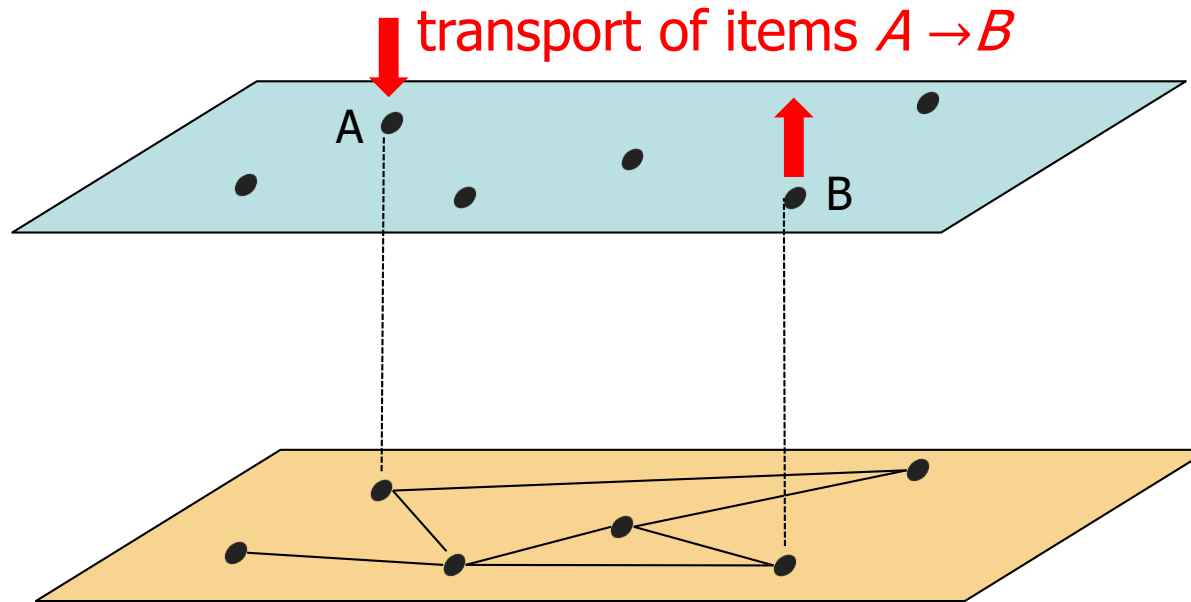# Epidemics on Networks

Piet Van Mieghem

in collaboration with
Eric Cator, Caterina Scoglio, Ruud van de Bovenkamp, Cong Li, Stojan Trajanovski, Dongchao Guo, Zhidong He, Qiang Liu, Annalisa Socievole, Bastian Prasse, Massimo Achterberg, Mattia Sensi and Huijuan Wang

University of Virginia, Charlottesville, 27 June 2022

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Network = Process + Graph

transport of items $A \rightarrow B$

Process (Function)

Software, service

Graph (Structure)

Hardware, Topologie
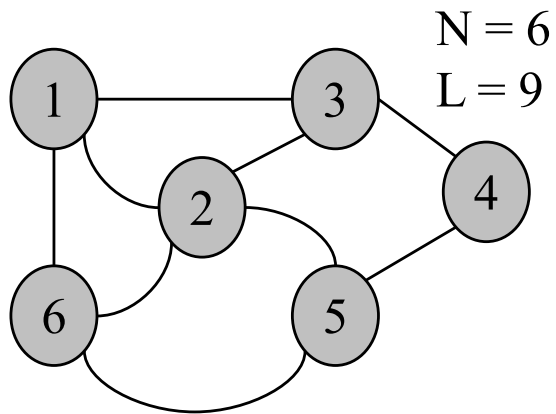Relationship between items
and/or processes

Network Science: Theory of processes on/in graphs

Duality between **process** and **graph** is cornerstone

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Three equivalent representations of an undirected graph

Topology domain

N = 6
L = 9

$$A_{N \times N} = \begin{bmatrix} 0 & 1 & 1 & 0 & 0 & 1 \\ 1 & 0 & 1 & 0 & 1 & 1 \\ 1 & 1 & 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 & 1 & 0 \\ 0 & 1 & 0 & 1 & 0 & 1 \\ 1 & 1 & 0 & 0 & 1 & 0 \end{bmatrix}$$
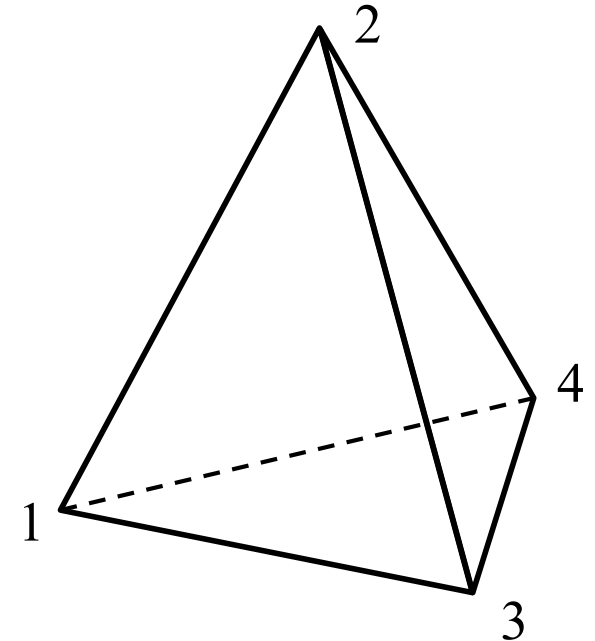
Spectral domain

$$A = A^T = X \Lambda X^T$$

$X_{N \times N}$: orthogonal eigenvector matrix

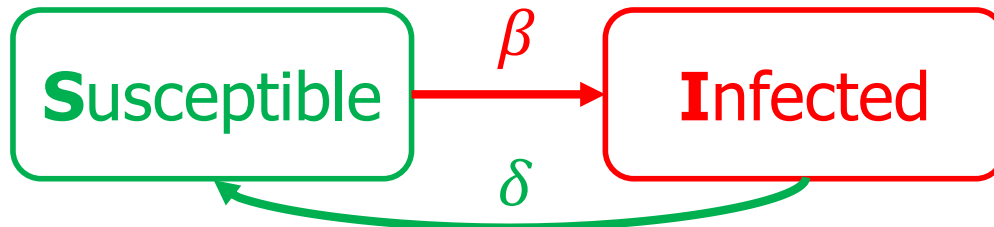$\Lambda_{N \times N}$: diagonal eigenvalue matrix

Geometric domain

Each undirected graph with N nodes
= a simplex in Euclidean
(N-1)-dimensional space

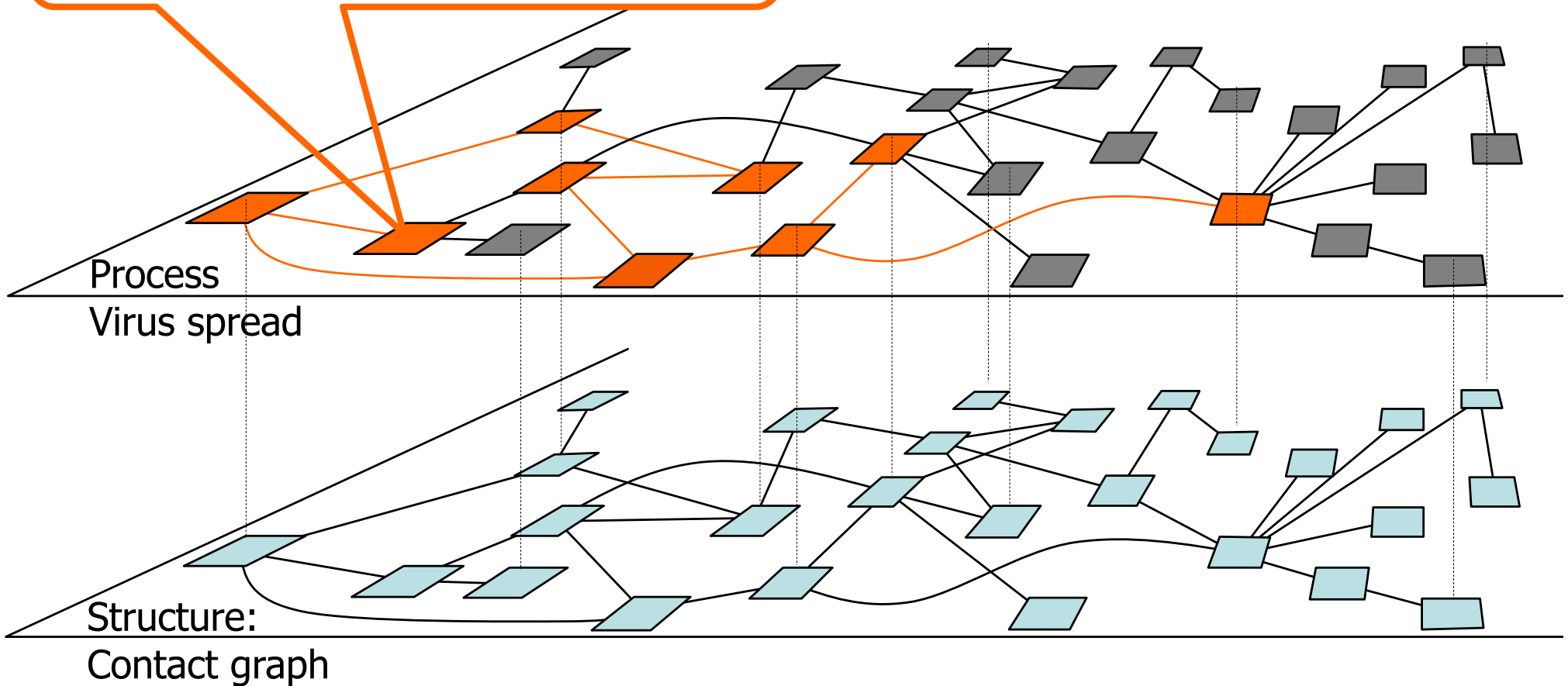**TU**Delft

Epidemic compartments

Single disease realization

$$\text{Susceptible} \xrightarrow{\beta} \text{Infected} \xrightarrow{\delta} \text{Removed}$$

Diseases with re-infections

$$\text{Susceptible} \xrightarrow{\beta} \text{Infected}$$
$$\text{Infected} \xrightarrow{\delta} \text{Susceptible}$$
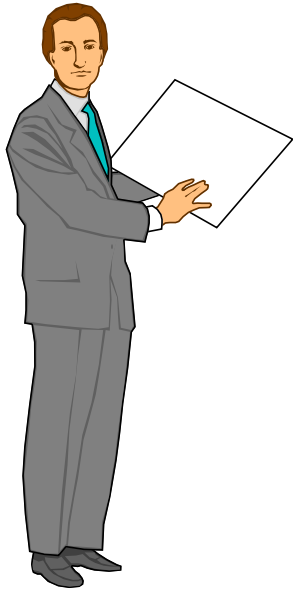
Essence: item can be only in 1 compartment at time t

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Local Rule – Global emergent behavior

While infected until recovered then do infect healthy neighbor

Process
Virus spread

Structure:
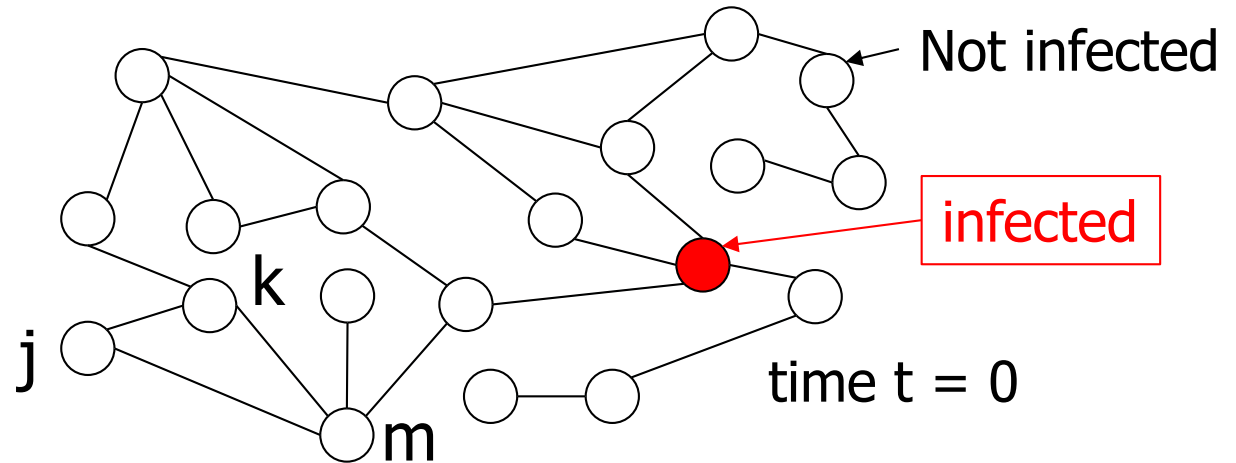Contact graph

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Outline

Theory of epidemics on networks

Recent developments

➢ Non-Markovian epidemics
➢ Inferring the graph

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SIS Virus spread in networks

Given:

Not infected
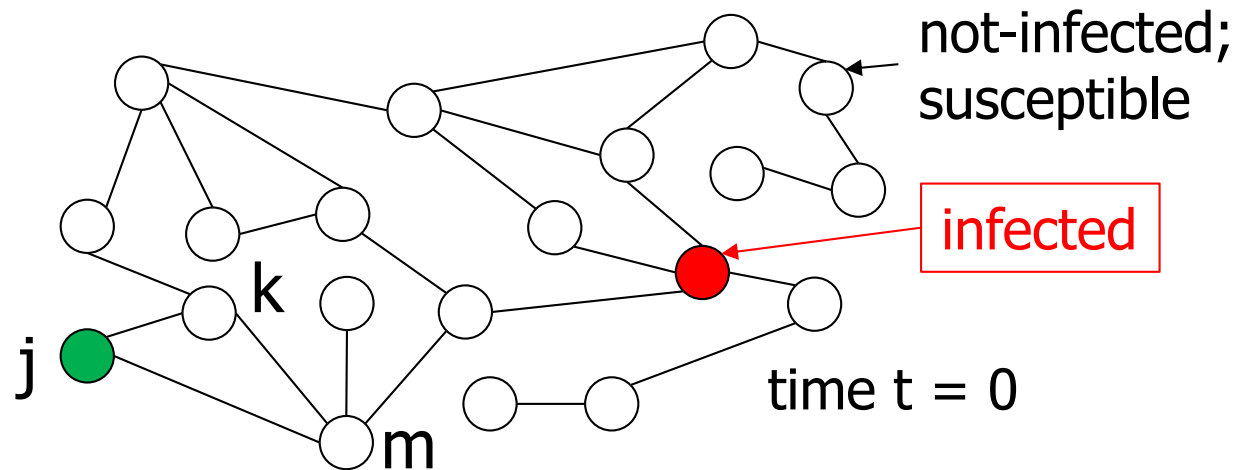
infected

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 processen are independent Poisson processes
4. infection and curing have constant strength
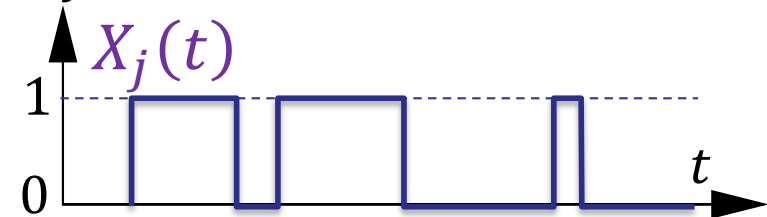(not time-varying, no mutations)

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SIS Virus spread in networks

not-infected; susceptible

infected

time t = 0

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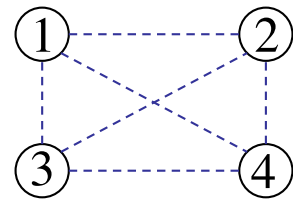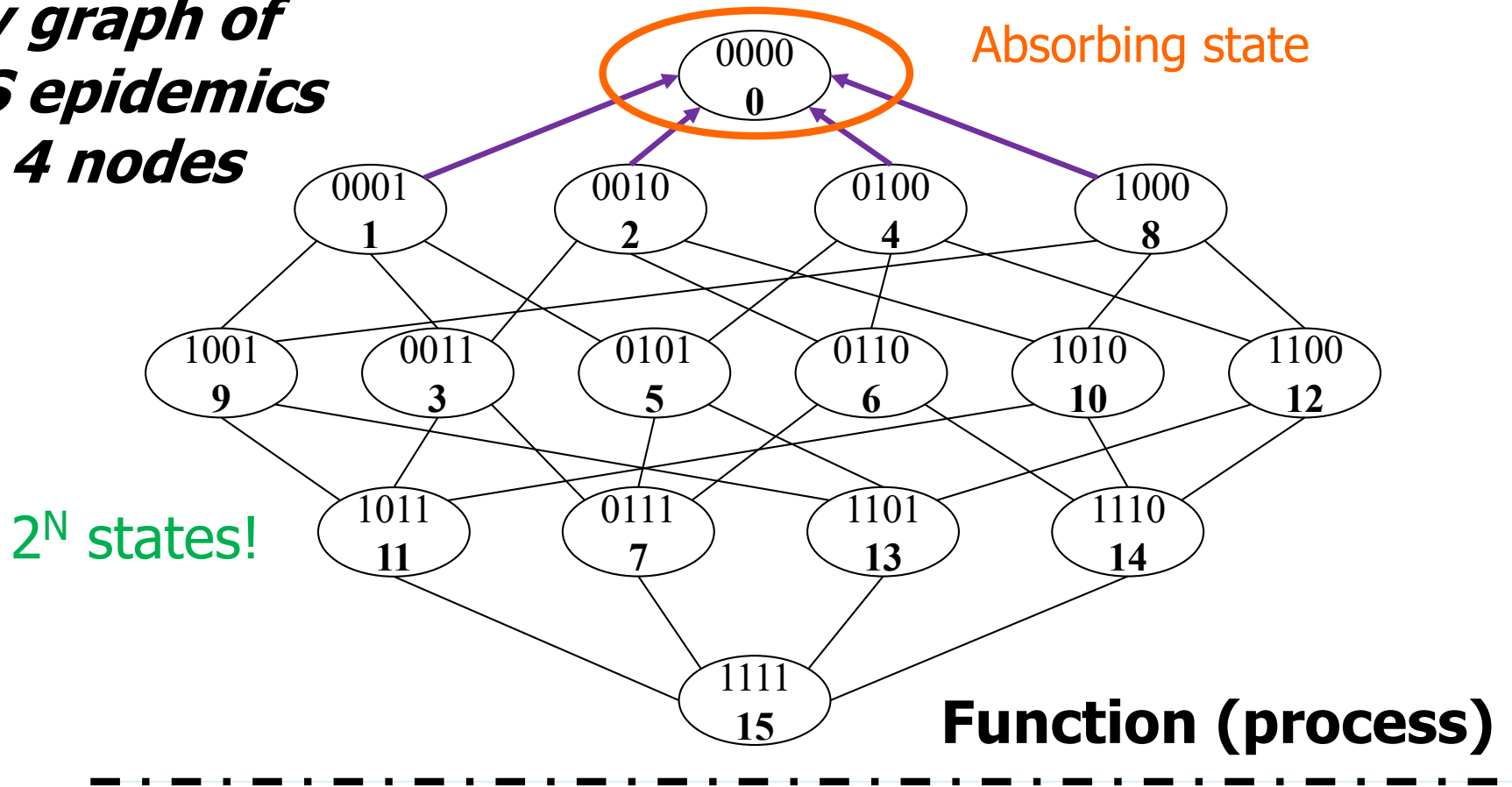$X_j(t) = 1$: node j is infected at time t

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

Observation (SIS): Bernoulli r.v. $\qquad Pr[X_j(t) = 1] = E[X_j(t)]$

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

Markov graph of the SIS epidemics on N = 4 nodes

Absorbing state

2^N states!

Function (process)

Structure (graph)

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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Governing Markovian SIS equation for node j

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

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

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

Complication

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

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Mean-field approximation:
replace random variable by its mean

NIMFA

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

$$X_j \Longrightarrow E[\breve{X}_j] = w_j$$

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

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

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Viral SIS dynamics

$$\frac{dv_j(t)}{dt} = -\delta v_j + \beta \sum_{k=1}^{N} a_{kj} v_k - \beta \sum_{k=1}^{N} a_{kj} E[X_j X_k]$$

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

Neglect last, non-negative sum:

$$\frac{dV(t)}{dt} \leq (\beta A - \delta I)V(t) \qquad \Longrightarrow \qquad V(t) \leq e^{(\beta A - \delta I)t}V(0)$$

Eigenvalues of a symmetric matrix are real and can be ordered:

$$\lambda_1(A) \geq \lambda_2(A) \geq \cdots \geq \lambda_N(A)$$

Two regimes or phases:

$$\beta \lambda_1(A) - \delta > 0 \qquad \Longrightarrow \qquad \textit{Initial} \text{ exponentional increase}$$

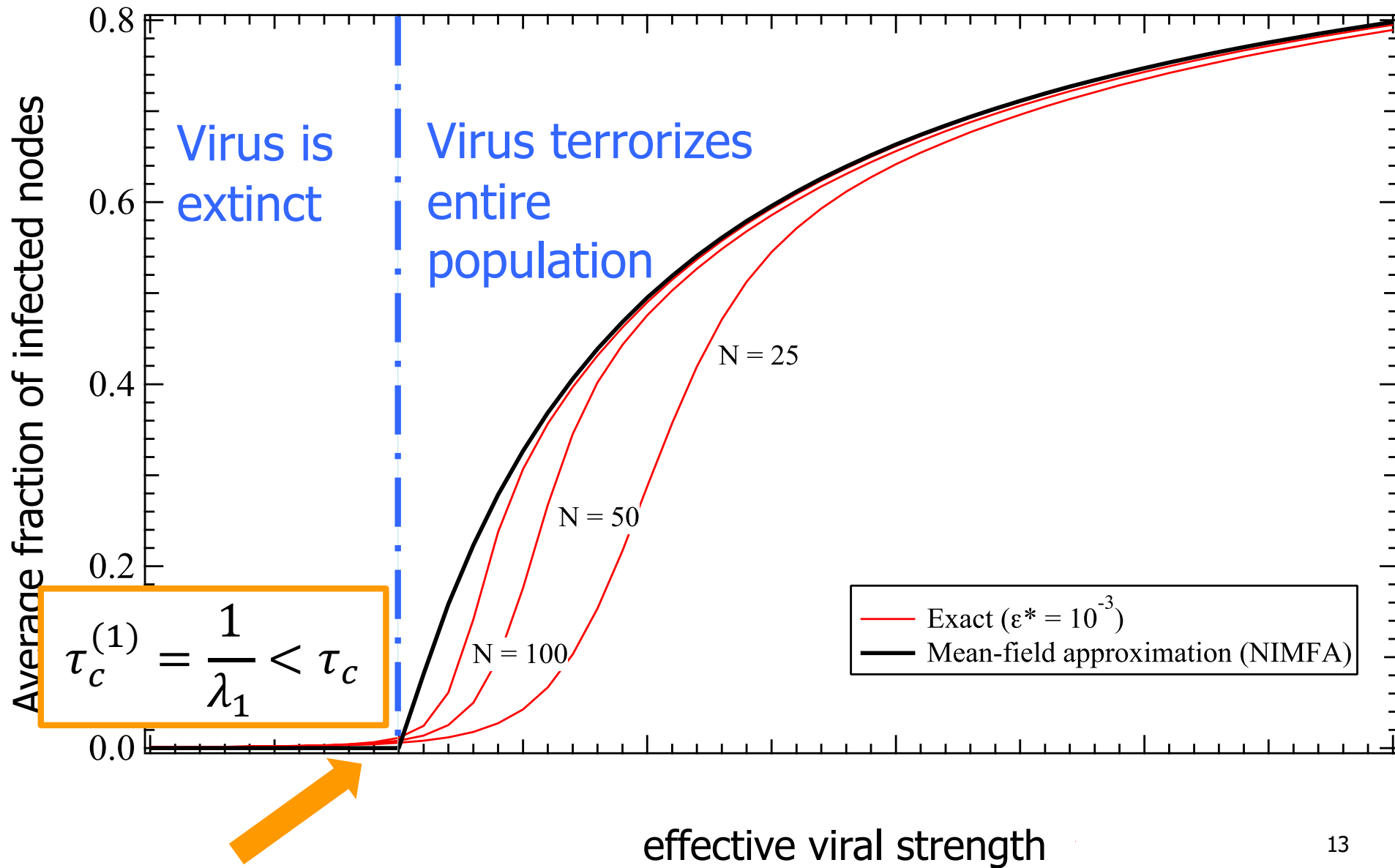$$\beta \lambda_1(A) - \delta < 0 \qquad \Longrightarrow \qquad \text{Exponential extinction}$$

Epidemic threshold τ_c : $\quad \tau = \dfrac{\beta}{\delta} < \dfrac{1}{\lambda_1(A)} = \tau_c^{(1)} < \tau_c \qquad\qquad R_0 = \dfrac{\tau}{\tau_c^{(1)}} = \tau \lambda_1(A)$

Prevalence: $\quad y(t) = \dfrac{1}{N} \sum_{j=1}^{N} v_j(t) \sim e^{(\beta \lambda_1(A) - \delta)t} = e^{(\tau \lambda_1(A) - 1)(\delta t)} = e^{(R_0 - 1)t^*}$

time $t^* = \delta t = \dfrac{t}{\delta^{-1}}$ in units of the average curing time δ^{-1}

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$$e^{(\beta A - \delta I)t} = \sum_{k=1}^{N} e^{(\beta \lambda_k(A) - \delta)t} x_k x_k^T \approx e^{(\beta \lambda_1(A) - \delta)t} x_1 x_1^T$$

SIS prevalence

Average fraction of infected nodes (y-axis)

effective viral strength (x-axis)

Virus is extinct

Virus terrorizes entire population

$$\tau_c^{(1)} = \frac{1}{\lambda_1} < \tau_c$$

N = 25

N = 50

N = 100

—— Exact ($\varepsilon^* = 10^{-3}$)
—— Mean-field approximation (NIMFA)

Epidemic threshold heavily depends on graph structure

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Extensions of NIMFA

- **In-homogeneous**: each node i has own β_i and δ_i:

  P. Van Mieghem & J. Omic, 2008, "In-homogeneous Virus Spread in Networks", arXiv.1306.2588

- **SAIS** (Infected, Susceptible, Alert) and **SIR** instead of SIS:

  F. Darabi Sahneh & C. Scoglio, 2011,"Epidemic Spread in Human Networks", 50th IEEE Conf. Decision and Contol, Orlando, Florida.
  M. Youssef & C. Scoglio, 2011, "An individual-based approach to SIR epidemics in contact networks" Journal of Theoretical Biology 283, pp. 136-144.

- Generalized Epidemic mean-field model (**GEMF**): extension of NIMFA to m compartments (includes both SIS, SAIS, SIR,...):

  F. Darabi Sahneh, C. Scoglio, 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.
  S. A. Moon, F. Darabi Sahneh, C. Scoglio, 2021, Group-Based General Epidemic Modeling for Spreading Processes on Networks: GroupGEM, IEEE Transactions on Network Science and Engineering, Vol. 8, No. 1.

- NIMFA on **Interdependent networks**

  Wang, H., Q. Li, G. D'Agostino, S. Havlin, H. E. Stanley and P. Van Mieghem, 2013, "Effect of the Interconnected Network Structure on the Epidemic Threshold", Physical Review E, Vol. 88, No. 2, August, p. 022801.

- **Universal SIS mean-field framework**: NIMFA is close to optimal

  Devriendt, K. & P. Van Mieghem, 2017, "Universal mean-field framework for SIS epidemics on networks, based on graph partitioning and the isoperimetric inequality", Physical Review E, Vol. 96, No. 5, p. 052314.

- **Exact** NIMFA solution for the complete graph (with self-infections) and discrete-time

  Prasse, B. and P. Van Mieghem, 2019, "The Viral State Dynamics of the Discrete-Time NIMFA Epidemic Model", IEEE Transactions on Network Science and Engineering, Vol. 7, No. 3, pp. 1667-1674, July-September (DOI 10.1109).
  Prasse, B. and P. Van Mieghem, 2020, "Time-Dependent Solution of the NIMFA Equations around the Epidemic Threshold", Journal of Mathematical Biology, Vol. 81, December, pp. 1299-1355.
  Prasse, B., K. Devriendt and P. Van Mieghem, 2021, "Clustering for epidemics on networks: a geometric approach", Chaos: An Interdisciplinary Journal of Nonlinear Science, vol. 31, No. 6, p. 063115
  Achterberg, M. A., B. Prasse and P. Van Mieghem, 2022, "An exact analysis of continuous-time Markovian epsilon-SIS epidemics on networks", Physical Review E, Vol. 105, No 5, p. 054305.
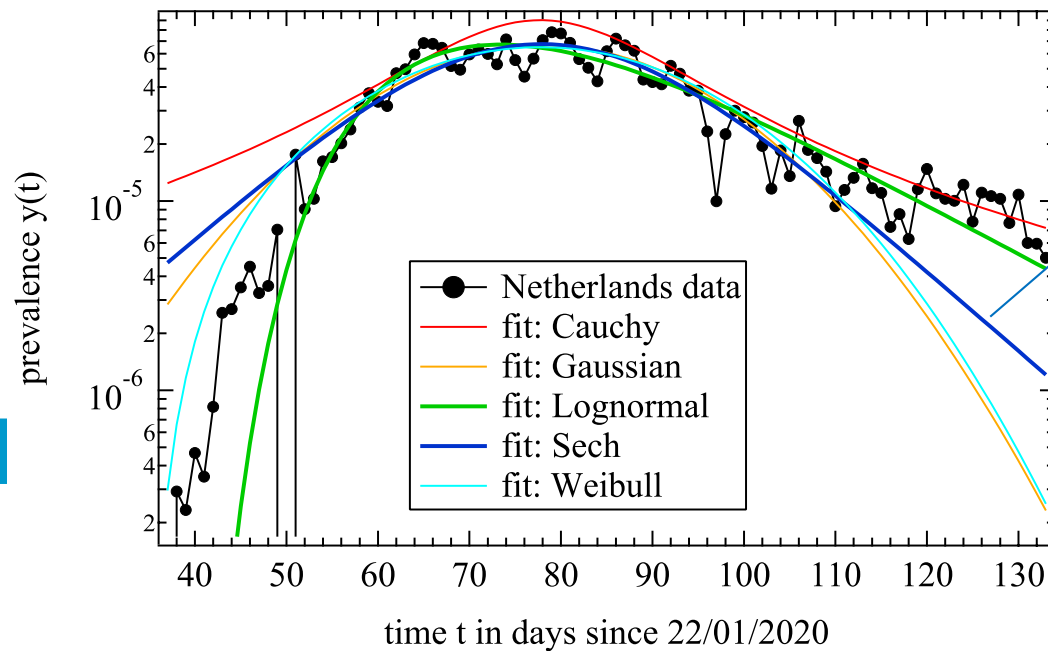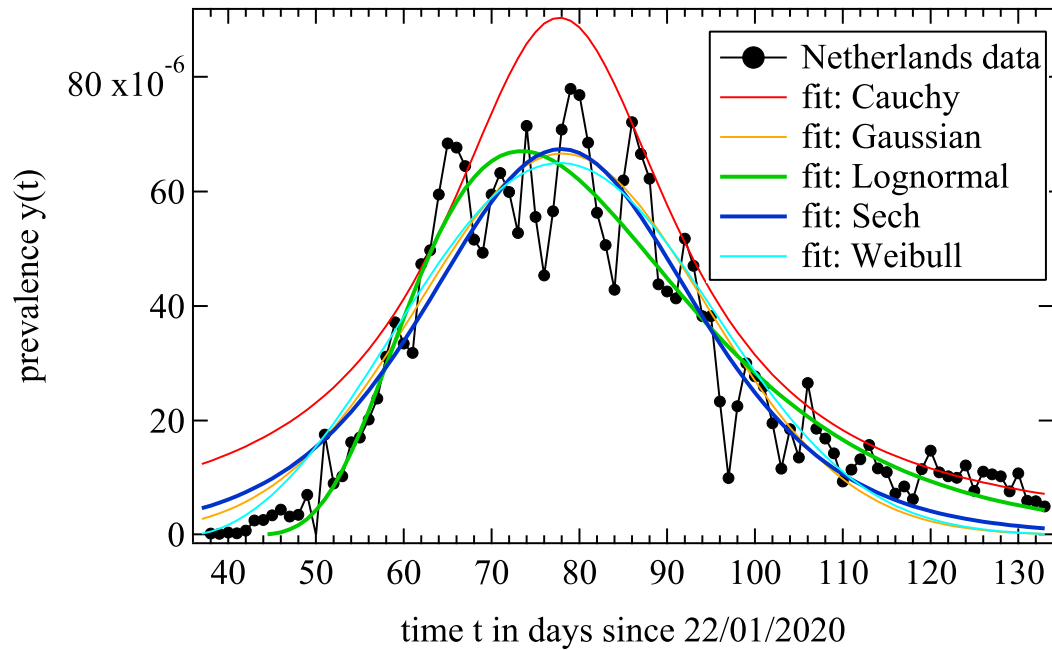
Outline
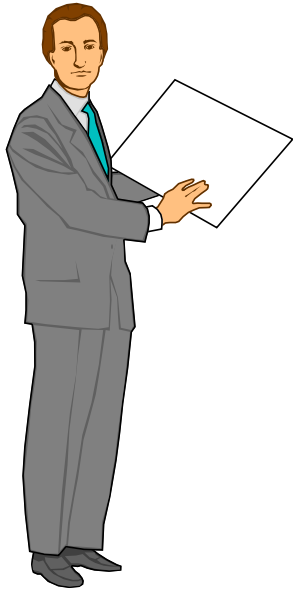
Theory of epidemics on networks

Recent developments

 ➢ **Non-Markovian epidemics**
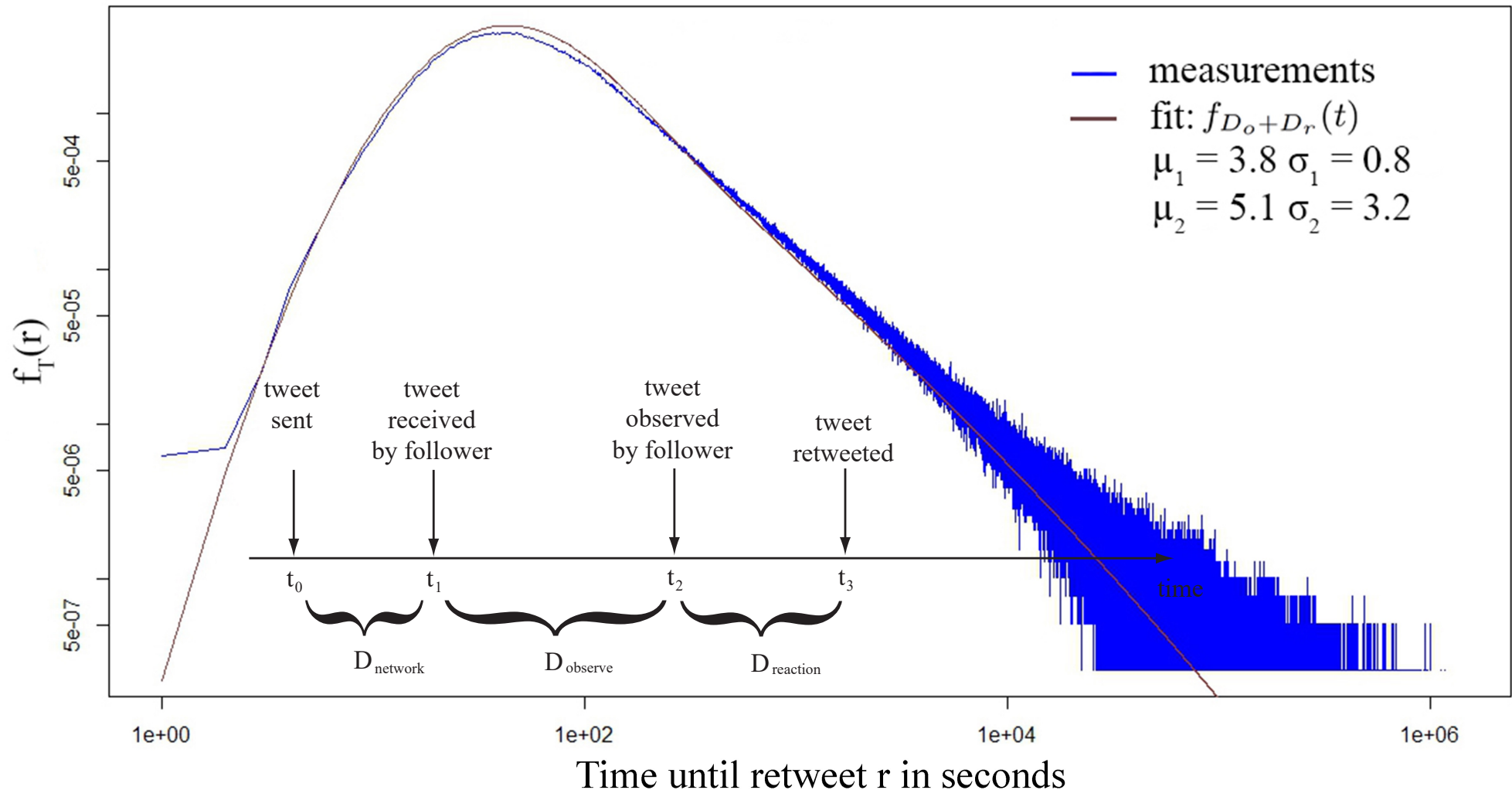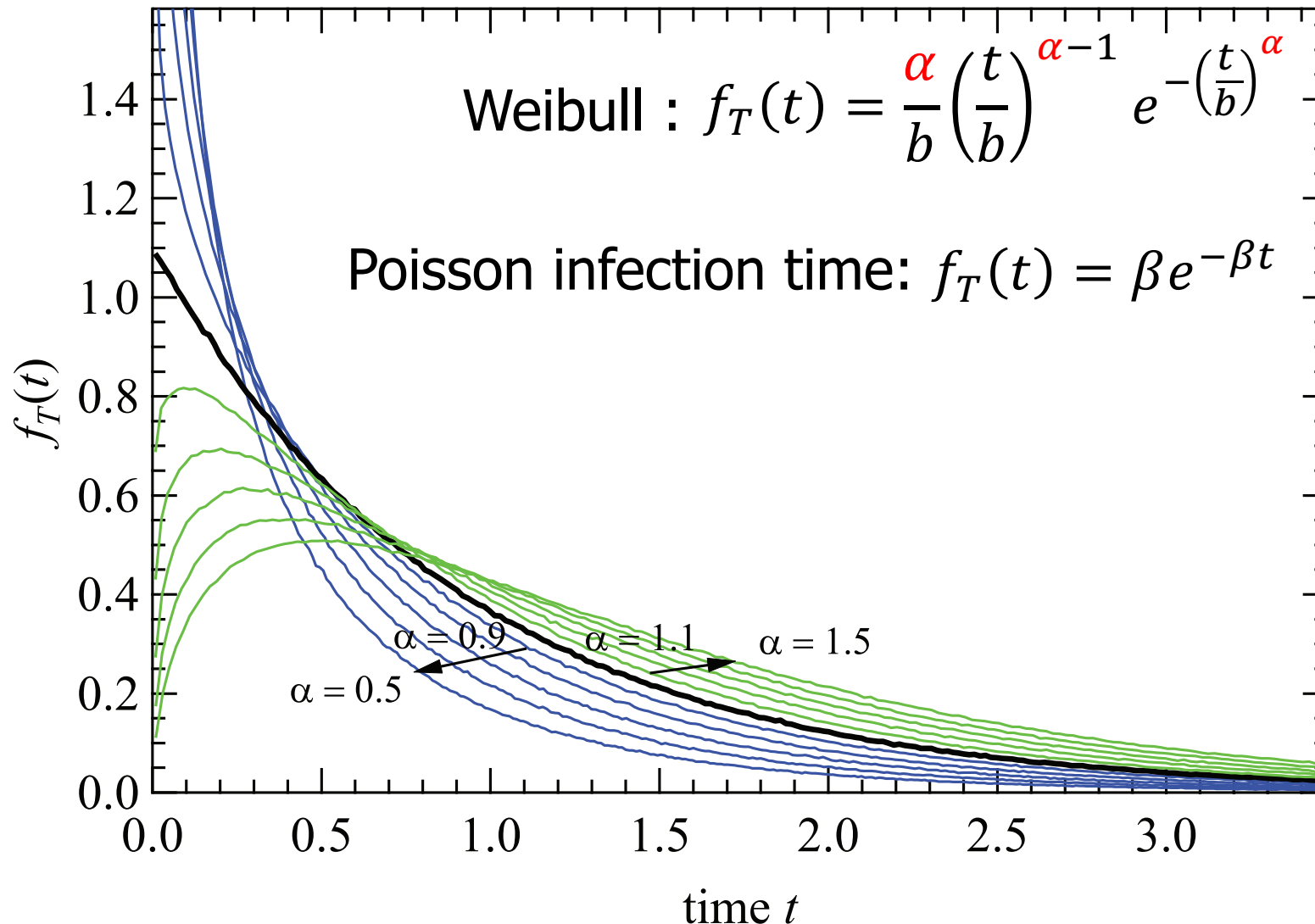 ➢ Inferring the graph

RIVM (Dutch CDC) data (begin Covid-19)

Exponential?

$$y(t) \approx e^{(R_0-1)t^*}$$

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Twitter Epidemic times are not exponential

Time until retweet r in seconds

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Non-Markovian infection times

Weibull : $f_T(t) = \dfrac{\alpha}{b}\left(\dfrac{t}{b}\right)^{\alpha-1} e^{-\left(\frac{t}{b}\right)^{\alpha}}$

α: shape parameter

Poisson infection time: $f_T(t) = \beta e^{-\beta t}$
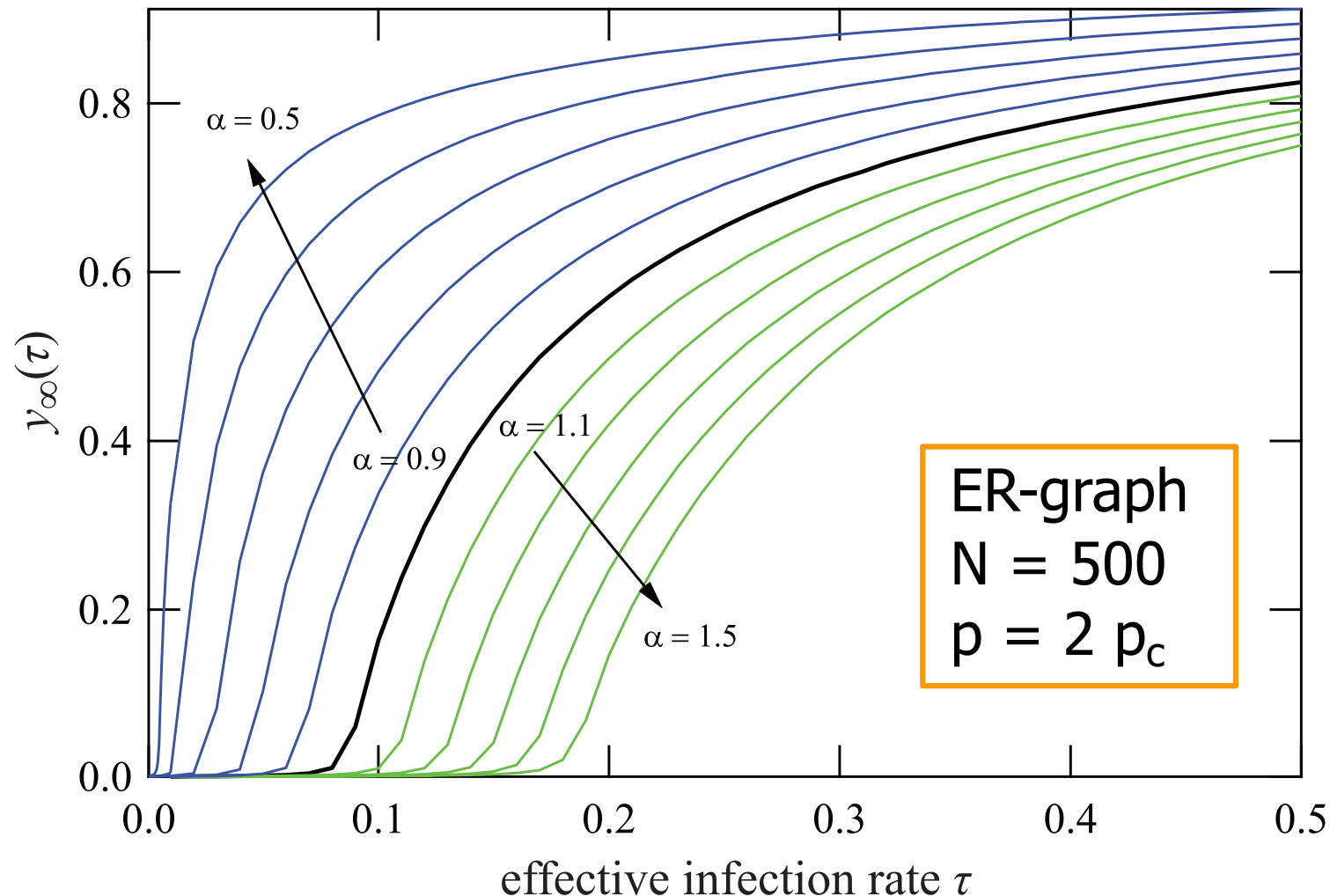
Each Weibull distribution has the same mean

$$E[T] = \frac{1}{\beta}$$

$$\frac{1}{b} = \beta \Gamma\left(1 + \frac{1}{\alpha}\right)$$

$\alpha = 0.5$ $\alpha = 0.9$ $\alpha = 1.1$ $\alpha = 1.5$

T is time to infect a neighboring node
$f_T(t)$ is probability density of T: $\Pr[t \le T \le t + \Delta t]$

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Non-Markovian epidemic threshold

| Non-exponential infection time has a dramatic influence! |

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Epidemic threshold $\tau_c^{(1)}(\alpha)$ versus α

Legend:
- ◇ ER network $\lambda_1 = 8.5232$
- ○ Rectangular grid $\lambda_1 = 3.9642$
- ✳ Scale-free network $\lambda_1 = 11.9944$
- —— Theory
- - - - Asymptotic expansion of the theory

$\tau_c^{(1)}(1) = \dfrac{1}{\lambda_1}$

Rectangular grid: $1/\ln(1+\lambda_1) = 0.6242$

ER: $1/\ln(1+\lambda_1) = 0.4437$

Scale-free: $1/\ln(1+\lambda_1) = 0.3899$

Lagrange series for $\tau_c^{(1)}(\alpha)$

$$\frac{1}{\tau_c^{(1)}(\alpha)} = \ln(1+\lambda_1) + \frac{1}{2}\frac{\left(\Gamma''(1)-\gamma^2\right)}{\left(\alpha\Gamma\left(1+\frac{1}{\alpha}\right)\right)^2}\ln^2(1+\lambda_1) + O\left(\frac{1}{\alpha^3}\right)$$

Axis labels: Epidemic threshold (y-axis), Shape parameter α (x-axis)

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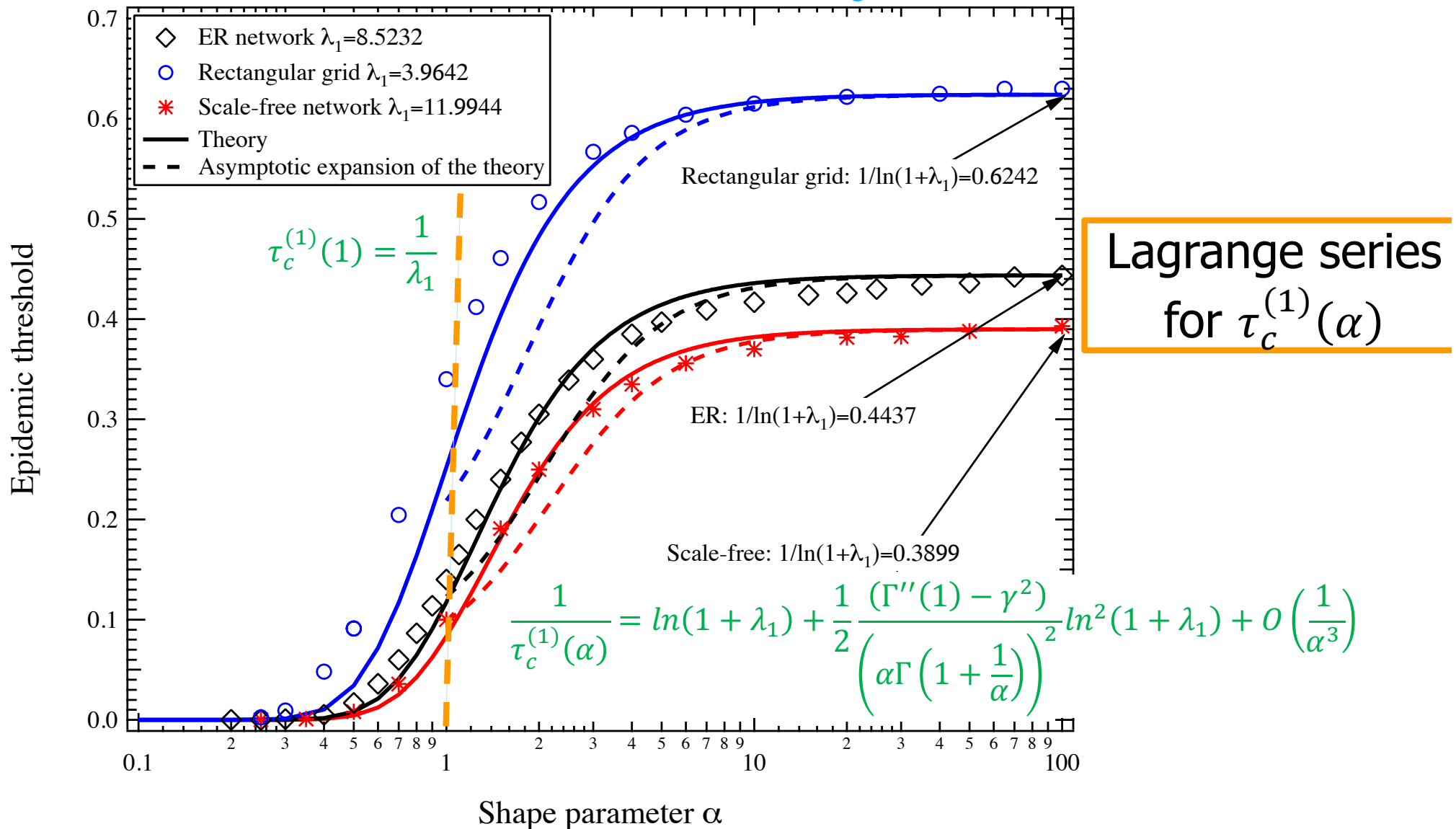
Fractional Calculus for non-Markovian epidemics?

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

$0 < \alpha \leq 1$

Replace $D = \frac{d}{dt}$ by

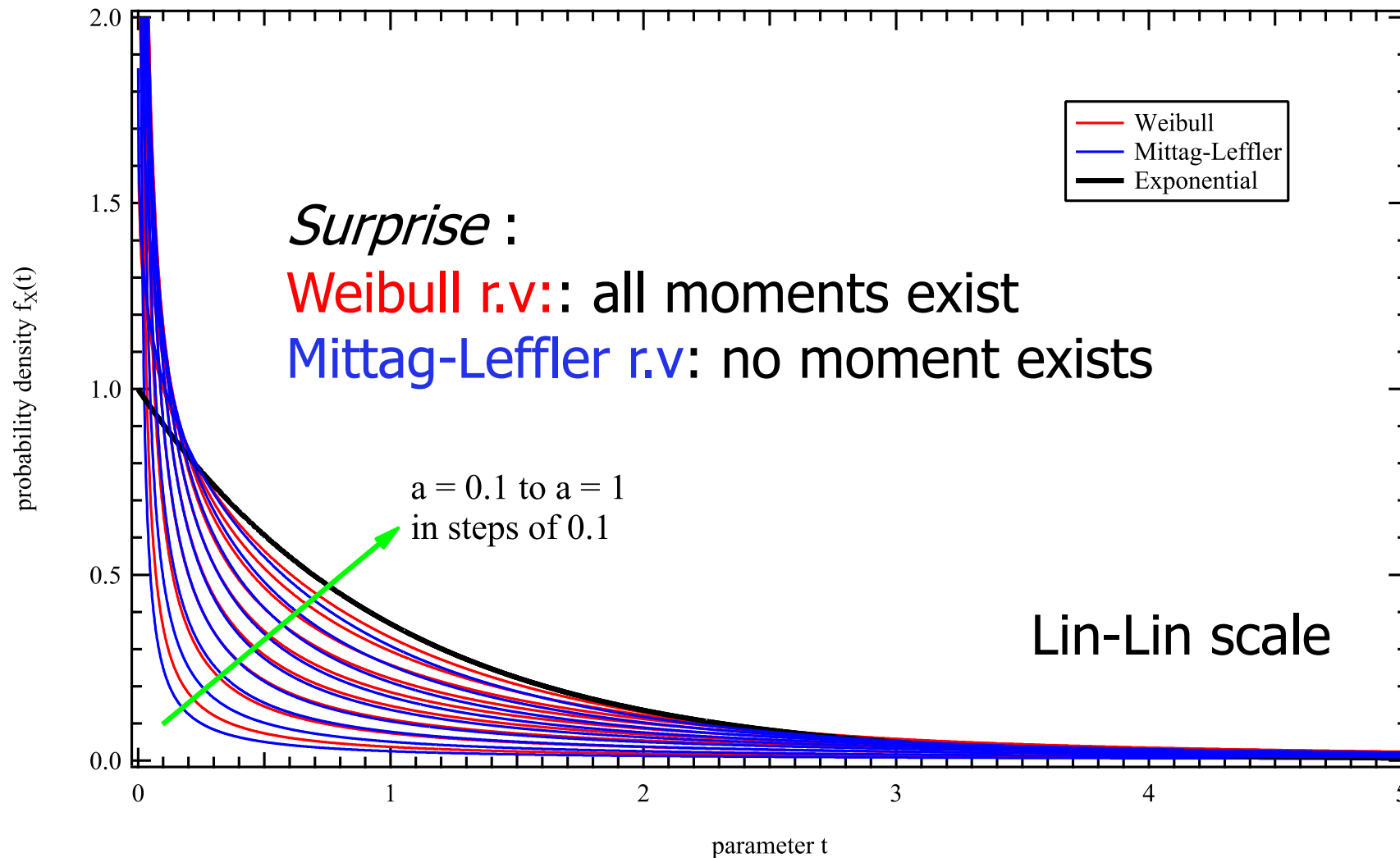Caputo fractional derivative D^α

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

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

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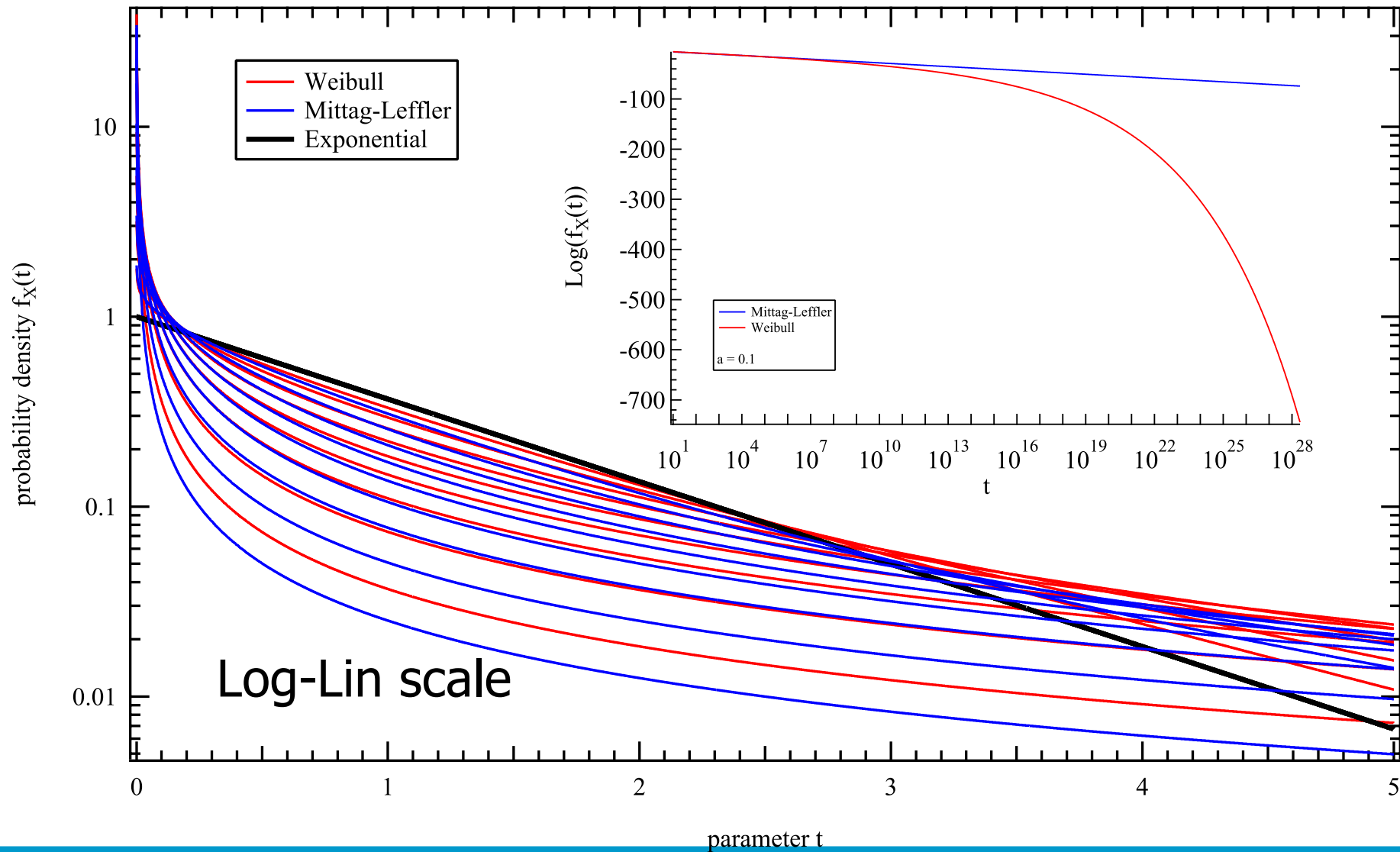
$$E_{1,1}(z) = e^z$$

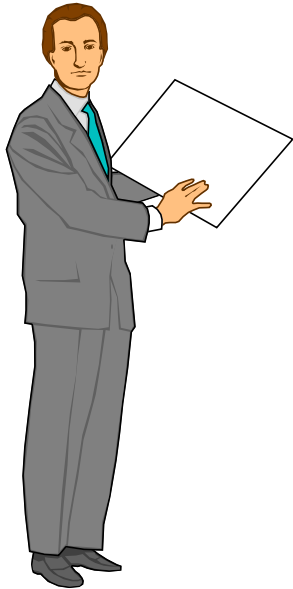**Open problem**: find sojourn time for α-fractional non-Markovian process

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Weibull and Mittag-Leffler pdf

Surprise :

Weibull r.v:: all moments exist

Mittag-Leffler r.v: no moment exists

a = 0.1 to a = 1
in steps of 0.1

Lin-Lin scale

probability density $f_X(t)$

parameter t

Weibull
Mittag-Leffler
Exponential

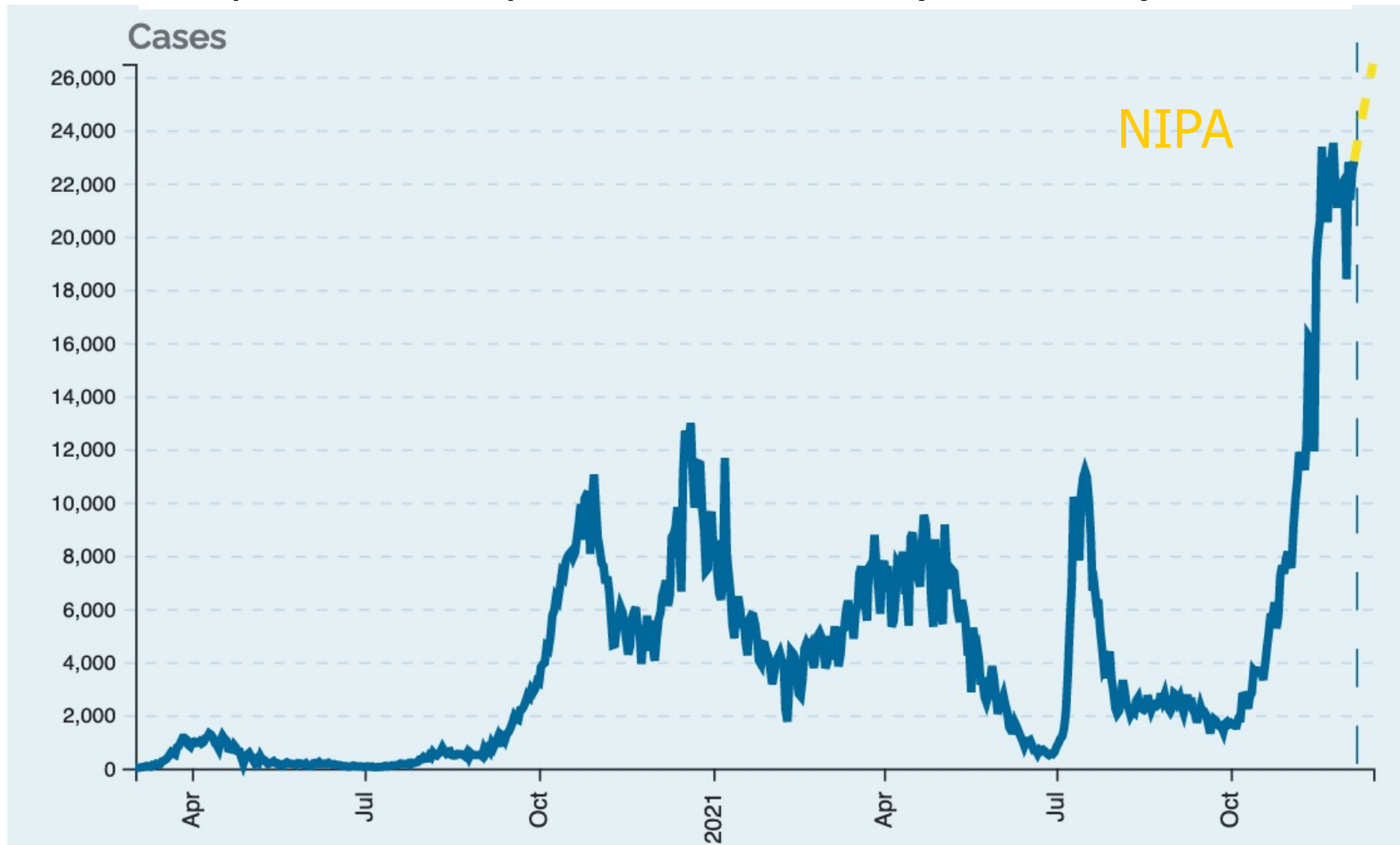TUDelft

Weibull and Mittag-Leffler pdf

Outline

Theory of epidemics on networks

Recent developments

  ➢ Non-Markovian epidemics
  ➢ **Inferring the graph**

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Confirmed infections per day in NL

Daily automatically loaded from RIVM (Dutch CDC)
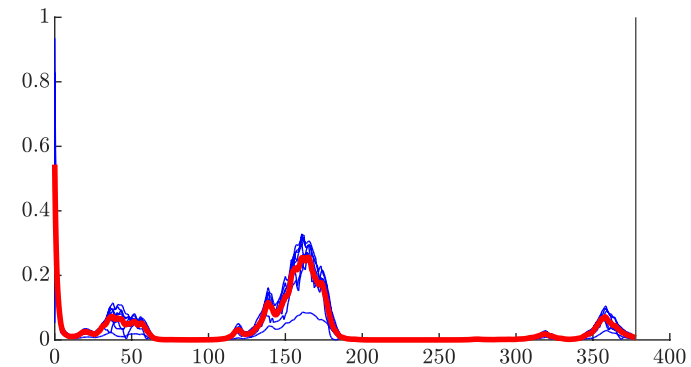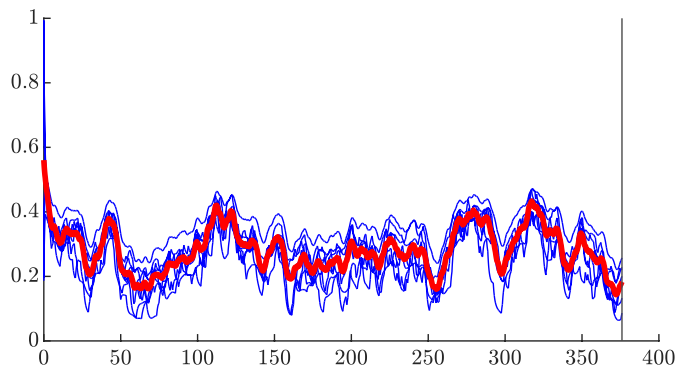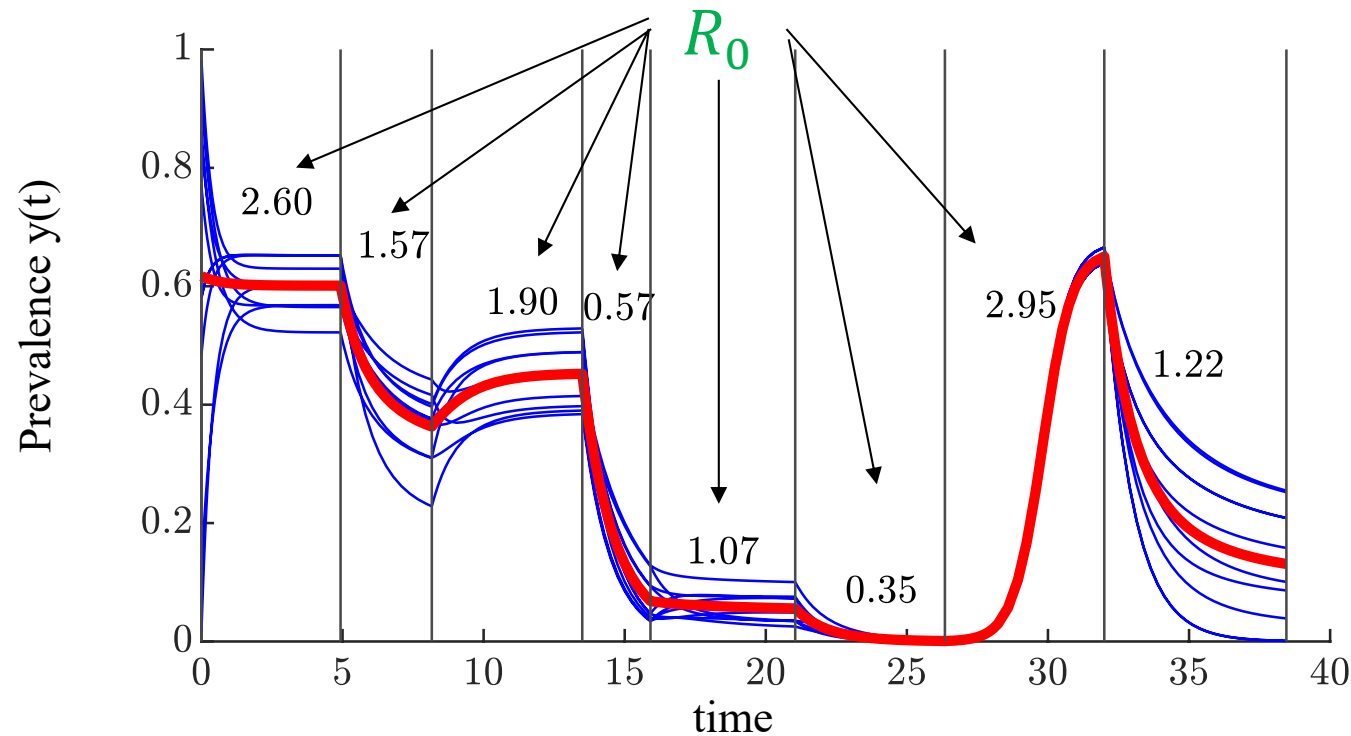
Achterberg, M. A., B. Prasse, L. Ma, S. Trajanovski, M. Kitsak and P. Van Mieghem, 2020, "Comparing the Accuracy of Several Network-based COVID-19 Prediction Algorithm", International Journal of Forecasting, to appear. (DOI: j.ijforecast.2020.10.001)

SIS prevalence in a temporal contact graph

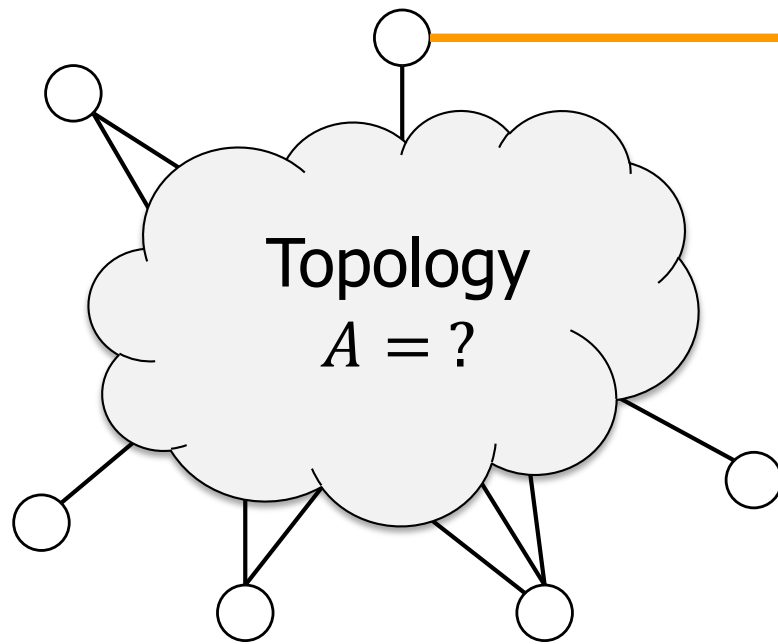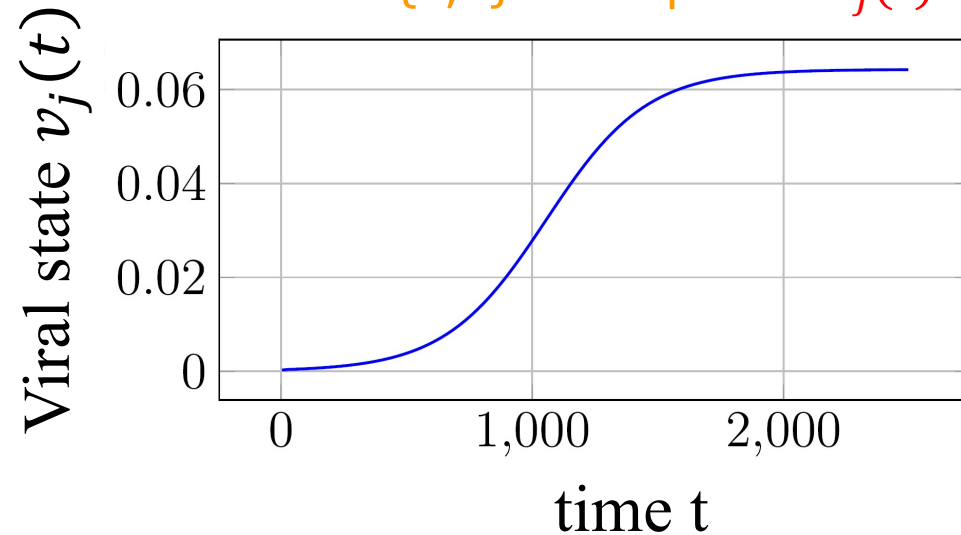Viral parameters β and δ do not change

Influence of spectral radius λ_1

$$y(t) \approx e^{(R_0 - 1)t^*}$$

$$R_0 = \tau \lambda_1 = \frac{\tau}{\tau_c^{(1)}}$$

Graph Reconstruction from epidemics

Topology
$A = ?$

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

Viral state $v_j(t)$

0.06

0.04

0.02

0

0   1,000   2,000

time t

Aim: Determine the N×N adjacency matrix A of the contact graph from a series of infection probabilities over time of all nodes

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.

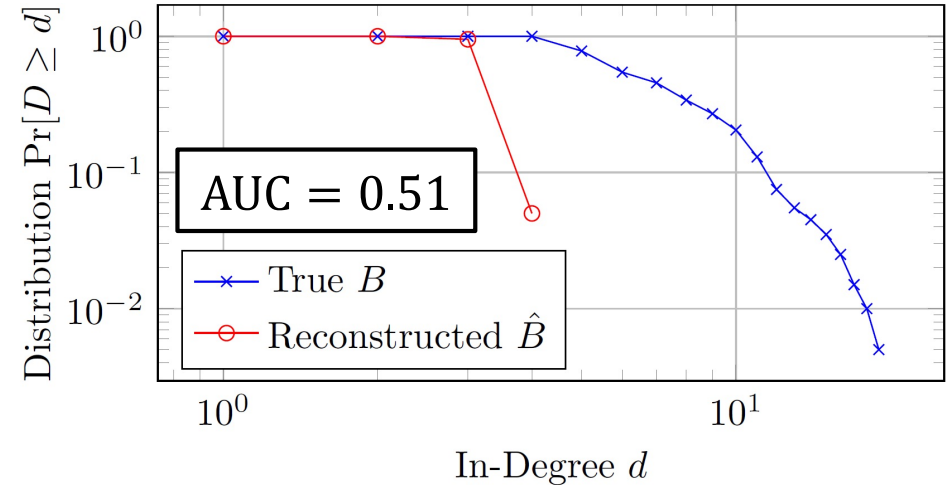T U Delft

Accurate prediction of epidemic outbreaks *without* accurate network reconstruction

Prediction
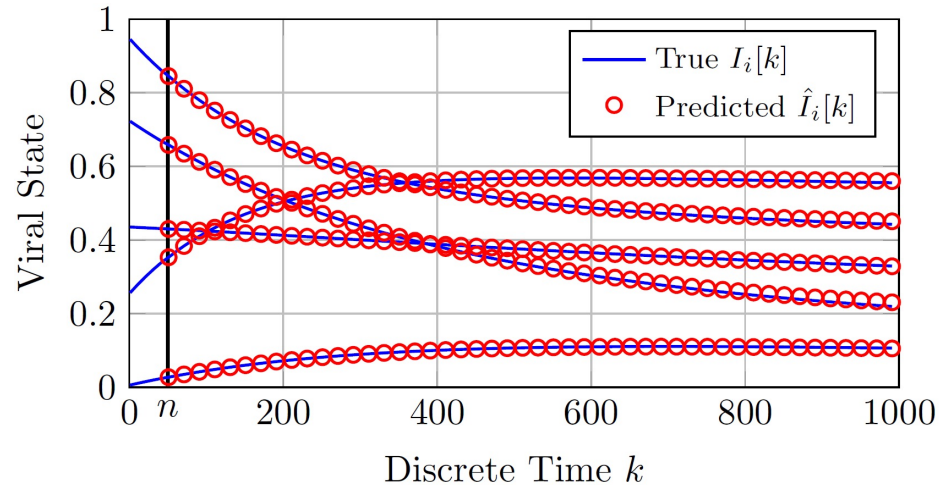
Reconstruction

Process: only a few eigenmodes   Graph: nearly all 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

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Contact graph

- Generated by human mobility:
  - Not static, but result of a yet unknown process
  - Hardly models; lot of scenario's

- **"Meten is weten" (Simon Stevin, 1548-1620)**: develop digital technology

- Corona app (BETIS: Bayesian Estimation for Tracing Infection States)
  - BETIS learns continuously over time
  - BETIS alarms in real-time when infected person approaches
  - BETIS is very effective in computer simulaties

    ➤ Implementiaton possible in practice (inclusive secured privacy)
    ➤ No interest of society (but from companies)

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Conclusion

- Theory of virus spread in networks: fascinating!
  - ○ "local-rule, global emergent" processes & phase transitions
- Nobody can 1% accurately predict a few days ahead
  - ○ Contact graph must be measured
- All hope on vaccination, barely digital technology
  - ○ Digital technology (BETIS): fraction of cost w.r.t vaccination

- Freedom & Privacy = basic right in a democracy:
  - ○ Individual freedom has an epidemic cost:
    - ➢ each contact increases the spectral radius λ_1 and lowers the epidemic threshold $\tau_c^{(1)} = \frac{1}{\lambda_1}$
    - ➢ *An infection somewhere, increases the infection chance for us all*
  - ○ In the Free west: Freedom is an ally of Covid-19
    - ➢ World-wide mortility (dec. 2021) = $\frac{5.262.000}{265.419.382} \approx 0.0198 < 2\%$
    - ➢ If 5 x higher mortality & uniformly over all ages: no freedom discussion anymore

E. Cator and P. Van Mieghem, **2014**, "Nodal infection in Markovian SIS and SIR epidemics on networks are non-negatively correlated," **Physical Review E, Vol. 89, No. 5, p. 052802.**

Open PhD & Postdoc positions

ERC VISiON (Virus Spread on Networks) is seeking

- 5 PhD students
- 2 Postdocs

Starting from 1 September 2022

Details: see news on https://www.nas.ewi.tudelft.nl

email: Professor P. Van Mieghem at p.f.a.vanmieghem@tudelft.nl

Thank You

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P.F.A.VanMieghem@tudelft.nl

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