
Load L	1000	1000	991	951	875	765
BEDS	92	80	60	40	28	18

Assume that there were 50 hospital beds available. Then if $c > 0.5$ (1/2) then this would have a serious detrimental impact on hospitals. The lower the value of c, the less contact between infected and susceptible then the number of days S_T to the peak infection is dramatically increased and this gives more time for authorities to take measures to reduce the effects of the epidemic.

The greater the number of contacts between an infected person and susceptible people per day, then the higher the number of people that become infected. So, isolation of infected individuals and restricting the movement of susceptible people is a good strategy of limiting the severity of the disease.

The effective reproduction number R_e is a useful parameter that is helpful in signally the worst of the epidemic is over. This occurs when $R_e < 1$ and the susceptible population falls below the threshold susceptible population S_T. A summary of a simulation is displayed in the Python Figure Window. For example,

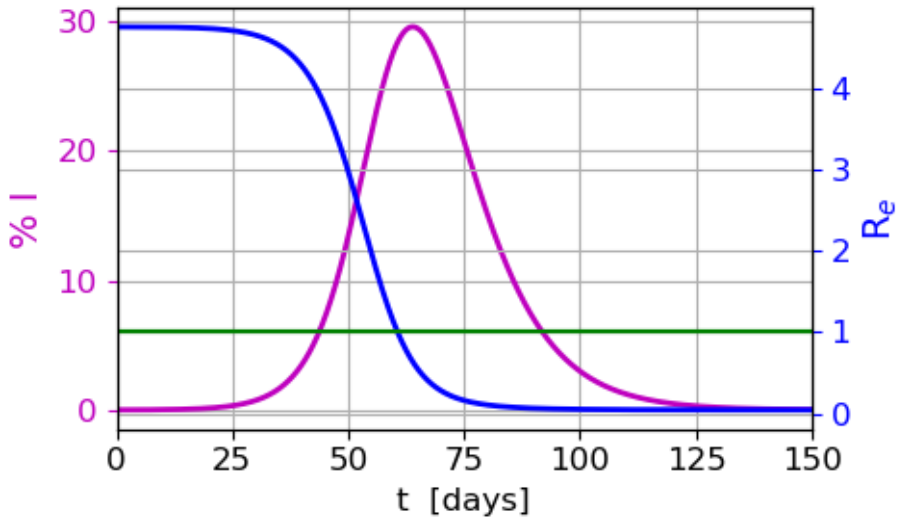


Fig. 4.2. Infections and effective reproduction number R_e.

$p = 0.95$, $c = 1/2 = 0.5$, $R_0 = 4.75$. When $R_e < 1$ the number of infections decrease and the worst of the epidemic is over.

By implementing strategies such as using masks, washing hands, and limiting movement of people can be very effective in preventing the wide-spread propagation of the disease.

SIMULATION 5 People die in an epidemic

In an epidemic such as measles, people die especially young children. A death rate given by the parameter d is incorporated into the mSIR model to study the population dynamics as shown in figures 5.1 and 5.2.

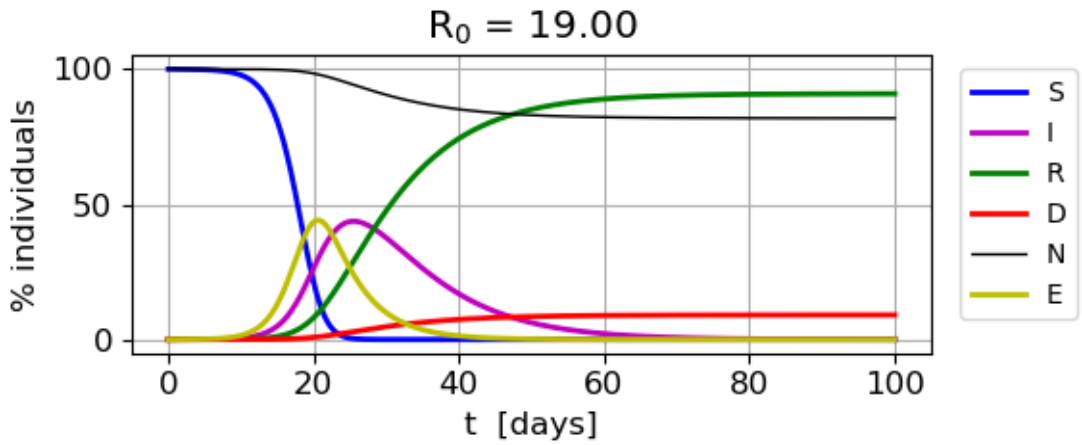


Fig. 5.1. Population dynamics $d = 0.01$, $p = 0.95$, $c = 2$, $R_0 = 19$ $D = 9$ %, $R = 91$ %. All people are infected by the disease with 91 % recovering and 9 % deaths.

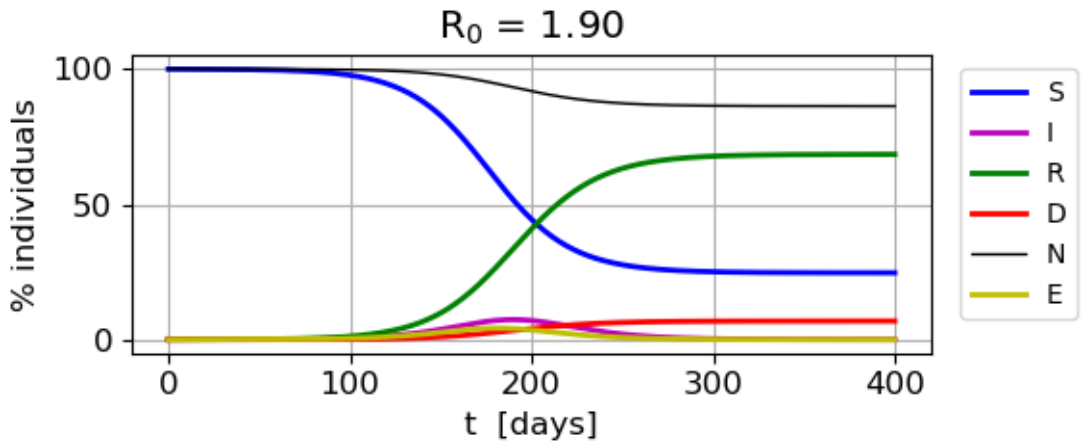


Fig. 5.2. Population dynamics $d = 0.01$, $p = 0.95$, $c = 1/5$, $R_0 = 1.9$ $D = 6.8$%, $R = 68.5$ %. 24.7 % of the population are not infected by the disease with 68.5 % recovering and 6.8 % deaths.

Even with strict control measures in place, still about 7 % of the population die. Only if $R_0 < 1$ does the number of deaths drop to zero since only a very small percentage of the population becomes infected.

SIMULATION 6 REMOVAL RATE

Different diseases have different recovery periods. The average duration is given by the parameter T_b where $b = 1/T_b$ is the removal coefficient - rate at which an individual has recovered or died from the infection. What difference does it make to evolution of the populations? Figures 6.1 and 6.2 shows the population dynamics for $T_b = 14$ days and $T_b = 7$ days ($p = 0.95$, $c = 2$).

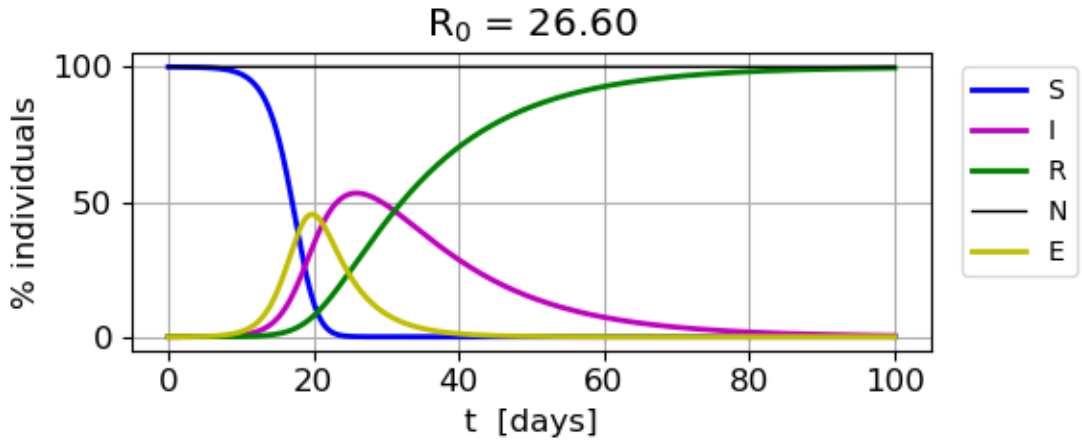


Fig. 6.1. Population dynamics T_b = 14 days, I_{peak} = 53% and load L = 1394.

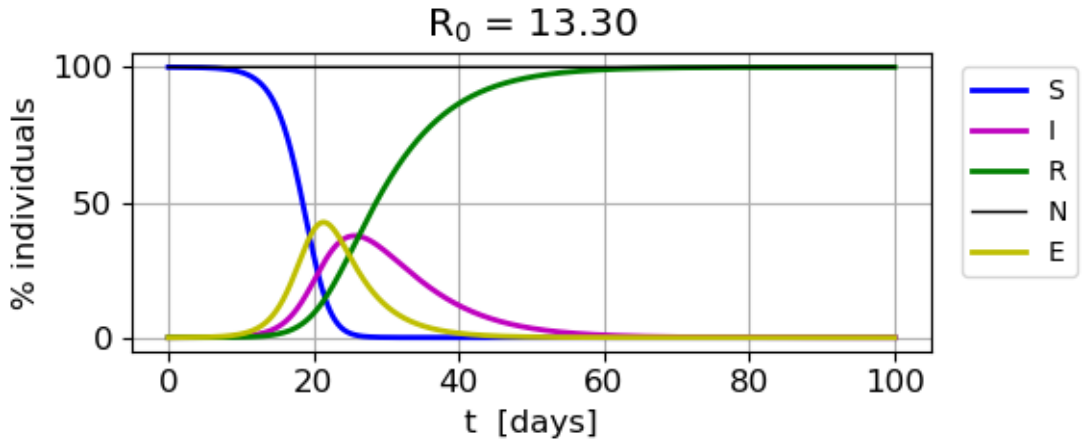


Fig. 6.2. Population dynamics T_b = 7 days, I_{peak} = 38% and load L = 700.

When the removal period is longer, the epidemic will last longer and the peak number of infections is much greater and with a significantly greater load factor.

SIMULATION 7 VACCINATIONS

Vaccination can prevent the infection of an individual. In addition, it can also protect a population from epidemics, even if not all individuals are vaccinated (this is the concept of herd immunity). We can use this simple mSIR model to examine the effectiveness of vaccinations by determining the proportion of the population that should be vaccinated in order to prevent the initial spread of the disease. In this model, vaccination is equivalent to the transfer of individuals from the susceptible compartment to the removed compartment, since a vaccinated individual cannot infect or be infected. We can run a simulation experiment to find the percentage of the population that needs to be vaccinated so that the daily maximum number of infected individuals is small. Figure 1 shows examples for different percentage of people who have been vaccinated and are immune to the disease. This is done by setting the initial value of the removed population, $R[0]$.

Figure 7 clearly shows the value of a vaccination program in helping reduce the number of injections in the course of an epidemic. For an initial infected population of 1/1000 individuals, we can conclude that more than 80% of the susceptible population would have to be vaccinated so that less than 5% of the population are not infected during the course of the epidemic. The number of infections is very sensitive to the vaccination rate. R[0] = 94% then the peak daily

infection is 0.04% , while if R[0] = 93% then the peak daily infection is 0.16%, 4 times greater.

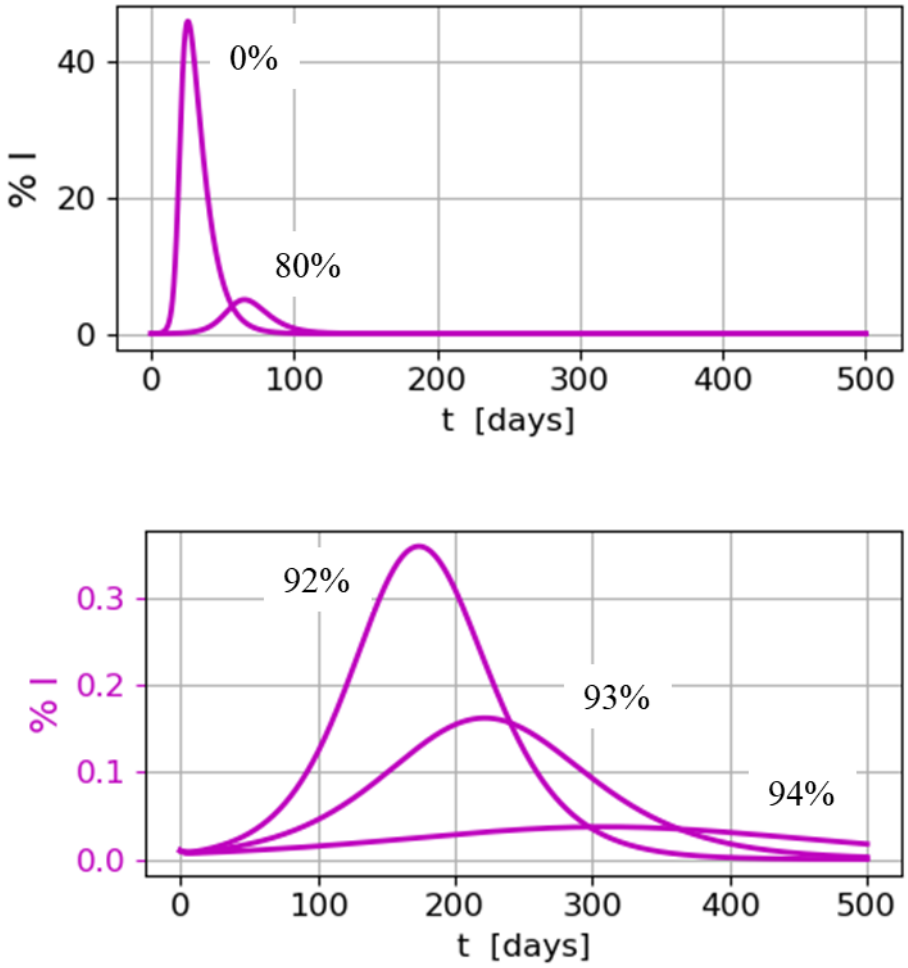


Fig. 7. Vaccination percentages and the infected populations.

To prevent the spread of measles, at least 95% of the population needs to be vaccinated to achieve herd immunity. This high vaccination rate is necessary because measles is highly contagious, and vaccination is the most effective way to protect vulnerable individuals in the community. To prevent the spread of polio, about 85% of a population needs to be vaccinated, though some sources cite a higher threshold of 95%.

SIMULATION 8

Breakout – surges susceptible and infections populations

In an epidemic there is often a new source of infected individuals and new communities of susceptible individuals in a short period of time.

The Ruby Princess cruise ship was the centre of a major COVID-19 outbreak in Sydney in March 2020. The Ruby Princess departed Sydney on March 8, 2020, for a 13-day cruise to New Zealand, returning early on March 19 as borders began to close due to the emerging pandemic. Despite 13 passengers on board being tested for COVID-19 symptoms, nearly 2,700 passengers were permitted to disembark at Circular Quay without proper health screening or isolation orders before their test results were known. The incident became the single largest source of COVID-19 infections in Australia at the time, with over 600 confirmed cases among passengers and crew, and ultimately linked to 28 deaths.

We can incorporate this feature of an epidemic by adding to the susceptible and infected populations. The surge in populations occurs on day 20. The surge at day 20 is defined by the susceptible population increasing by 50% and the infected population by 1%.

```
if n == 2000: S[n+1] = S[n+1] + 50;  I[n+1] = I[n+1] + 1
```

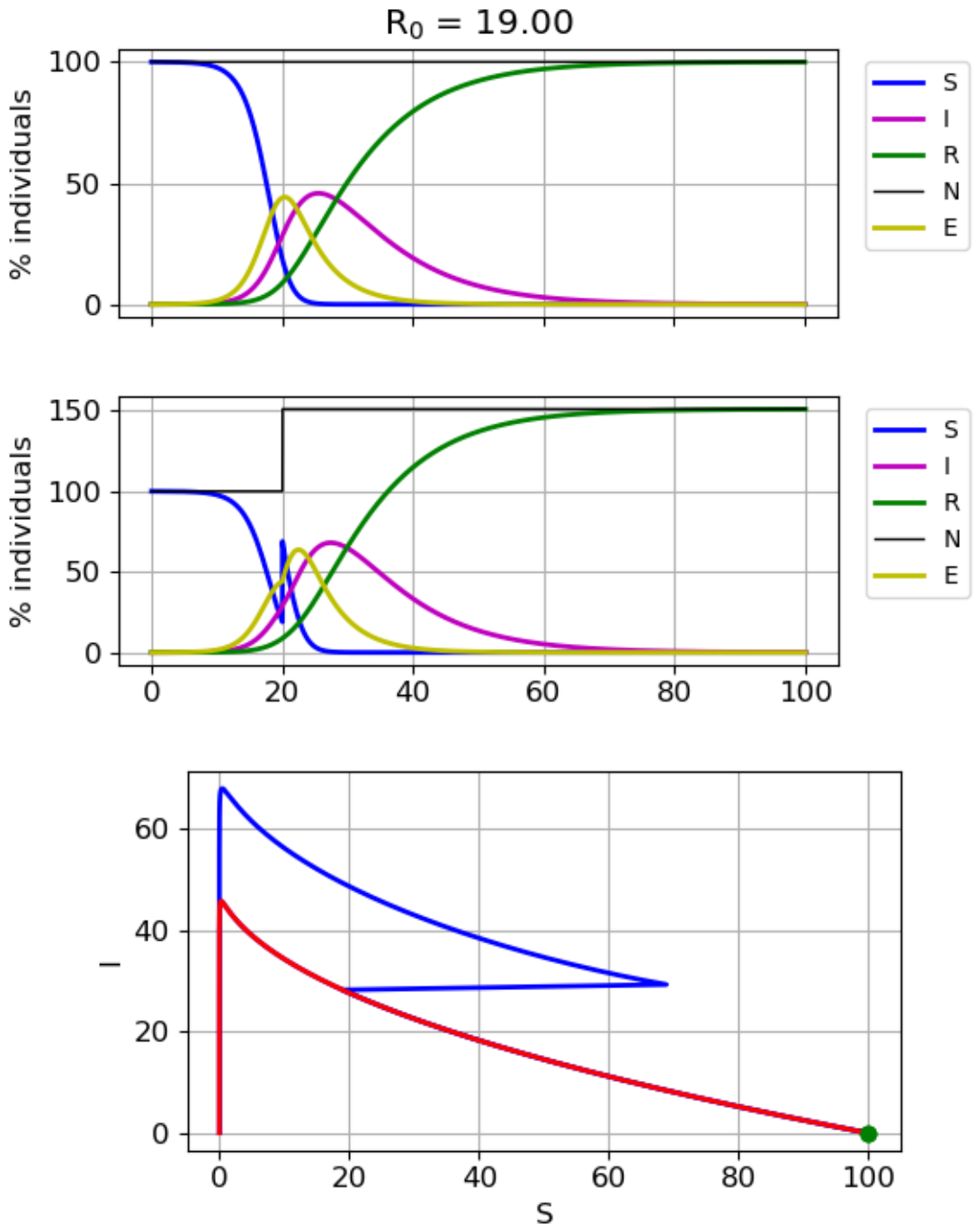


Fig. 8.1. Population dynamics with and without surges in the injected or susceptible populations. Due to the surge the infection load *L* increases from 1000 to 1509 and the peak daily infection from 46% to 68%.

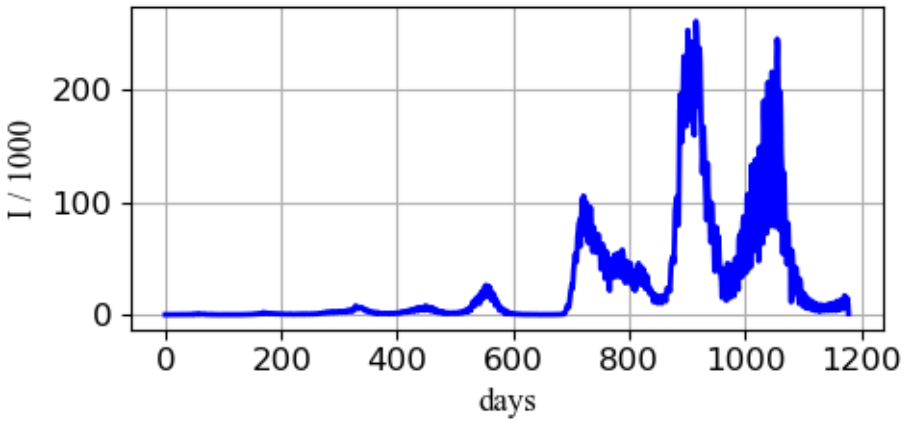


Fig. 8.2. Daily active COVID19 infections in Japan for 1200 days from February 2020. The peaks in the Japanese infections are due to surges in the infected and susceptible populations due to the mobility of infected people travelling within in Japan and arriving from overseas.

SIMULATION 9 NO IMMUNITY

Diseases such as the measles after being infected, an individual completely recovers and is immune from the disease and cannot transmit the disease to other people. However, other disease such as influenza (contagious respiratory illness caused by influenza viruses that can range from mild to severe) there is no immunity. If a person is infected again, then they are able to transmit the disease to others.

The parameter *s* specifies the proportional of the removed population that has not died that become susceptible again at each time step.

Model input parameters

p = 0.95 c = 2.00 a = 1.90 Te = 5.00 e = 0.20
Tb = 10.00 b = 0.10 d = 0.00 R0 = 19.00
Initial populations
Sf = 99.99 Ef = 0.00 If = 0.01 Rf = 0.00 Df = 0.00

Figures 9.1 and 9.2 clearly shows that the epidemic persists with a non-zero infectious population since there is always a supply of susceptible people.

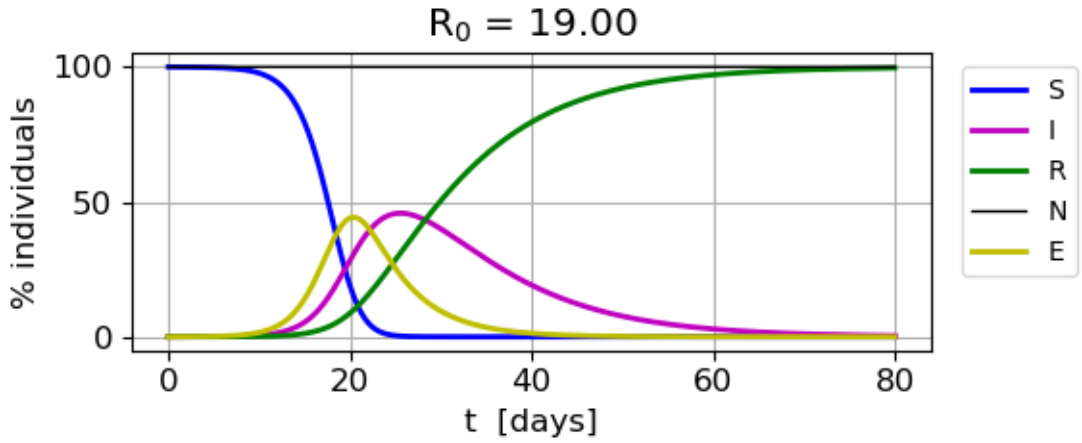


Fig. 9.1. Population dynamics s = 0.

Sf = 0.0 Ef = 0.0 If = 0.4 Rf = 99.6

Smax = 100.0 Emax = 44.3 **Imax = 45.8** Rmax = 99.

Peak: ST = 0.3 tST = 25.6 days Infection load: **L = 996**

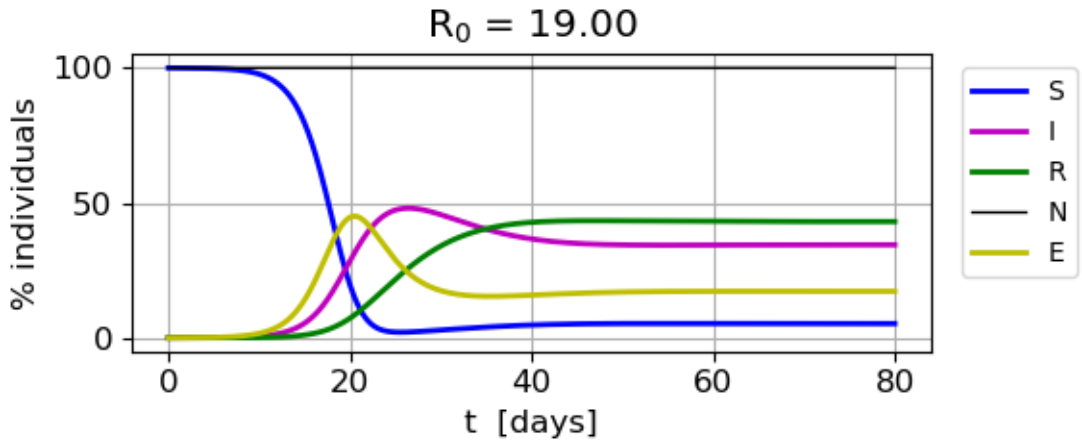


Fig. 9.2. Population dynamics s = 0.08.

Sf = 5.3 Ef = 17.2 **If = 34.5** Rf = 43.1

Smax = 100.0 Emax = 45.1 Imax = 48.0 Rmax = 43.4

Peak: ST = 2.1 tST = 26.4 days Infection load: **L = 2315**

SIMULATION 10 A more virulent virus

When a virus is described as "more virulent," it means it has an increased capacity to cause severe disease or harm to its host
It typically leads to more severe clinical signs, significant tissue or organ damage, and potentially higher rates of host mortality. In essence, a more virulent virus is better equipped to overcome a person's defences and cause a higher degree of damage. We can simulate a virus mutating and becoming more virulent by changing the probability parameter during the period of the epidemic as shown in figure 10. The initial value is $p = 0.20$ and changed to $p = 0.95$ at times 20 days, 40 days, and 50 days. The increase in the number of daily infections increases with the higher value of p. However, the increase in infections is time dependent. The increase in infections is greatest for a larger susceptible population as shown in figure 10.

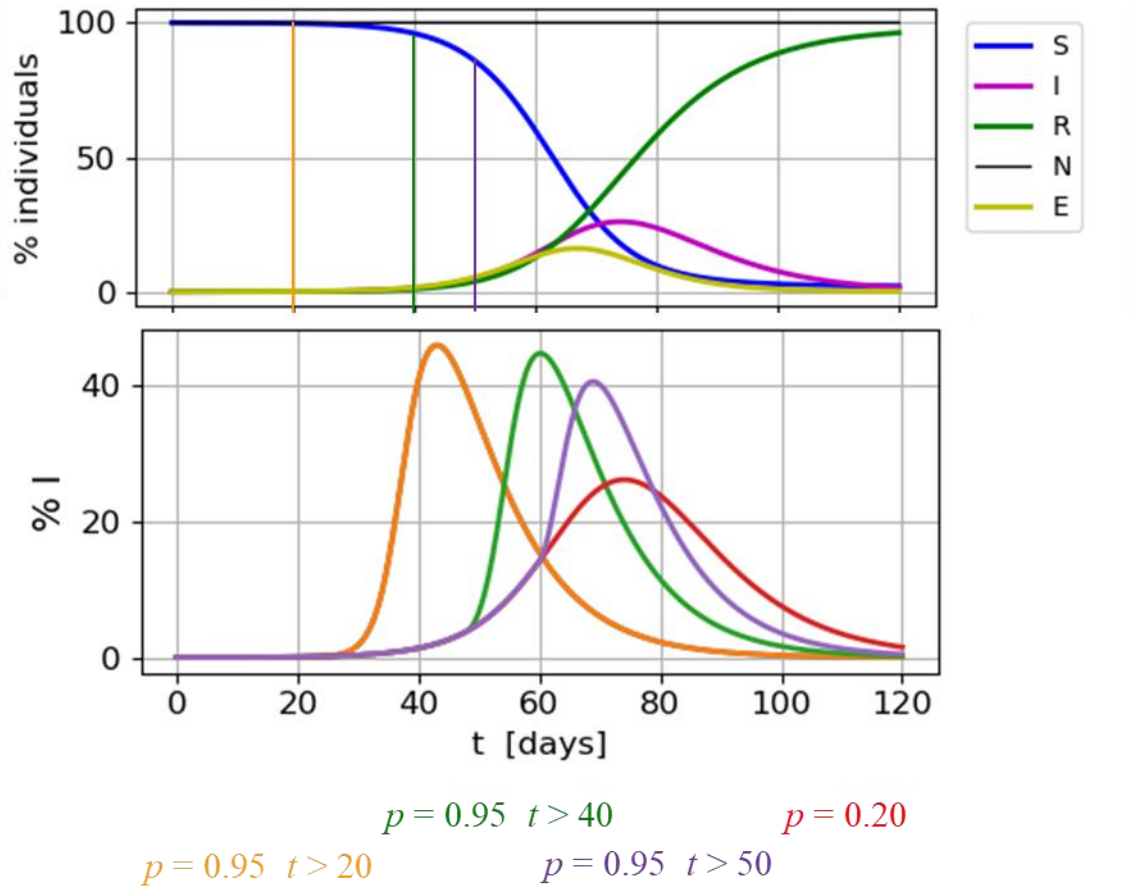


Fig. 10. Population dynamics for an abrupt change in the virulence of the virus.

SIMULATION 11 COVID 19 JAPAN dsEC19.py

The COVID-19 pandemic in Japan resulted in 33,803,572 confirmed cases of COVID-19 and 74,694 deaths, along with 33,728,878 recoveries. Figure 11.1 shows the daily active infections for 1200 days starting from 15 February 2020. The two large peaks occurred around August 2022 and January 2023 where the daily number infected people was in the order of 250 000. The mSIR model can be used to explain the most likely reason why these peaks occurred.

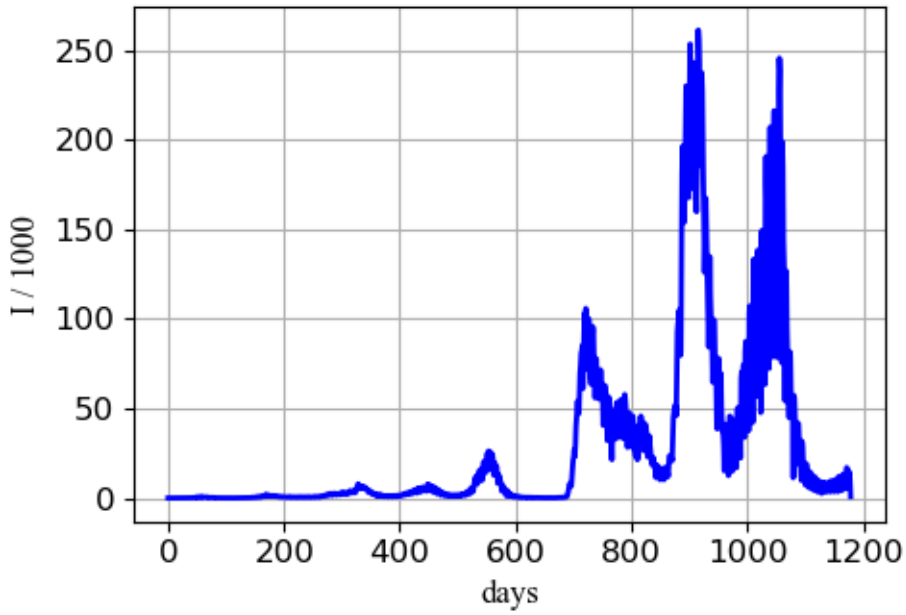


Fig. 11.1. The daily infected active cases of Covid19 in Japan starting on 15 February 2020.

The simulation experiment using the Python Code **dsEC1919.py** used the following input parameters to find solutions that would account for the major peaks in the infected population of figure 11.1. The simulation did not take into account any deaths.

p = 0.50 c = 1.00 a = 0.50 Te = 14.00 e = 0.07
Tb = 14.00 b = 0.07 d = 0.00 s = 0.00 R0 = 7.00
Initial populations
So = 10.00 Eo = 0.00 Io = 0.00 Ro = 0.00 Do = 0.00

It is assumed that the model parameters p, c, T_e and T_b are constant during the epidemic. To match the model predictions with the real data, the susceptible population S was increment at specific times in a trail-and-error approach;

```
if n == 3000: S[n+1] = S[n+1] + 80
if n == 4300: S[n+1] = S[n+1] + 50
if n == 5400: S[n+1] = S[n+1] + 400
if n == 5600: S[n+1] = S[n+1] + 100
if n == 6900: S[n+1] = S[n+1] + 1200
if n == 8100: S[n+1] = S[n+1] + 1400
```

Figure 11.2 shows the plots of the real data and the model predictions (bottom plot) and the ratio $S(t) / S_o$ (top plot).

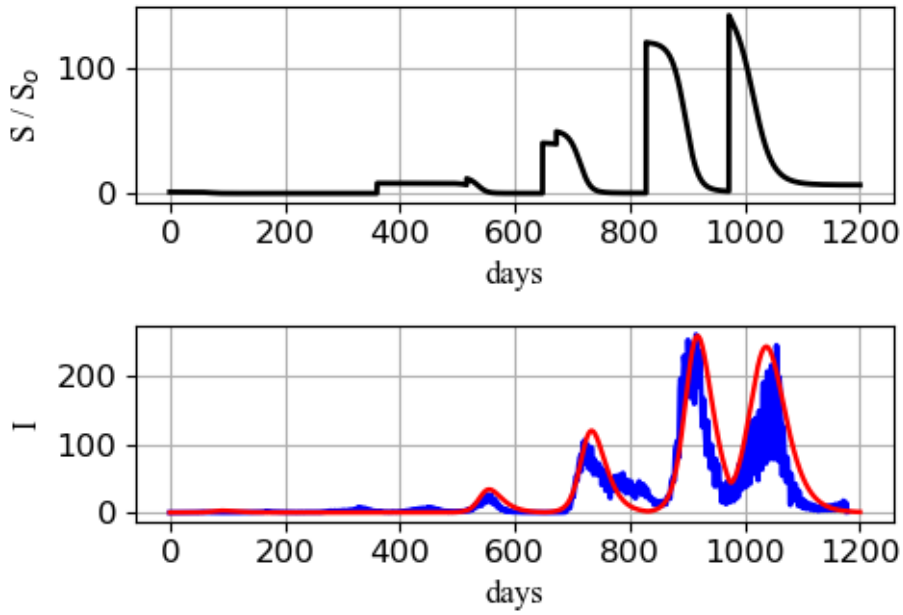


Fig. 11.2. Susceptible and infected populations.

We can conclude that the huge peaks in the infected population were caused by 100-fold increases in the susceptible population compared with the initial susceptible population. In Japan at the time of the virus infected people were not restricted in their movements they rapidly spread the virus into new communities, and hence the "sky-rocketing" increase in the susceptible population. This movement of people

throughout the county was due to the Japanese government lifting too early travel restrictions in place at the time.

Better model predictions could be made by adjusting other parameters to get better agreement with the real data.

We can conclude that using models such as the proposed mSIR model can give insights on how epidemics can be better managed.