

Markovian Epidemics on Networks without Re-infections

Piet Van Mieghem

in collaboration with
Massimo Achterberg

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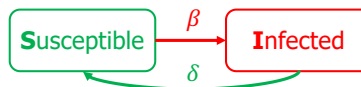
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Epidemic compartments

Single disease realization



Diseases with re-infections



Essence: item can be only in 1 compartment at time t



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Local Rule – Global Emergent behavior

While infected until recovered
 then do infect healthy neighbors

Process: Virus spread

Structure: Contact graph

LRGE dynamics:

$$\frac{dx_i(t)}{dt} = f_i(x_i(t)) + \sum_{j=1}^N a_{ij} g(x_i(t), x_j(t))$$

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Outline

Markovian epidemics on networks

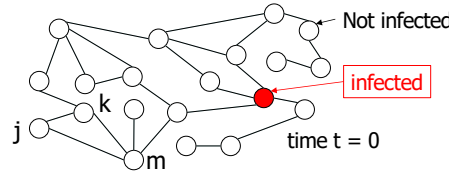
SIR

Non-Markovian epidemic on networks

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SIS Virus spread in networks

Given:



Not infected

time $t = 0$

Infection process: Poisson with infection strength β_{jk}
 Curing process: Poisson with curing strength δ_j

Compute: Probability that node j is infected at time $t > 0$

Assumptions:

1. SIS model: only 2 compartments: S & I
2. graph is static (not time-varying) and known
3. all processes are independent Poisson processes
4. infection and curing have constant strength (not time-varying, no mutations)

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Markovian SIS epidemics in networks

Susceptible
 $X_j = 0$

β

δ

Infected
 $X_j = 1$

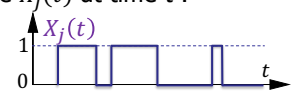
Markov state $X_j \in \{0,1\}$ of node j is a **Bernoulli random variable**

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

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 : $v_j(t) = \Pr[X_j(t) = 1]$

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

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

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



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

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

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

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

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



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Continuous-time Markov process

Chapman-Kolmogorov governing equation of a continuous-time Markov process with m states is a **linear** differential equation:

$$\frac{ds(t)}{dt} = -Qs(t)$$

with solution $s(t) = e^{-Qt} s(0)$
 where

$s(t)$: $m \times 1$ vector with $s_i(t) = \Pr[X(t) = i]$

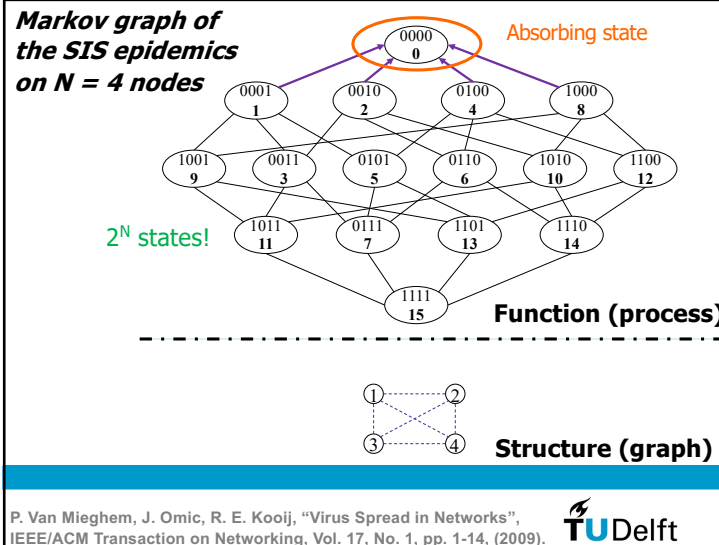
Q : $m \times m$ weighted, directed Laplacian of the Markov graph
 = - infinitesimal generator

Epidemics with c compartments in a graph with N nodes: $m = c^N$

All transition times (infection, curing, etc.) are *exponential* random variables

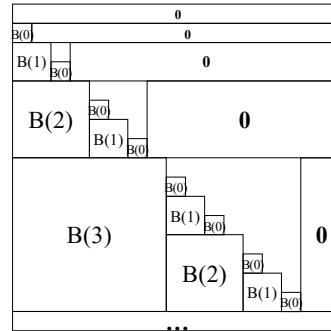
Sahneh, F. D., C. Scoglio and P. Van Mieghem, 2013, "Generalized Epidemic Mean-Field Model for Spreading Processes over Multi-Layer Complex Networks", IEEE/ACM Transactions on Networking, Vol. 21, No. 5, pp. 1609-1620.

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SIS infinitesimal generator: lower triangular part



Only function
of curing rate δ

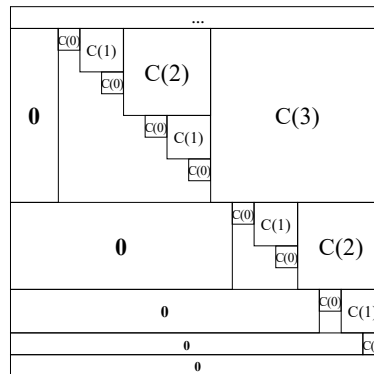
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P. Van Mieghem, J. Omic, R. E. Kooij, "Virus Spread in Networks",
IEEE/ACM Transaction on Networking, Vol. 17, No. 1, pp. 1-14, (2009).



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SIS infinitesimal generator: upper triangular part



Contains network links
and infection rates β_{ij}

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Van Mieghem, P. and E. Cator, 2012, "Epidemics in networks with nodal
self-infection and the epidemic threshold", Physical Review E, vol. 86,
No. 1, July, p. 016116.



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Idea

When is the infinitesimal generator $-Q$ a triangular matrix?

If Q is a triangular matrix:

- Diagonal elements of Q are eigenvalues
- Dynamics can be analytically solved

Solution due to Massimo Achterberg:

the infinitesimal generator Q is a triangular matrix

if the compartment graph does not contain loops

Thus, for epidemics without re-infections (SI, SIR,...)

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Markovian epidemics on networks

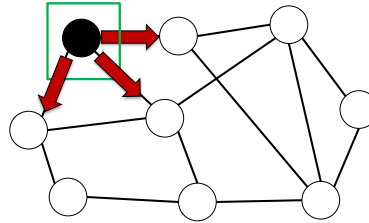
SIR

Non-Markovian epidemic on networks



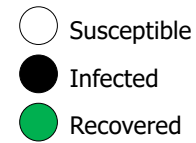
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SIR epidemics on a network



Two types of events

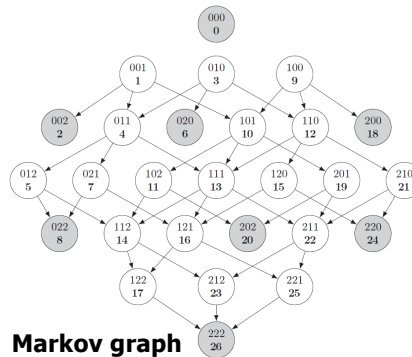
- Infection process
- Curing process



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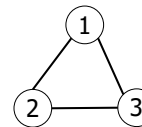
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SIR epidemics – Markov graph



Each node is either:

- Susceptible = 0
- Infected = 1
- Recovered = 2



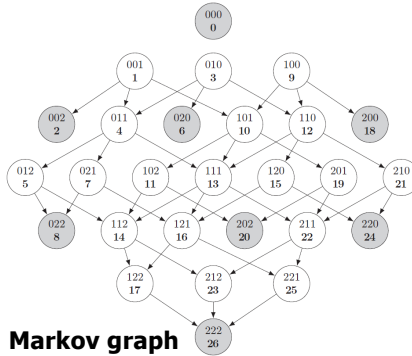
Markov graph

Contact graph

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SIR epidemics – Markov graph



Markov graph

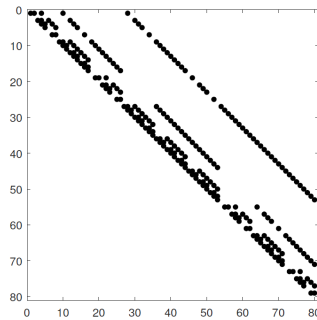
Procedure:

- Trinary numbering of states
- Number of states 3^N
- If infection times are exponential, then the process is Markovian
- Exact, analytic solution possible!

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SIR infinitesimal generator Q



$$s = \begin{pmatrix} (000) \\ (001) \\ (002) \\ (010) \\ \dots \\ (222) \end{pmatrix}$$

$$\frac{ds}{dt} = -Qs$$

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If configuration $i = (0,1,2)$, then $z_{2,0}(i) = z_{2,2}(i) = 0$ and $z_{2,1}(i) = 1$

$$z_{k,c}(i) = \mathbf{1}_{\{\text{node } k \in C_c \text{ in config } i\}}$$

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State space Markovian SIR

N	3^N
1	3
2	9
3	27
4	81
5	243
6	729
7	2187
8	6561
9	19683
10	59049

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Linear differential equations $\frac{ds}{dt} = -Qs$

Solution (if all infection rates β_{ij} are different):

$$s(t) = \sum_{i=0}^{3^N-1} c_i e^{-\lambda_i t} v_i$$

λ_i eigenvalues of Q
 v_i right-eigenvectors of Q

Prevalence (average fraction of infected nodes)

$$y(t) = \sum_{i=0}^{3^N-1} \tilde{c}_i e^{-\lambda_i t}$$

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Eigenvalue λ_i of configuration i

\circ Susceptible
 \bullet Infected
 \bullet Recovered

$\lambda_i = \text{sum over the cut-set between } S \text{ and } I \text{ nodes} + \text{sum over curing rates of infected nodes in config. } i$

$$\lambda_i = \sum_{k=1}^N \sum_{l=1}^N \beta_{kl} z_{k,1}(i) z_{l,0}(i) + \sum_{k=1}^N \delta_k z_{k,2}(i)$$

$$z_{k,c}(i) = 1_{\{\text{node } k \in C_c \text{ in config } i\}}$$

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Epidemic peak

- The epidemic peak time important for decision makers
- The epidemic peak can be determined up to arbitrary precision!

prevalence y
 time t

— Exact solution
 * Monte Carlo simulations
 - - Mean-field approximation

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Epidemic peak

The epidemic peak t_p satisfies $y'(t_p) = 0$:

- Newton-Raphson $t_{k+1} = t_k - \frac{y'(t_k)}{y''(t_k)}$

- 2nd-order Newton-Raphson

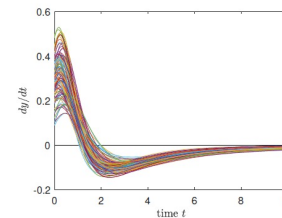
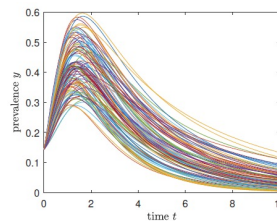
$$t_{k+1} = t_k - \frac{y''(t_k) \mp \sqrt{(y''(t_k))^2 - 2y'(t_k)y'''(t_k)}}{y'''(t_k)}$$

- If NR converges, then $t_p = \lim_{K \rightarrow \infty} t_k$

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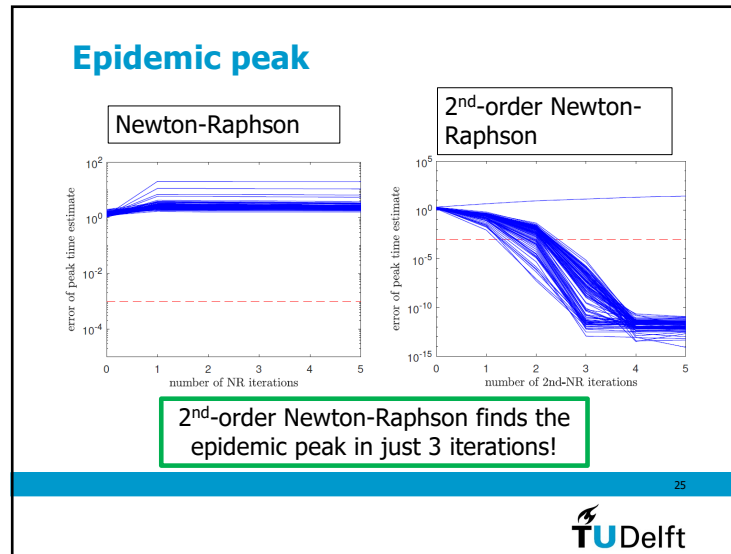
Epidemic Peak



- Graph with 7 nodes:
 - Infection rates uniformly $\in [0.05, 0.85]$
 - Curing rates uniformly $\in [0.1, 0.9]$
- Initially 1 infected node, the others susceptible
- 100 realizations

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Fractional Calculus for non-Markovian epidemics?

Chapman-Kolmogorov governing equation of a continuous-time Markov process with N states:

$$\frac{ds(t)}{dt} = -Qs(t)$$

with solution $s(t) = e^{-Qt} s(0)$

$s(t)$: $N \times 1$ vector with $Pr[X(t) = i]$
 Q : $N \times N$ weighted Laplacian Markov graph
 = - infinitesimal generator

$0 < \alpha \leq 1$ ↓ Replace $D = \frac{d}{dt}$ by Caputo fractional derivative D^α

$$D^\alpha s(t) = -Q^\alpha s(t)$$

with solution $s(t) = E_{\alpha,1}(-(Qt)^\alpha) s(0)$

$E_{a,b}(z) = \sum_{k=0}^{\infty} \frac{z^k}{\Gamma(a k + b)}$: Mittag-Leffler function
 $E_{1,1}(z) = e^z$

Open problem: physical explanation of α -fractional non-Markovian process

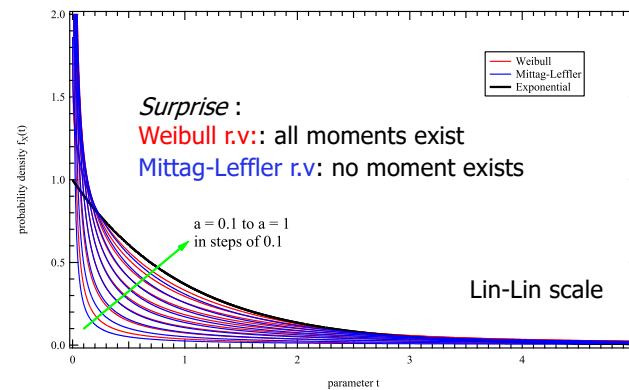
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Van Mieghem, P., "Origin of the fractional derivative and fractional non-Markovian continuous-time processes", Physical Review Research, Vol 4, No. 2, June 2022, p. 023242.



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Weibull and Mittag-Leffler pdf

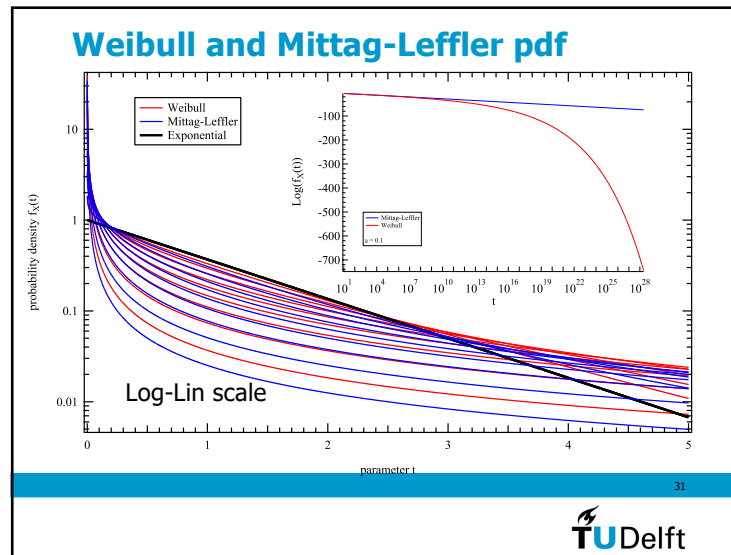


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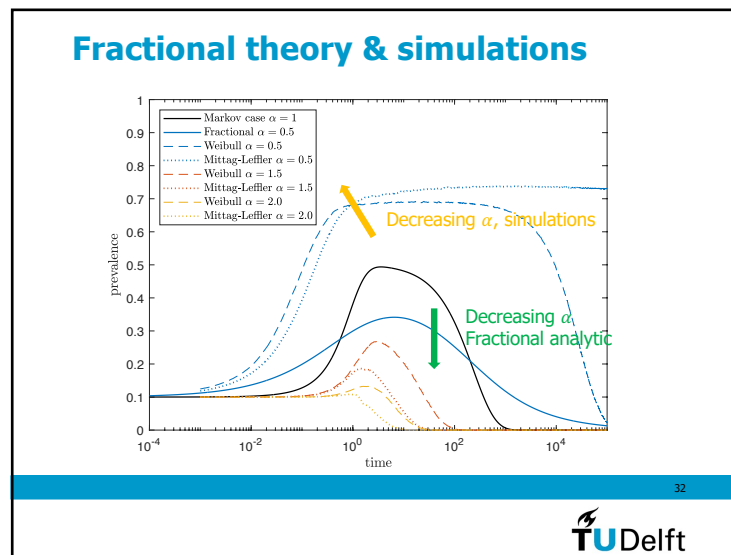
Van Mieghem, P., 2020, "The Mittag-Leffler function", Delft University of Technology, report20200528 (<http://arxiv.org/abs/2005.13330>).



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Conclusions

- Markovian epidemics without re-infections (as SIR, SI) are analytically computable
- Non-Markovian fractional epidemics are still a mystery

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