

Epidemic model with four compartments and retarded transition rates

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The first modern approach of epidemic dynamics appeared almost a century ago in the seminal work of Kermack and Mc Kendrick who introduced the ‘SIR - model’ considering three states (‘compartments’) of health (susceptible, infected, recovered) [1]. This presentation is devoted to an epidemic model for a constant population by taking into account four compartments of individuals characterizing their states of health. Each individual is in one of the compartments susceptible (S); incubated – infected yet not infectious (C), infected and infectious (I), and recovered – immune (R). An infection is ‘visible’ only when an individual is in state I. Upon infection, an individual performs the transition pathway $S \rightarrow C \rightarrow I \rightarrow R \rightarrow S$ remaining in each compartments C, I, and R for certain random waiting time t_C, t_I, t_R , respectively. The waiting times for each compartment are independent and drawn from specific probability density functions (PDFs) introducing memory effects into the model [2] generalizing our previous model [3].

In the first part we introduce the macroscopic SCIRS model. We derive memory evolution equations involving convolutions (time derivatives of general fractional type). We consider several cases. The memoryless case is represented by exponentially distributed waiting times. Cases of long waiting times with fat-tailed (power-law) waiting time distributions are considered as well where the SCIRS evolution equations take the form of time-fractional ODEs. We obtain formulae for the endemic equilibrium and a condition of its existence for cases when the waiting time PDFs have existing means. We analyze the stability of healthy and endemic equilibria and derive conditions for which the endemic state becomes oscillatory (Hopf) unstable.

In the second part we present computer simulations of a simple multiple random walker’s approach (microscopic model of Brownian motion of Z independent walkers) with above random SCIRS waiting times where PYTHON programming language is used. Infections occur with a certain probability by collisions of infectious with susceptible walkers. We compare the endemic states predicted in the macroscopic model with the numerical results of the simulations and find accordance of high accuracy. We conclude that a simple random walker’s approach offers an appropriate microscopic description for the macroscopic SCIRS model.

References

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Supplementary materials (Simulation films and Python codes):
<https://sites.google.com/view/scirs-model-supplementaries/accueil>
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