On the Analysis and Observability of a Networked Competitive Multi-Virus SIR Model

Ciyuan Zhang*, Sebin Gracy†, Tamer Başar‡, Philip E. Paré†

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

*Department of Electrical and Computer Engineering, Rice University, Houston, TX, USA

†Coordinated Science Laboratory at the University of Illinois at Urbana-Champaign, IL, USA

**Ciyuan Zhang

The Center for Education and Research in Information Assurance and Security

On the Analysis and Observability of a Networked Competitive Multi-Virus SIR Model

Ciyuan Zhang*, Sebin Gracy†, Tamer Başar‡, Philip E. Paré†

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

*Department of Electrical and Computer Engineering, Rice University, Houston, TX, USA

†Coordinated Science Laboratory at the University of Illinois at Urbana-Champaign, IL, USA

Objectives

• Propose an epidemic model which captures the spread of multiple competitive computer viruses over a network
• Provide a sufficient condition which ensures that each computer virus dies out in exponential time
• Estimate the infection level of each computer virus with an observation model

System Model

Networked competitive multi-virus Susceptible-Infected-Recovered (SIR) epidemics model proposed in [1]:

\[ s_i[t+1] = s_i[t] - h s_i[t] \sum_{j=1}^{m} \beta_{ij} x_j[t] \]

\[ x_i[t+1] = x_i[t] + h \left( s_i[t] \sum_{j=1}^{m} \beta_{ij} x_j[t] - \gamma_i x_i[t] \right) \]

\[ r_i[t+1] = r_i[t] + h \sum_{j=1}^{m} \gamma_j x_j[t] \]

The competing SIR networked model

Assumption 1

For all \( i \in [n], \ k \in [m] \), we assume that \( s_i[0], x_i[0], r_i[0] \in [0,1]\), \( s_i[0] + \sum_{k=1}^{m} x_i^k[0] + r_i[0] = 1\), \( \beta_{ij} \geq 0\), \( \gamma_i > 0\), \( h \sum_{k=1}^{m} x_i^k \leq 1\), and \( h \sum_{k=1}^{m} \gamma_i^k \leq 1\).

• Let \( M^k = I - h \beta^k + h \beta^k \) where, \( S[t] = diag(s_i[t])\), \( B^k \) is a matrix with \( (i,j)-th \) entry \( \beta_{ij}^k \) and \( \Gamma^k[t] = diag(\gamma_i^k) \)

• We let \( \rho(M^k) \) denote the spectral radius of \( M^k \), which can be interpreted as the reproduction number of virus \( k \) over the network

Simulation

- Both computer viruses die out eventually
- The estimation error converges to zero before the viruses die out
- The magnitude of the estimation error of each virus in each company is less than 10% of its infected proportion

Virus I

Deleting files
Random shutdown
Storage shortage
Symptoms of two computer viruses

Virus II

The observation model is written as

\[ y_i[t] = \sum_{k=1}^{m} c_i^k x_i^k[t] \]

where \( c_i^k > 0\), for all \( i \in [n], \ k \in [m] \).

Theorem 1

Under Assumption 1, if \( \rho(M^k) < 1\), then the \( k \)-th virus dies out in exponential time, and this holds for all \( k \in [m] \).

State Observation Model

We use the following Luenberger observer:

\[ x_i^k[t+1] = x_i^k[t] + h \left( \gamma_i x_i^k[t] - y_i[t] \right) \]

\[ r_i^k[t+1] = r_i^k[t] + h \left( \gamma_i x_i^k[t] - y_i[t] \right) \]

where \( \gamma_i^k + \rho \sum_{k=1}^{m} \beta_{ij} x_j^k[t] \) in which the recovered level is estimated through

\[ r_i^k[t+1] = r_i^k[t] + h \sum_{j=1}^{m} \gamma_j x_j^k[t] \]

at each time step, recursively.

Estimation Algorithm

The estimation error

\[ \epsilon_i^k[t] = x_i^k[t] - x_i^k[t] \]

for all \( i \in [n], \ k \in [m] \).

Theorem 2

Under Assumption 1, if, for each \( i \in [n], \ y_i^k \) is a distinct value for all \( k \in [m] \), the competing virus model is locally observable at \( s_i[t] = 0\), for all \( i \in [n] \).

Evolution of proportion of computers infected by virus I in each company (left)
Evolution of proportion of computers infected by virus II in each company (right)

Estimation error of the infected proportion of computers by virus I in each company (left)

Estimation error of the infected proportion of computers by virus II in each company (right)