

Prediction of processes on networks

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Network Architectures and Services

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Outline



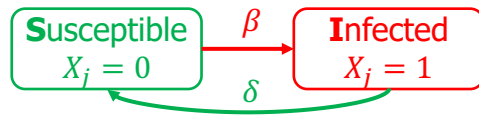
Prediction of epidemic on a fixed graph,
given past infection data

Prediction of future temporal graphs,
given its graph sequence in the past



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Markovian SIS epidemics in networks



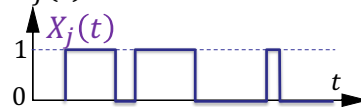
Markov state $X_j \in \{0,1\}$ of node j is a **Bernoulli random variable**

$$\Pr[X_j(t) = 1] = E[X_j(t)]$$

Each node j possesses a health state $X_j(t)$ at time t :

$X_j(t) = 0$: node j is **not** infected at time t

$X_j(t) = 1$: node j is infected at time t



Infection probability of node j at time t : $v_j(t) = \Pr[X_j(t) = 1]$

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Infection process: Poisson with infection strength $\beta_{jk} = \beta$ (per link)
 Curing process: Poisson with curing strength $\delta_j = \delta$ (per node)

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Governing Markovian SIS equation for node j

$$\frac{dE[X_j(t)]}{dt} = E \left[-\delta X_j(t) + (1 - X_j(t)) \left\{ \beta \sum_{k \in \text{neighbor}(j)} X_k(t) \right\} \right]$$

time-change of
 $E[X_j] = \Pr[X_j = 1]$
 probability that
 node j is infected

if *infected* ($X_j = 1$):
 probability of
 curing per
 unit time

if *not infected* ($X_j = 0$):
 probability of infection per
 unit time from
 infected neighbors

$$\frac{dE[X_j]}{dt} = -\delta E[X_j] + \beta \sum_{k=1}^N a_{kj} E[X_k] - \beta \sum_{k=1}^N a_{kj} E[X_j X_k]$$

Complication

$$E[X_j X_k] = \Pr[X_j = 1, X_k = 1]$$

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R. Pastor-Satorras, C. Castellano, P. Van Mieghem and A. Vespignani,
 "Epidemic processes in complex networks", Review of Modern Physics,
 Vol. 87, No. 3, pp. 925-979, 2015

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Mean-field approximation: replace random variable by its mean

NIMFA



$$\frac{dE[X_j]}{dt} = E \left[-\delta X_j + (1 - X_j)\beta \sum_{k=1}^N a_{kj} X_k \right]$$



$$X_j \Rightarrow E[X_j] = w_j$$

$$\frac{dw_j}{dt} = -\delta w_j + (1 - w_j)\beta \sum_{k=1}^N a_{kj} w_k$$

From 2^N linear Markov differential equations to
 N non-linear mean-field **approximating** diff. equations

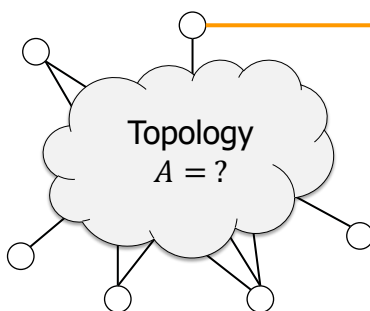
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P. Van Mieghem, "The N-Intertwined SIS epidemic network model",
Computing (Springer), Vol. 93, Issue 2, p. 147-169, 2011

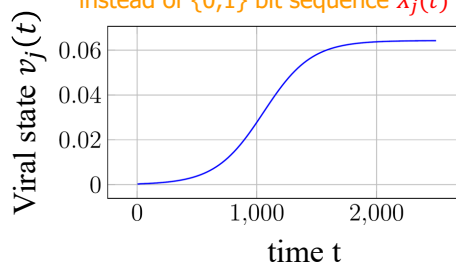


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Graph Reconstruction from epidemics



Viral state observation = infection probability $v_j(t) = \Pr[X_j(t) = 1]$ over time, instead of $\{0,1\}$ bit sequence $X_j(t)$



Aim: Determine the $N \times N$ adjacency matrix A of the contact graph from a given the time series of infection probabilities of all N nodes *and* the governing equations of epidemic spread on a graph (i.e. NIMFA)

Solution: *only partially possible*

Prasse, B. and P. Van Mieghem, 2018, "Exact Network Reconstruction from Complete SIS Nodal State Infection Information Seems Infeasible", IEEE Transactions on Network Science and Engineering, Vol. 6, No. 4, October-December, pp. 748-759.



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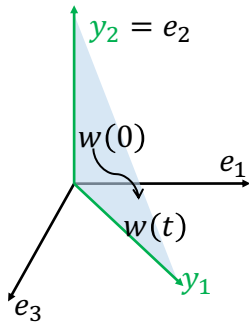
Agitation modes

Proper orthogonal decomposition (POD) of the viral state vector

$$w(t) \approx \sum_{i=1}^m c_i(t) y_i$$

y_1, \dots, y_m : orthonormal agitation modes

$$c_i(t) = y_i^T w(t): \text{scalar, projection of } w(t) \text{ on } y_i$$



If the POD is accurate with $m < N$, we do not need N differential equations:

$$N \text{ differential equations } \frac{dw_i(t)}{dt} = f_{\text{SIS},i}(w(t)), \quad i = 1, \dots, N$$

↓ Projection on agitation modes y_l

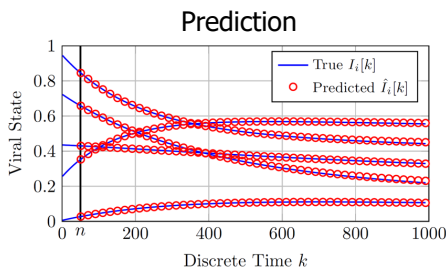
$$m < N \text{ differential equations } \frac{dc_l(t)}{dt} \approx y_l^T f_{\text{SIS}}(\sum_{i=1}^m c_i(t) y_i), \quad l = 1, \dots, m$$

Prasse, B. and P. Van Mieghem, 2022, "Predicting network dynamics without requiring the knowledge of the interaction graph", Proceedings of the National Academy of Sciences (PNAS), Vol. 119, No. 44, e2205517119

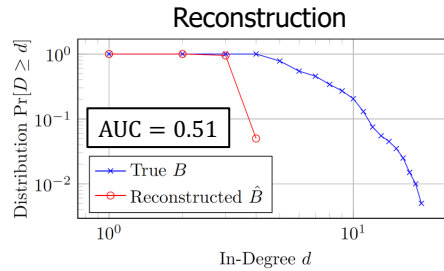


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Accurate prediction of epidemic outbreaks *without* accurate network reconstruction



Process: only a few agitation modes



Graph: nearly all N eigenmodes

Basis of the **Network Inference Prediction Algorithm (NIPA)**

Real-time data loading from RIVM (Dutch ministry of health):

<https://www.nas.ewi.tudelft.nl/nipa/covid-prediction>

B. Prasse and P. Van Mieghem, 2020, "Network Reconstruction and Prediction of Epidemic Outbreaks for General Group-Based Compartmental Epidemic Models", IEEE Transactions on Network Science and Engineering, Vol. 7, No. 4, October-December, pp. 2755-2764



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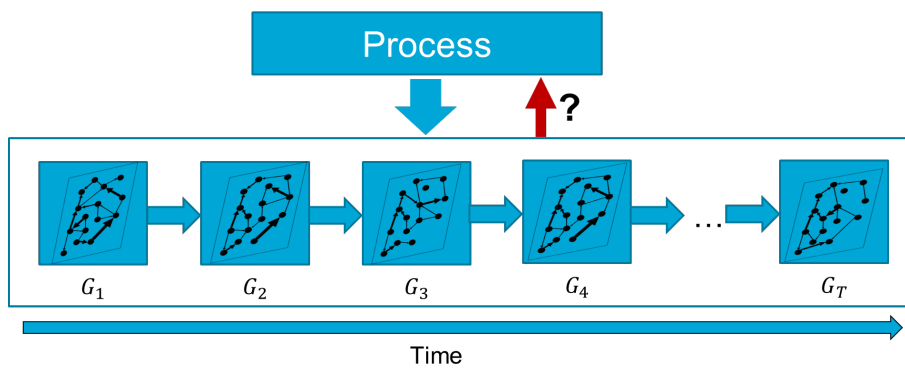
Outline



Prediction of epidemic on a graph,
given past infection data

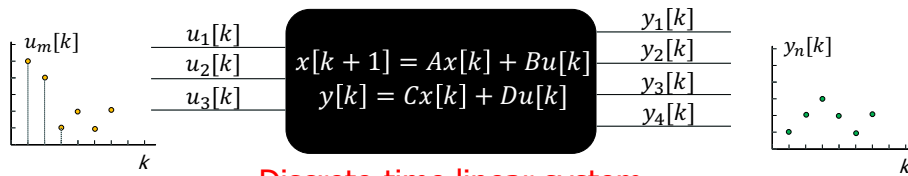
Prediction of future temporal graphs,
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Problem Statement



What can we infer about the process? How can we model the observed dynamics of the network?

Data is generated by a process



Discrete-time linear system

Given: input vectors $\{u[1], u[2], \dots, u[K]\}$ and matrices A, B, C, D
 → output vectors $\{y[1], y[2], \dots, y[K]\}$ can be computed

Inverse process

Given: $\{u[1], u[2], \dots, u[K]\}$ and $\{y[1], y[2], \dots, y[K]\}$
 Find : matrices A, B, C, D

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De Moor, B., J. Vandewalle, M. Moonen, L. Vandenberghe and P. Van Miegheem, "A Geometrical Strategy for the Identification of State Space Models of Linear Multivariable Systems with Singular Value Decomposition", Proceedings of the 8th IFAC/IFORS Symposium on Identification and System Parameter Estimation, Beijing Aug. 27-31, 1988, pp. 493-497.



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Linear Time-invariant State Space model

$$\begin{aligned} x[k+1] &= Ax[k] + Bu[k] \\ y[k] &= Cx[k] + Du[k] \end{aligned}$$

Matrix Form

$$\begin{bmatrix} x[k+1] \\ y[k] \end{bmatrix} = \begin{bmatrix} A & B \\ C & D \end{bmatrix} \begin{bmatrix} x[k] \\ u[k] \end{bmatrix}$$

Blocksystem matrix

$$Q = \begin{bmatrix} A & B \\ C & D \end{bmatrix}$$

$$\begin{bmatrix} x[k+1] \\ y[k] \end{bmatrix} = Q \begin{bmatrix} x[k] \\ u[k] \end{bmatrix}$$

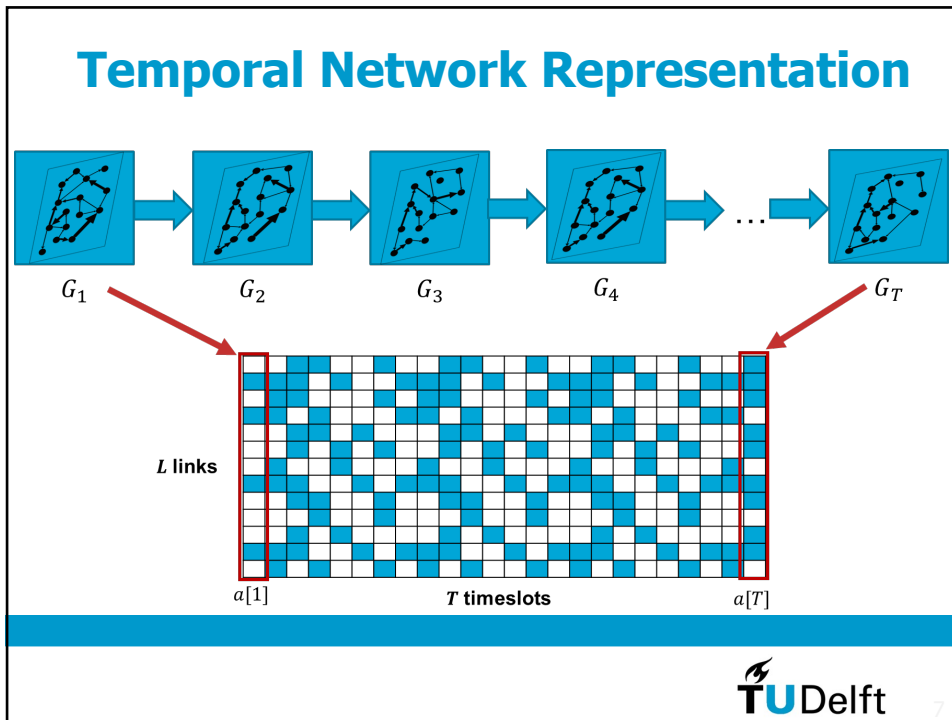
$u[k]$: $m \times 1$ input vector at (discrete) time k
 $y[k]$: $l \times 1$ output vector at (discrete) time k
 $x[k]$: $n \times 1$ state vector at (discrete) time k

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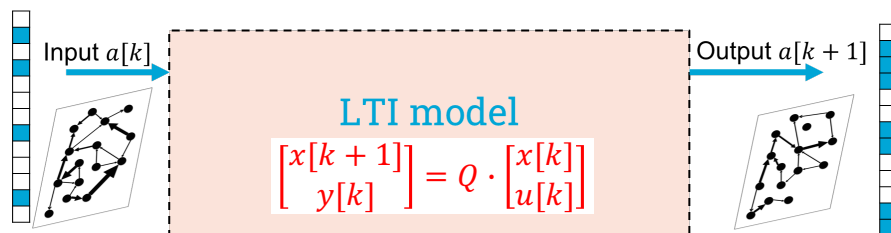
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Temporal Network Representation



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Linear Time-invariant State Space model applied to Temporal Graphs



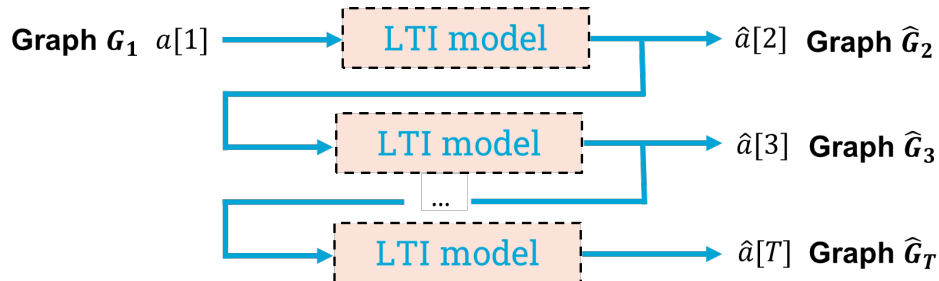
Input: Graph G_k , $L \times 1$ binary vector.

Output: Graph G_{k+1} , $L \times 1$ binary vector.

How to generate more than 1 graph?

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Subspace Graph Generator (SG-Gen)



$$\begin{bmatrix} x[k+1] \\ y[k] \end{bmatrix} = Q \cdot \begin{bmatrix} x[k] \\ u[k] \end{bmatrix} \quad u[k] = y[k-1] = \hat{a}[k] \quad \text{and} \quad u[1] = a[1]$$

k -th output:
$$\begin{bmatrix} x[k+1] \\ \hat{a}[k+1] \end{bmatrix} = Q^k \begin{bmatrix} x[1] \\ a[1] \end{bmatrix}$$

All eigenvalues of Q must lie on the unit circle

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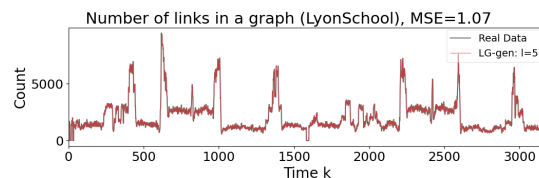
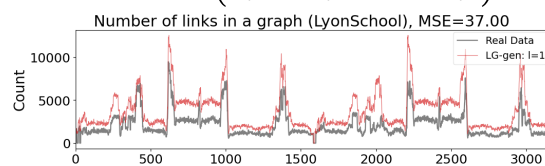
LG-gen: Real Data

Datasets: Hospital data, LyonSchool, InVS13 (sociopatterns.org)

- Dynamics of real networks can be accurately approximated by a small number of periodic graph sequences;
- Exponential decrease in the MSE if $G_k \approx \text{round}(G_k^{(1)} + G_k^{(2)} + \dots + G_k^{(l)})$;

Example:

- For $l = 5$, the MSE is 1.07 (≈ 1 incorrect contact per timestamp).
- For $l = 11$, the LG-gen generates the LyonSchool network exactly.



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Summary prediction

- Prediction of "local-rule, global emergent" dynamics:
 - Possible without knowing the (assumed fixed) interaction graph!
 - Explanation of success of "deep learning methods"
 - Autonomous dynamic in high dimensions only evolves in a small subspace
- Emulation (or reproduction) of a sequence of temporal graphs is possible with high accuracy
 - Prediction is depressingly bad
 - Is it possible to predict, given only one realization (i.e. one sequence of temporal graph)?

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Thank You

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