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 $a, b, c, \dots$ 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 ≈ years.

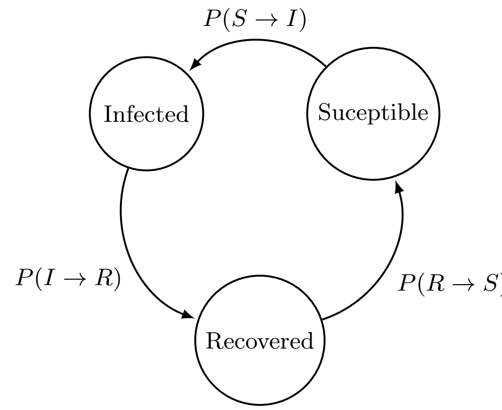

FIG. 1: The SIRS Model

RESULTS AND DISCUSSIONS

Implementation

CONCLUSIONS

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

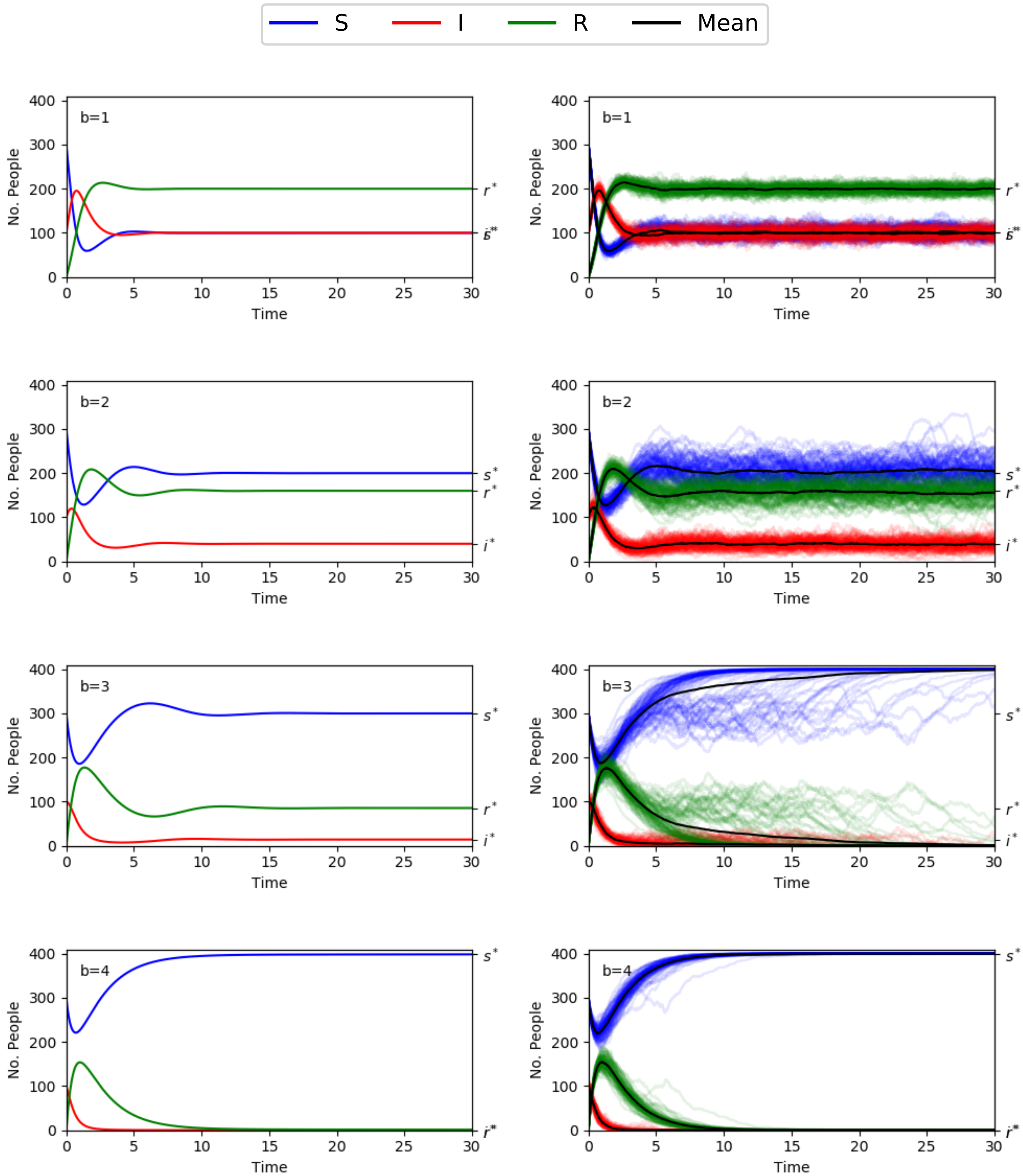

FIG. 2: Solutions for SIRS model described by Eqn. (REF TO EQN) (a - d) and Monte Carlo solution (e - h) for $b = 1, 2, 3, 4$ (rate of recovery)

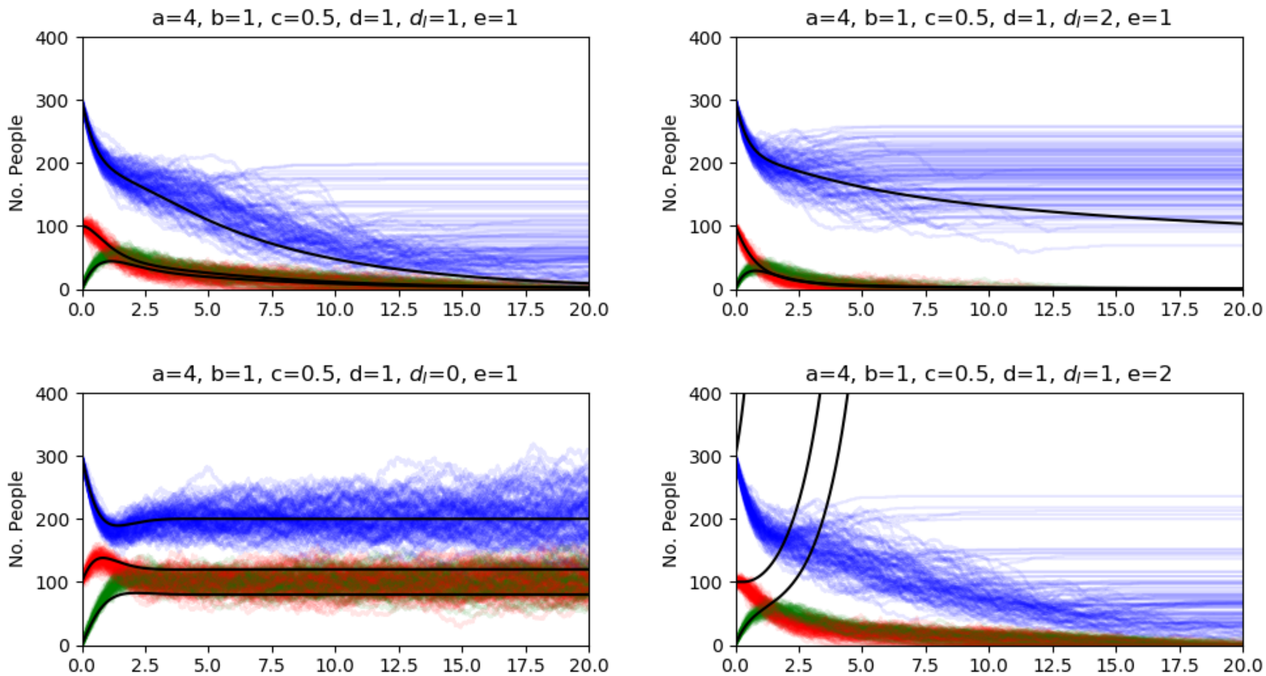
a=4, b=1, c=0.5, d=1, d_I=1, e=1
a=4, b=1, c=0.5, d=1, d_I=2, e=1
a=4, b=1, c=0.5, d=1, d_I=0, e=1
a=4, b=1, c=0.5, d=1, d_I=1, e=2
No. People

FIG. 3

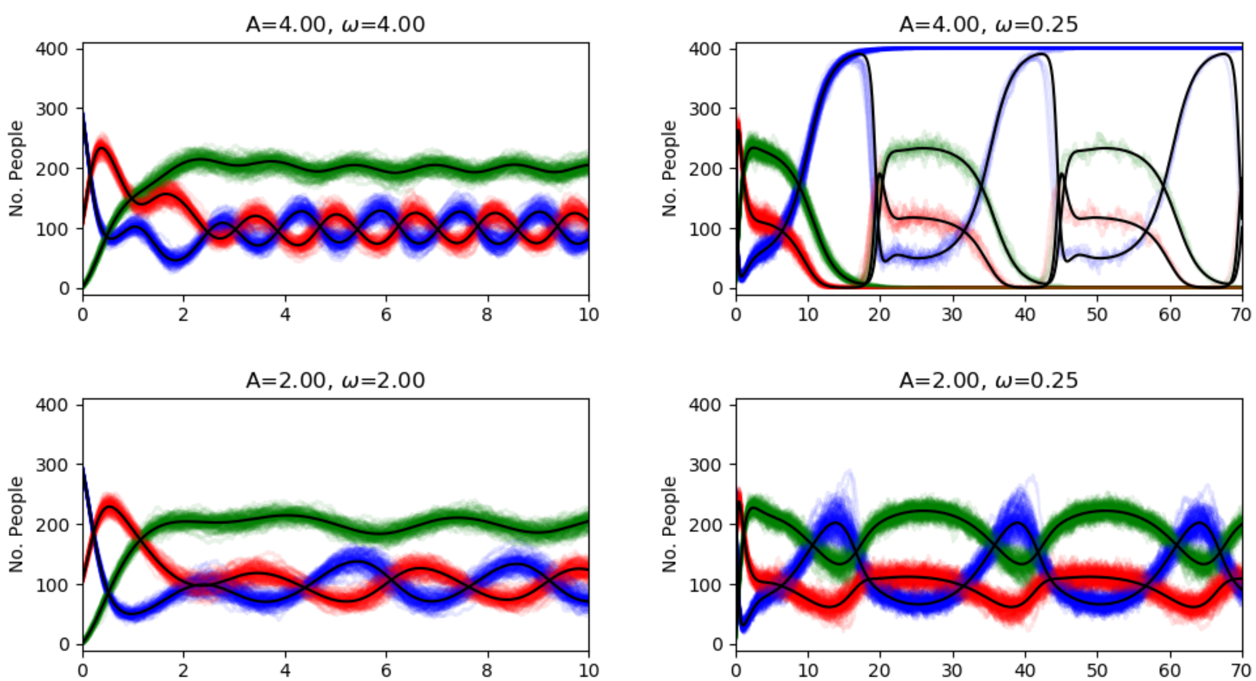
A=4.00, ω=4.00
A=4.00, ω=0.25
A=2.00, ω=2.00
A=2.00, ω=0.25
No. People

FIG. 4