The background, development and evaluation of the SIRVD-Modell

Project Report – Scientific Computing in Mathematica

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1. Introduction

With relatively recent advancements in medicine, many diseases that were previously incredibly dangerous have become non-problematic. Smallpox and rinderpest for example have entirely been eradicated thanks to vaccines. Once commonly spreading through many premodern cities and countries wreaking havoc, diseases in general became a non-issue in current times compared to what they once were. Especially in developed nations, many people did not know life-threatening and fast-spreading diseases. In fact, the possibility of a pandemic occurring was something many people disregarded as plausible, even though a variety of experts or other influential figures have predicted such a thing.

But with the power of hindsight, the reader should already be aware of the Covid-19 pandemic and how it has defied these expectations. As a result, scientific research regarding pandemics have experienced an increase since the start of the Covid-19 pandemic. The public's interest has accordingly spiked as well.

As a result, many new methods to estimate the course of any given pandemic have been developed. However, with all the varying factors influencing the spreading of a disease, doing so accurately is very difficult. One of the models often used as a baseline for such simulations is the SIR-model. It is not a new concept and was already suggested as a plausible model for pandemics since the 20^{th} century. But since then, this model has seen a variety of new adaptations to make it more accurate.

2. The SIR-Model

The SIR-model is a compartmental model. Therefore, the population is classified into several different, usually very generalized, separate and non-overlapping compartments. The basic SIR-model classifies any given person as either **S**usceptible, **I**nfectious or **R**emoved and models the transitions via a set of differential equations.

2.1. The basics of SIR-like-Models

As already mentioned, many models use the standard SIR-model as a baseline and add additional features to it. Accordingly, understanding the basics of the SIR-model is crucial to further follow the adaptations that will be made. The underlying mechanism of the SIR-model can be modelled as such:

Figure 1: Standard SIR-model

Where B substitutes the transfer of people from the category susceptible to infected and Γ similarly expresses the flow from infected to removed. In this case, the compartment "Removed" represents all people that are not labeled as either susceptible or infected, meaning that the model does not differentiate between recovered or deceased individuals. Furthermore, the model uses the following system of differential equations:

$$\begin{cases} \frac{dS}{dt} = -\frac{\beta\, I\, S}{N}, \\ \frac{dI}{dt} = \frac{\beta\, I\, S}{N} - \gamma\, I, \\ \frac{dR}{dt} = \gamma\, I, \end{cases}$$

in which S, I and R are the stock of the susceptible, the infected and the removed population respectively, while N is the total of the population. Additionally, β is the rate at which the disease is transmitted, while γ is the rate at which infected people are removed.

Notably, when examining the system mentioned above it can be concluded that

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0$$

holds true. This is because the system ignores so called vital dynamics, such as births or deaths unrelated to the pandemic, resulting in a static population.

3. Problem formulation

Accurately simulating a pandemic via equation-based analysis in which the entire population is treated uniformly in respect to certain parameters. These parameters include a distinction between recovered and deceased individuals, vaccination rate and development time of an effective vaccine. A successful recovery from the disease shall only temporarily grant immunity, resulting in a potentially cyclic model of infection.

4. My Variation of the SIR-Model

As outlined in the problem formulation, a simulation of a pandemic should respect a set of basic parameters that are not included in the SIR-model. Hence, the model implemented in Mathematica will be more complex. It can be modelled as such:

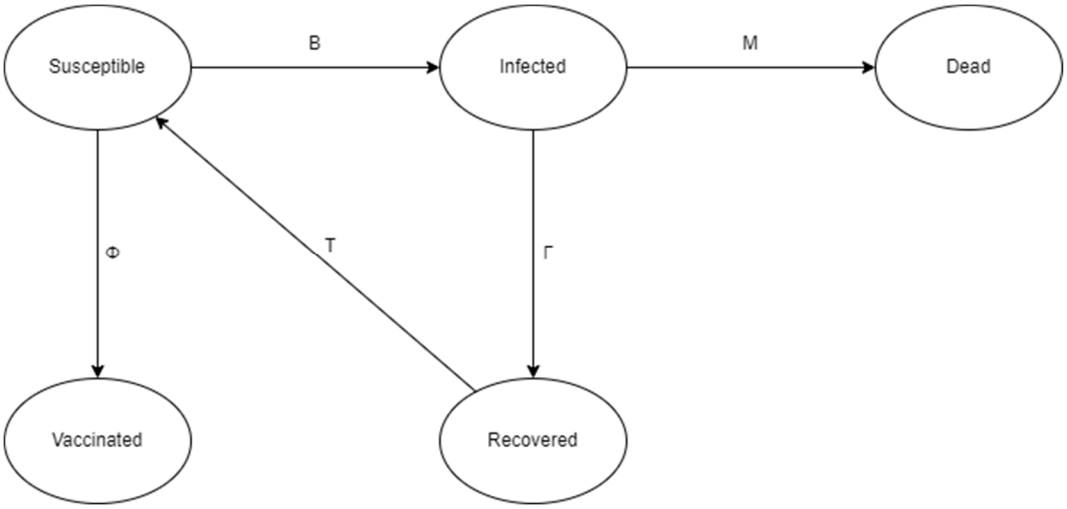

Figure 2: The SIRVD-model

In the graphic above, the compartment "Removed" has now been split up to represent both deceased and recovered people. Additionally, a new classification for the vaccinated population has been added. Once more, B expresses the transfer of susceptible people to the category "Infected". In contrast, Γ and M only model the recovery and the mortality rate of the infected population respectively. Moreover, Φ is the rate of vaccination, while T represents the rate of recovery. The system of differential equations employed for such a model is the following:

$$\begin{cases} \frac{dS}{dt} = -\frac{\beta\, I\, S}{N} - \phi\, S\, Vs + \tau\, R, \\ \frac{dI}{dt} = \frac{\beta\, I\, S}{N} - \gamma\, I - \mu\, I, \\ \frac{dR}{dt} = \gamma\, I - \tau\, R, \\ \frac{dV}{dt} = \phi\, S\, Vs, \\ \frac{dD}{dt} = \mu\, I, \end{cases}$$

In which S, I, R, V and D are the stock of susceptible, infected, recovered, vaccinated and dead population respectively. N represents the total population still alive, meaning: $N = S + I + V + R$. Again, β is the rate at which the disease is transmitted.

Likewise, γ, μ, ϕ and τ express the rate of recovery, mortality, vaccination and the loss of immunity of the recovered population to the disease. The variable Vs is an abbreviation for "Vaccination start" and indicates at what point during the simulation a vaccine is fully developed and in usage. The model remains static, resulting in the equation

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} + \frac{dV}{dt} + \frac{dD}{dt} = 0$$

being a tautology. From this point onward the presented model will be referred to as the SIRVD-model.

5. Development and Evaluation of the SIRVD-Model

The development of the SIRVD-model was relatively straight-forward. Using the standard SIR-model as a basis, the main task was to addon additional features in a sensible fashion. Identifying these features and formulating their requirements in regard to the already existing model, without impeding the remaining components, was the most extensive task.

5.1. Specifying the desired features of the SIRVD-Model

One of the first additions that was necessary for a rational model was the splitting of the "Removed" compartment of the standard SIR-model into both a "Recovered" and "Dead" category. Afterall, it is incredibly unrealistic that during a pandemic there are no casualties. Even if we assume a recovery rate of 100 percent, the absence of any deaths is still an interesting statistic. Summarizing recoveries and deaths simultaneously denies access to this kind of information.

Next in order: Vaccinations. In modern times medicine has advanced tremendously and can relatively quickly develop vaccines, as was the case with Covid-19. Vaccines have become a powerful tool to combat diseases and their impact on slowing any pandemic outbreak cannot be understated. Therefore, to more accurately depict the course of a pandemic, another compartment ("Vaccinated") in the SIRVD-model was needed. This is not uncommon for many compartmental models. However, often these models assume that the rate of vaccination is a constant and that vaccination immediately begins when the first person is infected. And while vaccine development can be swift, it is not instant. Hence, the SIRVD-model adds another modification: the ability to set the required duration for the vaccine development.

Lastly, many SIR-like-models tend to have a very linear flow between the compartments. This results in the majority of the population quickly and permanently becoming immune to further infections. Because of that, these models are only capable of approximating non-cyclical pandemics. On the contrast, the SIRVD-model has the capability of simulating a cyclic evolution of a disease.

5.2. Shortcomings of the SIRVD-Model

The most glaring problem with the SIRVD-model is the fact that many relevant factors of a pandemic are not represented. Social distancing, quarantining and incubation period of the disease for example are all very important for the development of real pandemics. Yet, the SIRVD-model does not directly respect theses aspects. And while the SIRVD-model can indirectly integrate these factors, it is difficult and cumbersome to do so in an even slightly reasonable fashion.

Furthermore, the model assumes certain simplifications usually not present in reality:

Vaccinations provide instant, permanent and perfect immunity to the disease after just one dose. While a person is marked as “Recovered” it is impossible for them to get infected again or to infect other people. Vital dynamics, such as birth and death rates, are completely ignored. Superspreading events are non-existent, resulting in unrealistically smooth infection curves. The population is perfectly homogenous.

All of these simplifications result in a model, that is unable to accurately predict reality. Moreover, the absence of vital dynamics results in a steady, non-replenishing flow of the population into the compartments “Vaccinated” and “Dead”. Ultimately, this causes the SIRVD-Model to become more inaccurate the larger the timeframe of a simulation is.

6. Conclusion

The SIRVD-model is useful for roughly simulating the course of a pandemic. Its predictions are believable and, more importantly, logically sound in regard to the factors that are included in the model. Nevertheless, as already outlined, the SIRVD-model is a severe simplification of reality and should only be used when an equally simplified simulation of a pandemic is desirable or sufficient. Yet, the developed model is still much more accurate than many other SIR-like-models, since it combines a higher number of variables than usual, mimicking reality more closely.

Sources:

1. W.O. Kermack and A.G. McKendrick. *A Contribution to the Mathematical Theory of Epidemics.* Royal College of Physicians, Edinburgh, 1927.
2. Herbert W. Hethcote. *The Mathematics of Infectious Diseases.* Society for Industrial and Applied Mathematics, 2000.
3. Ross Beckley, Cametria Weatherspoon, Michael Alexander, Marissa Chandler, Anthony Johnson and Ghan S Bhatt. *Modeling epicdemics with differential equations.* 2013.

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SIRVD-Model

Relevant parameters for the simulation are:
1. Total initial population (initPop)
2. Total number of infected people (initInf) during initialization (Healthy peopl
3. Exposure rate (β).
4. Recovery rate (γ).
The recovery rate is equal to 1/n, with n being the average duration of
5. Transition rate (τ) from status recovered back to susceptible of any given ind
Again, the transition rate can also be denoted as 1/n, with n being the
immune to the disease after having recovered from the disease previously
6. Vaccination rate (ϕ).
7. Mortality rate (μ).
8. Number of iterations (iterations) during the simulation.

In[49]:=
```
(*Clearing all variables*)
Clear["Global`*"];

(*Starting parameters. Edit here to change the outcome of the simulation*)
initPop = 100 000;
initInf = 10;
β = exposureRate = 0.3;
γ = recoveryRate = 1 / 14;
τ = transRate = 1 / 50;
ϕ = vacinationRate = 1 / 100;
μ = mortalityRate = 1 / 56;
startVac = 50;
iterations = 200;

(*Defining the neccessary differential equations
 according to the theory presented in the paper*)
totalPop = s[t] + i[t] + v[t] + r[t];
eqS = s '[t] == -(β i[t] × s[t]) / totalPop - ϕ s[t] Min[1, Max[0, t - startVac]] + τ r[t];
eqI = i '[t] == (β i[t] × s[t]) / totalPop - γ i[t] - μ i[t];
eqR = r '[t] == γ i[t] - τ r[t];
eqV = v '[t] == ϕ s[t] Min[1, Max[0, t - startVac]];
eqD = d '[t] == μ i[t];

(*Solving the differential equation system with the given start parameters*)
sol = NDSolve[{
    (*Defining the functions that should be solved*)
    eqS,
```

```
    eqI,
    eqR,
    eqV,
    eqD,

    (*Defining proper starting values*)
    (*Number of susceptible people during initialization is the total
     population without the initial number of infected individuals*)
    s[0] == 1. initPop - initInf,
    i[0] == 1. initInf,
    r[0] == 0.,
    v[0] == 0.,
    d[0] == 0.
    (*Starting values are initialized as floats. The
     Hardware is usually more efficient when working with floats*)
   },
   {s, i, r, v, d},
   {t, iterations}];

(*Parsing the solutions of the differential
 equation system into more easily usable forms*)
solS = First[s /. sol];
solI = First[i /. sol];
solR = First[r /. sol];
solV = First[v /. sol];
solD = First[d /. sol];

(*Plotting the simulation*)
Plot[{solS[t], solI[t], solR[t], solV[t], solD[t]}, {t, 0, iterations},
 PlotStyle → {Black, Orange, Blue, Green, Red},
 PlotRange → Automatic,
 Filling → None,
 AxesLabel → {"Iterations", "Number of people"},
 PlotLabel → "Simulation",
 PlotLegends → {"Susceptible", "Infected", "Recovered", "Vaccinated", "Dead"}
]

(*Plotting the numerical change of each compartment each iteration*)
Plot[{solS[t + 1] - solS[t], solI[t + 1] - solI[t], solR[t + 1] - solR[t],
  solV[t + 1] - solV[t], solD[t + 1] - solD[t]}, {t, 0, iterations},
 PlotStyle → {Black, Orange, Blue, Green, Red},
 PlotRange → All,
 Filling → Axis,
```

```
  AxesLabel → {"Iterations", "Number of people"},
  PlotLabel → "Numerical change of each compartment each iteration",
  PlotLegends → {"Susceptible", "Infected", "Recovered", "Vaccinated", "Dead"}
]
```

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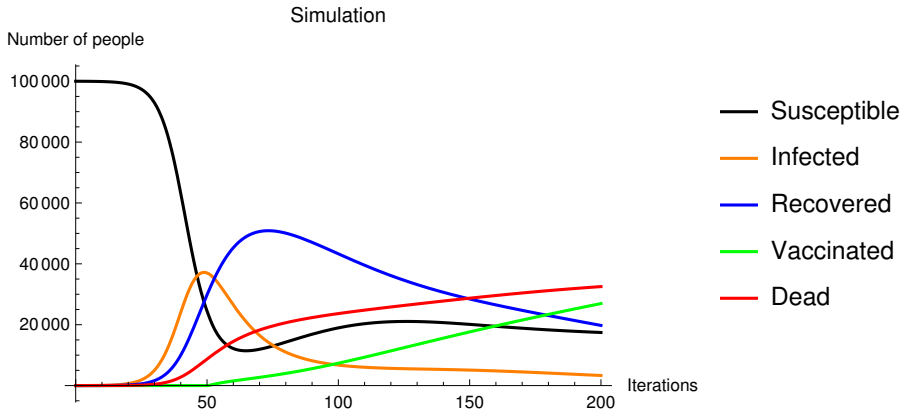

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