A Mathematical Model of a Pandemic

Mikołaj Bartkowiak · 148164 (I1.1)
mikolaj.bartkowiak@student.put.poznan.pl
Szymon Stanisławski · 150192 (I6.2)
szymon.stanislawski@student.put.poznan.pl

This project's aim is to model the progression of a pandemic in a population given certain initial parameters. In order to accomplish this, a basic SIR (*Susceptible-Infectious-Recovered*) model [1] was used to construct a new mathematical model that is able to model the pandemic's progression with some accuracy. The model is by default based on mathematical models that have been used to model the COVID-19 pandemic, although the modularity of its parameters allow it to be used as a general model.

1 Model

In order to mathematically model the course of the pandemic, an SIRDV model[1] was constructed.

In this model the population N is divided into five compartments: the susceptible compartment S, the infected compartment I, the recovered compartment R, the deceased compartment D and the vaccinated compartment V. The transmission of people from susceptible compartment into infected compartment is determined by the rate of infection β, which can be reduced by employing face coverings or lockdown measures by certain part of the population, thus reducing the number of infections. The maximum effectiveness of mask use and lockdown measures was determined as the result of studies on the effectiveness of these measures in the case of the COVID-19 pandemic: face masks amount to 50% reduction in effective transmission, while lockdown measures to 85% [2].

For simplicity no non-pandemic demographic impact was assumed, i.e. the birth rate is equal to the non-pandemic death rate.

1.1 Variables

The variables used in the model relate to the specified population compartments:

- $S(t)$ — susceptible compartment: number of people susceptible to infection,

[1] *Susceptible-Infectious-Recovered-Deceased-Vaccinated model.*

- $I(t)$ — infected compartment: number of infected people,
- $R(t)$ — recovered compartment: number of people that have successfully recovered from disease and have obtained temporary immunity,
- $D(t)$ — deceased compartment: number of deaths due to disease,
- $V(t)$ — vaccinated compartment: number of vaccinated people.

The total alive population N at time t is determined by the following sum:

$$N(t) = S(t) + I(t) + R(t) + V(t). \tag{1}$$

1.2 Parameters

Parameters used in the model:

- β — basic infection rate,
- γ — recovery rate,
- μ — mortality rate,
- σ — immunity loss rate,
- ϕ — percentage of people correctly employing face masks ($0 \leq \phi \leq 1$),
- θ — effectiveness of face coverings defined as the effect on the reduction of infection rate ($0 \leq \theta \leq 1$); in this project assumed $\theta = 0.5$,
- δ — percentage of people undergoing social isolation ($0 \leq \delta \leq 1$),
- η — effectiveness of social isolation defined as the effect on the reduction of infection rate ($0 \leq \eta \leq 1$); in this project assumed $\eta = 0.85$,
- λ — vaccination rate defined as the percentage of vaccinated people per unit of time,
- α — vaccine efficacy index ($0 \leq \alpha \leq 1$).

1.3 Differential equations

Differential equations used in the model:

$$\begin{aligned}
\frac{dS}{dt} &= -(1-\phi\theta)(1-\delta\eta)\beta\frac{IS}{N} + \sigma R - \lambda S, \\
\frac{dI}{dt} &= (1-\phi\theta)(1-\delta\eta)\beta\left(\frac{IS}{N} + (1-\alpha)\frac{IV}{N}\right) - (\gamma+\mu)I, \\
\frac{dR}{dt} &= \gamma I - \sigma R, \\
\frac{dD}{dt} &= \mu I, \\
\frac{dV}{dt} &= \lambda S - (1-\phi\theta)(1-\delta\eta)(1-\alpha)\beta\frac{IV}{N}.
\end{aligned} \tag{2}$$

Using the equation (1), the change in total alive population N is described by the equation

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

which, after using the substitutions (2) simplifies to:

$$\frac{dN}{dt} = -\mu I. \tag{3}$$

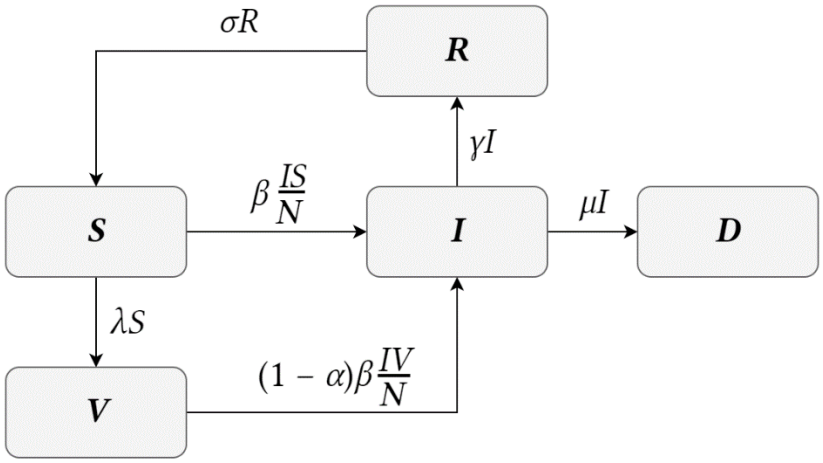

Figure 1. Flowchart of the formulated model.

1.4 Constraints

Since each of the variables represents a non-negative quantity, i.e. the population of a given compartment, the model is subject to the following constraints:

$$\begin{aligned} S(0) &\geq 0, \\ I(0) &\geq 0, \\ R(0) &\geq 0, \\ D(0) &\geq 0, \\ V(0) &\geq 0. \end{aligned}$$

Furthermore under the above constraints all states of variables are non-negative for all time $t > 0$, thus the model is epidemiologically meaningful and its dynamics can be considered in the region below:

$$\Omega = \left\{(S, I, R, D, V) \in \mathbb{R}_+^5\right\}.$$

The basic reproduction number R_0 represents the expected number of new cases generated by an infected individual in a completely susceptible population $\left(\frac{S}{N} \approx 1\right)$ [3] and can be calculated using the following formula:

$$R_0 = \frac{\beta}{\gamma + \mu}.$$

R_0 represents the pure transmission rate of the disease and does not take into account what proportion of the current population is susceptible or the reduction in transmission caused by isolation measures and mask use.

Assuming non-zero vaccine efficacy[2] ($\alpha > 0$), herd immunity threshold p_c (i.e. the percentage of population that needs to be vaccinated to stop the spread of the pandemic) is defined as:

$$p_c = \frac{1 - 1/R_0}{\alpha}.$$

[2] As vaccine efficacy tends to zero, the limit $\lim_{\alpha \to 0^+} p_c = \infty$, i.e. there is no such percentage that grants herd immunity in the case of a vaccine with 0% efficacy.

Conversely, the reproduction number R_t at a time t depends on the proportion of the susceptible population and measures taken after the onset of a pandemic. R_t varies over the course of a pandemic and takes into account the proportion vaccinated individuals, who have lesser risk of contracting the disease:

$$R_t = \frac{(1-\phi\theta)(1-\delta\eta)\left(\frac{S}{N} + (1-\alpha)\frac{V}{N}\right)\beta}{\gamma+\mu}.$$

1.5 Difference equations

Using the following relationship

$$\frac{df}{dt} = \lim_{\Delta t \to 0} \frac{f(t+\Delta t) - f(t)}{\Delta t} \approx \frac{f(n+1) - f(n)}{T_p} = \frac{\Delta f(n)}{T_p}$$

the differential equations (2) were transformed into their respective discrete difference equations:

$$\begin{aligned}
\frac{\Delta S(n)}{T_p} &= -(1-\phi\theta)(1-\delta\eta)\beta\frac{I(n)S(n)}{N(n)} + \sigma R(n) - \lambda S(n), \\
\frac{\Delta I(n)}{T_p} &= (1-\phi\theta)(1-\delta\eta)\beta\left(\frac{I(n)S(n)}{N(n)} + (1-\alpha)\frac{I(n)V(n)}{N(n)}\right) - (\gamma+\mu)I(n), \\
\frac{\Delta R(n)}{T_p} &= \gamma I(n) - \sigma R(n), \\
\frac{\Delta D(n)}{T_p} &= \mu I(n), \\
\frac{\Delta V(n)}{T_p} &= \lambda S(n) - (1-\phi\theta)(1-\delta\eta)(1-\alpha)\beta\frac{I(n)V(n)}{N(n)}.
\end{aligned} \tag{4}$$

Similarly, total alive population (3) was transformed into the following discrete form:

$$\frac{\Delta N(n)}{T_p} = -\mu I(n).$$

T_p is the sampling period and it is defined as the duration for which the discretisation of the model is performed, expressed in days. For the purposes of the simulation $T_p = 1$ was assumed, as realistically most epidemiological data are given on a daily basis.

2 Implementation

The described model was implemented using Python programming language along with Flask web framework and SQLAlchemy serving as an SQL toolkit. The charts were generated using open-source JavaScript library Chart.js.

The app structure is relatively straightforward. `routes.py` describes the routing used for serving pages using the HTML templates specified in the `templates` subfolder. `models.py` is used to construct an SQL database; the initial values of the parameters are taken from `values.py`. Finally, `maths.py` contains the description of the mathematical model using the designated difference equations (4).

2.1 Database structure

The SQL database structure is defined as follows:

database
id
infection_rate
recovery_rate
mortality_rate
immunity_loss_rate
mask_rate
social_distancing_rate
mask_effectiveness
social_distancing_effectiveness
vaccination_rate
vaccine_efficacy
_time

The `id` field acts as a primary key in order to differentiate between consecutive simulations differing by the values of the parameters provided by the user.

3 Literature

[1] I. Cooper, A. Mondal and C. G. Antonopoulos, "A SIR model assumption for the spread of COVID-19 in different communities," *Chaos, Solitons & Fractals,* vol. 139, 2020.

[2] S. Talic, S. Shah, H. Wild, D. Gasevic, A. Maharaj, Z. Ademi, X. Li, W. Xu, I. Mesa-Eguiagaray, J. Rostron, E. Theodoratou, X. Zhang, A. Motee, D. Liew and D. Ilic, "Effectiveness of public health measures in reducing the incidence of covid-19, SARS-CoV-2 transmission, and covid-19 mortality: systematic review and meta-analysis," *BMJ,* vol. 375, 2021.

[3] J. Jones, "Notes on R0," Stanford University.