

The SIR Model



INTRODUCTION

Infectious diseases have accompanied the human species throughout recorded history. Their emergence and re-emergence constitute a worldwide health challenge. Some of these diseases, such as Polio, can inflict mortality on their hosts. HIV, for example, has accumulated a death toll of over 40 million people since its widespread emergence in 1981 (WHO, 2022).



Figure 1: The SIR Model (Gounane et. al, 2021)

OBJECTIVE/METHODOLOGY

The question my paper seeks to answer is; how do the elements of the SIR model affect predictions made about disease dynamics, from both a mathematical and epidemiological perspective? This is done using numerical experiments analyzing the effect of model parameters β and γ on the S, I and R curves and how elements such as time stepping, rounding and computational cost of Runge-Kutta integrators interact when solving the basic SIR model. The experiments are done using R and Excel

THE SIR MODEL

The SIR model uses 3 differential equations to mathematically express the movement of individuals from the susceptible to the infected and lastly to the recovered group. When taking vital dynamics (birth and death rates) into account, three parameters are used when setting up the three equations; the recovery rate γ , e.g. ,the average rate at which individuals leave the infected class, the transmission rate β , e.g., the average rate at which individuals enter the infected class, and the per capita birth/death rate μ .

The SIR equations can be solved for S, I and R using numerical integration. This entails using an algorithm to approximate future values using initial values and their derivatives, stepwise.

$$\begin{aligned} \frac{dS}{dt} &= \mu - \beta SI - \mu S, \\ \frac{dI}{dt} &= \beta IS - \gamma I - \mu I, \\ \frac{dR}{dt} &= \gamma I - \mu R. \end{aligned}$$

Figure 2: The SIR equations



Figure 3: The basic reproduction number ($R_0=2$)

R_0

In epidemiology, β/γ denotes the basic reproduction number R_0 and is understood as the average number of secondary cases arising from an average primary case in an entirely susceptible population.

If $R_0 > 1$, disease invasion occurs.
If $R_0 < 1$, disease invasion does not occur.

The effective reproduction number $R(E)$ denotes the average number of secondary cases per infectious individual in a non-fully susceptible population and can be approximated by multiplying the basic reproduction number R_0 with the fraction of susceptible in the host population.

RESULTS

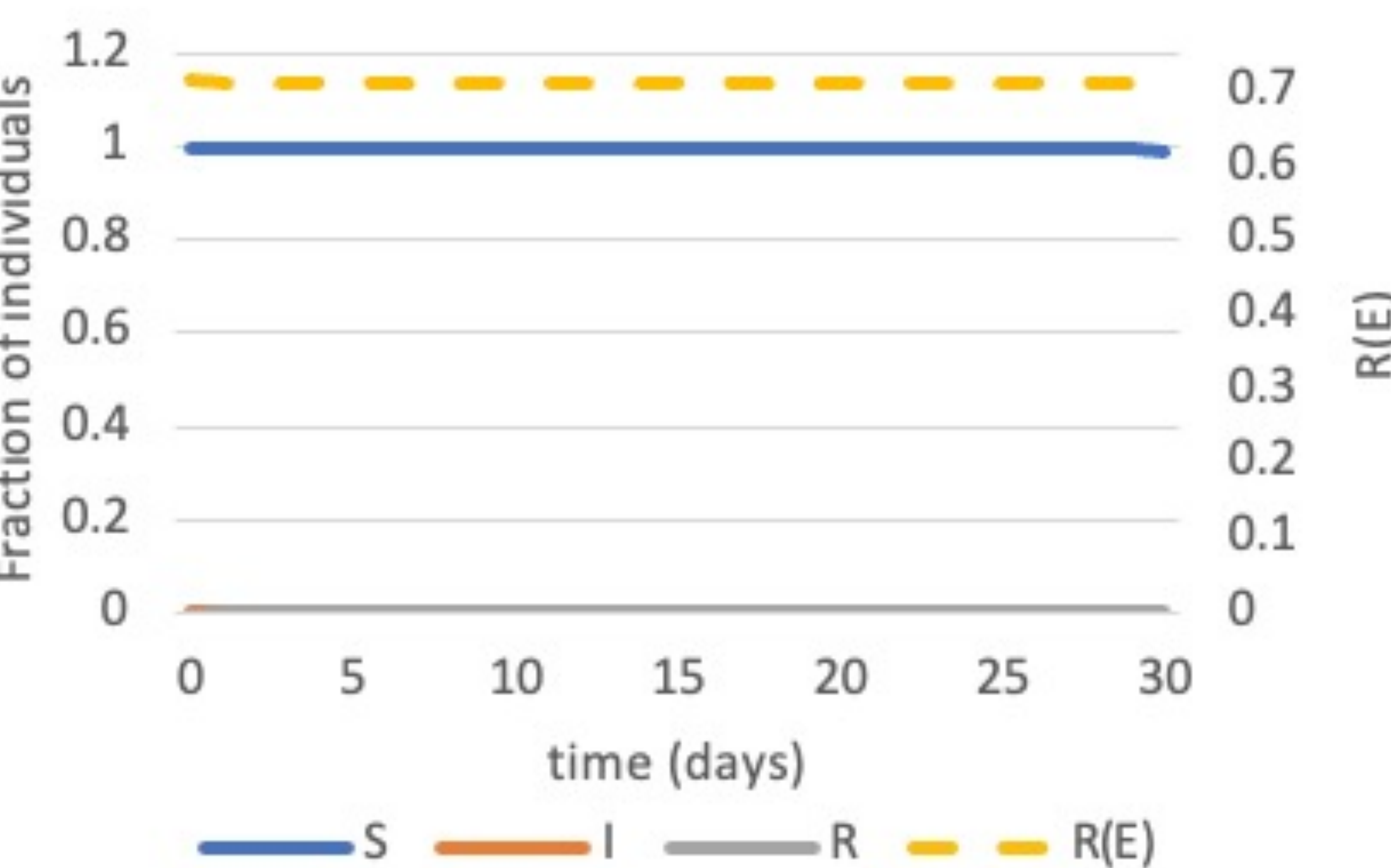


Figure 4: Simulation for $\beta=0.5, \gamma=0.7$

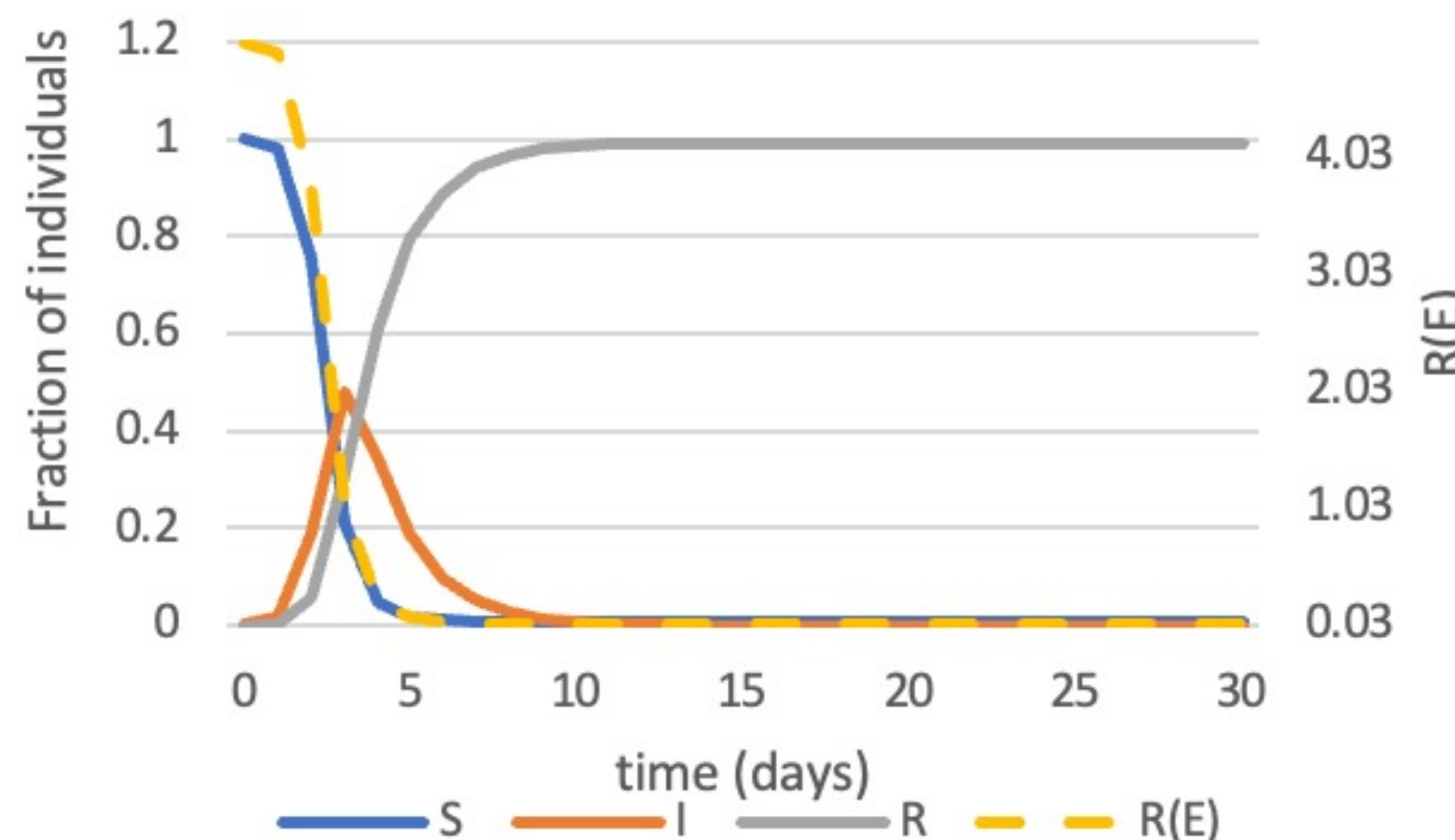


Figure 5: Simulation for $\beta=3.5, \gamma=0.7$

ANALYSIS OF RESULTS

Above the results for the parameter experimentation are presented. Two scenarios are shown; $R_0 > 1$ and $R_0 < 1$. In figure 4, all curves are stagnant. This is due to the transmission rate being smaller than the recovery rate ($0.5 < 0.7$); more people leave the infectious class on average per time than enter. This leads to the infection not being able to proliferate, as seen by the flat infectious curve..

Figure 5 shows an extreme example where $R_0=5$. This means the disease spreads rapidly, which is reflected in the maximum of infected at a little less than half the population infected being reached after only 3 days. This shows that a higher R_0 leads to a higher maximal number of infected. Because the basic reproduction number is so high, virtually all susceptible become infected, as can be seen in the number of susceptible at the stable endemic equilibrium. After reaching its height ($R(E)=1$), the infectious curve dies down to 0, at which point approximately the total population is comprised of recovered individuals. It is also noteworthy that for each simulation, the total population is conservative.

Sources

WHO. (2022). *HIV*. Retrieved from who.int: <https://www.who.int/data/gho/data/themes/hiv-aids>

Gounane, Said, Barkouch, Yassir, Atlas, Abdelghafour, Bendahmane, Mostafa, Karami, Fahd and Meskine, Driss. "An adaptive social distancing SIR model for COVID-19 disease spreading and forecasting" *Epidemiologic Methods*, vol. 10, no. s1, 2021,. <https://doi.org/10.1515/em-2020-0044>

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