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Distributed Reproduction Numbers of Networked Epidemics

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***Abstract*—Reproduction numbers are widely used for the estimation and prediction of epidemic spreading processes over networks. However, reproduction numbers do not enable estimation and prediction in individual communities within networks, and they can be difficult to compute due to the aggregation of infection data that is required to do so. Therefore, in this work we propose a novel concept of *distributed reproduction numbers* to capture the spreading behaviors of each entity in the network, and we show how to compute them using certain parameters in networked SIS and SIR epidemic models. We use distributed reproduction numbers to derive new conditions under which an outbreak can occur. These conditions are then used to derive new conditions for the existence, uniqueness, and stability of equilibrium states. Finally, in simulation we use synthetic infection data to illustrate how distributed reproduction numbers provide more fine-grained analyses of networked spreading processes than ordinary reproduction numbers.**

I. Introduction

Reproduction numbers are some of the most critical quantities in infectious disease epidemiology [1]. Reproduction numbers are often among the quantities most urgently estimated for emerging infectious diseases in outbreak situations, since it is easy for policy-makers to explain the reproduction numbers to the general public, and their values can also be used to design control interventions during an established pandemic [2]. There are two types of most commonly used reproduction numbers. *Basic reproduction numbers* describe the number of secondary infected cases generated by one infected case in the full susceptible population. Meanwhile, *effective reproduction numbers* capture the number of secondary infected cases generated by one infected case in a mixed susceptible and infected population [1]. The critical value of a reproduction number is 1, since epidemic spreading processes will exhibit different spreading behaviors if the reproduction number is less than or greater than 1.

In control theory, researchers have used reproduction numbers to model, analyze, and design control strategies for epidemic mitigation problems [3]–[6]. Recent work has constructed threshold conditions at 1 to analyze the transient and steady-state behaviors of spreading processes based on basic and effective reproduction numbers being less than or greater than 1 [7]–[10]. Researchers have also extended the idea of constructing threshold conditions at 1 from the classic networked SIS models [11] to some recent novel networked spreading models, e.g., networked bi-virus models [12] and coupled networked spreading models [3]. These threshold conditions are typically in terms of the reproduction numbers of the overall network spreading processes.

However, networked compartmental models often exhibit high heterogeneity in both spreading parameters and local network structures. Hence, it can be challenging to use the reproduction numbers of the overall network to characterize the spreading behaviors of individual entities within the network. For instance, the spreading behavior of COVID-19 in different regions was different across the United States, in terms of infection growth, peak infection date, etc. [13].

In addition, different regions have different ways of collecting and representing infection data. Along with privacy issues, it is arduous to aggregate data from many communities to construct network-level reproduction numbers [14]. Therefore, while existing network-level reproduction numbers capture the overall epidemic spread in a network, we require new reproduction numbers for each entity in a network that can be locally computed and characterize local spreading.

To achieve this goal, we first introduce the classic networked SIS and SIR models and their reproduction numbers, which we refer to as "network-level reproduction numbers." Then, we propose a group of novel distributed reproduction numbers to capture the spreading behavior of individual communities. We develop threshold conditions as the function of these distributed reproduction numbers to study the classic networked SIS and SIR models. In simulation, we illustrate that the distributed reproduction numbers can be estimated locally via synthetic data. This simulation also shows that distributed reproduction numbers can be used to infer spreading trends within and between communities, which network-level reproduction numbers cannot do.

To summarize, our contributions are:

- We introduce a new group of distributed reproduction numbers. Unlike the network-level reproduction number, we illustrate the distributed reproduction numbers can capture spreading behaviors of individual entities within the network (e.g., individual communities);
- We show that not only can distributed reproduction numbers capture epidemic spread within individual entities, but can also facilitate the analysis of the transient and

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steady-state behaviors of overall networked spreading;
- We leverage synthetic infection data to estimate distributed reproduction numbers, and we illustrate that distributed reproduction numbers capture more detailed spreading properties within and between the entities in a network than network-level reproduction numbers.

The rest of the paper is organized as follows. We introduce the background and problem statements in Section II. In Section III, we propose and study distributed reproduction numbers. In Section IV, we illustrate the effectiveness of the distributed reproduction numbers using synthetic infection data. Then Section V concludes. Note that a detailed version of this work, including all proofs and one simulation example, can be found in [15].

Notation

Let $\underline{n}$ denote the index set $\{1, 2, 3, \ldots, n\}$. For a matrix $\mathcal{A} \in \mathbb{R}^{n\times n}$, we use $[\mathcal{A}]_{ij}$ to denote the ij^{th} entry of $\mathcal{A}$. We use $\rho(\mathcal{A})$ to represent the spectral radius of the matrix $\mathcal{A}$. For a vector $x \in \mathbb{R}^n$, we use $\text{diag}(x) \in \mathbb{R}^{n\times n}$ to denote the diagonal matrix with the ith diagonal entry being x_i for all $i \in \underline{n}$. For two vectors $x, y \in \mathbb{R}^n$, we use $x > y$ (or $x \geq y$) to denote that there exists at least one $i \in \underline{n}$ such that $x_i > y_i$ (or $x_i \geq y_i$). Denote $\mathbf{0}$ and $\mathbf{1}$ as the zero vector and one vector with the corresponding dimension given by context. Let $[a, b]^n$ denote a closed cube and $(a, b)^n$ denote an open cube, for any $a, b \in \mathbb{R}$.

II. Problem Formulation

This section provides background on two existing networked spreading models and the standard threshold conditions for their network-level reproduction numbers. Then we formulate the problems that are the focus of this work.

A. Background: SIR and SIS Models

The networked SIS and SIR models are popular in modeling and analyzing epidemic spreading processes [7]–[10], and we study them throughout the paper. We consider epidemic processes on strongly connected graphs of n communities. For all $i \in \underline{n}$, let s_i, x_i, and r_i represent the susceptible, infected, and recovered proportions of the population of community i, respectively. We use $s_i(t)$ and s_i interchangeably. The classic networked SIS model is

$$\frac{ds_i}{dt} = -\sum_{j\in\underline{n}} s_i\beta_{ij}x_j + \gamma_i x_i, \tag{1a}$$

$$\frac{dx_i}{dt} = \sum_{j\in\underline{n}} s_i\beta_{ij}x_j - \gamma_i x_i, \tag{1b}$$

and the classic networked SIR model is

$$\frac{ds_i}{dt} = -\sum_{j\in\underline{n}} s_i\beta_{ij}x_j, \tag{2a}$$

$$\frac{dx_i}{dt} = \sum_{j\in\underline{n}} s_i\beta_{ij}x_j - \gamma_i x_i, \tag{2b}$$

$$\frac{dr_i}{dt} = \gamma_i x_i. \tag{2c}$$

In these models, $\beta_{ij} \geq 0$ denotes the transmission rate from community j to community i for all $i, j \in \underline{n}$, and $\gamma_i > 0$ denotes the recovery rate of community i for all $i \in \underline{n}$. Further, we define $\mathcal{B} \in \mathbb{R}^{n\times n}_{\geq 0}$ such that $[\mathcal{B}]_{ij} = \beta_{ij}$ for all $i, j \in \underline{n}$ as the *transmission matrix*. We define the diagonal matrix $\mathcal{D} \in \mathbb{R}^{n\times n}_{\geq 0}$ such that $[\mathcal{D}]_{ii} = \gamma_i > 0$ for all $i \in \underline{n}$ as the *recovery matrix*.

Definition 1. *At any healthy (disease-free) equilibrium, $x^* = \mathbf{0}$. At any endemic equilibrium, $x^* \in (0, 1)^n$.*

Note that at an endemic equilibrium one cannot have $x_i^* = 0$ or $x_i^* = 1$ for any $i \in \underline{n}$ [7]. Inspired by the use of reproduction numbers to construct threshold conditions for the analysis of non-networked epidemic models, researchers have studied the spreading behaviors of the networked SIS and SIR models in (1) and (2) using thresholds conditions [7]–[10]. These threshold conditions are defined in terms of the *reproduction numbers of networks* (namely the network-level reproduction numbers).

Definition 2. *(Reproduction Numbers of Networks) Define the basic reproduction numbers of the networked SIS and SIR models as $R^0 = \rho(\mathcal{D}^{-1}\mathcal{B})$. Define the effective reproduction numbers of the networked SIS and SIR models as $R^t = \rho(diag(s)\mathcal{D}^{-1}\mathcal{B})$.*

Further, we can leverage both reproduction numbers of networks in Definition 2 to characterize the spreading behaviors of the network, illustrated by the following two lemmas.

Lemma 1. *[7, Thm. 4.2 , 4.3] The networked SIS model in* (1) *has a unique equilibrium which is the globally asymptotically stable healthy equilibrium if and only if $R^0 \leq 1$. The SIS model has a unique endemic equilibrium that is globally asymptotically stable if and only if $R^0 > 1$.*

It is less useful to analyze the existence of equilibria of the networked SIR model, since SIR models have an infinite number of healthy equilibria but cannot have any endemic equilibria. Instead, we are more interested in studying the transient behavior of the SIR model. Thus, we use w to denote the normalized left eigenvector of the matrix $\mathcal{D} - \mathcal{B}$, and the following lemma summarizes the transient behavior of the networked SIS and SIR models.

Lemma 2. *[7, Thm. 5.2 , 5.4] [16, Thm. 2.7, Lemma 2.4] The weighted average $w^\top x$ is decreasing if and only if $R^t < 1$. The weighted average $w^\top x$ is increasing if and only if $R^t > 1$. The weighted average $w^\top x$ remains unchanging if and only if $R^t = 1$.*

Note that the original theorems [7, Thm. 4.2, 4.3] and [7, Thm. 5.2, 5.4] capture the case of homogeneous transmission rates in a network. However, the results for heterogeneous transmission networks listed in Lemma 1 and Lemma 2 can be obtained through the similar proofs given by [7, Thm. 4.2, 4.3] and [7, Thm. 5.2, 5.4].

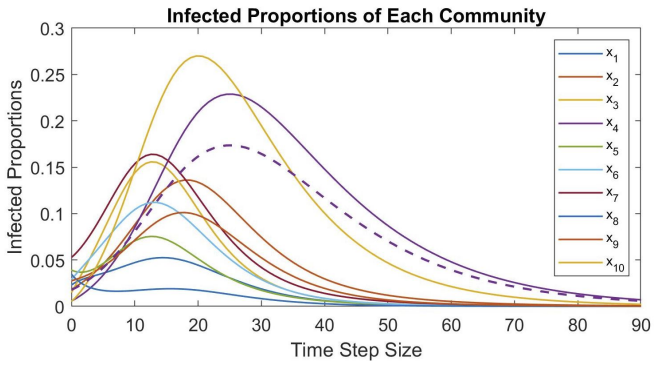

Figure 1: Infected Proportions of Each Community

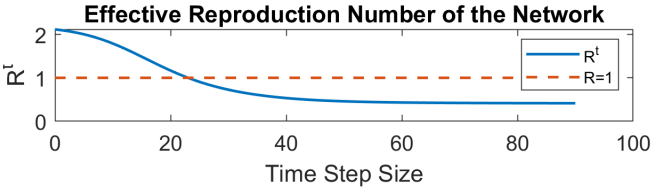

Figure 2: Effective Reproduction Number of the Networked Epidemic

B. Motivation and Problem Statements

Lemma 1 and Lemma 2 characterize the spreading behaviors of the networked models in (1) and (2) through the *reproduction numbers of the network*, i.e., R^0 and R^t. However, these reproduction numbers of the network may fail to capture the spreading behavior of individual entities within the network. To illustrate this point, Fig. 1 presents the infected proportion of each community in a networked SIR model over ten communities in a strongly connected graph. The dashed line indicates $w^\top x$. Fig. 2 shows the corresponding effective reproduction number of the network, i.e., R^t. The effective reproduction number $R^t > 1$ until roughly timestep 20. However, the infected proportions of most communities, including x_1, x_2, and x_6, already start decreasing by timestep 20. Therefore, if we aim to analyze an individual community or a subnetwork of connected communities within the network, the reproduction numbers of the network, R^0 and/or R^t, may fail to capture the spreading behavior, since both thresholds in Lemmas 1 and 2 characterize network-level spreading only.

Motivated by this discussion of the reproduction numbers of networks, we formulate the following problem statements.

Question 1. *How can we define distributed reproduction numbers to capture the spreading behaviors within individual communities and between the communities within a network?*

Question 2. *Compared to the network-level reproduction numbers of a network, can we use the distributed reproduction numbers to study the spreading processes at both the individual-level and the network-level?*

Question 3. *When capturing epidemic spreading processes in application, what are the advantages of leveraging the distributed reproduction numbers developed?*

We will answer Questions 1-3 in the next two sections.

III. Distributed Reproduction Numbers

In this section, we define distributed reproduction numbers for the networked SIS and SIR models, which answers Question 1. We will leverage the distributed reproduction numbers to study the transient and steady-state behaviors of the spreading models. In order to answer Question 2, we will bridge the gap between the distributed reproduction numbers and the network-level reproduction numbers by showing that the distributed reproduction numbers can capture the spreading behavior at both the individual- and network-levels.

A. Definition of Distributed Reproduction Numbers

One way to study epidemic spreading processes is to leverage reproduction numbers to indicate the change of the infected population (e.g., increasing, decreasing, unchanging.). As indicated in Lemmas 1 and 2, network-level reproduction numbers can capture the overall spreading behavior within a network. However, the spreading behavior of an individual community might not be captured by the reproduction numbers of the network. Thus, based on the intuition that the infected population of community i will increase if the effective reproduction number of community i is greater than 1, and vice versa, we introduce the following definition of distributed reproduction numbers.

Definition 3 (Distributed Reproduction Numbers)**.** *For each $i \in \underline{n}$, define $R^0_{ii} = \frac{\beta_{ii}}{\gamma_i}$ as the basic reproduction number within community i itself, and define $R^0_{ij} = \frac{\beta_{ij}}{\gamma_i}$ as the basic reproduction number from community j to community i for each $j \in \underline{n}$. For each $i \in \underline{n}$, define $R^t_{ii} = \frac{s_i\beta_{ii}}{\gamma_i}$ as the effective reproduction number within community i, and define $R^t_{ij} = \frac{s_i\beta_{ij}}{\gamma_i}$ for each $j \in \underline{n}$ as the pseudo-effective reproduction number from community j to community i. In addition, we define $I_{ij} = \frac{x_j}{x_i}$ with $x_i, x_j \in (0, 1]$ as the infection ratio from the infected proportions of community j to community i. Then, we define the effective reproduction number from community j to community i as $\bar{R}_{ij} = R^t_{ij} I_{ij}$.*

In order to explain the intuition behind Definition 3, we consider the group compartmental SIS and SIR models with β and γ being the transmission and recovery rates, respectively [7]. Note that the two models admit $\frac{\beta}{\gamma}$ and $\frac{s(t)\beta}{\gamma}$ as the basic and effective reproduction numbers, respectively. Based on these terms, we then choose to use $R^0_{ij} = \frac{\beta_{ij}}{\gamma_i}$ and $R^t_{ij} = \frac{s_i(t)\beta_{ij}}{\gamma_i}$ for the basic and pseudo-effective reproduction numbers of the infected proportion x_{ij}, where x_{ij} denotes the infected proportion in community i generated by the infected proportion in community j for all $i, j \in \underline{n}$. Through the definition, we have $\frac{dx_{ij}}{dt} > 0$ if and only if $R^t_{ij} > 1$, and vice versa. Further, we define the scaled infected proportion $\bar{x}_{ij} = x_{ij} I_{ij}$ for all $i, j \in \underline{n}$. Note that the scaled infected proportion $\bar{x}_{ij}$ can be considered as a normalized infected proportion of $\bar{x}_{ij}$ with respect to community i. When computing effective reproductions of

community i, it is necessary to evaluate the infections from different resources at the same scale. The following lemma shows the use of $\bar{R}_{ij}^t = R_{ij}^t I_{ij}$.

Lemma 3. *The scaled infected proportion generated by community j in community i, denoted by $\bar{x}_{ij}$ for all $i, j \in \underline{n}$, are increasing if and only if $\bar{R}_{ij}^t > 1$, and they are decreasing if and only if $\bar{R}_{ij}^t < 1$.*

Based on Lemma 3, the pseudo-effective reproduction numbers together with the infection ratios, i.e., $\bar{R}_{ij}^t = R_{ij}^t I_{ij}$, are used as the effective reproduction number from community j to community i for all $i, j \in \underline{n}$. The basic reproduction number captures the situation where $s_i \approx 1$ for all $i \in \underline{n}$, and the effective reproduction number captures cases in which $x_i \in (0, 1]$ for all $i \in \underline{n}$. Definition 3 proposes distributed reproduction numbers by separating the infected cases generated in community i in two ways: (i) the new cases that are generated through the infected cases within the community itself, and (ii) the new cases that are generated through the infected cases from neighboring communities. Hence, we use two types of reproduction numbers, namely the reproduction numbers within a community (R_{ii}^0 and R_{ii}^t) and the reproduction numbers from one community to another community (R_{ij}^0 and $\bar{R}_{ij}^t$), to capture the two types of infection processes. In addition, similar to the reproduction numbers of group compartmental models, we have $R_{ii}^t = s_i R_{ii}^0$ within community i for all $i \in \underline{n}$. For the pseudo-effective reproduction numbers from community j to i, we have $R_{ij}^t = s_i R_{ij}^0$ for all $i, j \in \underline{n}$.

Definition 3 and Lemma 3 propose a way of explaining spread processes through the distributed reproduction numbers within and between communities. For the purpose of characterizing the spread process of a community, we further define the basic reproduction number and effective reproduction number of a community within the network, through the distributed reproduction numbers in Definition 3.

Definition 4 (Reproduction Numbers of Community i)**.** *For all $i \in \underline{n}$, let R_i^0 denote the basic reproduction number of community i, and let R_i^t denote the effective reproduction number of community i, where*

$$R_i^0 = \sum_{j=1}^{n} R_{ij}^0, \tag{3}$$

$$\bar{R}_i^t = \sum_{j=1}^{n} \bar{R}_{ij}^t = \sum_{j=1}^{n} R_{ij}^t I_{ij}. \tag{4}$$

Remark 1. *The reproduction numbers defined in* (3) *and* (4) *quantify the relationship between the infection within community i and the infections in other communities. Specifically, the basic and effective reproduction numbers of a community are built upon the distributed reproduction numbers from Definition 3. Eq.* (3) *indicates that the basic reproduction number of community i within the network is the sum of the basic reproduction number within the community i itself and the basic reproduction numbers introduced by its neighbors. Similarly, Eq.* (4) *indicates that the effective reproduction number of community i within the network is the sum of the effective reproduction number within community i itself and the effective reproduction numbers introduced by its neighbors. Further, the effective reproduction numbers introduced by its neighbors are scaled by the infection ratio I_{ij}. For instance, if community i has a lower infected proportion than community j (i.e., $x_i < x_j$), then the effective reproduction number from community j to community i will be scaled up by I_{ij}. Hence, the effective reproduction number of community i ($\bar{R}_i^t$) can be high, even if the effective reproduction number within community i (R_{ii}^t) and the pseudo-effective reproduction numbers from community j to community i (R_{ij}^t) are low, since the weights I_{ij} can be large.*

B. Properties of Distributed Reproduction Numbers

Through the distributed reproduction numbers introduced in Definition 3 and Lemma 3, we can compose the reproduction numbers of an individual community through the sum of the distributed reproduction numbers, as shown in Definition 4. Compared to the effective reproduction number of the network (R^t), the effective reproduction number of an individual community ($\bar{R}_i^t$) can facilitate the study of the spreading behavior of community i for all $i \in \underline{n}$.

Theorem 1. *When the infected population in community i is nonzero, i.e., $x_i(t) > 0$, the effective reproduction number $\bar{R}_i^t > 1$ if and only if the infected proportion x_i increases; $\bar{R}_i^t < 1$ if and only if x_i decreases; $\bar{R}_i^t = 1$ if and only if x_i remains unchanged.*

Theorem 1 demonstrates that the definition of the effective reproduction numbers exhibits thresholding behavior, and thus that we can leverage the effective reproduction numbers of communities to capture the spreading behavior within and between them. In addition, recall that the effective reproduction number of the whole network, R^t, is monotonically non-increasing, since for all $i \in \underline{n}$, the value of s_i is monotonically non-increasing [7]. However, for all $i \in \underline{n}$ the value of $\bar{R}_i^t$ can be non-monotonic.

Lemma 4. *For all $i \in \underline{n}$, the effective reproduction number $\bar{R}_i^t$ of community i can be non-monotonic.*

Theorem 1, Lemma 3, and Lemma 4 demonstrate that we can leverage the distributed reproduction numbers to capture spreading behaviors of individual communities. Hence, we have answered Question 1 from Section II. In order to answer Question 2, we connect distributed reproduction numbers to the network-level reproduction numbers of networks, namely R^0 and R^t. First we define the distributed reproduction number matrices.

Definition 5 (Distributed Reproduction Number Matrices)**.** *The distributed basic and effective reproduction number matrices are*

$$\mathcal{R}^0 = \begin{bmatrix} R_{11}^0 & R_{12}^0 & \cdots & R_{1n}^0 \\ R_{21}^0 & R_{22}^0 & \cdots & R_{2n}^0 \\ \vdots & \vdots & \ddots & \vdots \\ R_{n1}^0 & R_{n2}^0 & \cdots & R_{nn}^0 \end{bmatrix}, \tag{5}$$

and

$$\mathcal{R}^t = \begin{bmatrix} R^t_{11} & R^t_{12} & \cdots & R^t_{1n} \\ R^t_{21} & R^t_{22} & \cdots & R^t_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ R^t_{n1} & R^t_{n2} & \cdots & R^t_{nn} \end{bmatrix}, \tag{6}$$

respectively.

Remark 2. *The distributed basic reproduction number matrix $\mathcal{R}^0 = \mathcal{D}^{-1}\mathcal{B}$ is the next generation matrix [17] of the networked SIS/SIR models. Thus, the distributed effective reproduction number matrix $\mathcal{R}^t$ is equal to $diag(s(t))\mathcal{R}^0$. However, the advantage of viewing $\mathcal{R}^0$ and $\mathcal{R}^t$ as the composition of distributed reproduction numbers in* (5) *and* (6) *is that we can construct these matrices through the distributed reproduction numbers directly from data. For instance, in real-world epidemic spreading processes, when we need the network-level effective reproduction number $\rho(\mathcal{R}^t)$, instead of estimating the model parameters β_{ij}, γ_i, and $s_i(t)$ to obtain $\mathcal{R}^0$ and $\mathcal{R}^t$, we only need the estimated distributed reproduction numbers R^t_{ij} to compose $\mathcal{R}^t$. We will further illustrate this idea in Section IV.*

Based on Definition 2, it can be observed that $\mathcal{R}^0 = \mathcal{D}^{-1}\mathcal{B}$ and $\mathcal{R}^t = \text{diag}(s)\mathcal{D}^{-1}\mathcal{B}$. Hence, the spectral radius of the distributed basic reproduction number matrix, denoted $\rho(\mathcal{R}^0)$, is the basic reproduction number of the network, i.e., $\rho(\mathcal{R}^0) = R^0$. Meanwhile, the spectral radius of the distributed effective reproduction number matrix, denoted $\rho(\mathcal{R}^t)$, is the effective reproduction number of the network, i.e., $\rho(\mathcal{R}^t) = R^t$. Further, for all $i \in \underline{n}$, the i^{th} row sum of the distributed basic reproduction number matrix is the reproduction number of community i, i.e., we have $\sum_{j=1}^{n}[\mathcal{R}^0]_{ij} = R^0_i$. Note that the i^{th} row sum of the distributed effective reproduction number matrix, $\mathcal{R}^t$, is not equal to R^t_i, since the weights I_{ij} are not included in $\mathcal{R}^t$.

Through studying the spreading behavior of the network, we connect the effective reproduction number of the network to the effective reproduction numbers of the communities.

Theorem 2. *When the epidemic states are not at a healthy equilibrium, the following statements hold:*

- *$\bar{R}^t_i = 1$ for all $i \in \underline{n}$ only if $\rho(\mathcal{R}^t) = 1$;*
- *$\bar{R}^t_i < 1$ for all $i \in \underline{n}$ only if $\rho(\mathcal{R}^t) < 1$;*
- *$\bar{R}^t_i > 1$ for all $i \in \underline{n}$ only if $\rho(\mathcal{R}^t) > 1$.*

Remark 3. *Theorem 2 bridges the gap between R^t and $\bar{R}^t_i$. Especially, for the case where the overall information of the network is unknown, we can leverage the distributed effective reproduction numbers of each community to indicate the effective reproduction number of the whole network, and further to determine the overall spreading behavior.*

Using Theorem 2 and Lemma 1, we can characterize the spreading behaviors of the SIS and SIR models through $\bar{R}^t_i$.

Corollary 1. *For the networked SIR model, the healthy equilibria are locally stable if $\bar{R}^t_i < 1$ for all $i \in \underline{n}$. For the networked SIS model, if $\bar{R}^t_i > 1$ for all $i \in \underline{n}$, then there must exist a unique endemic equilibrium, which is stable.*

Remark 4. *Corollary 1 provides a new way to analyze the spreading behavior of the classic SIS and SIR models, i.e., through the distributed reproduction numbers. For networked SIR models, if the reproduction number of every community in the network is less than* 1*, then we can ensure the epidemic is fading away. For networked SIS models, if the effective reproduction number of each community in the network is greater than* 1*, then there must be an endemic in the future.*

Lemmas 1 and 2 indicate that if $R^0 < 1$, then the weighted sum of the infected states will converge to zero. However, unlike the fact that $R^t \leq R^0$ for network-level reproduction numbers, if the basic reproduction number of community i is less than 1 for all $i \in \underline{n}$, then the effective reproduction number of community i can still be greater than 1. Hence, we have the following corollary.

Corollary 2. *There can be an outbreak within community i even under the condition that the basic reproduction number of the community is smaller than* 1*, i.e., $R^0_i < 1$ for all $i \in \underline{n}$.*

After demonstrating that we can use the distributed reproduction numbers to analyze spreading behaviors, we showed that the distributed reproduction numbers are closely related to the basic and effective reproduction numbers of the network in Theorem 2, Corollary 1, and Corollary 2. Hence we have answered Question 2 that not only can we use the distributed reproduction numbers to analyze spreading behaviors of individual entities within the network, but also we can use the distributed reproduction numbers to study the overall spreading behavior of the network as a whole.

IV. Applications

In this section, we use two examples to illustrate the importance of leveraging distributed reproduction numbers to study epidemic spread across entire networks and within each entity in a network. In the first example, we show the advantage of leveraging $\bar{R}^t_i$ for all $i \in \underline{n}$ instead of R^t in analyzing networked spreading processes. In the second example, we illustrate the potential of leveraging distributed reproduction numbers in data-driven applications. Due to the page limit, we show the second example in Section IV.B [15]. Together, these examples answer Question 3 from Section II.

Consider an epidemic spreading over ten strongly connected communities, as shown in Fig. 3. Suppose the epidemic spreads based on the classic networked SIR models in (2). We capture the spreading behavior in the plots in Fig. 4. Fig. 4 (Top) shows that the effective reproduction number of the whole network (R^t) is always less than 1. Thus, if a community uses this R^t for policy-making and forecasting, then the community might believe that the infected proportion of the population will decrease from time step zero.

However, there are still outbreaks over several communities, e.g., communities 3 and 5 in Fig. 4 (Bottom), where the infected proportions in fact increase for several timesteps at the beginning. These outbreaks can be explained through the distributed reproduction numbers of the communities, which are plotted in Fig. 4 (Middle). Through analyzing

Fig. 4 (Middle), $\bar{R}_3^t$ and $\bar{R}_5^t$ are greater than 1 at the beginning, which indicate outbreaks within them and thus that both communities should take actions against potential outbreaks. This simple case demonstrates that it is more informative to leverage distributed reproduction numbers when designing mitigation policies for individual community.

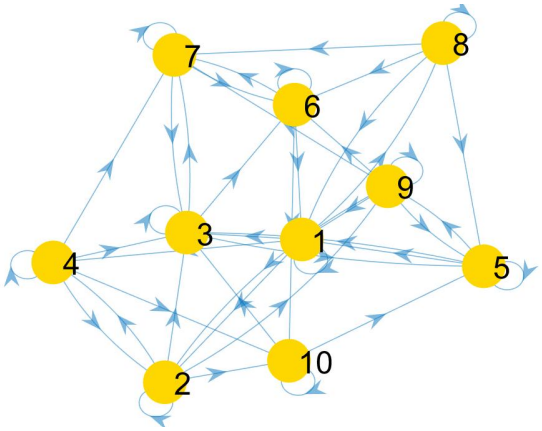

Figure 3: We consider an SIR model of an epidemic spreading over this strongly connected network of 10 communities.

V. Conclusion and Future Work

In this work, we defined distributed reproduction numbers to study spreading behaviors of networked epidemic models. In addition, we demonstrated that distributed reproduction numbers can capture both spreading behaviors of individual communities and networks as a whole. Compared to network-level reproduction numbers, we show that distributed reproduction numbers estimated from synthetic data can infer much more information about the spread of an epidemic. Future work will consider how we can leverage real-world networked testing and contact tracing data to estimate distributed reproduction numbers and how we can design distributed interventions by using these estimated distributed reproduction numbers.

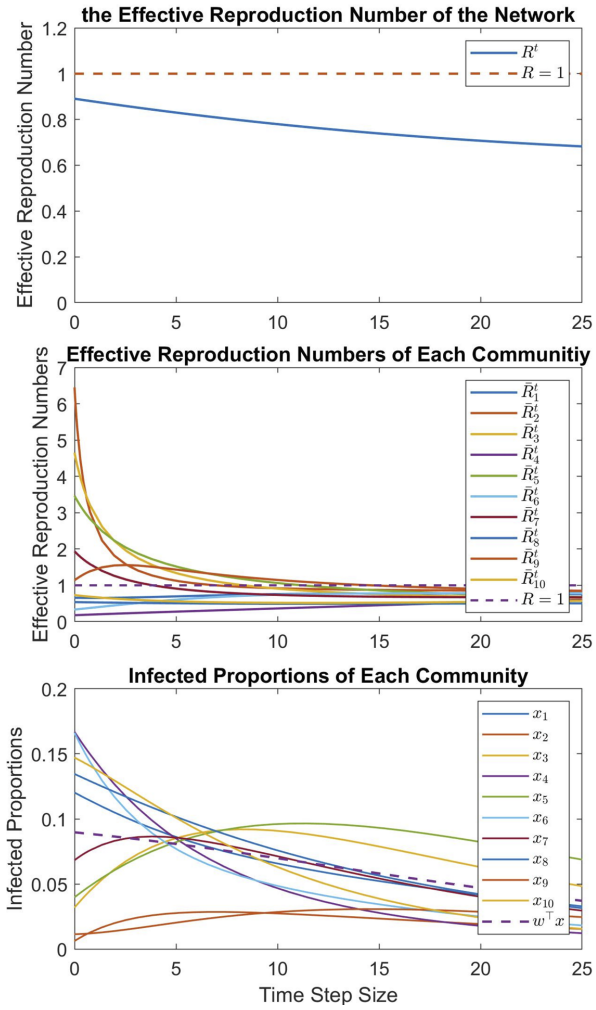

Figure 4: (Top) The effective reproduction number of the whole spread network. (Middle) The effective reproduction number of each community in the network, (Bottom) The infected proportion of each community. Note that the dashed line is the weighted sum of the infected proportions, and the trend of weighted sum is captured by R^t in the top figure.

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