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

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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]:

\[
\begin{align*}
\dot{s}_i(t) &= -s_i(t) \left( \sum_{j=1}^{N} [B]_{ij} x_j(t) + \sum_{j=1}^{N} [B_w]_{ij} w_j(t) \right) \\
\dot{x}_i(t) &= s_i(t) \left( \sum_{j=1}^{N} [B]_{ij} x_j(t) + \sum_{j=1}^{N} [B_w]_{ij} w_j(t) \right) - [D_w]_{ii} x_i(t) \\
\dot{r}_i(t) &= [D_w]_{ii} x_i(t) \\
\dot{w}_j(t) &= -[D_w]_{ij} w_j(t) + \sum_{i=1}^{N} [A_w]_{ij} x_i(t) + \sum_{i=1}^{N} [C_w]_{ij} x_i(t)
\end{align*}
\]

SIR networked model coupled with a server network

Reproduction Numbers
- **Global Effective Reproduction Number** \( R(t) = \rho(H(s(t))D_f^{-1}B_f) \)
- **Users DRNs (pair-wise)**
  \[ R_{ij}(t) = s_i(t) \frac{I_j^U(k, t)}{[D]_{ij} x_j(t)} \]
  where \( I_j^U(k, t) = \begin{cases} [B]_{ij} x_j(t), & \text{if } j \in V^U \\ [B_w]_{ij} w_j(t), & \text{if } j \in V^S \end{cases} \)
- **Servers DRNs (pair-wise)**
  \[ R_{jk}(t) = \frac{I_j^S(k, t)}{[D]_{ij} x_j(t)} \]
  where \( I_j^S(k, t) = \begin{cases} [C_w]_{kj} x_k(t), & \text{if } k \in V^U \\ [A_w]_{kj} w_k(t), & \text{if } k \in V^S \end{cases} \)
- **Local Effective Reproduction Numbers (LERNs)**
  \[ R_i(t) = \sum_{j \in V} R_{ij}(t) \]

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

[1] José I. Caiza, Junjie Qin, Philip E. Paré, "Global and Distributed Reproduction Numbers of a Multilayer SIR Model with an Infrastructure Network", submitted to CDC 2024. This material is based upon work supported in part by the National Science Foundation, grants # ECCS 2032258, ECCS 2238388