Analysis and Estimation of Networked SIR & SEIR Models with Transportation Networks

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Abstract

In this paper we present the discrete-time networked SIR and SEIR models and present assumptions under which they are well defined. We analyze the limiting behavior of the models and present necessary and sufficient conditions for estimating the spreading parameters from data. We illustrate these results via simulation.

I. INTRODUCTION

Given recent outbreaks, it is critical to be able to quickly track the spread of the virus and understand the mechanisms that are enabling their propagation. While the mode of transmission of recent novel viruses is not exactly known, human-to-human interaction appears to be a main factor [1]. A key component for transmission is the underlying transportation network, which acts as a propagator of the virus within and between communities.

In this work we extend the commonly used SIR [2] and SEIR [3] models for viral spread to consider spread over the network in the context of human interaction and transportation. We model the proportion of people in each county who have not been infected ($S$), those who have been infected but have not been confirmed via a test ($E$), test-confirmed infected cases ($I$), and those who have either recovered or died from the virus ($R$) and show that we are able to accurately model the evolution of such a virus, as well as how to recover the proper model parameter values from time series data of infections and recoveries.

Previous work has explored the networked SIR models [4], [5]. Specifically, the authors in [4] provide stability properties and asymptotic convergence, as well as a novel algorithm to compute the asymptomatic state of the network SIR system. More recently, the SEIR model has become popular for modeling epidemic spread (e.g., [6]). The model has also been extended to account for quarantine [7] and asymptomatic transmission [8]. We go beyond prior work by analyzing the limiting behavior of the network SEIR model and present estimation results of the spread parameters.

The remainder of the article is outlined as follows. The networked SEIR model is introduced in Section II and its limiting behavior is discussed in Section III. Parameter estimation for the networked SIR and SEIR models is discussed in Section IV and demonstrated in Section V.

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A. Notation

Given a vector $x$, the transpose is indicated by $x^\top$, $\bar{x}$ is the average of its entries, and $\text{diag}(\cdot)$ is a diagonal matrix with the argument on the diagonal. We use $0$ and $1$ to denote a vector or matrix of zeros and ones, respectively, of the appropriate dimensions. We define a directed graph $G = (\mathcal{V}, \mathcal{E}, w)$, where $\mathcal{V}$ is the set of nodes, $\mathcal{E} \subseteq \mathcal{V} \times \mathcal{V}$ is the set of edges, and $w : \mathcal{E} \to \mathbb{R}^+$ is a function mapping directed edges to their weightings, with $\mathbb{R}^+$ being the set of positive real values. Given $G$, we denote an edge from node $i \in \mathcal{V}$ to node $j \in \mathcal{V}$ by $(i, j)$. We say node $i \in \mathcal{V}$ is a neighbor of node $j \in \mathcal{V}$ if and only if $(i, j) \in \mathcal{E}$, and denote the neighbors of node $j$ as $\mathcal{N}_j$. We denote the weighted adjacency matrix associated with $G$ as $A$ with the nonzero entry $a_{ij}$ indicating the strength of edge $(i, j)$ as given by $w$.

II. Networked SIR & SEIR Models

Here we introduce the discrete-time networked SIR and SEIR models. In each case we assume that the virus spreads over $G = (\mathcal{V}, \mathcal{E}, w)$ with adjacency matrix $A$. Each node in $\mathcal{V}$ can be interpreted as a single individual or a subpopulation and the states are interpreted as probabilities or proportions, respectively, referred to as levels from here on out.

A. Networked SIR Model

For an SIR process spreading over $G$, node $i$’s levels of susceptibility $s^k_i$, infection $p^k_i$, and recovery $r^k_i$ evolve as

\begin{align*}
    s^{k+1}_i &= s^k_i - hs^k_i \left( \sum_{j \in \mathcal{N}_i} a_{ij} p^k_j \right), \\
    p^{k+1}_i &= p^k_i + h \left( s^k_i \beta_i \sum_{j \in \mathcal{N}_i} a_{ij} p^k_j - \gamma_i p^k_i \right), \\
    r^{k+1}_i &= r^k_i + h \gamma_i p^k_i,
\end{align*}

where $k$ is the time step, $h$ is the sampling parameter, and $\beta_i$ and $\gamma_i$ are node $i$’s infection and recovery parameters, respectively. The SIR discrete-time model can be expressed in matrix form as follows

\begin{align*}
    p^{k+1} &= p^k + h \left( (I - P^k - R^k)BA - \gamma \right) p^k, \\
    r^{k+1} &= r^k + h \gamma p^k,
\end{align*}

where $P^k = \text{diag}(p^k)$, $R^k = \text{diag}(r^k)$, $B = \text{diag}(\alpha_i)$, and $\gamma = \text{diag}(\gamma^k_i)$. For this model to be well-defined we need the following assumptions.

Assumption 1. For all $i \in [n]$, we have $0 < h \gamma_i < 1$ and $h \sum_{j \in \mathcal{N}_i} \beta_i a_{ij} < 1$.

Lemma 1. Consider the model in (1) under Assumption 1. Suppose $s^0_i, p^0_i, r^0_i \in [0, 1]$ and $s^0_i + p^0_i + r^0_i = 1$ for all $i \in [n]$. Then, for all $k \geq 0$ and $i \in [n]$, $s^k_i, p^k_i, r^k_i \in [0, 1]$ and $s^k_i + p^k_i + r^k_i = 1$. 
B. Networked SEIR Model

For the discrete-time SEIR model spreading over \( G \) with \( s^k_i = 1 - e^k_i - p^k_i - r^k_i \), the exposed level of \( e^k_i \) and other states evolve as

\[
\begin{align*}
    s^{k+1}_i &= s^k_i - h s^k_i e^k_i, \\
    e^{k+1}_i &= e^k_i + h s^k_i e^k_i - h \sigma_i e^k_i, \\
    p^{k+1}_i &= p^k_i + h (\sigma_i e^k_i - \gamma_i p^k_i), \\
    r^{k+1}_i &= r^k_i + h (\gamma_i p^k_i),
\end{align*}
\]

where

\[
\begin{align*}
    i^k_i &= \beta_i^E \sum_{j \in N_i} a_{ij} e^k_j + \beta_i \sum_{j \in N_i} a_{ij} p^k_j,
\end{align*}
\]

\( \beta_i^E \) is infection parameter associated with the \( e^k_i \) state, \( \sigma_i \) captures the rate at which the exposed become confirmed infected cases.

For transportation model we define

\[
\dot{\imath}^k_i = \dot{i}^k_i + \sum_{l \in \mathcal{L}} \left( \beta_i^{E,l} \sum_{j \in N_i} \bar{a}_{ij} e^k_j + \beta_i^l \sum_{j \in N_i} \bar{a}_{ij} p^k_j \right),
\]

where \( \mathcal{L} \) is the set of transportation networks, \( \bar{a}_{ij} \) is the transportation network, and \( \beta_i^{E,l} \) and \( \beta_i^l \) are the corresponding infection rates, for the \( l \)th transportation network.

The SEIR discrete-time model can also be expressed in matrix form as follows

\[
\begin{align*}
    e^{k+1} &= e^k + h \left( S^k (B^E A e^k + B A p^k) - \sigma e^k \right), \\
    p^{k+1} &= p^k + h (\sigma e^k - \gamma p^k), \\
    r^{k+1} &= r^k + h (\gamma p^k),
\end{align*}
\]

where \( S^k = \text{diag}(s^k_i) \), \( B^E = \text{diag}(\beta_i^E) \), and \( \sigma = \text{diag}(\sigma_i) \).

For the discrete-time SEIR model to be well-defined we need the following assumptions.

**Assumption 2.** For all \( i \in [n] \), we have \( 0 < h \gamma_i < 1 \), \( 0 < h \sigma_i \leq 1 \), and \( 0 \leq h(\beta_i^E + \beta_i) \sum_{j \in N_i} a_{ij} < 1 \).

\( \beta_i^E, \beta_i, a_{ij} \geq 0 \) for all \( i, j \in [n] \).

**Lemma 2.** Consider the model in (3)-(4) under Assumption 2. Suppose \( s^0_i, e^0_i, p^0_i, r^0_i \in [0, 1] \), \( s^0_i + e^0_i + p^0_i + r^0_i = 1 \) for all \( i \in [n] \). Then, for all \( k \geq 0 \) and \( i \in [n] \), \( s^k_i, e^k_i, p^k_i, r^k_i \in [0, 1] \) and \( s^k_i + e^k_i + p^k_i + r^k_i = 1 \).

**Proof.** We prove this result by induction. By assumption, it holds for the base-case \( k = 0 \). We follow the proof by showing the induction-step, that is, assume \( s^k_i, e^k_i, p^k_i, r^k_i \in [0, 1] \) and \( s^k_i + e^k_i + p^k_i + r^k_i = 1 \), for all \( i \in [n] \), and we now show that this holds also for time-step \( k + 1 \). By Assumption 2 and (3a), \( s^{k+1} \geq s^k_i + h \left[ -s^k_i (\beta_i^E + \beta_i) \sum_{j \in N_i} a_{ij} \right] = s^k_i \left[ 1 - h(\beta_i^E + \beta_i) \sum_{j \in N_i} a_{ij} \right] \geq 0 \). We have \( s^{k+1} \leq s^k \leq 1 \) since
Theorem 2. Consider the model in (3a) under Assumption 2. Suppose $s_i^0, e_i^0, p_i^0, r_i^0 \in [0, 1]$, $s_i^0 + e_i^0 + p_i^0 + r_i^0 = 1$ for all $i \in [n]$, $BA$ is irreducible, $s_i^0 > 0$ for all $i \in [n]$, and $p_i^0 > 0$ for some $i$. Then, for all $i \in [n]$,

1) $s_i^{k+1} \leq s_i^k$, for all $k \geq 0$,
2) $\lim_{k \to \infty} e_i^k = 0$, and
3) $\lim_{k \to \infty} p_i^k = 0$, and
4) $\lambda_{\text{max}}$ is monotonically decreasing as a function of $k$,
5) there exists $\tilde{k}$ such that $\lambda_{\text{max}} < 1$ for all $k \geq \tilde{k}$, and
6) $\lambda_{\text{max}}$ is monotonically decreasing as a function of $k$.

Proof. We present the proof for each part of the theorem, starting with 1).

1) By Lemma 2 and Assumption 2, we have that $h \left[ -s_i^k \left( \sum_{j \in \mathcal{N}_i} \beta_i j e_j^k + \sum_{j=1}^k \beta_i a_i j p_i^j \right) \right] \leq 0$ for all $i \in [n]$ and $k \geq 0$. Therefore, from (3a), we have $s_i^{k+1} \leq s_i^k$. 

III. Analysis of Models

In this section we discuss the limiting behavior of the networked models from Section II

A. SIR Model

For the matrix $I + h \operatorname{diag}(s^k)BA - h \gamma$, define its dominant eigenvalue as $\lambda_{\text{max}}$.

Theorem 1. [5] Consider the model in (1) with Assumption 7. BA irreducible, $s_i^0 > 0$ for all $i \in [n]$, and $p_i^0 > 0$ for some $i$. Then, for all $i \in [n]$,

1) $s_i^{k+1} \leq s_i^k$, for all $k \geq 0$,
2) $\lim_{k \to \infty} e_i^k = 0$,
3) $\lim_{k \to \infty} p_i^k = 0$, and
4) $\lambda_{\text{max}}$ is monotonically decreasing as a function of $k$,
5) there exists $\tilde{k}$ such that $\lambda_{\text{max}} < 1$ for all $k \geq \tilde{k}$, and
6) $\lambda_{\text{max}}$ is monotonically decreasing as a function of $k$.

B. SEIR Model

Let $\lambda_{\text{max}}^M_k$ be the dominant eigenvalue of $M_k$, where $M_k$ is defined as

$$M_k = \begin{bmatrix} (I + h \operatorname{diag}(s^k)BA - h \sigma) & h \operatorname{diag}(s^k)BA \cr h \sigma & (I - h \gamma) \end{bmatrix}. \quad (7)$$

Observe that $z^{k+1} := \begin{bmatrix} e_i^{k+1} \\ p_i^{k+1} \end{bmatrix} = M_k \begin{bmatrix} e_i^k \\ p_i^k \end{bmatrix}$.

Theorem 2. Consider the model in (3a) under Assumption 2. Suppose $s_i^0, e_i^0, p_i^0, r_i^0 \in [0, 1]$, $s_i^0 + e_i^0 + p_i^0 + r_i^0 = 1$ for all $i \in [n]$, $BA$ is irreducible, $s_i^0 > 0$ for all $i \in [n]$, and $p_i^0 > 0$ for some $i$. Then, for all $k \geq 0$ and $i \in [n]$,

1) $s_i^{k+1} \leq s_i^k$,
2) $\lim_{k \to \infty} e_i^k = 0$ and $\lim_{k \to \infty} p_i^k = 0$,
3) $\lambda_{\text{max}}^M_k$ is monotonically decreasing as a function of $k$,
4) there exists $\tilde{k}$ such that $\lambda_{\text{max}}^M_k < 1$ for all $k \geq \tilde{k}$, and
5) there exists $\tilde{k}$, such that $p_i^k$ converges linearly to 0 for all $k \geq \tilde{k}$ and $i \in [n]$.

Proof. We present the proof for each part of the theorem, starting with 1).

1) By Lemma 2 and Assumption 2, we have that $h \left[ -s_i^k \left( \sum_{j \in \mathcal{N}_i} \beta_i j e_j^k + \sum_{j=1}^k \beta_i a_i j p_i^j \right) \right] \leq 0$ for all $i \in [n]$ and $k \geq 0$. Therefore, from (3a), we have $s_i^{k+1} \leq s_i^k$. 

h \left[ -s_i^k \left( \sum_{j \in \mathcal{N}_i} \beta_i j e_j^k + \sum_{j=1}^k \beta_i a_i j p_i^j \right) \right] \leq 0. By Assumption 2 and (3b), $e_i^{k+1} \geq (1 - h \sigma_i) e_i^k \geq 0$. Moreover, by the assumption $e_i^k, p_i^k \leq 1$ for all $j \in [n]$, Assumption 2 and (3b), $e_i^{k+1} \leq e_i^k + s_i^k h \beta_i j e_j^k \leq e_i^k + s_i^k \leq 1$. By Assumption 2 and (3d), $p_i^{k+1} \leq p_i^k + h \sigma_i e_i^k \leq p_i^k + e_i^k \leq 1$. By Assumption 2 and (3d), $p_i^{k+1} \geq r_i^k \geq 0$, and $r_i^{k+1} \leq r_i^k + p_i^k$. 

Thus, by the principle of mathematical induction we have that, if $s_i^0, e_i^0, p_i^0, r_i^0 \in [0, 1]$ and $s_i^0 + e_i^0 + p_i^0 + r_i^0 = 1$ for all $i \in [n]$ then $s_i^k, e_i^k, p_i^k, r_i^k \in [0, 1]$ and $s_i^k + e_i^k + p_i^k + r_i^k = 1$ for all $k \in \mathbb{N}$. \qed
2) Since the rate of change of $s^k$, $-h \text{diag}(s^k) [B^E A e^k + B A p^k]$, is non-positive for all $k \geq 0$ and $s^k$ is lower bounded by zero, by Lemma 2 we conclude that $\lim_{k \to \infty} s^k$ exists. Therefore,

$$\lim_{k \to \infty} -h \text{diag}(s^k) [B^E A e^k + B A p^k] = 0. \quad (8)$$

Therefore, $\lim_{k \to \infty} e^{k+1} - e^k = \lim_{k \to \infty} -h \sigma e^k$. Thus, by Assumption 2, $h \sigma_i > 0$ for all $i \in [n]$, $\lim_{k \to \infty} e_i^k = 0$ for all $i \in [n]$.

Similarly, we show that $\lim_{k \to \infty} p_i^k = 0$ for all $i \in [n]$. We have that $\lim_{k \to \infty} p_i^{k+1} - p_i^k = \lim_{k \to \infty} h \left( \sigma e^k - \gamma p^k \right) = \lim_{k \to \infty} -h \gamma p^k$, where we used that $\lim_{k \to \infty} e^k = 0$. By assumption $h \gamma_i > 0$ for all $i \in [n]$, thus $\lim_{k \to \infty} p_i^k = 0$ for all $i \in [n]$.

3) By assumption $s_i^0 > 0$ for all $i \in [n]$, and from the proof of Lemma 2 we can see that $s_i^k > 0$ for all $i \in [n]$, $k \geq 0$. Therefore, since we have that $B A$ is irreducible, from (7), the matrix $M_k$ is irreducible, and non-negative by Assumption 2 for all finite $k$. Thus by the Perron-Frobenius Theorem for irreducible non-negative matrices we have that $\lambda_{M_{\max}}^{M_k} = \rho(M_k)$. Since $\rho(M_k)$ increases when any entry increases [9, Theorem 2.7] and by 1) of this theorem, we have that $\rho(M_k) \geq \rho(M_{k+1})$, that is $\lambda_{M_{\max}}^{M_k} \geq \lambda_{M_{\max}}^{M_{k+1}}$.

4) There are two possible equilibria: i) $\lim_{k \to \infty} s^k = 0$, and ii) $\lim_{k \to \infty} s^k = s^* \neq 0$. We explore the two cases separately.

i) If $\lim_{k \to \infty} s^k = 0$,

$$\lim_{k \to \infty} M^k = \begin{bmatrix} I - h \sigma & 0 \\ h \sigma & I - h \gamma \end{bmatrix}.$$ 

Therefore, by Assumption 2 there exists a $\bar{k}$ such that $\lambda_{M_{\max}}^{M_k} < 1$ for all $k \geq \bar{k}$.

ii) If $\lim_{k \to \infty} s^k = s^* \neq 0$, then, by 2), for any $(s^0, e^0, p^0, r^0)$ the system converges to some equilibrium of the form $(s^*, 0, 0, 1 - s^*)$. Define

$$\epsilon_s^k := s^k - s^* \text{ and } \epsilon_p^k := z^k - 0_{2n}. \quad (9)$$

By 1) and Lemma 2 respectively we know that $\epsilon_s^k \geq 0_n$ and $\epsilon_p^k \geq 0_{2n}$ for all $k \geq 0$. Furthermore, we know that $\epsilon_s^{k+1} \leq \epsilon_s^k$ for all $k \geq 0$, $\lim_{k \to \infty} \epsilon_s^k = 0_n$, and $\lim_{k \to \infty} \epsilon_p^k = 0_{2n}$. where the last equality comes from 2).

Linearizing the dynamics of $\epsilon_s^k$ and $\epsilon_p^k$ around $(s^*, 0_{2n})$ gives

$$\epsilon_s^{k+1} = \epsilon_s^k - h \text{diag}(s^*) [B^E A] \epsilon_s^k, \quad (10a)$$

$$\epsilon_p^{k+1} = M_k \epsilon_p^k, \quad (10b)$$

Let $\lambda_{M_{\max}}^{M^*}$ be the maximum eigenvalue of

$$M^* = \begin{bmatrix} (I + h \text{diag}(s^*) B^E A - h \sigma) & h \text{diag}(s^*) B A \\ h \sigma & (I - h \gamma) \end{bmatrix}$$

with corresponding normalized eigenvector $w^*$, that is,

$$w^{\ast \top} M^* = \lambda_{M_{\max}}^{M^*} w^{\ast \top}. \quad (12)$$
If $\lambda_{\text{max}}^M > 1$, then the system in (10) is unstable. Therefore, by Lyapunov’s Indirect Method, $\lim_{k \to \infty} (\epsilon^k, \epsilon^k_p) \neq (s^*, 0_{2n})$, which is a contradiction.

Now consider the case where $\lambda_{\text{max}}^M = 1$. Define

$$\tilde{M}_k = \begin{bmatrix} h\text{diag}(\epsilon_k^s)BA & h\text{diag}(\epsilon_k^s)B^E A \\ 0 & 0 \end{bmatrix}. \quad (13)$$

Then we can write $M_k = M^* + \tilde{M}_k$, observe that all entries in $\tilde{M}$ are non-negative. Using (9) and left multiplying the equation of $\epsilon^{k+1}_p$ in (10b) by $w^*\top$ we get

$$w^*\top \epsilon^{k+1}_p = w^*\top M \epsilon^k_p = \lambda_{\text{max}}^M w^*\top \epsilon^k_p + w^*\top \tilde{M}_k \epsilon^k_p.$$  

Thus,

$$w^*\top (\epsilon^{k+1}_p - \epsilon^k_p) = w^*\top \tilde{M}_k \epsilon^k_p \geq 0,$$  \quad (14)

where the last inequality holds since all elements are non-negative. This contradicts that $\lim_{k \to \infty} z^k = 0_{2n}$, that is 2). Therefore, there exists a $\bar{k}$ such that $\lambda_{\text{max}}^M_k < 1$ for all $k \geq \bar{k}$.

5) Since, by 4), there exists a $\bar{k}$ such that $\lambda_{\text{max}}^M_k < 1$ for all $k \geq \bar{k}$, and we know that $\lambda_{\text{max}}^M_k = \rho(M_k) \geq 0$ by Assumption 2, we have

$$\lim_{k \to \infty} \frac{\|p^{k+1}\|}{\|p^k\|} = \frac{\|M_k p^k\|}{\|p^k\|} = \lambda_{\text{max}}^M_k < 1. \quad (15)$$

Therefore, for $k \geq \bar{k}$, $p^k$ converges linearly to $0_n$. \hfill \Box

IV. Estimating Model Parameters

In this section we discuss estimating the parameters of the networked models from Section II using data. Note that these results are similar to the ones for the networked SIS model in [10, 11].

A. Networked SIR Model

We first explore conditions for estimating the model parameters for the homogeneous model, that is, where every node has the same infection and healing parameters. In order to do so we define the following matrices:

$$\Phi = \begin{bmatrix} hS^0 A p^0 & -h p^0 \\ \vdots & \vdots \\ hS^{T-1} A p^{T-1} & -h p^{T-1} \end{bmatrix}_a,$$

and

$$\Gamma = \begin{bmatrix} 0 & b \end{bmatrix}_b. \quad (16)$$

$$\Phi = \begin{bmatrix} hS^0 A p^0 & -h p^0 \\ \vdots & \vdots \\ hS^{T-1} A p^{T-1} & -h p^{T-1} \end{bmatrix}_a,$$  \quad (16)

$$\Gamma = \begin{bmatrix} 0 & b \end{bmatrix}_b. \quad (17)$$
Using the above matrices we construct 
\[ Q = \begin{bmatrix} \Phi \\ \Gamma \end{bmatrix} \] 
and write (1b) and (1c) as
\[
\begin{bmatrix}
  p^1 - p^0 \\
  \vdots \\
  p^T - p^{T-1} \\
  r^1 - r^0 \\
  \vdots \\
  r^T - r^{T-1} \\
\end{bmatrix} = Q \begin{bmatrix} \beta \\ \gamma \end{bmatrix}.
\] (18)

We find the least squares estimates \( \hat{\beta} \) and \( \hat{\gamma} \) by employing the pseudoinverse of \( Q \).

**Theorem 3.** Consider the model in (1) with homogeneous virus spread, that is, \( \beta \) and \( \gamma \) are the same for all \( n \) nodes.

Assume that \( s^k, p^k, r^k \), for all \( k \in [T] \cup \{0\} \), and \( h \) are known, with \( n > 0 \). Then, the parameters of the spreading process can be identified uniquely if and only if \( T > 0 \), and there exist \( i_1, i_2 \in [n] \) and \( k_1, k_2 \in [T-1] \cup \{0\} \) such that

\[
  p^1_{i_1} \neq 0, \\
  (S^{k_2} A p^{k_2})_{i_2} \neq 0.
\] (19a)

**Proof.** Using (16) and (17) we can write \( Q \) as follows
\[
Q = \begin{bmatrix} a & -b \\ 0 & b \end{bmatrix} = \begin{bmatrix} I & -I \\ 0 & I \end{bmatrix} \begin{bmatrix} a & 0 \\ 0 & b \end{bmatrix}.
\]

If the assumptions in (19) hold, \( a \) and \( b \) each have at least one element that is nonzero, therefore \( \tilde{Q} \) has full column rank. Clearly \( D \) has full rank which implies that the rank for \( Q \) is equal to the rank of \( \tilde{Q} \). Therefore, there exists a unique solution to (18) using the inverse or pseudoinverse.

If one of the assumptions in (19) is not met, \( Q \) will have a nontrivial nullspace. Therefore, in that case, (18) does not have a unique solution.

Note that we do not need to know all \( s^k, p^k, r^k \) but only the entries \( s^k_j, p^k_j, r^k_j \), for \( j \in \mathcal{N}_{i_1} \cup \mathcal{N}_{i_2} \cup \{i_1, i_2\} \) is sufficient, where \( i_1, i_2 \) satisfy (19).

To estimate the spreading parameters for the discrete-time SIR model from Section II-A in the heterogeneous
In the homogeneous case, we form the following matrices:

\[
\Phi_i = \begin{bmatrix}
  h s_i^0 \sum_{j \in N_i} a_{ij} p_j^0 & -h p_i^0 \\
  \vdots & \vdots \\
  h s_i^{T-1} \sum_{j \in N_i} a_{ij} p_j^{T-1} & -h p_i^{T-1}
\end{bmatrix}, \quad \text{and}
\]

\[
\Gamma_i = \begin{bmatrix}
  0 & b_i
\end{bmatrix}.
\]

Using the above matrices we construct

\[
Q_i = \begin{bmatrix}
  \Phi_i \\
  \Gamma_i
\end{bmatrix}.
\]

For each \( i \), we find the least squares estimates \( \hat{\beta}_i \) and \( \hat{\gamma}_i \) by using the pseudoinverse of \( Q_i \).

We now explore conditions for estimating the SEIR model parameters in the homogeneous case. In order to do so we define the following matrices:

\[
\Phi^E = \begin{bmatrix}
  h S^0 A e^0 & h S^0 A p^0 & -h e^0 & 0 \\
  \vdots & \vdots & \vdots & \vdots \\
  h S^{T-1} A e^{T-1} & h S^{T-1} A p^{T-1} & -h e^{T-1} & 0
\end{bmatrix},
\]

\[
\Sigma^E = \begin{bmatrix}
  0 & 0 & h e^0 & -h p^0 \\
  \vdots & \vdots & \vdots & \vdots \\
  0 & 0 & h e^{T-1} & -h p^{T-1}
\end{bmatrix},
\]

\[
\Gamma^E = \begin{bmatrix}
  0 & 0 & 0 & d^E
\end{bmatrix}.
\]
Using the above matrices we construct \( Q^E = \begin{bmatrix} \Phi^E \\ \Sigma^E \\ \Gamma^E \end{bmatrix} \) and write (3)-(4) as

\[
\begin{bmatrix}
 e^1 - e^0 \\
 \vdots \\
 e^T - e^{T-1} \\
p^1 - p^0 \\
 \vdots \\
p^T - p^{T-1} \\
r^1 - r^0 \\
 \vdots \\
r^T - r^{T-1}
\end{bmatrix}
= Q^E \begin{bmatrix} \beta^E \\ \beta \\ \sigma \\ \gamma \end{bmatrix}.
\]  
(26)

We find the least squares estimates \( \hat{\beta}^E, \hat{\beta}, \hat{\sigma}, \) and \( \hat{\gamma} \) using the pseudoinverse of \( Q^E \).

**Theorem 4.** Consider the model in (3)-(4) with homogeneous virus spread, that is, \( \beta^E, \beta, \sigma, \) and \( \gamma \) are the same for all \( n \) nodes. Assume that \( s^k, e^k, p^k, r^k \) for all \( k \in [T] \cup \{0\} \), and \( h \) are known, with \( n > 1 \). Then, the parameters of the spreading process can be identified uniquely if and only if \( T > 0 \), and there exist \( i_1, i_2, i_3, i_4 \in [n] \) and \( k_1, k_2, k_3, k_4 \in [T-1] \cup \{0\} \) such that

\[
p^k_{i_1} \neq 0, e^k_{i_2} \neq 0, \tag{27a}
\]

\[
g_{i_3}^{k_3}(e^{k_3})g_{i_4}^{k_4}(p^{k_4}) \neq g_{i_4}^{k_4}(e^{k_4})g_{i_3}^{k_3}(p^{k_3}), \tag{27b}
\]

where \( g^k_i(x) = s^k_i \sum_{j \in N_i} a_{ij} x_j. \)

**Proof.** Using (23)-(25), we can write \( Q^E \) as follows

\[
Q^E = \begin{bmatrix}
 I & -I & 0_{n \times nT} \\
 0_{nT \times n} & I & -I \\
 0_{nT \times nT} & 0_{nT \times nT} & I
\end{bmatrix}
\begin{bmatrix}
a^E & b^E & 0 & 0 \\
0 & 0 & c^E & 0 \\
0 & 0 & 0 & d^E
\end{bmatrix}.
\]  
(28)

Since \( n > 1 \), \( \Phi^E = \begin{bmatrix} a^E & b^E \end{bmatrix} \) has at least two rows, and given that (27b) holds, \( \Phi^E \) has column rank equal to two. Moreover, if (27a) holds \( c \) and \( d \) each have at least one element that is nonzero. Thus, \( \tilde{Q}^E \) has full column rank. Clearly \( D^E \) has full rank which implies that the rank of \( Q^E \) is equal to the rank of \( \tilde{Q}^E \) [12]. Therefore, there exists a unique solution to (26) using the pseudoinverse.

If one of the assumptions in (27a)-(27b) is not met, \( Q^E \) will have a nontrivial nullspace. Therefore, in that case, (26) does not have a unique solution. \( \square \)
Similar to the SIR model and the heterogeneous case it is not necessary to know all entries of \( s^k, e^k, p^k, r^k \). It is sufficient to know only \( s^j, e^j, p^j, r^j \), for \( j \in \mathcal{N}_i \cup \mathcal{N}_{i_2} \cup \mathcal{N}_{i_3} \cup \mathcal{N}_{i_4} \cup \{i_1, i_2, i_3, i_4\} \), where \( i_1, i_2, i_3, i_4 \) satisfy (27).

To estimate the spreading parameters for the discrete-time, heterogeneous SEIR model from Section II-B we define:

\[
\Phi_i^E = \begin{bmatrix}
hs_i^0 \sum_{j \in \mathcal{N}_i} a_{ij} e_j^0 & hs_i^0 \sum_{j \in \mathcal{N}_i} a_{ij} p_j^0 & -he_i^0 & 0 \\
\vdots & \vdots & \vdots & \vdots \\
hs_i^{T-1} \sum_{j \in \mathcal{N}_i} a_{ij} e_j^{T-1} & hs_i^{T-1} \sum_{j \in \mathcal{N}_i} a_{ij} p_j^{T-1} & -he_i^{T-1} & 0 \\
\end{bmatrix},
\]

\[
\Sigma_i^E = \begin{bmatrix}
\begin{bmatrix} a_i^E & he_i^0 -hp_i^0 \\
\end{bmatrix} & \begin{bmatrix} 0 \\
\end{bmatrix} \\
\vdots & \vdots \\
\begin{bmatrix} he_i^{T-1} & -hp_i^{T-1} \\
\end{bmatrix} & \begin{bmatrix} 0 \\
\end{bmatrix} \\
\end{bmatrix},
\]

and

\[
\Gamma_i^E = \begin{bmatrix}
0 & 0 & 0 & d_i^E
\end{bmatrix}.
\]

Using the above matrices we construct \( Q_i^E = \begin{bmatrix} \Phi_i^E \\ \Sigma_i^E \\ \Gamma_i^E \end{bmatrix} \) and write (3)-(4) as

\[
\begin{bmatrix}
e_i^1 - e_i^0 \\
e_i^T - e_i^{T-1} \\
p_i^1 - p_i^0 \\
p_i^T - p_i^{T-1} \\
r_i^1 - r_i^0 \\
r_i^T - r_i^{T-1} \\
\end{bmatrix} = \begin{bmatrix}
\beta_i^E \\
\sigma_i \\
\gamma_i \\
\end{bmatrix}.
\]

We find the least squares estimates \( \beta_i^E, \sigma_i, \gamma_i \) using the pseudoinverse of \( Q_i^E \).

**Theorem 5.** Consider the model in (3)-(4). Assume that \( s^k, e^k, p^k, r^k \), for all \( j \in \mathcal{N}_i \cup \{i\}, k \in [T-1] \cup \{0\} \), \( e_i^T, p_i^T, r_i^T \), and \( h \) are known. Then, the parameters of the spreading process for node \( i \) can be identified uniquely if and only if \( T > 1 \), and there exist \( k_1, k_2, k_3, k_4 \in [T-1] \cup \{0\} \) such that

\[
\begin{align}
p_i^{k_1} &\neq 0, e_i^{k_2} \neq 0, \\
g_i^{k_3}(e_i^{k_3}) &\neq g_i^{k_4}(e_i^{k_4}),
\end{align}
\]

where \( g_i^k(x) = s_i^k \sum_{j \in \mathcal{N}_i} a_{ij} x_j \) which only uses the entries \( x_j \) for which \( j \in \mathcal{N}_i \).
Using (29)-(31), we can write $Q_i^E$ as follows:

$$Q_i^E = \begin{bmatrix} I & -I & 0_{T \times T} \\ 0_{T \times T} & I & -I \\ 0_{T \times T} & 0_{T \times T} & I \end{bmatrix} \begin{bmatrix} a_i^E & b_i^E & 0 & 0 \\ 0 & 0 & c_i^E & 0 \\ 0 & 0 & 0 & d_i^E \end{bmatrix} \Phi_i^E.$$  

Since $T > 1$, $\Phi_i^E = [a_i^E \ b_i^E]$ has at least two rows, and given that (33b) holds, $\Phi_i^E$ has column rank equal to two. Moreover, if (33a) holds, $c$ and $d$ each have at least one element that is nonzero. Thus, $\tilde{Q}_i^E$ has full column rank. Clearly $D_i^E$ has full rank which implies that the rank of $Q_i^E$ is equal to the rank of $\tilde{Q}_i^E$ \eqref{eq:26}. Therefore, there exists a unique solution to \eqref{eq:26} using the pseudoinverse.

If one of the assumptions in (33a)-(33b) is not met, $Q_i^E$ will have a nontrivial nullspace. Therefore, in that case, \eqref{eq:32} does not have a unique solution.

V. Simulations

In this section we illustrate the analysis and parameter estimation results from Sections III-IV. For the adjacency matrix we use the nearest-neighbor network of counties in the northeast US with self-loops, namely, the counties in Massachusetts (MA), New Jersey (NJ), Rhode Islands (RI), Connecticut (CT), and New York (NY), combining the five counties that make up New York City into one.

To simulate the states for the SEIR model we use \eqref{eq:33} \eqref{eq:44}, with the following spread parameters $(\beta^E, \beta, \sigma, \gamma) = (0.04, 0.06, 0.4, 0.3)$ and the initial state $e_0^1 = 0.02, e_0^2 = 0.03, p_0^1 = 0.01$, with the rest of the initial conditions for the non-susceptible states are set to zero for each node. We correctly recover the spread parameters using \eqref{eq:26} and $e^k$, $p^k$, and $r^k$ for $k \in \{0,1\}$, as expected by Theorem \ref{thm:4}. Similarly, we correctly recover the spread parameters for the SIR model using $\beta, \gamma$, $p^0$, and $r^0$ to simulate $p^1$ and $r^1$ and recovering the spread parameters using \eqref{eq:18} and $p^k$ and $r^k$ for $k \in \{0,1\}$.

We add measurement noise to evaluate the sensitivity of the estimation results and assume that the perturbation on $e$ is greater than that on $p$ and $r$ since it is the most difficult of the three states to measure. The measured states are $\bar{e}$, $\bar{p}$, and $\bar{r}$, determined by $\bar{e}_k^e = e_k^e + \varepsilon(x_k^e)$ where $\varepsilon(x_i) \sim N(0,0.015x_i + 0.0001)$, $\bar{p}_k^e = p_k^e + \varepsilon(p_k^e)$, and

Fig. 1: Simulation of a homogeneous SEIR system with its measured states, and the recovered states to show how well the recovered states captures the average state of the system.
\( \hat{r}_i^k = r_i^k + \varepsilon(r_i^k) \) where \( \varepsilon(x_i) \sim \mathcal{N}(0, 0.008x_i + 0.00001) \). In order to emulate the difficulty of measuring the states at the beginning of an outbreak, we start measuring from \( k = 14 \), and recover the spread parameters by left multiplying \( E \) by the pseudo-inverse of \( Q^E \). The estimated states \( \hat{e}, \hat{p}, \) and \( \hat{r} \) are constructed using \( E \), the first set of measured states \( \tilde{e}_{14}^1, \tilde{p}_{14}^1, \) and \( \tilde{r}_{14}^1 \), and the recovered spread parameters. In Figure 1 we show how well the average states are recovered compared to the average of the actual states, \( e, p, \) and \( r \) using the measured states to recover the spread parameters. The recovered spread parameters are \( (\hat{\beta}^E, \hat{\beta}, \hat{\sigma}, \hat{\gamma}) = (0.0398, 0.0602, 0.4000, 0.3000) \).

The error of \( \hat{e}, \hat{p}, \) and \( \hat{r} \) are 0.0190, 0.0186, and 0.0055, respectively.

VI. CONCLUSION

In conclusion, the discrete time SIR and SEIR models are extended to capture virus spread on a network. The limiting behavior of each model is analyzed and sufficient conditions for estimating spread parameters from data are presented. The developed models are implemented in simulations. To extend this work and improve the performance of the model, we plan to incorporate asymptomatic transmission and apply the results to real data.

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