Exam, TFY4235 Computational physics

Number

Introduction

SIR, and the more advanced SEIIaR, are mathematical models that aim to capture how pandemics spread throughout a simulation. This paper documents the implementation and results of the simulation of these models in Python, as described in [1].

Implementation

All the different models used in this text follow the same basic form. The goal is to find $x(t)$, given initial conditions $x(t_0)$, and a equation of the form

$$f(x(t); \text{args}) = \frac{\mathrm{d}x(t)}{\mathrm{d}t}.$$

In the first part, $x = (S, I, R)$, while later $x = (S_{ij}, E_{ij}, I_{ij}, Ia_{ij}, R_{ij})$ where (ij) are different population groups. This is accomplished using function `integrate` in `utilities.py`. It takes as arguments the initial conditions `x0`, the functions `f` and `step`, the list `args` as well as the time step `dt` and total time `T` to simulate. It then creates a discrete approximation of $x(t)$ by taking time steps given by the function `step`. `step` is the particular *scheme* used, for example Runge-Kutta (4,5), while `f` defines the system.

The equations that give the asymptotic behavior are both of the type $x = f(x)$, and can thus be approximated by recursion, given that they converge. For $\mathcal{R}_0$ close to one, they converge increasingly slowly, and the program may reach maximum recursion depth. For the parameters in this exercise, however, this was not a problem

Results

Deterministic SIR model

The first model is the deterministic SIR model, given by a set of coupled ODEs [1]. In this text, the Runge-Kutta (4, 5) scheme was used, as it is both a simple yet precise scheme. Figure 1 demonstrates that S and R approaches the expected asymptotes, and that I grows exponentially in the beginning. Adjusting the β-parameter will affect how fast the virus spreads, thus "flattening the curve", as illustrated in Figure 2. This shows how far β must be reduced to ensure that the fraction infected stays below 0.2. Figure 3 shows the fraction of the population must be vaccinated *before* the outbreak to stop exponential growth. At the start of the simulation, the number of infected grows exponentially, i.e. $I \propto \exp(\alpha t)$ for some α. A partially vaccinated population can be modeled by setting $R(0)$ equal the proportion of the population that is vaccinated. The result shows that 60% or more must be vaccinated to avoid exponential growth, i.e. $\alpha \leq 0$

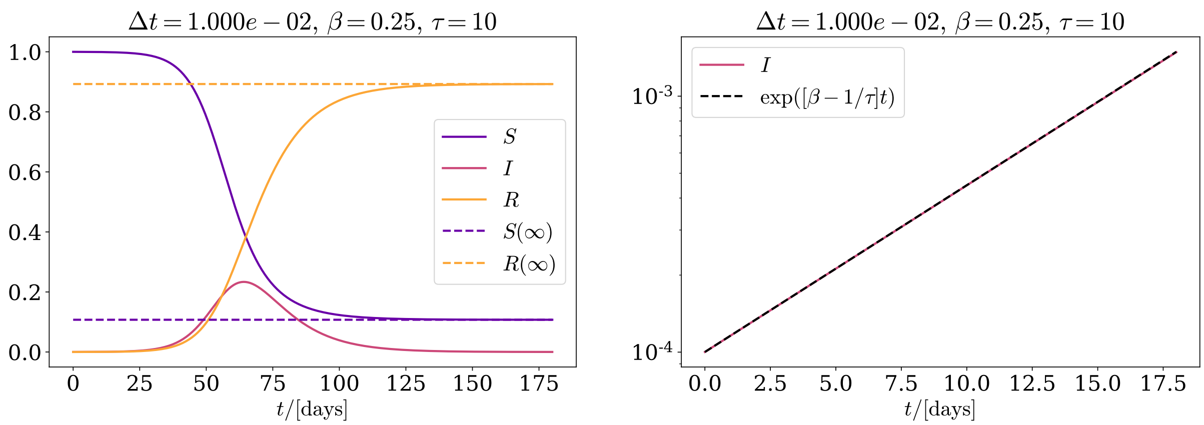

Figure 1: On the left, the fraction of the population that is in each group, over time. The plot on the right shows how the infection spreads exponentially in the begining

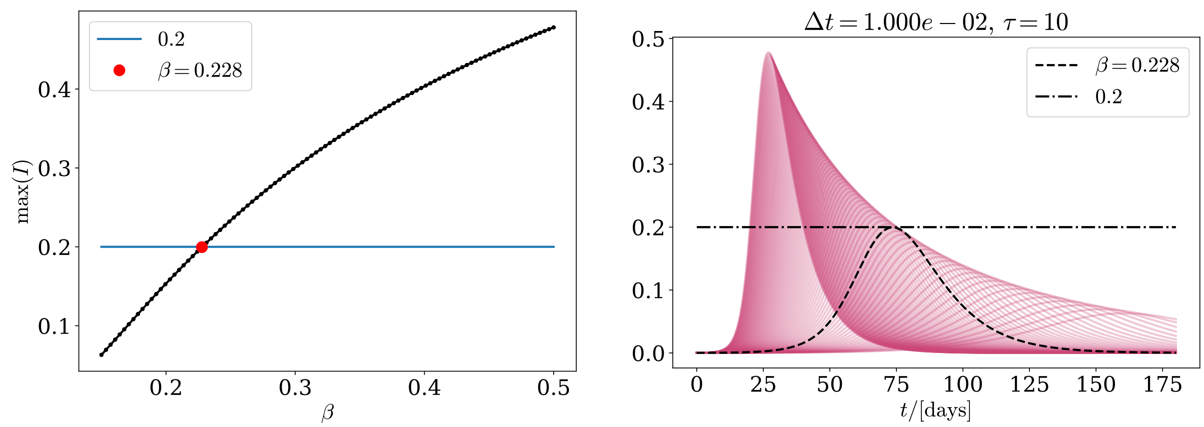

Figure 2: The figure on th eright shows the maximum fraction of infected, as a function of β. The largest value of β such that the maximum is beneth 0.2 is indicated. On the right, the corresponding infection curves.

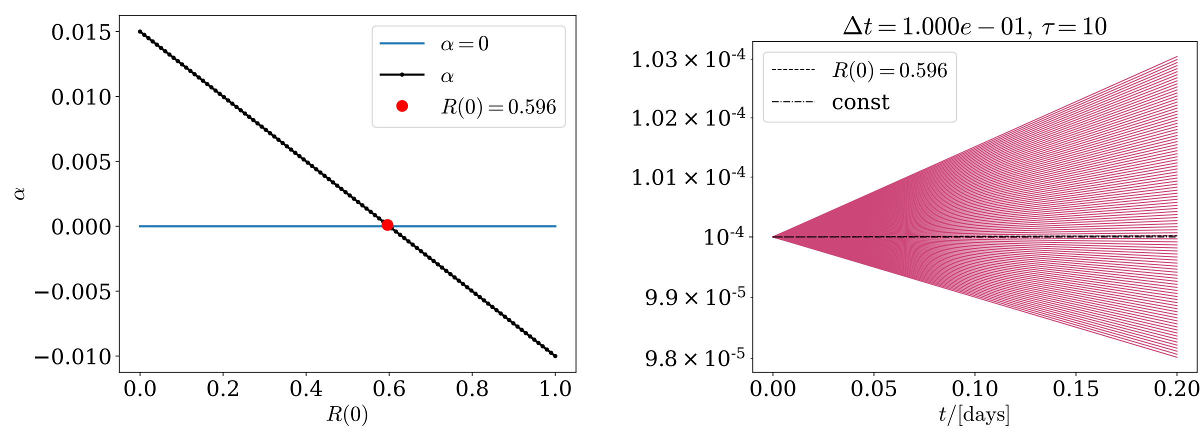

Figure 3: The plot on the left shows the maximu $R(0)$, i.e. fraction of vaccinated, that still gives exponential growth. The right shows a log-plot of the growht of infected at the very begining.

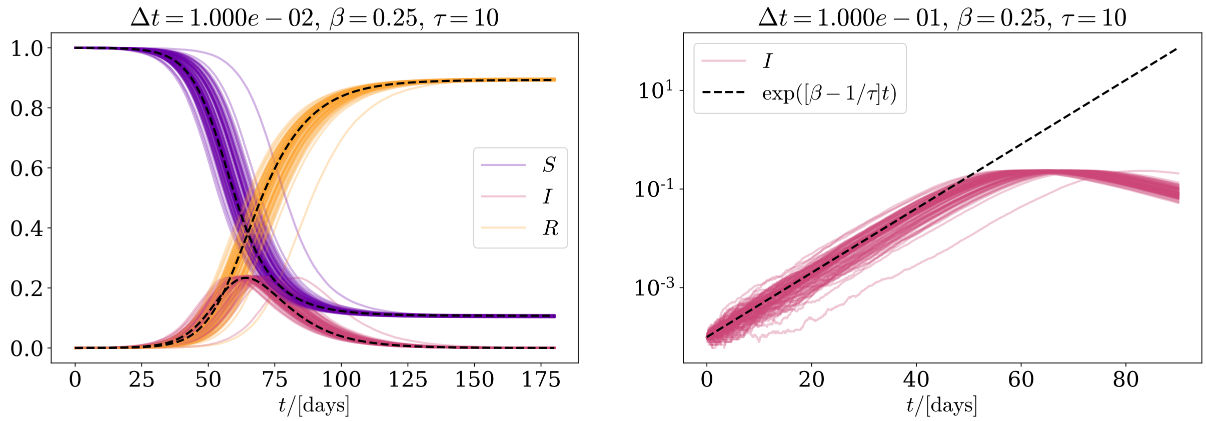

Figure 4: 100 runs of the stochastic SIR model. All runs are close to the deterministic, showed as dashed lines

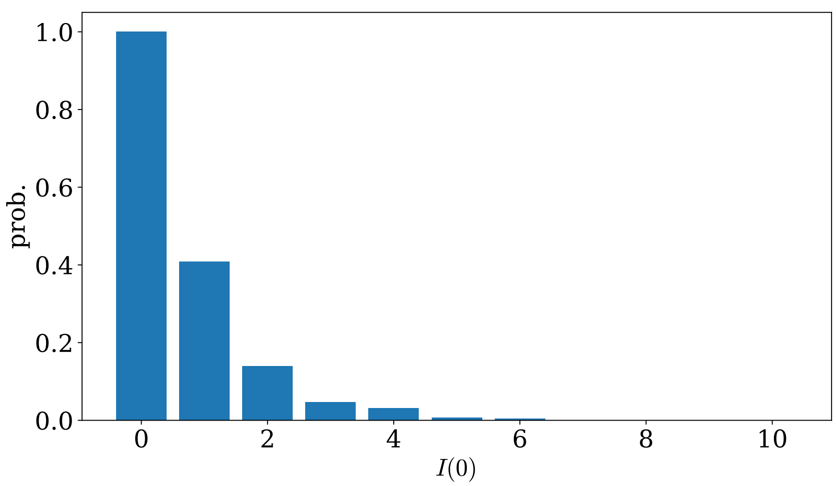

Figure 5: The probability that the infection dies, for different starting values of I.

Stochastic SIR model

Next, the stochastic version of SIR model is used. Figure 4 shows the result of 100 runs, which all give result close to that of the deterministic one. All simulation uses a population of 100 000, but the plots are normalized. (DISCUSS TIMESTEP) The stochastic nature of this model makes it possible for the infection to die out, even with $\mathcal{R}_0 > 1$, by pure chance. Figure 5 Shows the

References

[1] NTNU, Institutt for Fysikk. *Exam, TFY4235 Computational Physics*. 2021.