Math. Model. Nat. Phenom.
Vol. 9, No. 2, 2014, pp. 108–120
DOI: 10.1051/mmnp/20149207

Spectral Properties of the Connectivity Matrix and the SIS-epidemic Threshold for Mid-size Metapopulations

D. Juher[1]*, V. Mañosa[2]
[1]Dept. Informàtica, Matemàtica Aplicada i Estadística, Universitat de Girona, 17071, Girona, Spain
[2] Dept. Matemàtica Aplicada III, Universitat Politècnica de Catalunya, 08222, Terrassa, Spain

Abstract. We consider the spread of an infectious disease on a heterogeneous metapopulation defined by any (correlated or uncorrelated) network. The infection evolves under transmission, recovery and migration mechanisms. We study some spectral properties of a connectivity matrix arising from the continuous-time equations of the model. In particular we show that the classical sufficient condition of instability for the disease-free equilibrium, well known for the particular case of uncorrelated networks, works also for the general case. We give also an alternative condition that yields a more accurate estimation of the epidemic threshold for correlated (either assortative or dissortative) networks.

Keywords and phrases: SIS epidemic, complex networks

Mathematics Subject Classification: 05C82, 60J28, 37N25

1. Introduction

While the classical Susceptible-Infected-Removed (SIR) and Susceptible-Infected-Susceptible (SIS) epidemic models were based on the assumption of completely well-mixed populations, recent works have revealed the importance of considering some contact structure among populations at a geographical level (heterogeneous metapopulations). See for instance [8, 10, 11, 14, 16, 18, 21].

More precisely, one considers ensembles of local populations with a complex spatial arrangement which are pairwise connected by migration flows. So the formalism of complex networks arises [5–7, 15, 19, 22, 23]. In this paper we will deal with the following situation: the whole population is distributed inside a network of N nodes and L non-directed links. Without loss of generality we will assume that this network is connected, so that there is at least one path connecting any pair of nodes. Each node (or "patch") can be thought as a local population containing two types of individuals: S (susceptible) and I (infected). Within each patch, transmission and recovery occur between individuals of different type. Simultaneously, migratory flows take place among linked patches at constant rates. By assumption our model does not contain demography and, therefore, is only applicable to mild and fast epidemics on constant populations: the epidemic does not affect mortality and runs its course in a time small in comparison to the mean life of the affected individuals.

*Corresponding author. E-mail: `david.juher@udg.edu`