

Global and Distributed Reproduction Numbers (DRNs) of a Multilayer SIR Model

José I. Caiza, Junjie Qin, Philip E. Paré

Purdue University, School of Electrical and Computer Engineering, West Lafayette, IN, USA

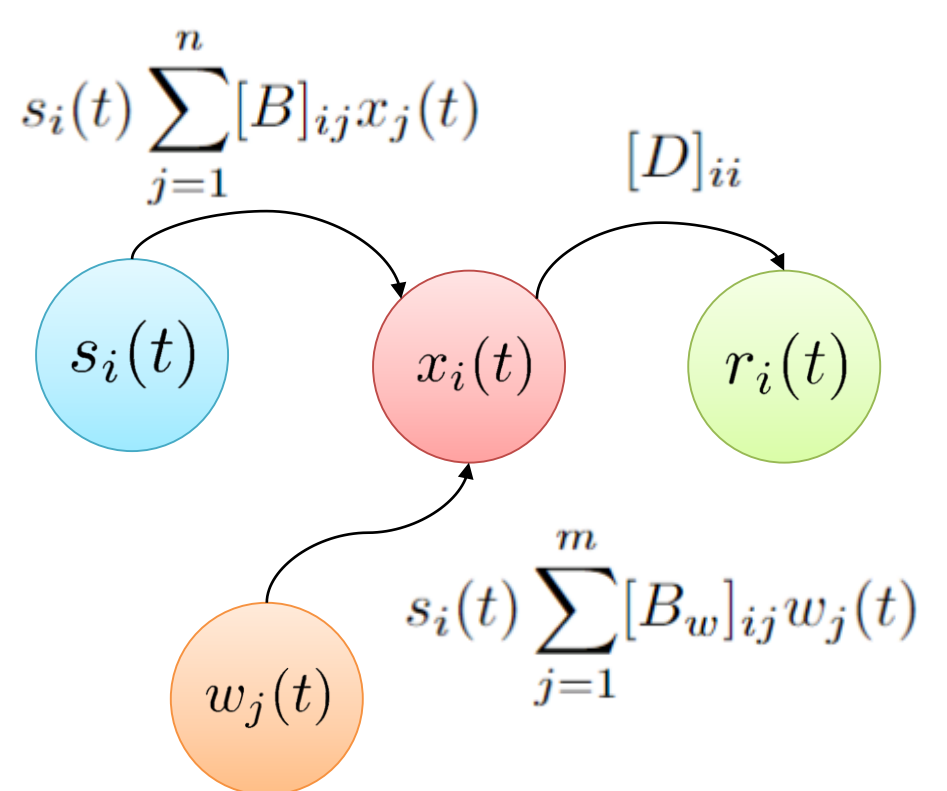
Objectives

- Propose a novel model that captures the spread of a virus in a computer network
- Provide conditions to predict the transient network-wide behavior based on the global reproduction number
- Define the DRNs and leverage their information to predict the behavior of the virus at the node level

Model

Multilayer Susceptible-Infected-Recovered (SIR) virus model with an Infrastructure Network proposed in [1]:

$$\begin{aligned} \dot{s}_i(t) &= -s_i(t) \left(\sum_{j=1}^n [B]_{ij} x_j(t) + \sum_{j=1}^m [B_w]_{ij} w_j(t) \right) \\ \dot{x}_i(t) &= s_i(t) \left(\sum_{j=1}^n [B]_{ij} x_j(t) + \sum_{j=1}^m [B_w]_{ij} w_j(t) \right) - [D]_{ii} x_i(t) \\ \dot{r}_i(t) &= [D]_{ii} x_i(t) \\ \dot{w}_j(t) &= -[D_w]_{jj} w_j(t) + \sum_{k=1}^m [A_w]_{kj} w_k(t) + \sum_{k=1}^n [C_w]_{kj} x_k(t) \end{aligned}$$



$$z(t) := \begin{bmatrix} x(t) \\ w(t) \end{bmatrix}, \quad H(s(t)) := \begin{bmatrix} \text{diag}(s(t)) & 0 \\ 0 & I_m \end{bmatrix}, \quad B_f := \begin{bmatrix} B & B_w \\ C_w & A_w \end{bmatrix}, \quad D_f := \begin{bmatrix} D & 0 \\ 0 & D_w \end{bmatrix}$$

Reproduction Numbers

- Global Effective Reproduction Number** $R(t) = \rho(H(s(t))D_f^{-1}B_f)$

- Users DRNs (pair-wise)**

$$R_{ij}(t) = s_i(t) \frac{I_i(j,t)}{[D]_{ii} x_i(t)}, \quad \text{where } I_i(j,t) = \begin{cases} [B]_{ij} x_j(t), & \text{if } j \in \mathcal{V}^U \\ [B_w]_{ij} w_j(t), & \text{if } j \in \mathcal{V}^S \end{cases}$$

- Servers DRNs (pair-wise)**

$$R_{jk}(t) = \frac{I_j^w(k,t)}{[D_w]_{jj} w_j(t)}, \quad \text{where } I_j^w(k,t) = \begin{cases} [C_w]_{kj} x_k(t), & \text{if } k \in \mathcal{V}^U \\ [A_w]_{kj} w_k(t), & \text{if } k \in \mathcal{V}^S \end{cases}$$

- Local Effective Reproduction Numbers (LERNs)**

$$R_i(t) = \sum_{j \in \mathcal{V}} R_{ij}(t)$$

Reproduction Numbers determine virus transient behavior:

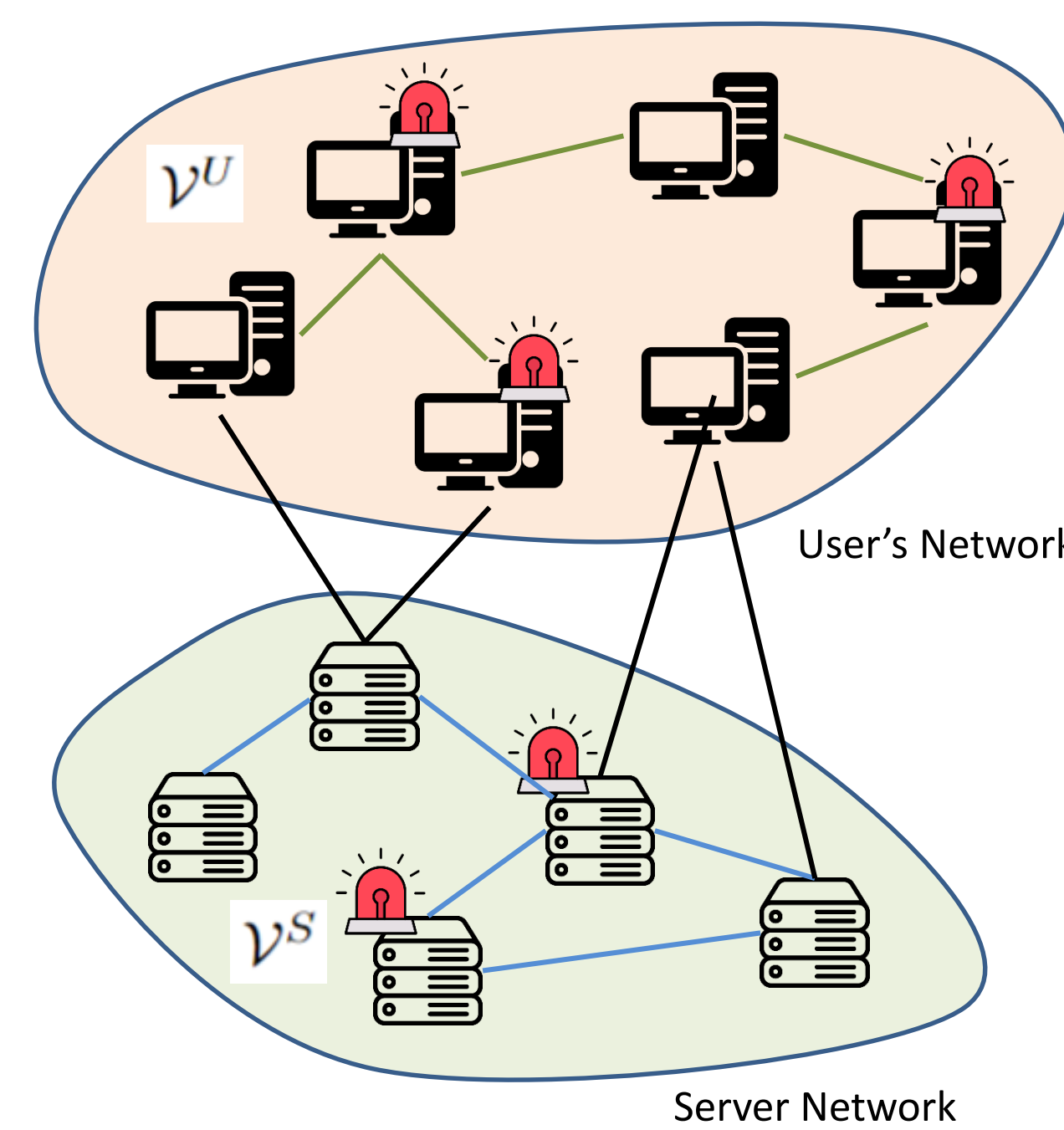
- Global Behavior: $R(t) > 1$ (growth), $R(t) \leq 1$ (decay)
- Local Behavior: $R_i(t) > 1$ (growth), $R_i(t) < 1$ (decay)

Networked Behavior from LERNs

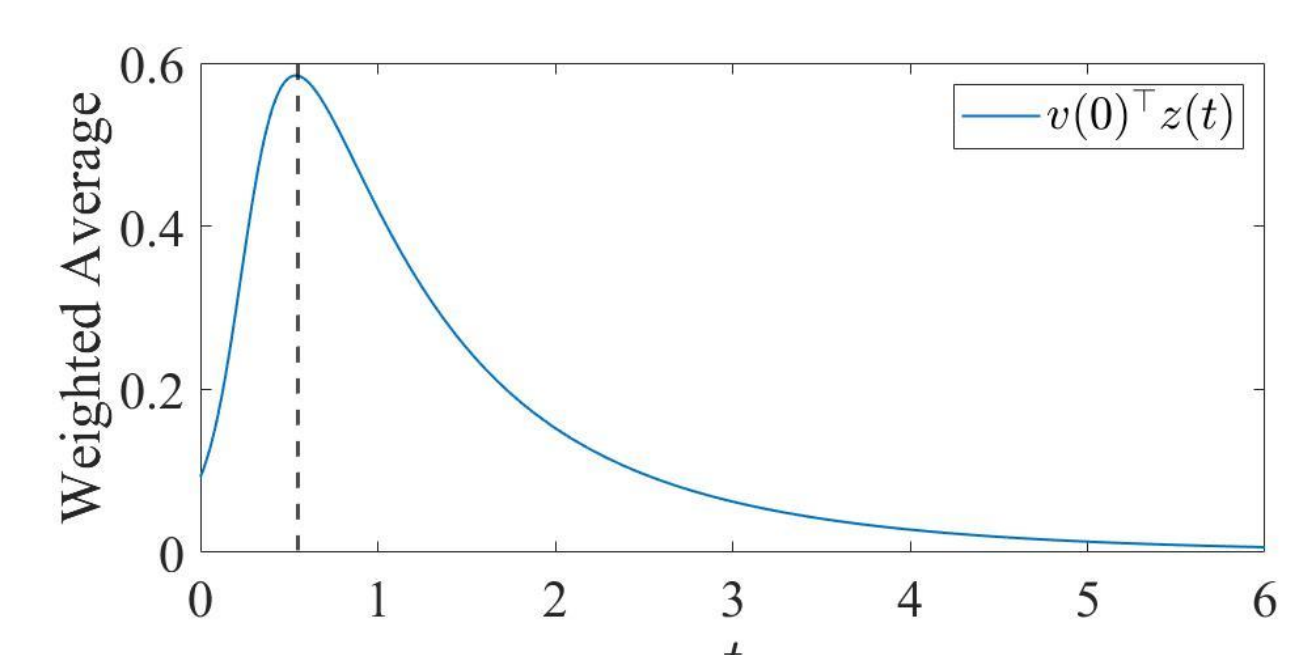
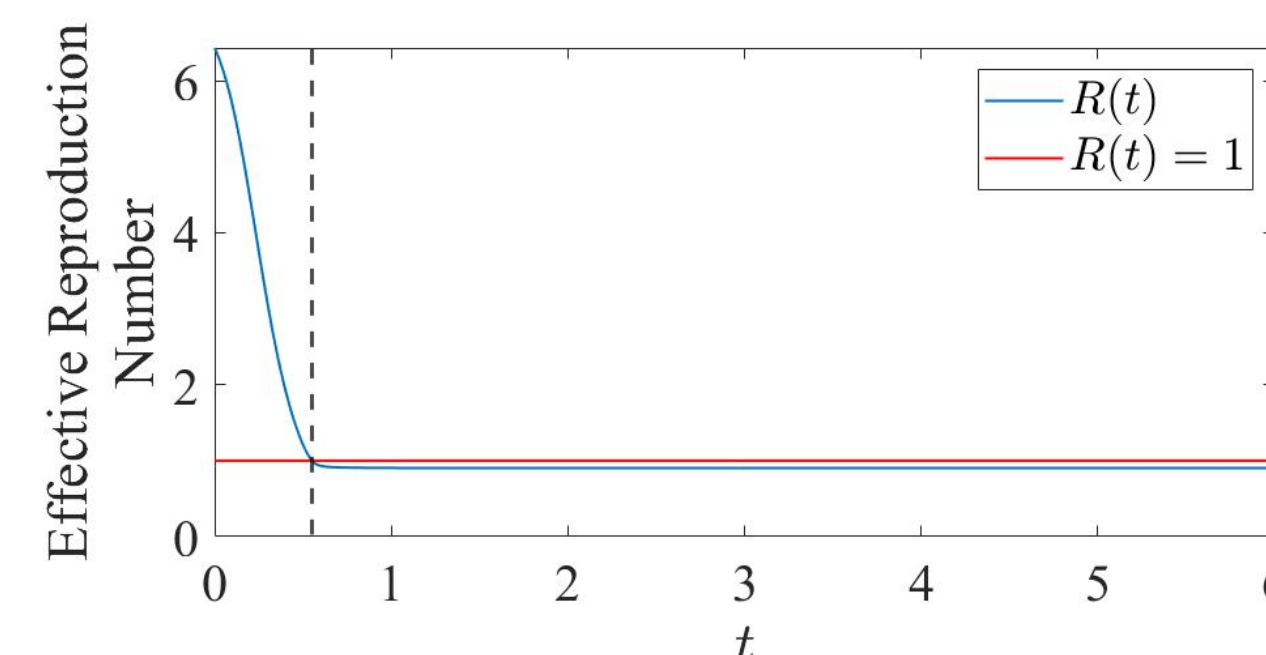
Assume the virus has not been eradicated from the system. The following claims hold:

- If $R_i(t) > 1$ for all users and servers, then $R(t) > 1$
- If $R_i(t) = 1$ for all users and servers, then $R(t) = 1$
- If $R_i(t) < 1$ for all users and servers, then $R(t) < 1$

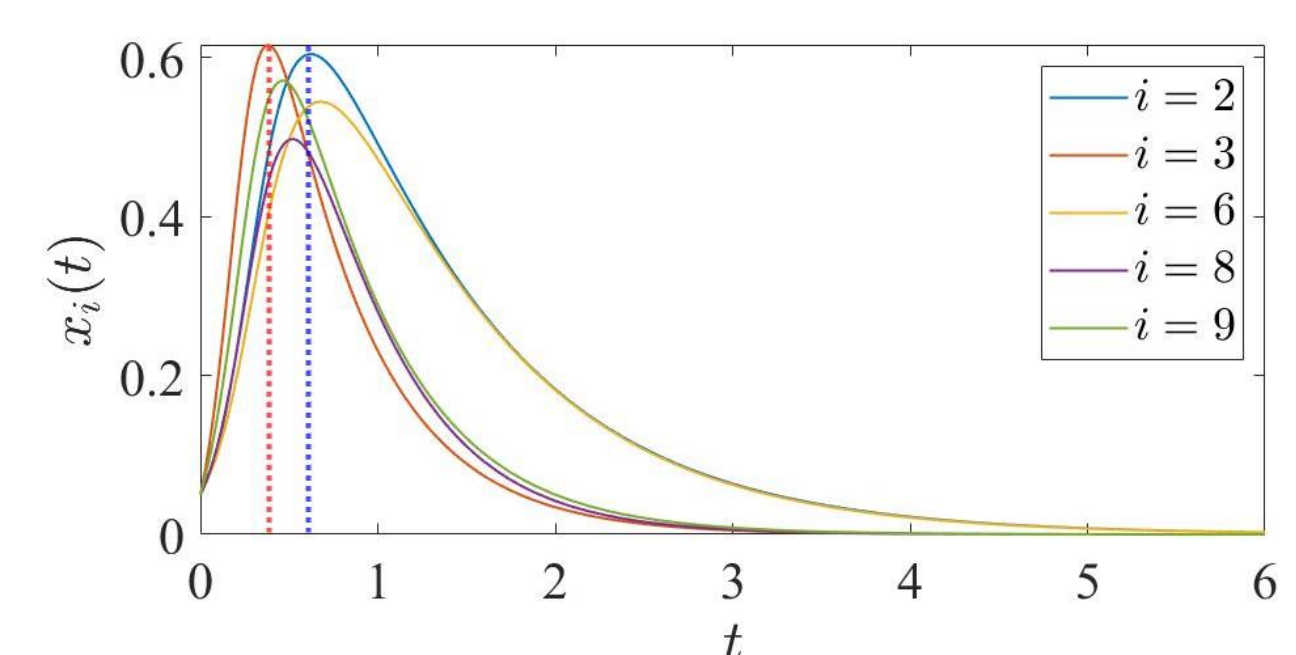
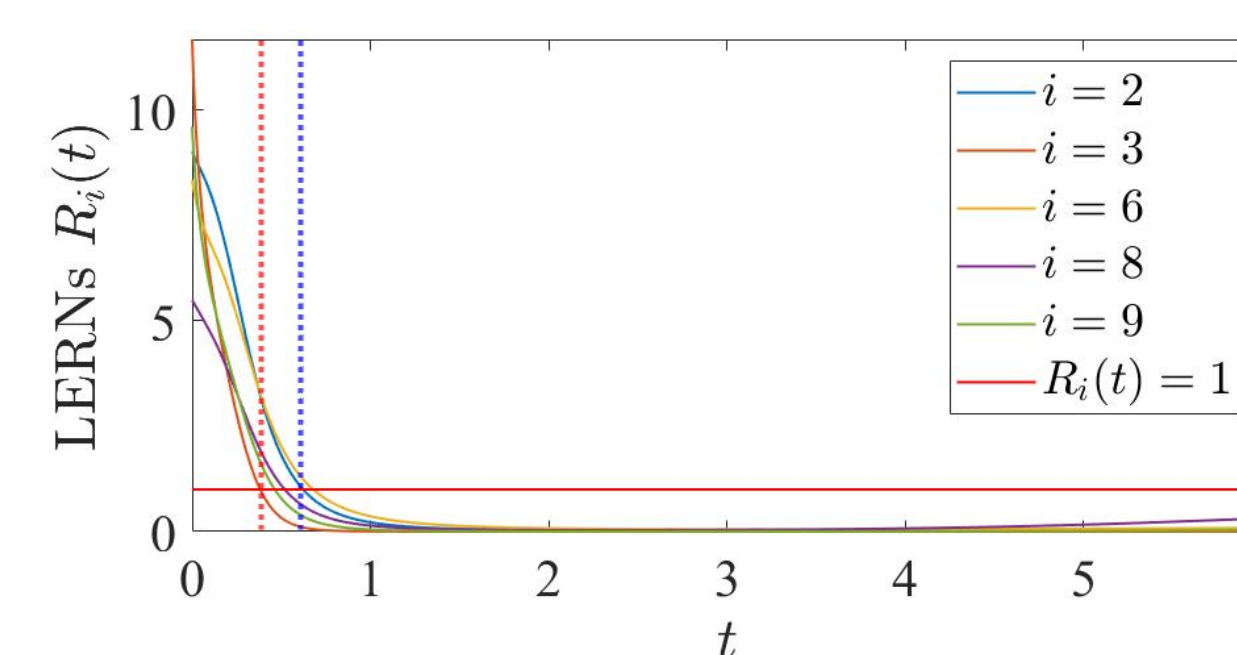
Simulation



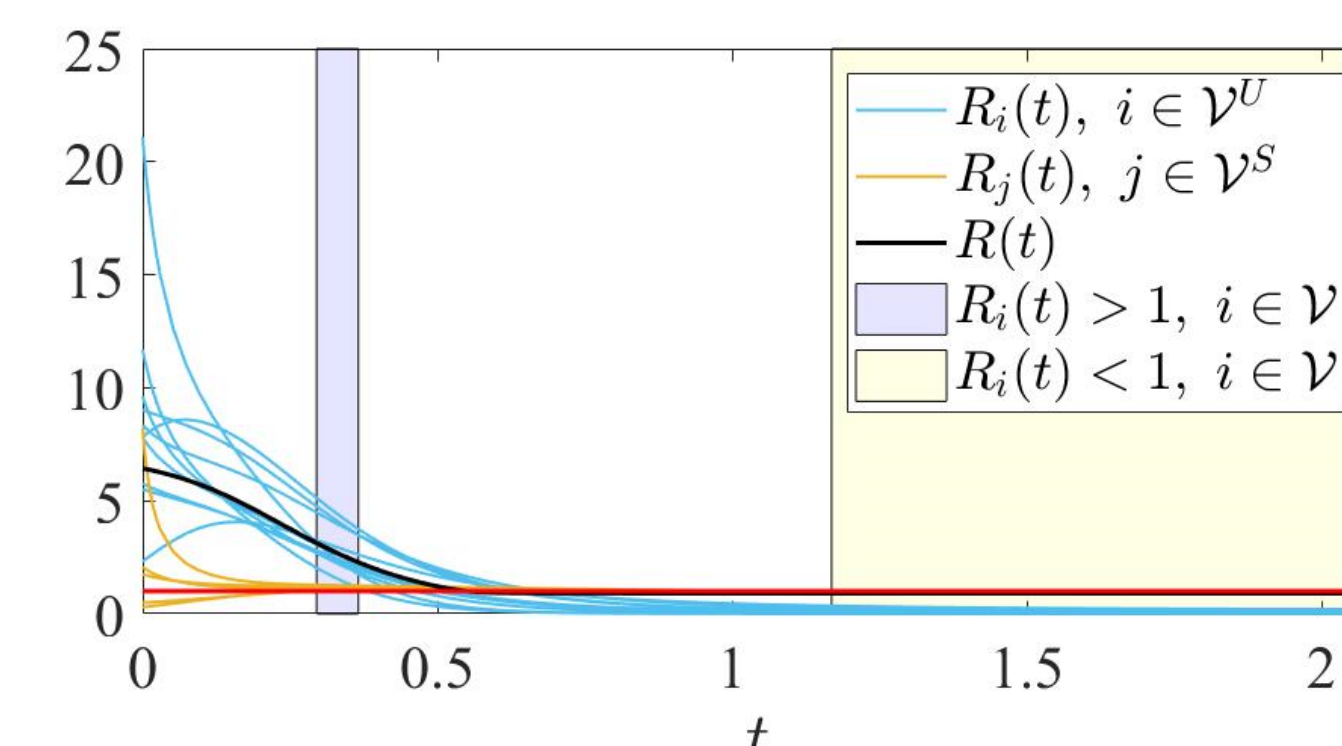
- Virus dies out in both the user and server network
- $R(t)$ is monotonic, $R_i(t)$ can be non-monotonic
- $R(t)$ crosses one much earlier than when all the LERNs are below one, i.e., **the infection is still increasing in more than half of the nodes**



Evolution of $R(t)$ (left) and the weighted average of the infected states



Evolution of LERNs (left) and the infected states of the user's network



$R_i(t) > 1$ for all users and servers (blue region)

$R_i(t) < 1$ for all users and servers (yellow region)