



A new epidemic modeling approach: Multi-regions discrete-time model with travel-blocking vicinity optimal control strategy



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ABSTRACT

First, we devise in this paper, a multi-regions discrete-time model which describes the spatial-temporal spread of an epidemic which starts from one region and enters to regions which are connected with their neighbors by any kind of anthropological movement. We suppose homogeneous Susceptible-Infected-Removed (SIR) populations, and we consider in our simulations, a grid of colored cells, which represents the whole domain affected by the epidemic while each cell can represent a sub-domain or region. Second, in order to minimize the number of infected individuals in one region, we propose an optimal control approach based on a travel-blocking vicinity strategy which aims to control only one cell by restricting movements of infected people coming from all neighboring cells. Thus, we show the influence of the optimal control approach on the controlled cell. We should also note that the cellular modeling approach we propose here, can also describes infection dynamics of regions which are not necessarily attached one to an other, even if no empty space can be viewed between cells. The theoretical method we follow for the characterization of the travel-locking optimal controls, is based on a discrete version of Pontryagin's maximum principle while the numerical approach applied to the multi-points boundary value problems we obtain here, is based on discrete progressive-regressive iterative schemes. We illustrate our modeling and control approaches by giving an example of 100 regions.

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1. Introduction

1.1. Main references and description of the problem

Kermack and McKendrick have contributed to the mathematical theory of epidemics by devising in 1927, the Susceptible-Infected-Removed (SIR) model which has represented a main reference for most mathematical modelers in epidemiology (Kermack & McKendrick, 1927). In SIR compartmental systems, and according to the disease transmission mechanism, a host

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population can be Susceptible, Infected, or Removed. Susceptible individuals are those who are healthy and do not carry the epidemic but can contract it from infected hosts. Infected hosts carry the contagion and are able to pass it on to susceptible hosts. Finally, removed hosts are those who are no longer infected and have acquired immunity from future infection.

In 2016, Zakary et al. published their first papers in (Zakary, Rachik, & Elmouki, 2016a, 2016b, 2016c; Zakary, Larrache, Rachik, Elmoukid, 2016) which have concerned new modeling and optimal control approaches applied to multi-regions SIR models in the continuous-time and discrete-time cases. Additionally, in these mentioned references, the authors supposed that all regions are connected, and then, the incidence rate depends on the number of infected people which come from all regions. However, a region is often infected due to the travel of infected people coming only from the neighboring regions, or generally in the case of detached regions, infection occurs when one or more infected individuals come from regions where there is a possibility to travel to the targeted region. Here, we are more interested in the study of infection dynamics in regions which are not necessarily all connected but in the case when there exists a direct mode of transport between them. For instance, in Fig. 1(a), region 5 is connected with all other regions, and that can represent connections case which has been studied in the references above. In the same figure, we can also see that region 1 is connected only with regions 2, 4 and 5, and such cases have motivated us to write this paper in order to present a new epidemic modeling approach which generalizes all possible cases of infection connections between regions.

More clearly, we propose a cellular representation of regions, assembled all together in one grid of cells, and we study the transmission dynamics of the epidemic in these regions with focusing on only one region, to show the impact of infection connections that relate it with other regions via travel. As illustrated in Fig. 1(b), we can see the example of all 9 regions presented in (a), how they can be converted to cells, assembled in one grid which represents a part of the earth as the global domain of interest.

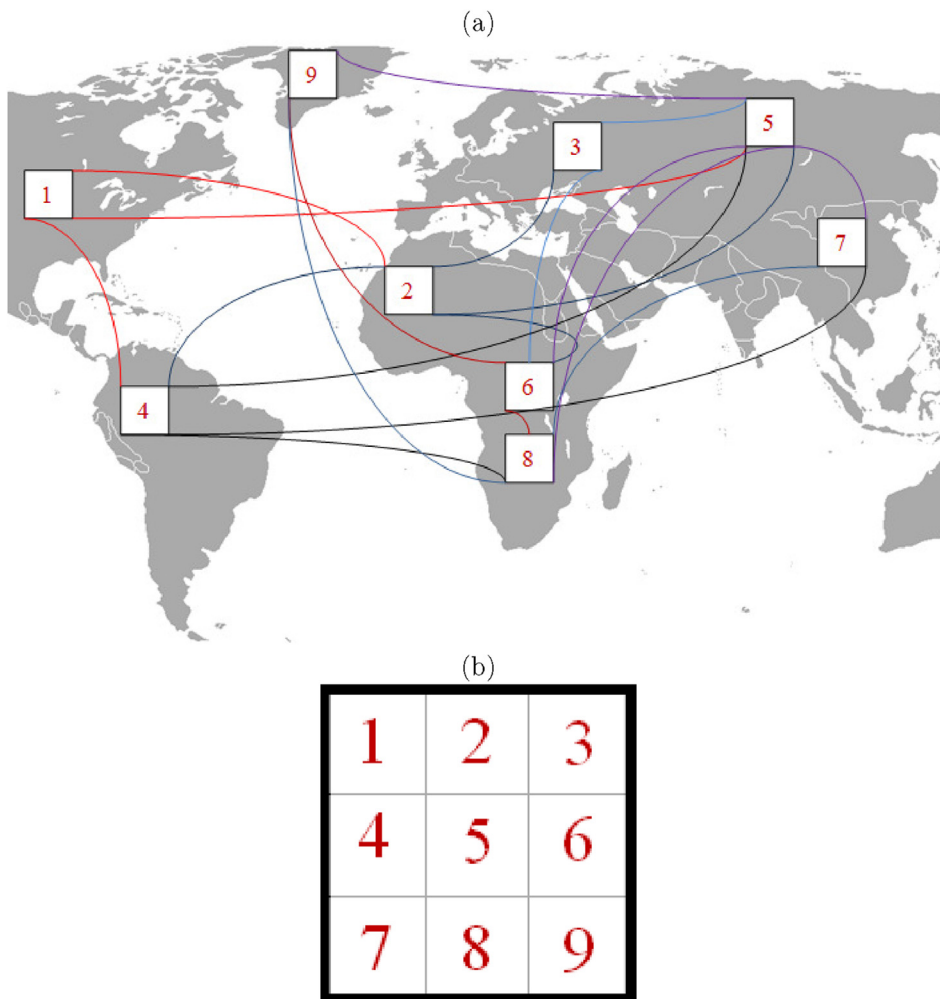


Fig. 1. (a): Infection travel connections between 9 separated geographical regions located at different continents. (b): Assembly of the regions in one grid of 9 numbered cells.

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