

# Disease Modeling - FYS3150 Computational Physics

Nicholas Karlsen

## 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  $P(x_i \rightarrow x_j)$ .

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.

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

The transition probabilities  $P(x_i \rightarrow x_j)$  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,  $\mathbf{x}_{k+1}$

$$M\mathbf{x}_k = \mathbf{x}_{k+1} \quad (2)$$

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  $k \rightarrow \infty$  characterized by

$$\mathbf{x}_k = \mathbf{x}_{k+1} \quad (3)$$

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  $S \rightarrow I \rightarrow R \rightarrow S$ .

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

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

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  $\Delta t$ , we can approximate the transition probabilities  $P(x_i \rightarrow x_j)$  from Eqn. 4

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

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

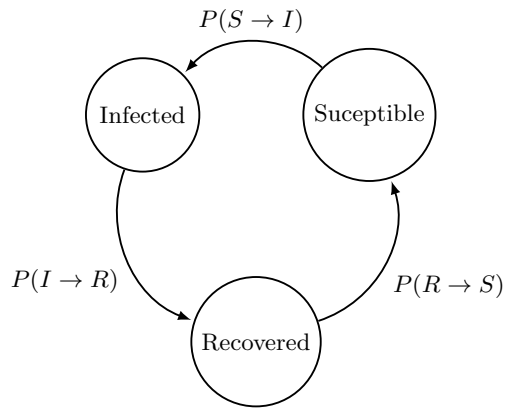


FIG. 1: The SIRS Model

## RESULTS AND DISCUSSIONS

## CONCLUSIONS

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

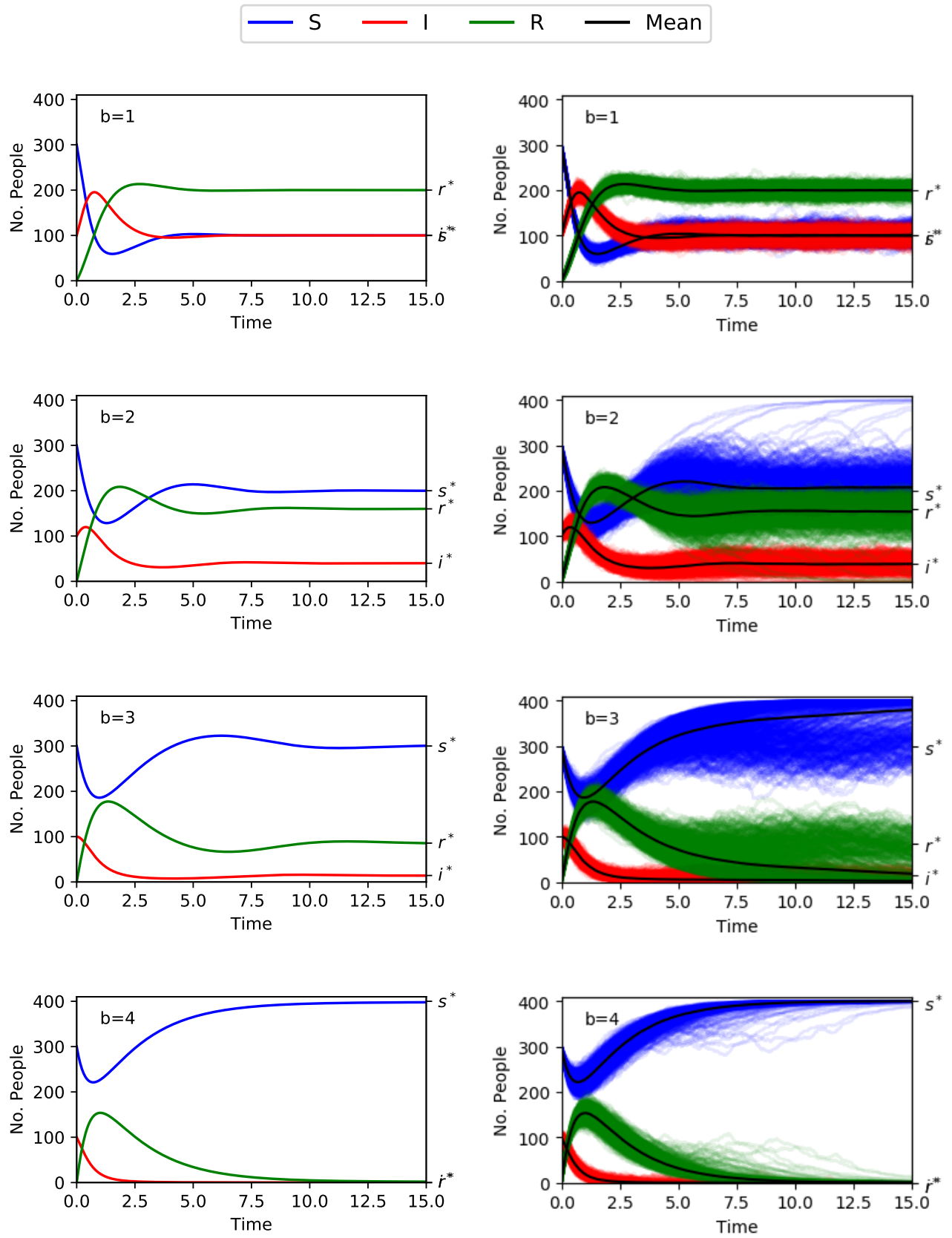


FIG. 2: Solutions for SIRS model described by Eqn. (REF TO EQN) (a - d) and Monte Carlo solution (e - h) for  $b = 1, 2, 3, 4$  (rate of recovery)