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The SIR metapopulation model in a temporal commuting network

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.

Networks:

Understanding complex systems requires comprehending the interactions among their components. A system's wiring diagram, represented by a network, provides a catalog of its components, referred to as nodes or vertices, along with their direct interactions, known as links or edges. This network representation serves as a universal language for studying diverse systems, regardless of their nature, appearance, or scope.

The number of nodes, denoted as N, corresponds to the total components within the system, often referred to as the network's size. Nodes are labeled as $i = 1, 2, ..., N$ to distinguish them from one another.

Meanwhile, the number of links, denoted as L, represents the total interactions between the nodes.

Unlike nodes, links are usually not individually labeled, as they can be identified based on the connected nodes. For instance, the (2, 4) link indicates the connection between nodes 2 and 4.

By analyzing the structure and properties of networks, researchers gain valuable insights into the behavior and dynamics of complex systems in various domains. Network theory provides a powerful framework for studying interconnected systems, ranging from social networks and biological networks to technological networks and transportation networks. **Networks can be categorized as directed or undirected based on the nature of their links.** Directed networks consist of directed links, while undirected networks have undirected links. However, certain networks can have a combination of both directed and undirected links. A prime example is the metabolic network, where some reactions are reversible (undirected) while others are irreversible (directed).

The representation of a system as a network heavily influences the effectiveness of applying network science to solve specific problems. The choices we make in network representation play a crucial role in determining our ability to utilize network science successfully.

The **adjacency matrix** is a common representation used in network analysis. It is particularly useful for describing the connections between nodes in a network. The structure and interpretation of the adjacency matrix differ for directed and undirected networks.

In a directed network, the adjacency matrix is a square matrix of size NN, where N represents the number of nodes in the network. Each element of

the matrix, denoted as A_{ij}, represents the presence or absence of a directed link from node j to node i. If there is a link from node j to node i, the value of A_{ij} is typically set to 1. On the other hand, if nodes i and j are not connected, the value of A_{ij} is usually set to 0. This binary representation allows us to determine the existence of directed connections between nodes.

In contrast, the adjacency matrix for an undirected network is also a square matrix of size N×N. However, in this case, each link is considered bidirectional, meaning it can be traversed in both directions. Therefore, an undirected network's adjacency matrix is symmetric. For example, if there is a link between nodes 1 and 2, the matrix entries A_{12} and A_{21} will both be set to 1, indicating the presence of a connection. Similarly, if nodes i and j are not connected, both A_{ij} and A_{ji} will be 0.

The adjacency matrix provides a comprehensive representation of the connections within a network, allowing for various analyses and computations to be performed efficiently. By examining the elements of the matrix, such as row or column sums, we can obtain valuable information about node degrees, identify connected components, and explore network properties in depth.

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

A **static network** is a network whose structure does not change over time. A **dynamic network** is a network whose structure changes over time.

Static networks are often used to model phenomena that are relatively stable, such as the social network of a group of friends. Dynamic networks are often used to model phenomena that are more dynamic, such as the spread of a disease through a population.

A **topological change** in a network is a change in the structure of the network. This can include the addition or removal of nodes, the addition or removal of edges, or the change in the weight of an edge.

Topological changes can be caused by a variety of factors, such as the addition or removal of nodes, the failure of links, or the change in the behavior of nodes.

Topological changes can have a significant impact on the behavior of a network. For example, the addition of a new node can increase the number of possible paths between nodes, while the removal of a node can decrease the number of possible paths. The failure of a link can also have a significant impact on the network, as it can disconnect nodes that were previously connected.

SIR model:

Proposed by William Ogilvy **Kermack** and Anderson Gray **McKendrick** as a special case of what we now call Kermack–McKendrick theory, and followed work McKendrick had done with Ronald **Ross**.

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

The transmission rate, β, is a measure of how likely an infected individual is to transmit the disease to a susceptible individual. It is typically measured in units of $1/time$. For example, if β is 0.1, then an infected individual is 10% likely to transmit the disease to a susceptible individual in a given time period.

The recovery rate, γ, is a measure of how quickly an infected individual recovers from the disease. It is typically measured in units of $1/time$. For example, if γ is 0.2, then an infected individual will recover from the disease in 5 days.

The units of β and γ are important because they determine the behavior of the SIR model. If β is greater than γ, then the disease will spread through the population. If β is less than γ, then the disease will die out.

The SIR model is a simple model, but it is a useful tool for understanding the spread of diseases. The model can be used to help public health officials make decisions about how to control the spread of diseases.

Here are some examples of how β and γ can be estimated:

- β can be estimated by looking at the number of

secondary infections caused by an infected individual.

- γ can be estimated by looking at the average time it takes for an infected individual to recover from the disease.

It is important to note that β and γ can vary depending on a number of factors, such as the type of disease, the population, and the environment.

1. $\frac{dS}{dt}$ represents the rate of change of the susceptible population over time. It is determined by the term $-\frac{\beta S I}{N}$, where β is the transmission rate of the disease, S is the number of susceptible individuals, I is the number of infected individuals, and N is the total population size. This term represents the rate at which susceptible individuals become infected due to contact with infected individuals.

2. $\frac{dI}{dt}$ represents the rate of change of the infected population over time. It consists of two terms. The first term, $\frac{\beta S I}{N}$, represents the rate at which new infections occur. It is determined by the transmission rate β, the number of susceptible individuals S, the number of infected individuals I, and the total population size N. The second term, γI, represents the rate at which infected individuals recover from the disease. Here, γ is the recovery rate.

3. $\frac{dR}{dt}$ represents the rate of change of the recovered population over time. It is determined solely by the term γI, indicating the rate at which individuals recover from the disease and become immune or removed from the susceptible and infected populations.

Secondly, we note that the dynamics of the infectious class depends on the following ratio:

$$R_0 = \frac{\beta}{\gamma},$$

the so-called **basic reproduction number** (also called basic reproduction ratio). This ratio is derived as the expected number of new infections (these new infections are sometimes called secondary infections) from a single infection in a population where all subjects are susceptible.

This idea can probably be more readily seen if we say that the typical time between contacts is $T_c = \beta^{-1}$, and the typical time until removal is $T_r = \gamma^{-1}$. From here it follows that, on average, the number of contacts by an infectious individual with others before the infectious has been removed is: T_r/T_c.

Metapopulations:

Metapopulation (the term metapopulation was coined by Richard Levins in 1969 to describe a model of population dynamics of insect pests in agricultural fields, but the idea has been most broadly applied to species in naturally or artificially fragmented habitats) 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.
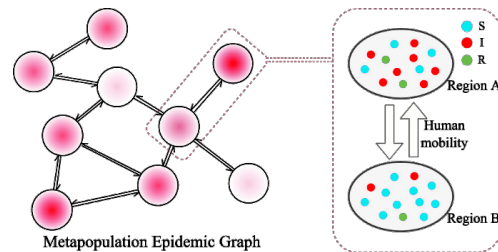

Figura 1: SIR model in a metapopulation network.

Host movement models:

Host movement models are mathematical models used to describe the movement patterns of hosts, such as animals or humans, in a given area. These models

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are used to understand how hosts move through space and time, and how this movement affects the spread of infectious diseases.

Eulerian and **Lagrangian** models are two types of movement models used in studying the spread of infectious diseases.

Eulerian models describe the rates at which hosts move from one location to another, without tracking individual behavior. These models are useful for understanding animal migration patterns.

Lagrangian models, on the other hand, follow individuals and track their movements over time. These models are useful for understanding human commuting behavior and can provide more detailed information about how diseases spread through populations.

Both types of models have their advantages and disadvantages, and the choice of model depends on the specific research question being addressed.

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

$$\frac{dN_i}{dt} = -\sum_{j=1}^{K} f_{i,j} N_i + \sum_{j=1}^{K} f_{j,i} N_j, \quad (2)$$

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 NxN matrix of travel rates) at which hosts move from site i to site j, with $f_{i,j}$ 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:

$$N = \sum_{i=1}^{K} N_i. \quad (3)$$

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

$$\begin{cases} \frac{dS_i}{dt} = -\beta_i \frac{S_i I_i}{N_i} - \sum_{j=1}^{K} f_{i,j} S_i + \sum_{j=1}^{K} f_{j,i} S_j, \\ \frac{dI_i}{dt} = \beta_i \frac{S_i I_i}{N_i} - \gamma I_i - \sum_{j=1}^{K} f_{i,j} I_i + \sum_{j=1}^{K} f_{j,i} I_j, \\ \frac{dR_i}{dt} = \gamma I_i - \sum_{j=1}^{K} f_{i,j} R_i + \sum_{j=1}^{K} f_{j,i} R_j. \end{cases}$$
$$(4)$$

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.