Disease Modeling - FYS3150 Computational Physics

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INTRODUCTION

THEORY, ALGORITHMS AND METHODS

Runge-Kutta methods

Markov Chains

A Markov Chain aims to model the behavior of stochastic processes, that is models which time-evolution of each parameter x_i is governed by a set of transition probabilities $P(x_i \to x_j)$.

The k-th state of the system is given by the state vector $\mathbf{x}_k$, a column vector with entries x_i for each parameter of the system.

$$\mathbf{x}_k = \begin{pmatrix} x_1 \\ \vdots \\ x_i \\ \vdots \\ x_n \end{pmatrix} \tag{1}$$

The transition probabilities $P(x_i \to x_j)$ are contained within a Stochastic matrix, M, an $n \times n$ matrix which columns are probability vectors that sum to unity. M is such that multiplying it by a state $\mathbf{x}_k$ determines the next state, $\mathbf{x}_{k+1}$

$$M\mathbf{x}_k = \mathbf{x}_{k+1} \tag{2}$$

From Theorem 18 in Lay [1, p. 277], if M is a regular stochastic matrix there exists a unique steady state vector $\mathbf{q}$ which the system will converge towards as $k \to \infty$ characterized by

$$\mathbf{x}_k = \mathbf{x}_{k+1} \tag{3}$$

Regardless of the initial state, $\mathbf{x}_0$.

SIRS Model

The SIRS model is a type of mathematical model describing how infectious disease evolves within a population, and is a part of a family of similar models in epidemiology with various different features. In the SIRS model, the total population (N) is divided into three groups

- Susceptible (S) : People who do not have the disease, and are not immune to it.
- Infected (I) : People who are infected with the disease.
- Recovered (R) : People who has recovered from the infection, and have developed immunity.

Where the permitted traversal from one group to another follows a cyclical pattern $S \to I \to R \to S$.

The rate of traversal is governed by a set of coupled differential equations,

$$\begin{aligned} S' &= cR - \frac{aSI}{N} \\ I' &= \frac{aSI}{N} - bI \\ R' &= bI - cR \end{aligned} \tag{4}$$

Where the constants a, b, c are governing the

- rate of transmission
- rate of recovery
- rate of immunity loss

respectively, with dimension inverse time. For the purposes of this report, we will not consider a specific unit of time, but rather the dynamics of the system, as the timescales at which different diseases operate on vary. However, based on data (INSERT CITATIONS) a lot of common diseases are observed to operate on a scale of days, whilst some operate on a scale of years.

This system can also be modelled as a Stochastic system described as a Markov Chain, shown as a Markov diagram in Fig. 1. If we consider a small, finite timeinterval Δt, we can approximate the transition probabilities $P(x_i \to x_j)$ from Eqn. 4

$$\begin{aligned} P(S \to I) &= \frac{aSI}{N}\Delta t \\ P(I \to R) &= bI\Delta t \\ P(R \to S) &= cR\Delta t \end{aligned} \tag{5}$$

It follows then, that the system will reach a steady state after a finite number of transitions for any set of initial conditions as discussed in Section

Units

Units of time, and the rates $a, b, c, \ldots$ isn't something i will pay much attention to in this report, as it is an

entirely separate topic on it's own. And ultimately, would be decided on a per-disease basis. But for the sake of discussion, and exploration of the model, i will consider the time-scale of order $\approx$ years.

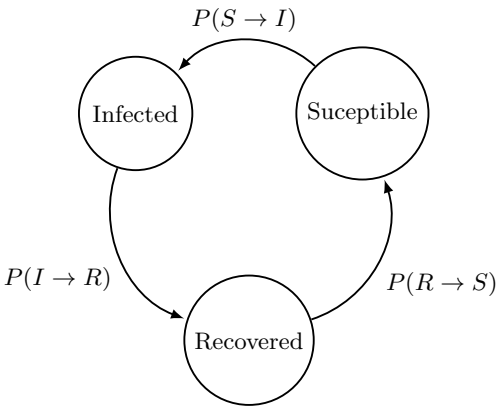

FIG. 1: The SIRS Model

Monte-Carlo Algorithm

The Monte-Carlo way of simulating the various SIRS-Models are outlined in the following for the simplest case

SIRS Monte-Carlo

```
for each MC-Cycle:
  for each t_i:
    Compute P(S → I)
    Compute P(I → R)
    Compute P(R → S)

    if P(S → I) > r and S_i > 0:
      S_{i+1} -= 1
      I_{i+1} += 1

    if P(I → R) > r and I_i > 0:
      I_{i+1} -= 1
      R_{i+1} += 1

    if P(R → S) > r and R_i > 0:
      R_{i+1} -= 1
      S_{i+1} += 1
```

We note here, a problem in the algorithm. That is; in what order do we evaluate the probabilities? Whether to consider $P(S \to I)$ or P$(R \to S)$ first is completely arbitrary, but may lead to a certain bias in smaller populations or when a group is nearing the lower limit of 0.

Another important issue, that is dealt with in the IF statements is the potential of negative population groups. Whilst the overall net population is easily conserved[1], we have to ensure that no groups goes below 0. This can be done in one of two ways. 1. By checking if any of the groups is > 0 after updating all the values. This is sufficient in an entirely cyclical SIRS-model, but for any of the non-cyclical model, it is not sufficient as we may have multiple movements from the same group per cycle. Therefore, the more robust method is to always check if the group that is being deducted is < 0, as seen in the IF statements above.

RESULTS AND DISCUSSIONS

Implementation

SIRS: Vital Dynamics

If we not turn to Fig. REF we see the plots for the vital dynamics system. For this model, we observe a significant mismatch between the ODE solution and and the MC solutions. Whilst this initially hits to

SIRS: Vaccination

CONCLUSIONS

The obvious next step in the analysis of the SIRS model, and the different features we have discussed is to consider the combination of all of these added features, described by

$$\begin{aligned} S' &= cR - (A\cos(\omega t) + a_0)\frac{SI}{N} - dS + eN - f \\ I' &= (A\cos(\omega t) + a_0)\frac{SI}{N} - bI - (d + d_I)I \\ R' &= bI - cR - dR + f \end{aligned} \tag{6}$$

Whilst the implementation of this model trivial[2], the analysis of it is likely a much more complicated due to how the different features will interact with each other.

[1] D. C. Lay, *Linear Algebra and Its Applications*, 5th ed. (Pearson, 2016).

[1] Mathematically, anyway.

[2] Armed with the experience of implementing, and understanding the individual features

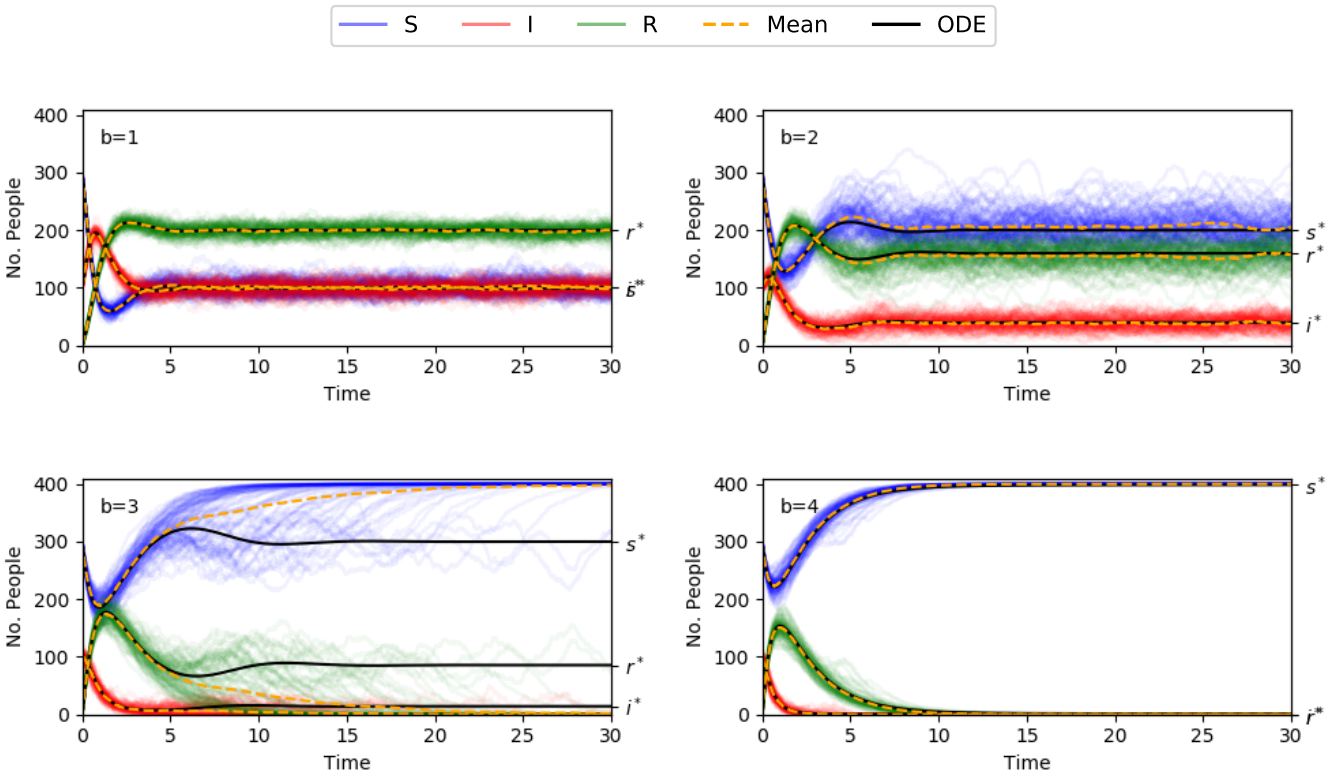

FIG. 2: fig:a b plots

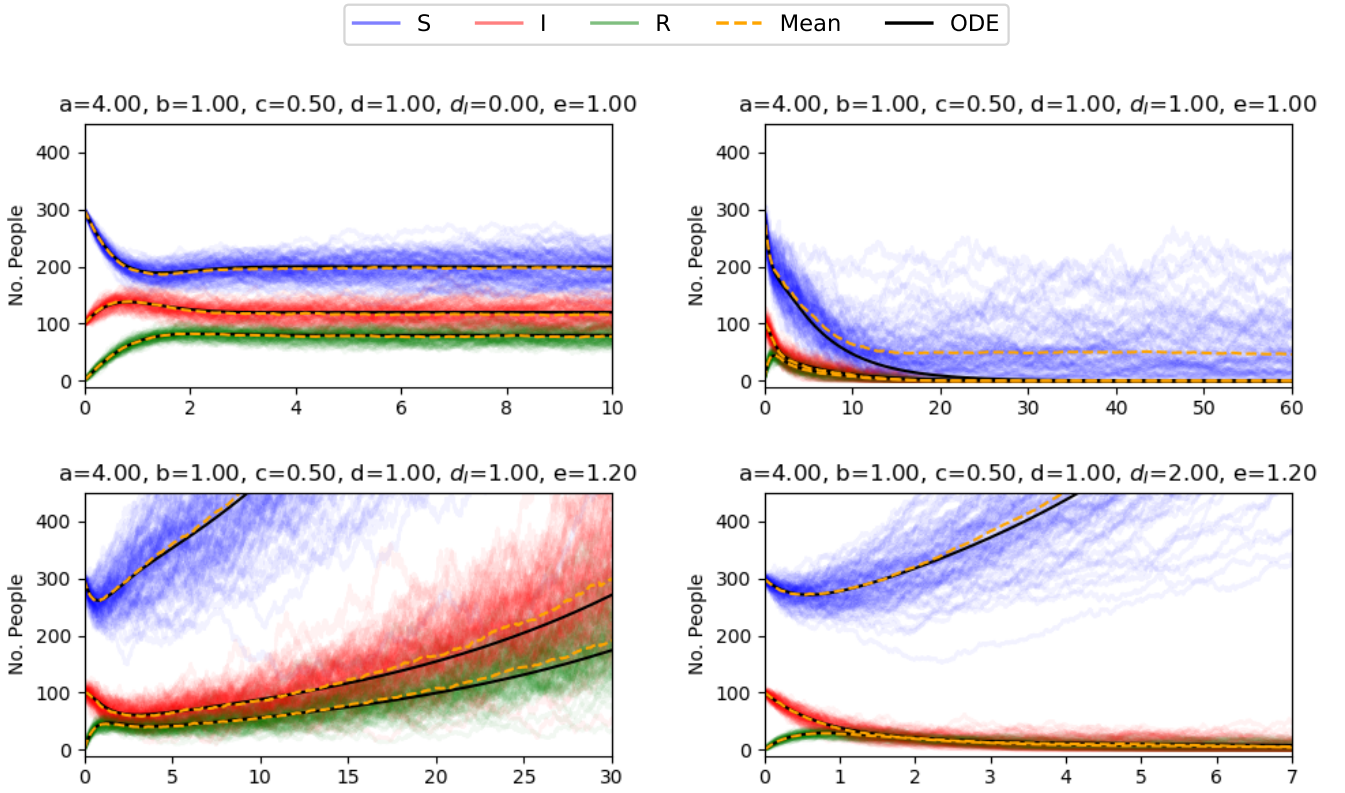

FIG. 3

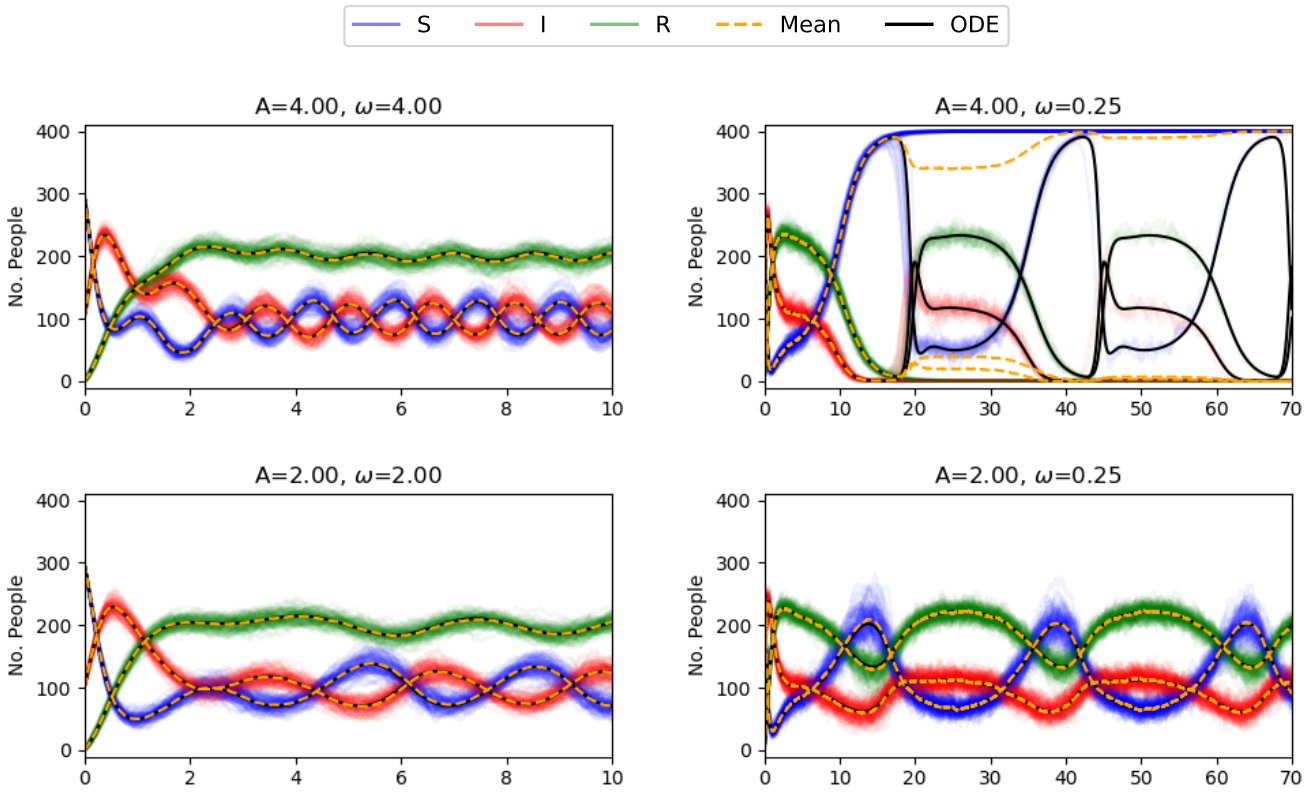
S
I
R
Mean
ODE
A=4.00, ω=4.00
A=4.00, ω=0.25
A=2.00, ω=2.00
A=2.00, ω=0.25
No. People

FIG. 4

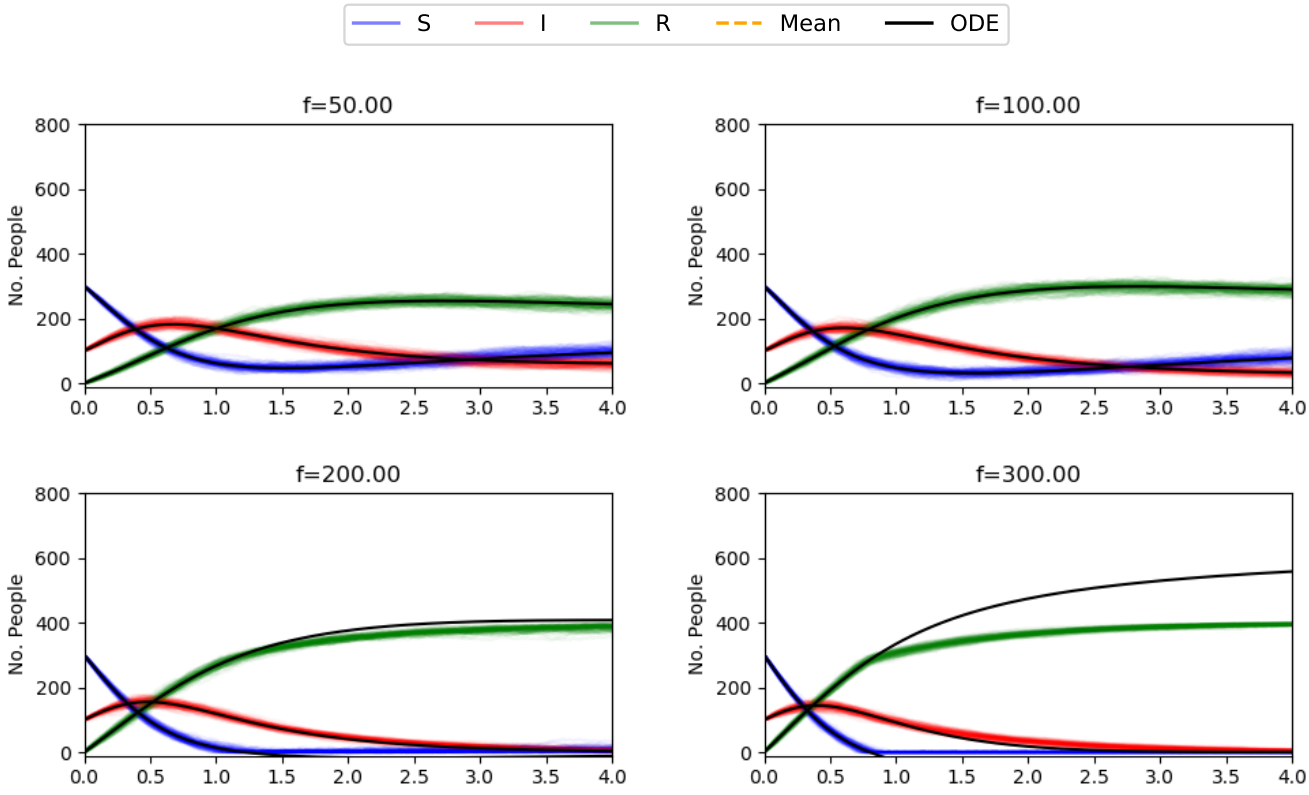
S
I
R
Mean
ODE
f=50.00
f=100.00
f=200.00
f=300.00
No. People

FIG. 5