

The SIR metapopulation model in a temporal commuting network

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2023 AUTUMN MEETING
BRAZILIAN PHYSICAL SOCIETY

Research objectives

1. Simulate the metapopulation SIR model in temporal mobility networks.
2. Compare results obtained from dynamic networks and static versions.
3. Quantify the differences between the simulated dynamics in the temporal network and its static version.
4. Investigate the tolerance in changing the network's time resolution in relation to its more refined version.
5. Analyze the correspondences between the changes in the dynamics with the topological changes of the network, in time.

Introduction

Networks

A network is a set of interconnected elements [4]. In graph theory and network science, networks are represented by a set of nodes interconnected by connections (or edges). Networks are a powerful way to represent and study complex systems in many areas, such as biology, sociology, technology, transportation, among others.

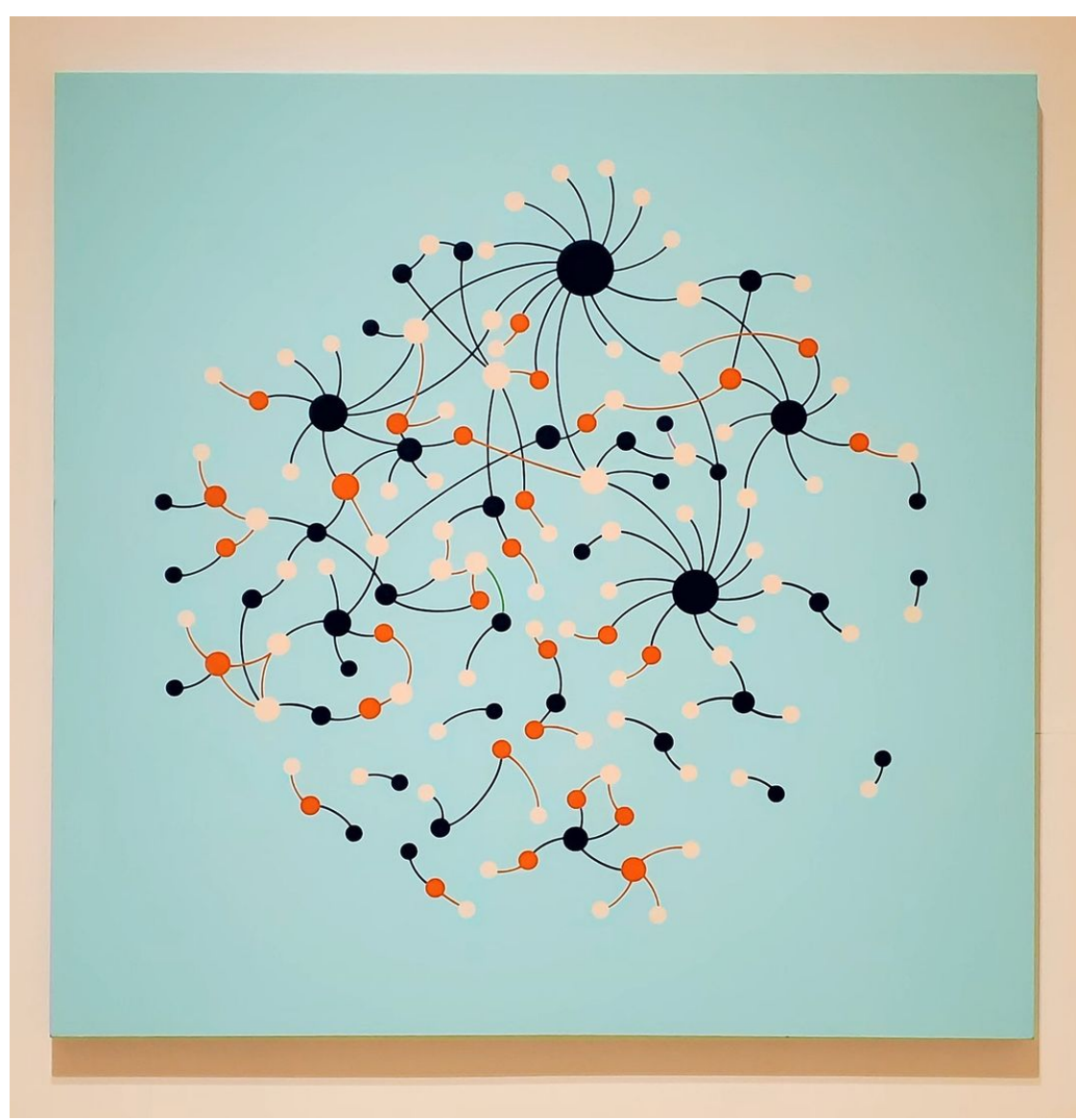


Figure 1: BarabasiLAB Art - Museum of Modern Art, MOMA. Source: Postmasters, <https://www.postmastersart.com>.

SIR model

The SIR model is a widely used mathematical framework for modeling and analyzing epidemics. It divides the population into three main groups: **susceptible (S)**, **infected (I)**, and **recovered (R)**. The model describes the spread of a disease over time, taking into account the rates of infection (β), recovery (γ), and contact between individuals.

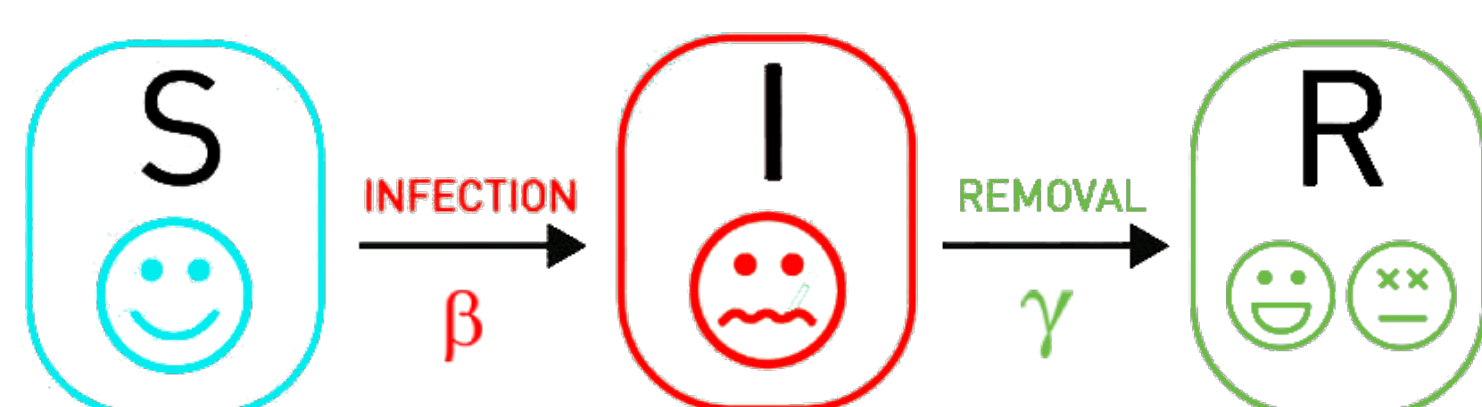


Figure 2: SIR schematic diagram.

The SIR model is a simple but powerful approach that can be used to simulate different scenarios of disease spread. For example, the model can be used to simulate the effects of different vaccination rates, contact tracing strategies, and quarantine policies.

The SIR model has been used to study a wide range of diseases, including measles, influenza, and COVID-19. The model has helped to inform public health policy and practice, and it has been used to develop new strategies for preventing and controlling the spread of disease.

The ordinary SIR model for a metapopulation with N hosts:

$$\begin{cases} \frac{dS}{dt} = -\frac{\beta SI}{N}, \\ \frac{dI}{dt} = \frac{\beta SI}{N} - \gamma I, \\ \frac{dR}{dt} = \gamma I. \end{cases} \quad (1)$$

Metapopulations

Metapopulation models represent geographically isolated host populations connected through movement. Assuming **homogeneous mixing** within local contexts, individuals within each population have random and equally probable contacts. Populations remain stable over time and can be calibrated using census data.

Disease transmission is assumed to be entirely local, with hosts from different subpopulations coming into contact only if they travel to the same location.

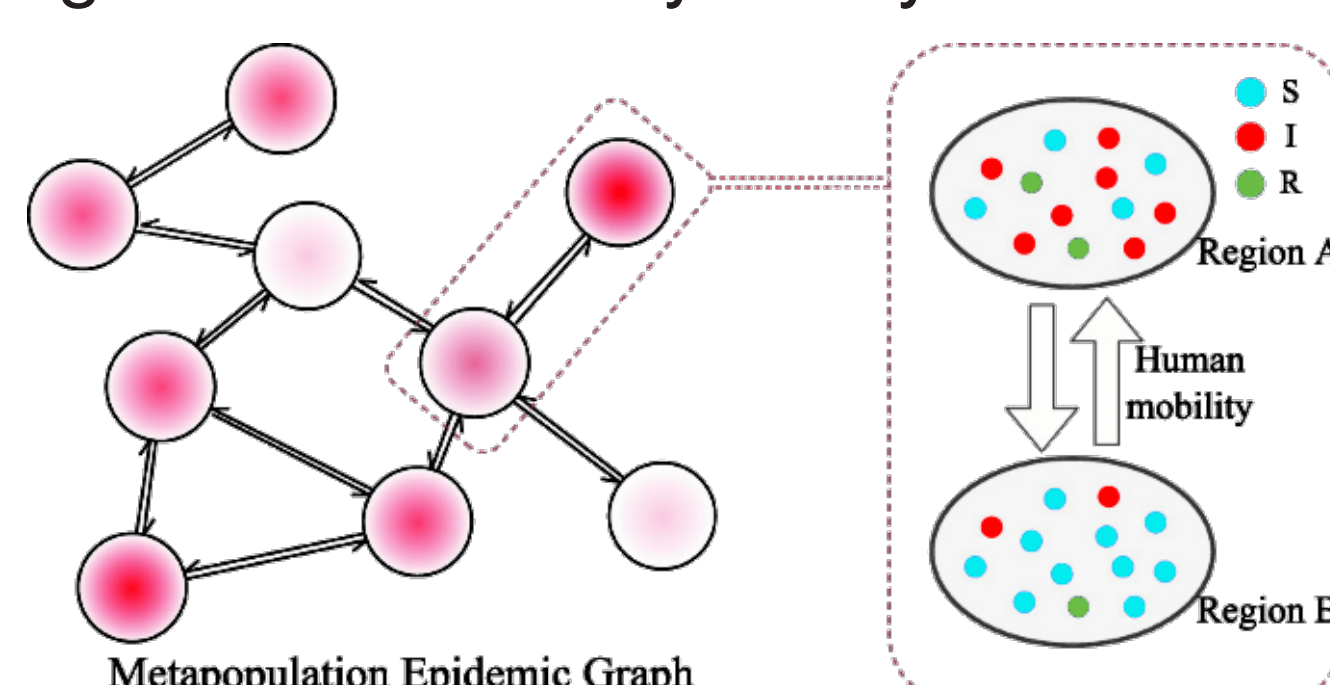


Figure 3: SIR model in a metapopulation network.

Methodology

Mobility and geographical data

We utilized the **Baidu Mobility Data** [1] from Jan-Feb 2020, before the official COVID-19 pandemic declaration. This dataset tracks daily movements between 340 Chinese cities [3].

The dataset includes two **adjacency matrices** for input and output streams. The input matrix shows the percentage of people moving from node i to node j , with node j representing the sum of all other entries. The output matrix behaves similarly. Each node has up to 100 neighbors.

The adjacency matrix of a directed network with N nodes is an $N \times N$ matrix. Its elements, denoted as $A_{i,j}$, are set to 1 if there is a directed link from node j to node i , and 0 if nodes i and j are not connected:

$$A_{i,j} = \begin{bmatrix} a_{1,1} & a_{1,2} & \cdots & a_{1,N} \\ a_{2,1} & a_{2,2} & \cdots & a_{2,N} \\ \vdots & \vdots & \ddots & \vdots \\ a_{N,1} & a_{N,2} & \cdots & a_{N,N} \end{bmatrix}. \quad (2)$$

Host movement models

Host movement models are utilized to simulate the movement of hosts within a metapopulation network. These models can be adapted to represent human mobility by tracking individuals movements between different locations or nodes. **Eulerian** and **Lagrangian** movement models are the two most commonly used classes of such models.

We specifically employed the Eulerian movement model [2], which describes the **diffusion** of hosts among metapopulation, with the following set of differential equations:

$$\frac{dN_i}{dt} = - \sum_{j=1}^K f_{i,j} N_i + \sum_{j=1}^K f_{j,i} N_j, \quad (3)$$

N_i represents the number of hosts currently located at site i , and K denotes the total number of populations. The term $f_{i,j}$ corresponds to the rate (our adjacency matrix here will correspond of $N \times N$ matrix of travel rates) at which hosts move from site i to site j , with $f_{i,i}$ accounting for movement within the same population. The model requires a total of $K(K-1)$ parameters for a complete specification. The total number of hosts remains constant over time:

$$N = \sum_{i=1}^K N_i. \quad (4)$$

Combining SIR model with Eulerian model, we obtain an analogous set of $3K$ equations, for K subpopulations (nodes):

$$\begin{cases} \frac{dS_i}{dt} = -\beta_i \frac{S_i I_i}{N_i} - \sum_{j=1}^K f_{i,j} S_i + \sum_{j=1}^K f_{j,i} S_j, \\ \frac{dI_i}{dt} = \beta_i \frac{S_i I_i}{N_i} - \gamma I_i - \sum_{j=1}^K f_{i,j} I_i + \sum_{j=1}^K f_{j,i} I_j, \\ \frac{dR_i}{dt} = \gamma I_i - \sum_{j=1}^K f_{i,j} R_i + \sum_{j=1}^K f_{j,i} R_j. \end{cases} \quad (5)$$

Conclusion

This project is currently a work in progress. We have successfully accomplished objective number one, and our focus has now shifted to objective number two. Throughout the course of our work, we encountered the formidable challenge of sourcing relevant temporal mobility data from national and international surveys, which consumed a significant amount of our research time.

References

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Acknowledgements

We would like to thank **CNPq** and **Universidade Federal de Ouro Preto**, for their financial support.