The role of directionality, heterogeneity & correlations in epidemic risk and spread

A CAUTIONARY TALE ON THE RISK OF IGNORING ASYMMETRY

Antoine Allard

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Disclaimer

- main results are not new by themselves (e.g. L. A. Meyers, M. E. J. Newman, J. C. Miller, and many more others)
- origin story of this work is worthwhile, and suggests that perhaps these known results put together had not yet fully percolated throughout the community
- full details can be found in a forthcoming paper by myself and many attendees of this workshop

The Role of Directionality, Heterogeneity, and Correlations in Epidemic Risk and Spread*

Antonie Allard[†]
Cristopher Moore[‡]
Samuel V. Scarpino[§]
Benjamin M. Althouse[¶]
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SIAM Review 65, 000–000 (2023; in press)

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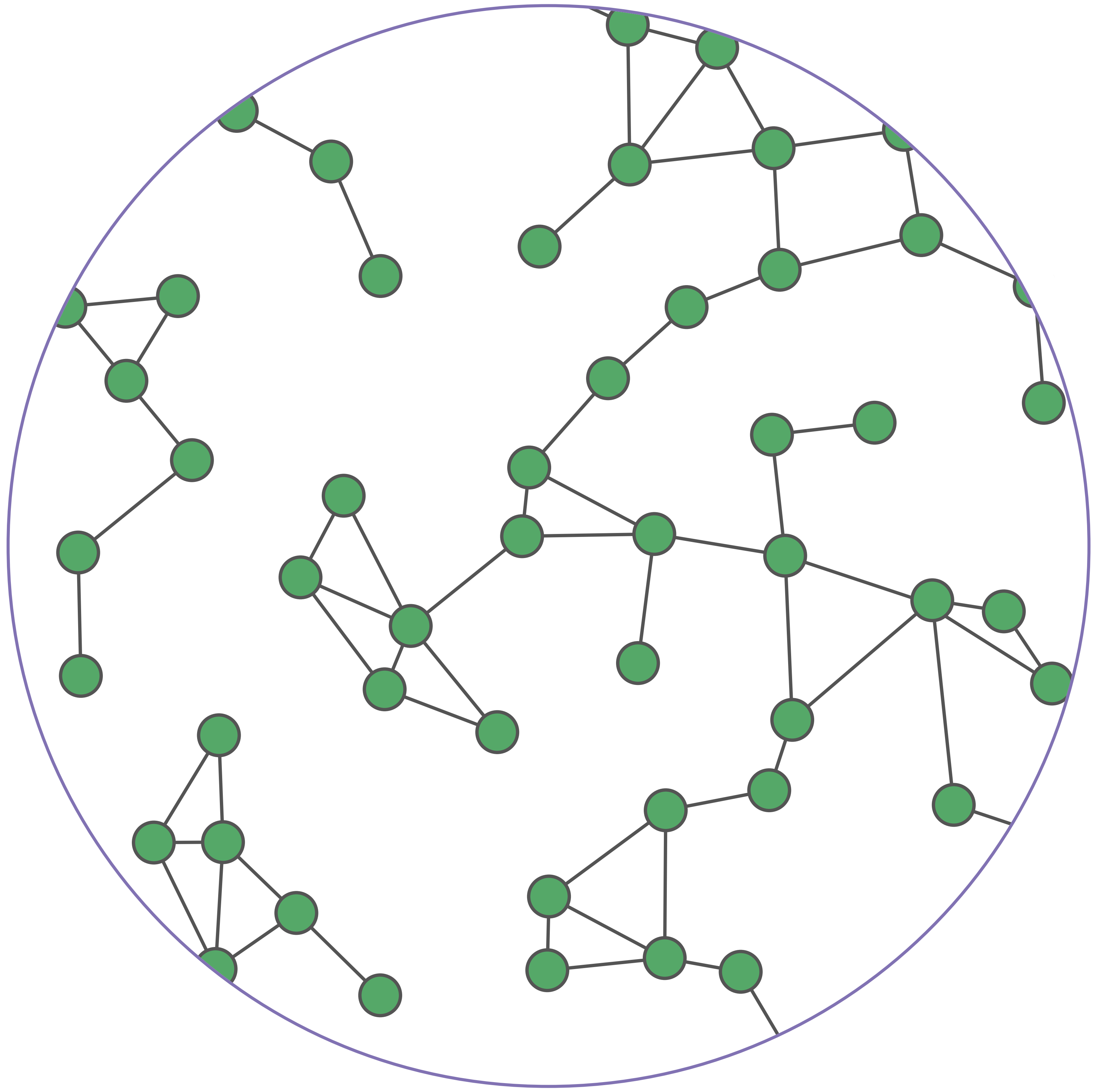

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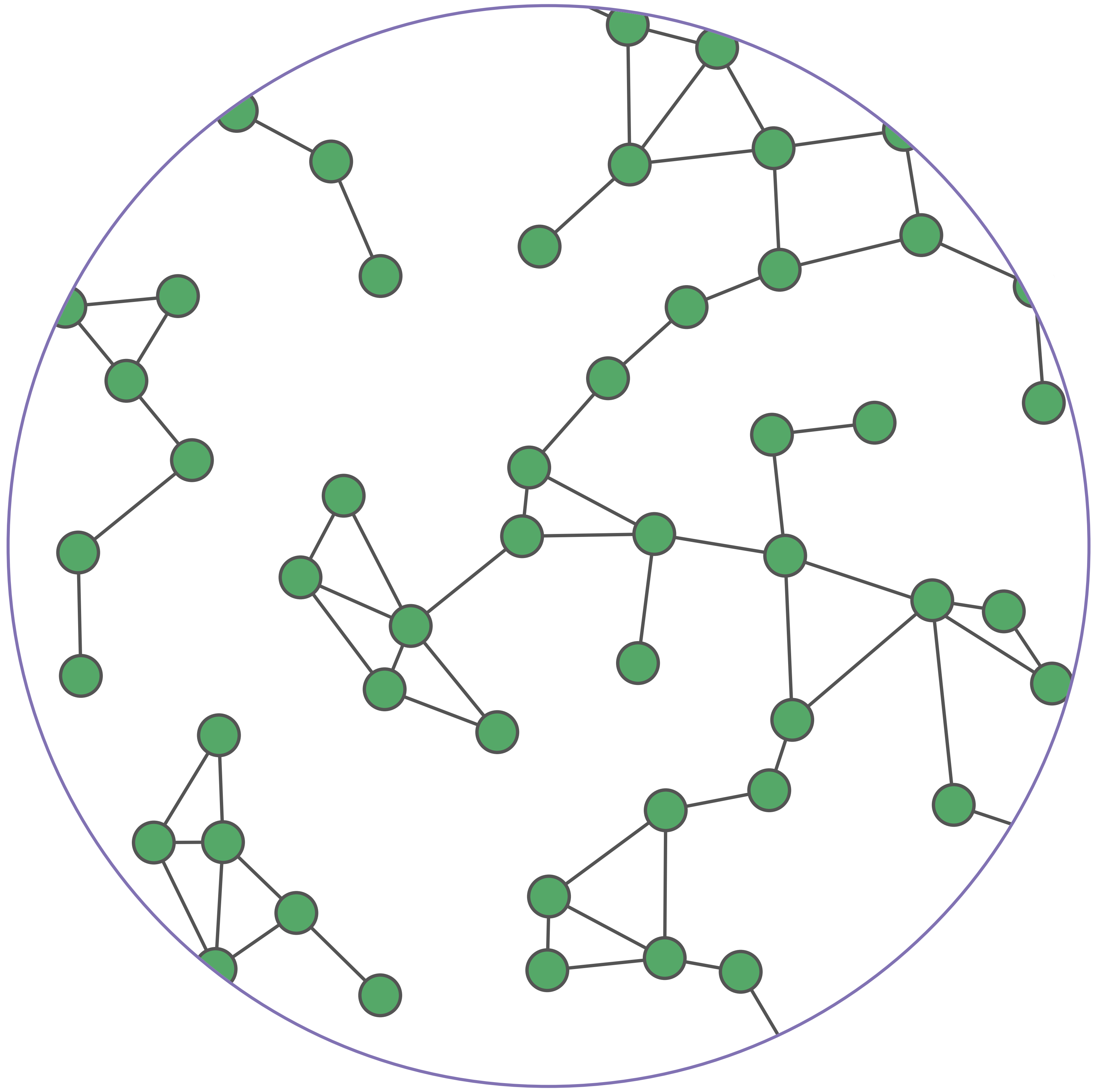

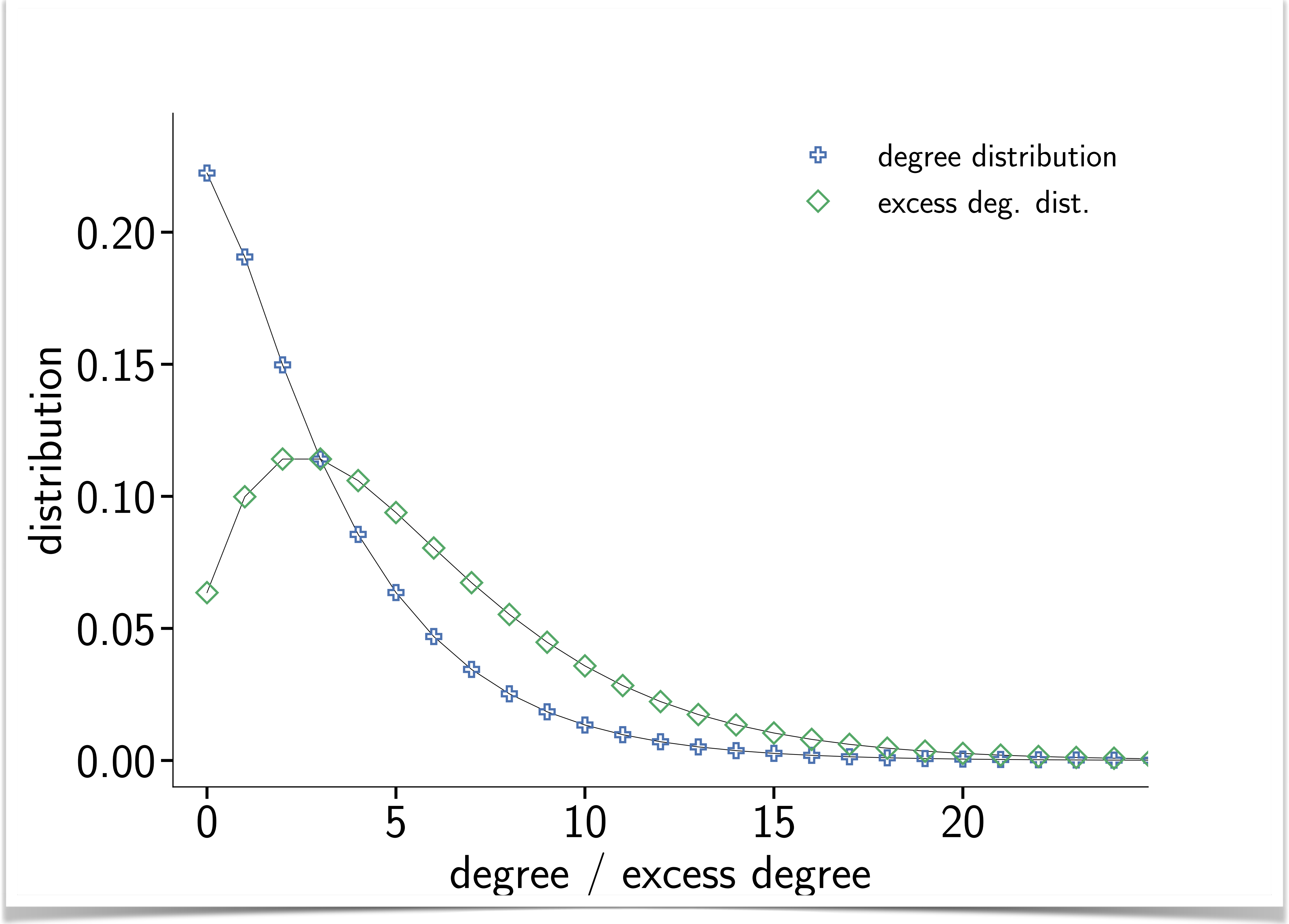

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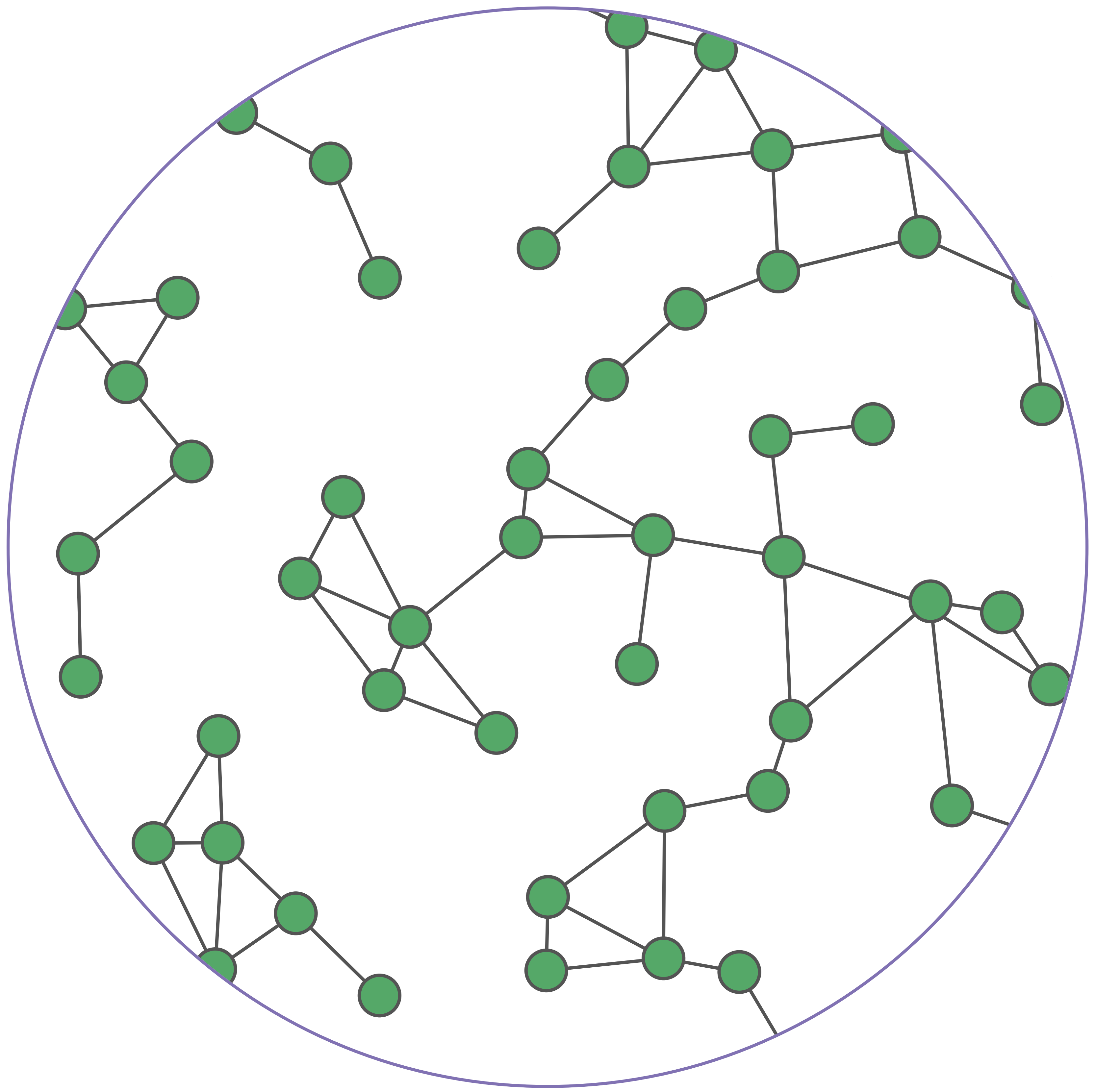

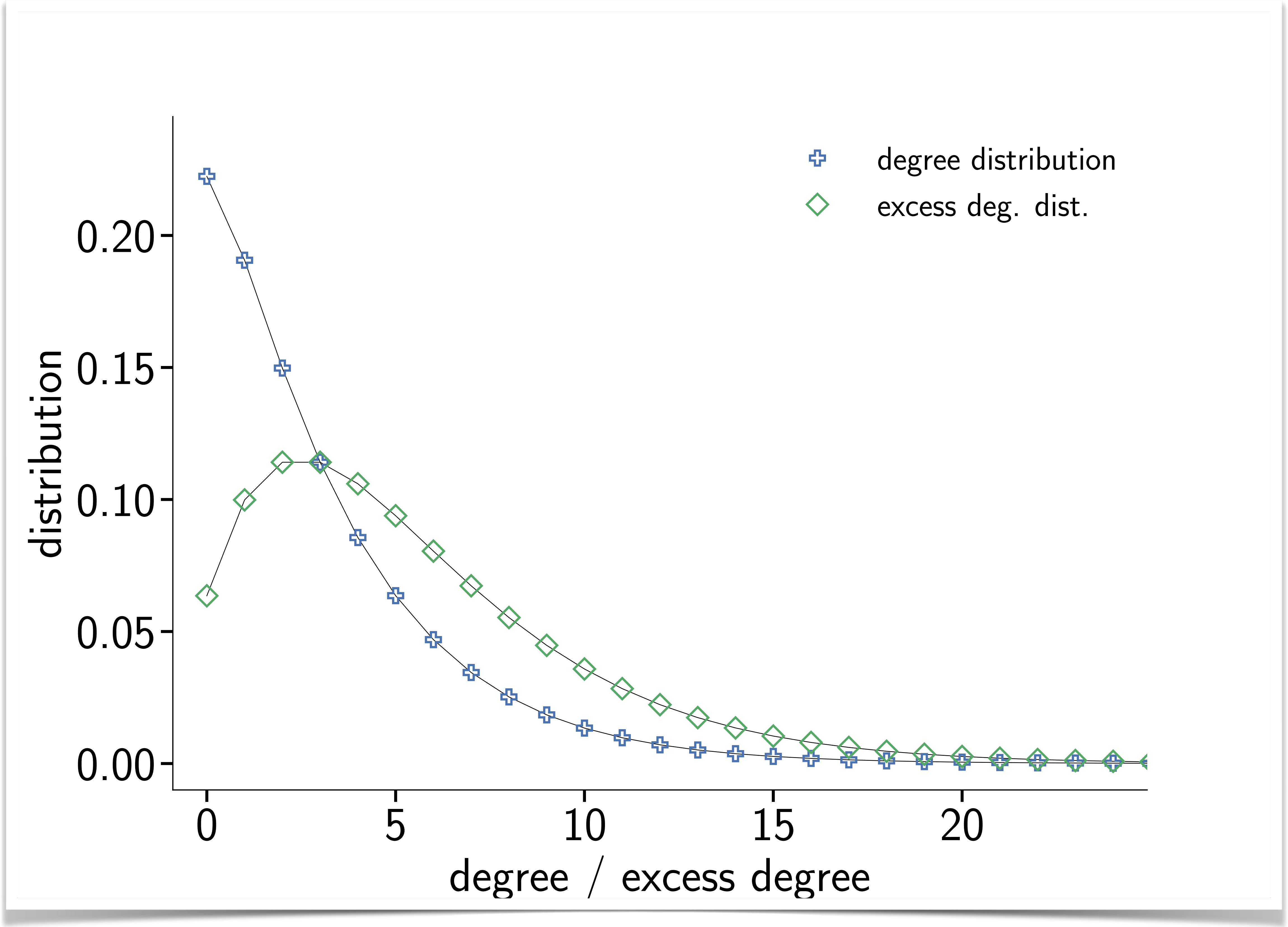

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. . . and then January 2020 came along.

statnews.com

Cause of Wuhan's mysterious pneumonia cases still unknown, Chinese officials say

By Helen Branswell Jan. 5, 2020

China CDC Weekly

Notes from the Field

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Wenjie Tan[1,2,#]; Xiang Zhao[1]; Xuejun Ma[1]; Wenling Wang[1]; Peihua Niu[1]; Wenbo Xu[1]; George F. Gao[1]; Guizhen Wu[1,2,#]

The NEW ENGLAND JOURNAL of MEDICINE

BRIEF REPORT

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Na Zhu, Ph.D., Dingyu Zhang, M.D., Wenling Wang, Ph.D., Xingwang Li, M.D., Bo Yang, M.S., Jingdong Song, Ph.D., Xiang Zhao, Ph.D., Baoying Huang, Ph.D., Weifeng Shi, Ph.D., Roujian Lu, M.D., Peihua Niu, Ph.D., Faxian Zhan, Ph.D., Xuejun Ma, Ph.D., Dayan Wang, Ph.D., Wenbo Xu, M.D., Guizhen Wu, M.D., George F. Gao, D.Phil., and Wenjie Tan, M.D., Ph.D., for the China Novel Coronavirus Investigating and Research Team

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Previously unknown virus may be causing pneumonia outbreak in China, WHO says | CBC News

Thomson Reuters · Posted: Jan 09, 2020 11:27 AM ET | Last Updated: January 9, 2020

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The health department of Wuhan initially reported 27 cases, but the tally stands at 59 as of 6 January

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China pneumonia outbreak: Mystery virus probed in Wuhan

3 January 2020

COMMENTARY

JOURNAL OF MEDICAL VIROLOGY WILEY

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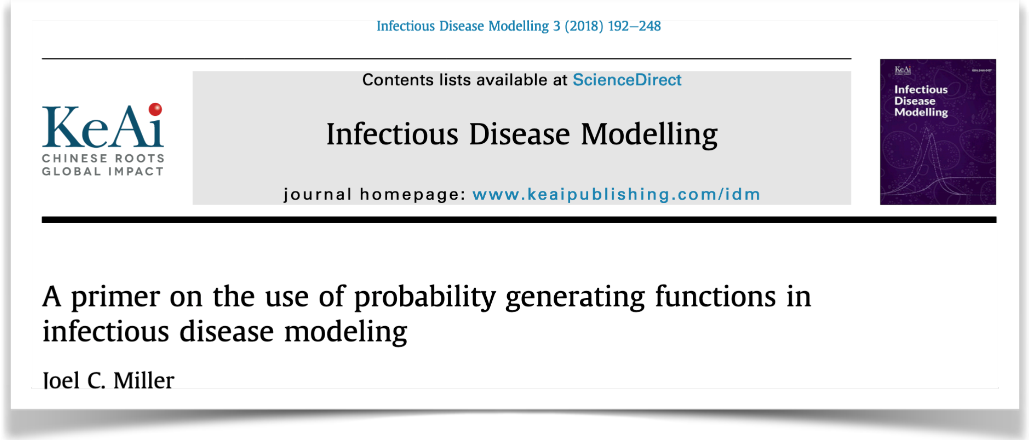
Contact network epidemiology


Infectious Disease Modelling 3 (2018) 192–248

Contents lists available at ScienceDirect

Infectious Disease Modelling

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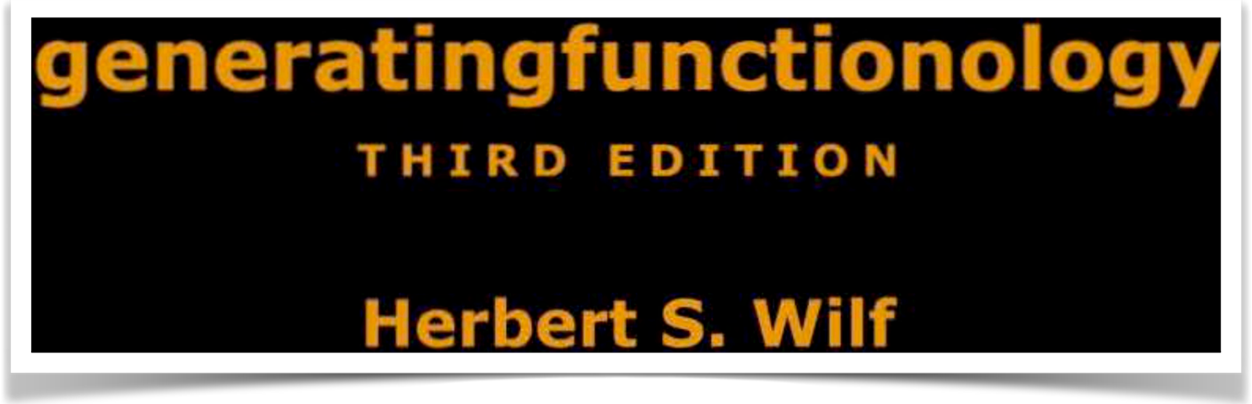
KeAi CHINESE ROOTS GLOBAL IMPACT

A primer on the use of probability generating functions in infectious disease modeling

Joel C. Miller



Probability generating functions (PGFs)

- a PGF is a formal power series whose coefficients are a probability mass function $\{a_n\}_{n\geq 0}$

$$A(x) = \sum_{n\geq 0}^{\infty} a_n x^n = a_0 + a_1 x + a_2 x^2 + a_3 x^3 + \dots$$

- computing the moments

$$A(1) = \sum_{n\geq 0}^{\infty} a_n = 1 \; ; \qquad \langle n \rangle = \sum_{n\geq 0}^{\infty} n\, a_n = \left.\frac{dA(x)}{dx}\right|_{x=1} = A'(1) \; ; \qquad \langle n^p \rangle = \sum_{n\geq 0}^{\infty} n^p\, a_n = \left(x\frac{d}{dx}\right)^p A(x)\Big|_{x=1}$$

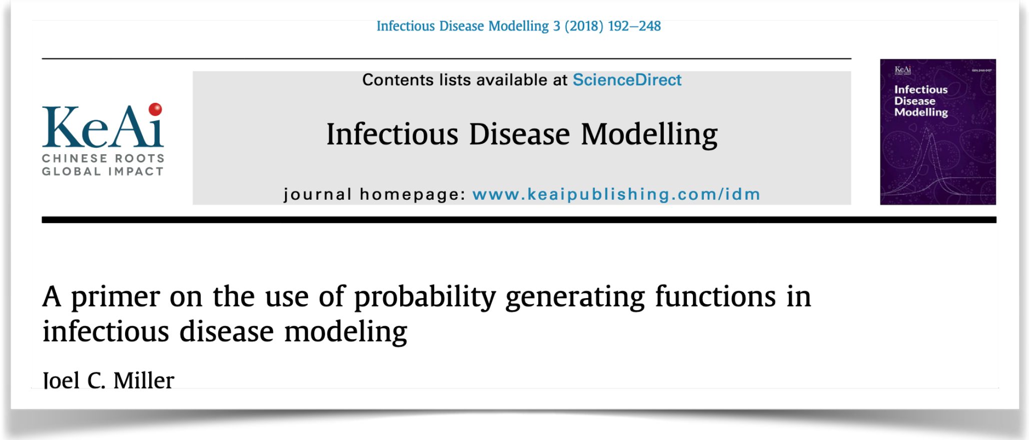
- extracting the coefficients

$$a_n = \frac{1}{n!}\left.\frac{d^n A(x)}{dx^n}\right|_{x=0} = \frac{1}{2\pi}\int_0^{2\pi} A(\mathrm{e}^{i\theta})\mathrm{e}^{-in\theta} d\theta$$

- sum of a fix/random number of variables drawn independently

$$B_2^{\text{fix}}(x) = \sum_{l\geq 0} b_l\, x^l = \sum_{l\geq 0}\sum_{n=0}^{l} a_n a_{l-n} x^l = \sum_{n\geq 0}^{\infty} a_n x^n \sum_{m\geq 0}^{\infty} a_m x^m = [A(x)]^2 \; ; \qquad B_p^{\text{fix}}(x) = [A(x)]^p \; ; \qquad C^{\text{rand}}(x) = \sum_{n\geq 0}^{\infty} a_n \big[A(x)\big]^n = A\big(A(x)\big)$$

Contact network epidemiology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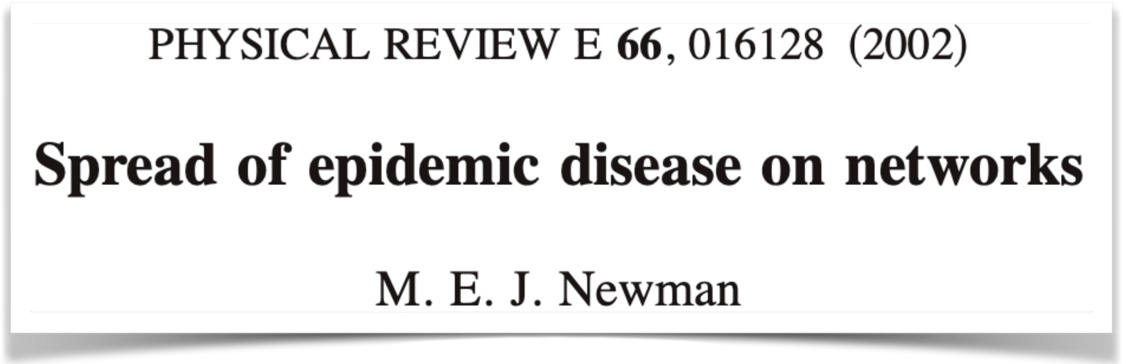
PHYSICAL REVIEW E **66**, 016128 (2002)

Spread of epidemic disease on networks

M. E. J. Newman

Probability generating functions (PGFs) formalism

- assuming a very, very large population (i.e. neglecting finite-size effects)
- patient zero causes k secondary infections with probability p_k (degree distribution of thfie network)

$$G_0(x) = \quad + \quad x + \quad x^2 + \quad x^3 + \ldots = \sum_{k\geq 0}^{\infty} p_k x^k \; ; \qquad \langle k \rangle = \sum_{k\geq 0}^{\infty} k\, p_k = G_0'(1) \; ; \qquad \langle k^2 \rangle = \sum_{k\geq 0}^{\infty} k^2\, p_k$$

- a newly infected individual causes k *new* infections with probability $(k+1)p_{k+1}/\langle k \rangle$ (*excess* degree distribution of the network)

$$G_1(x) = \quad + \quad x + \quad x^2 + \quad x^3 + \ldots = \sum_{k\geq 0}^{\infty} \frac{(k+1)p_{k+1}}{\langle k \rangle} x^k = \frac{G_0'(x)}{G_0'(1)}$$

- average number of secondary infections a newly infected individual causes

$$G_1'(1) = \frac{\langle k^2 \rangle - \langle k \rangle}{\langle k \rangle} \equiv R_0$$

- *all* outbreaks will eventually die out when $R_0 < 1$
- *some* outbreaks will eventually die out when $R_0 > 1$

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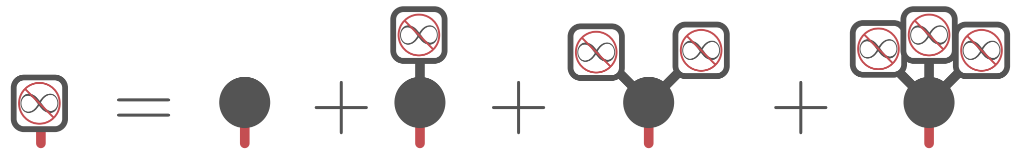
- probability u that an outbreak eventually dies out

$$u =$$



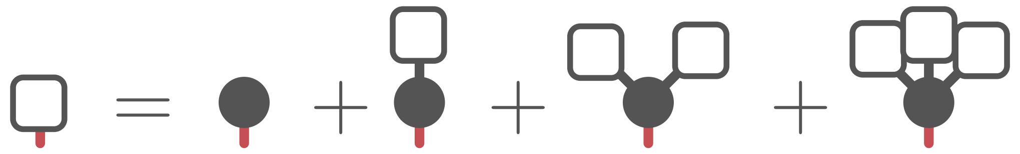
$$+ \dots = \sum_{k\geq 0}^{\infty} \frac{(k+1)p_{k+1}}{\langle k \rangle} u^k = G_1(u)$$

- the fraction of the population infected in an epidemic wave (and the probability of such wave) is

$$R(\infty) = \sum_{k\geq 0}^{\infty} p_k(1-u^k) = 1 - G_0(u)$$

- $H_0(x)$: PGF of the distribution of the size of outbreaks that will eventually die out

$$H_1(x) =$$



$$+ \dots = x \sum_{k\geq 0}^{\infty} \frac{(k+1)p_{k+1}}{\langle k \rangle} \left[H_1(x)\right]^k = xG_1\big(H_1(x)\big)$$

- the distribution of the size of outbreaks that will eventually die out can be extracted from

$$H_0(x) = xG_0\big(H_1(x)\big)$$

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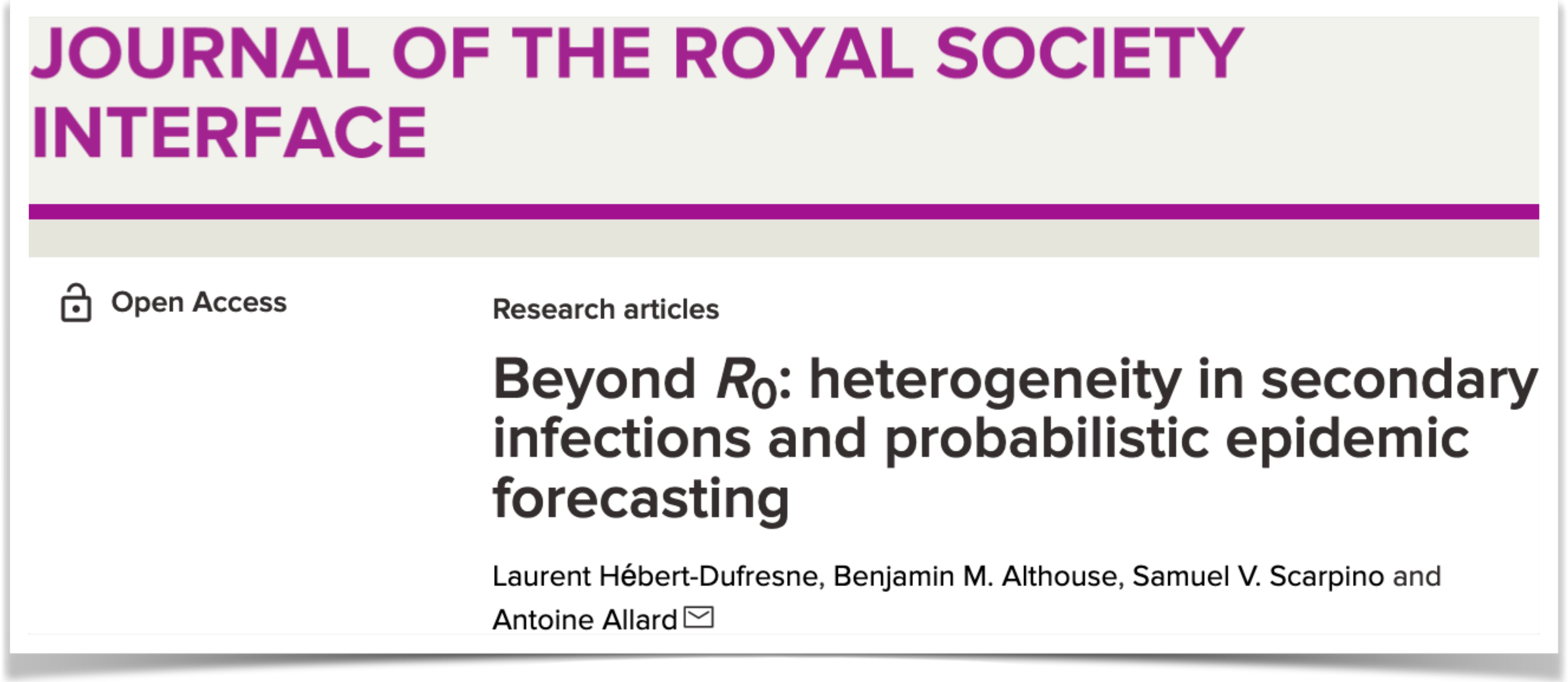
Laurent Hébert-Dufresne, Benjamin M. Althouse, Samuel V. Scarpino and Antoine Allard

Message #1 : the friendship paradox

- on average, your friends have more friends than you do
  - $\rightarrow$ a random individual has k friends with probability p_k
  - $\rightarrow$ however, their friends have k friends with probability $\propto kp_k$
- by spreading on a contact network, the disease naturally over-samples individuals more likely to cause a larger number of secondary infections
- ignoring this effect leads back to the mass-action assumption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Message #2 : the effect of superspreading events

- the PGF formalism falls back to the outcome of the SIR dynamics when p_k is a Poisson distribution

$$G_0(x) = G_1(x) = \mathrm{e}^{R_0(x-1)} \; ; \qquad R(\infty) = 1 - \mathrm{e}^{-R_0 R(\infty)}$$

- the mass-action assumption is not appropriate for diseases whose propagation is driven by superspreading events

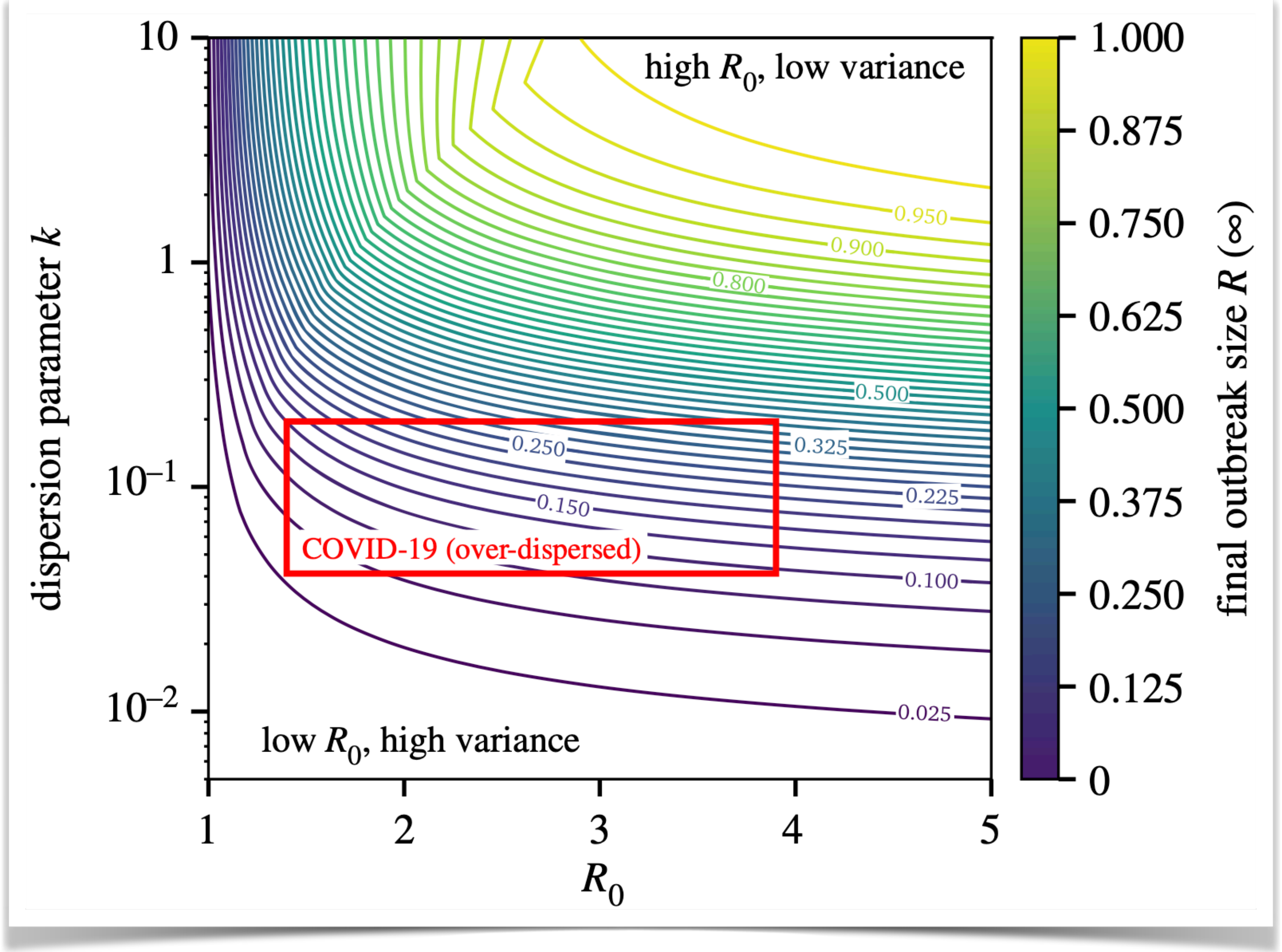
Message #3 : we need to look beyond R_0 for overdispersed infectious diseases like COVID-19

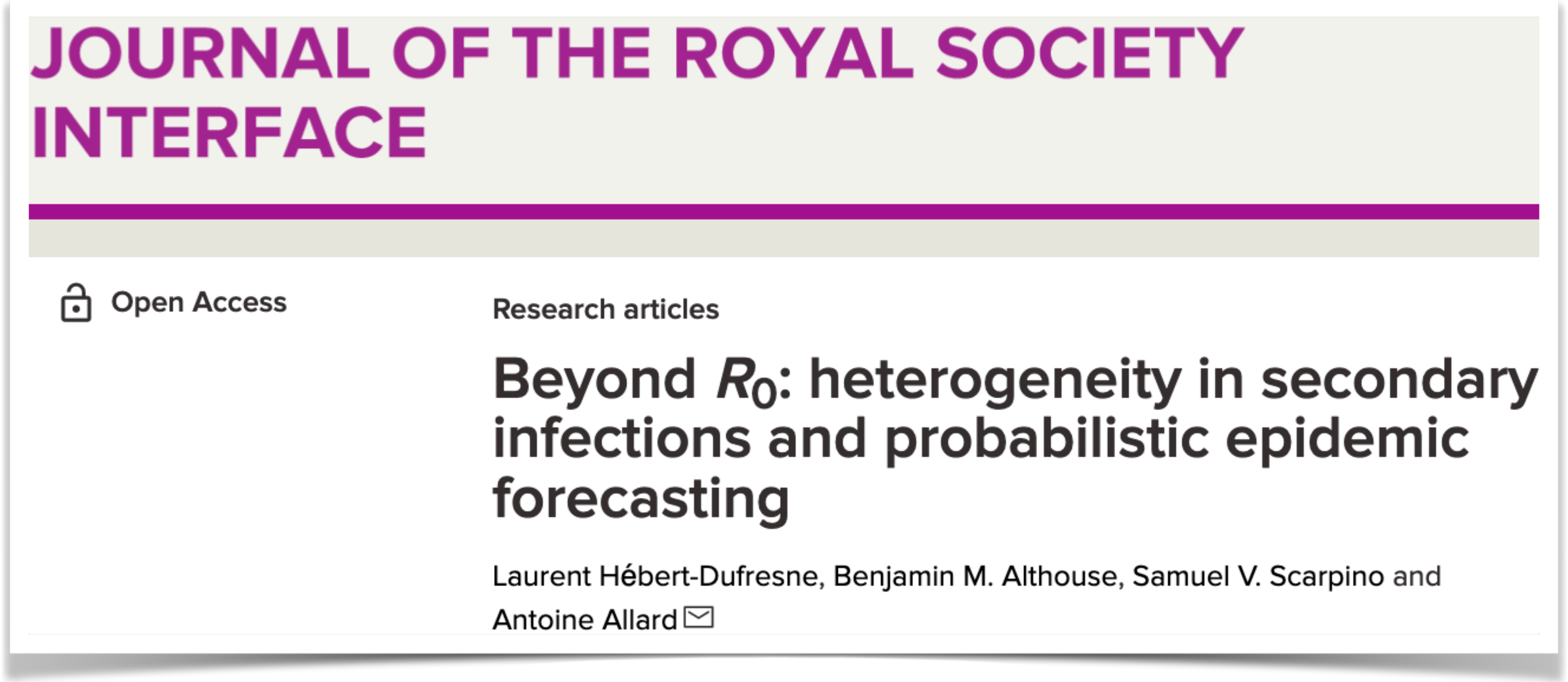
- negative binomial distribution for secondary cases

$$G_1(x) = \left[1 + \frac{R_0(x-1)}{\gamma}\right]^{-\gamma}$$

  shows the great impact overdispersion (small γ) has on the spreading dynamics

- in other words, if $R_0 > 1$, our attention should not be focused on whether R_0 equals 2.5 or 3.5, but rather be focused on figuring out how much heterogeneity there is behind it (what is γ?)





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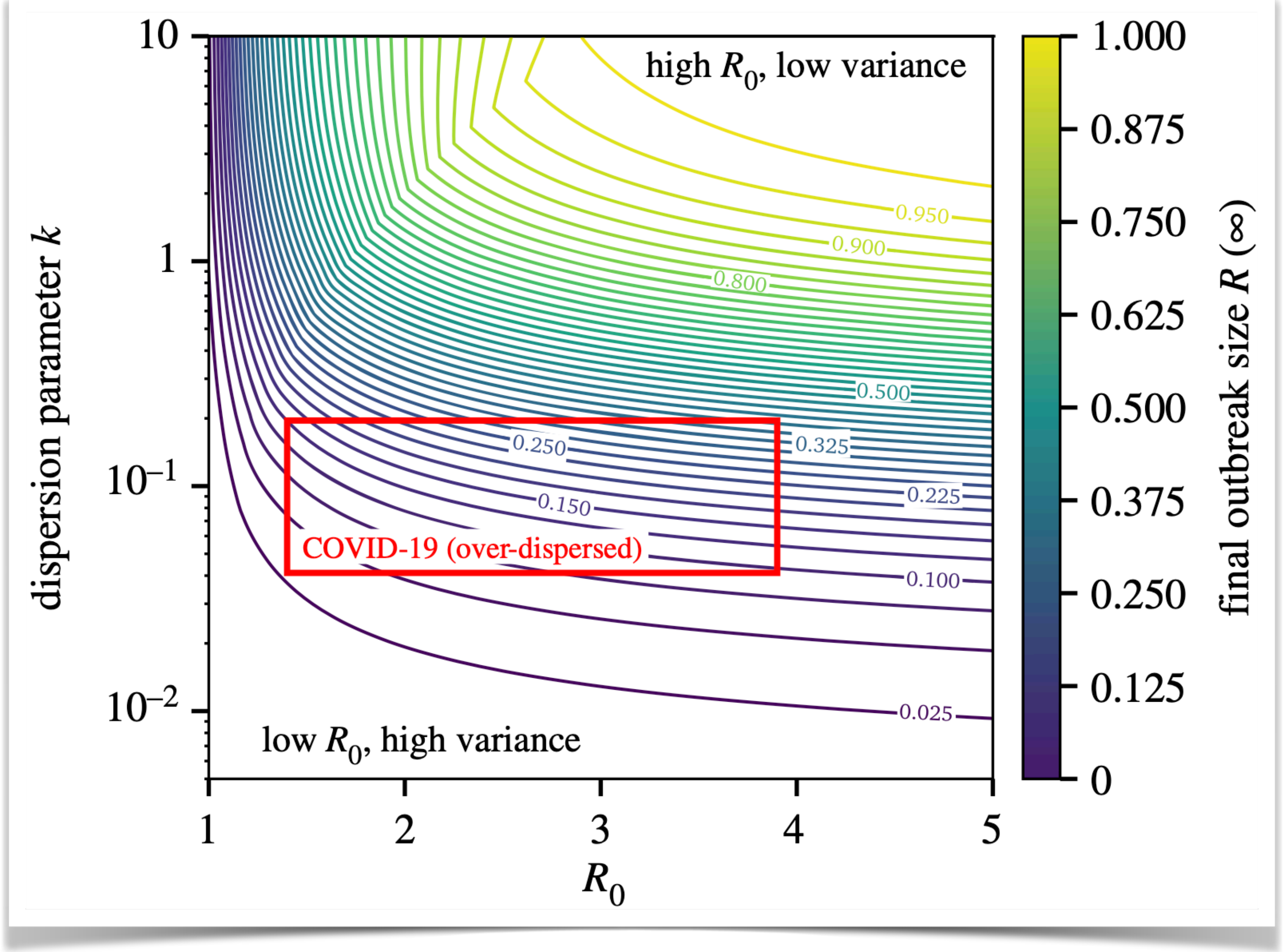

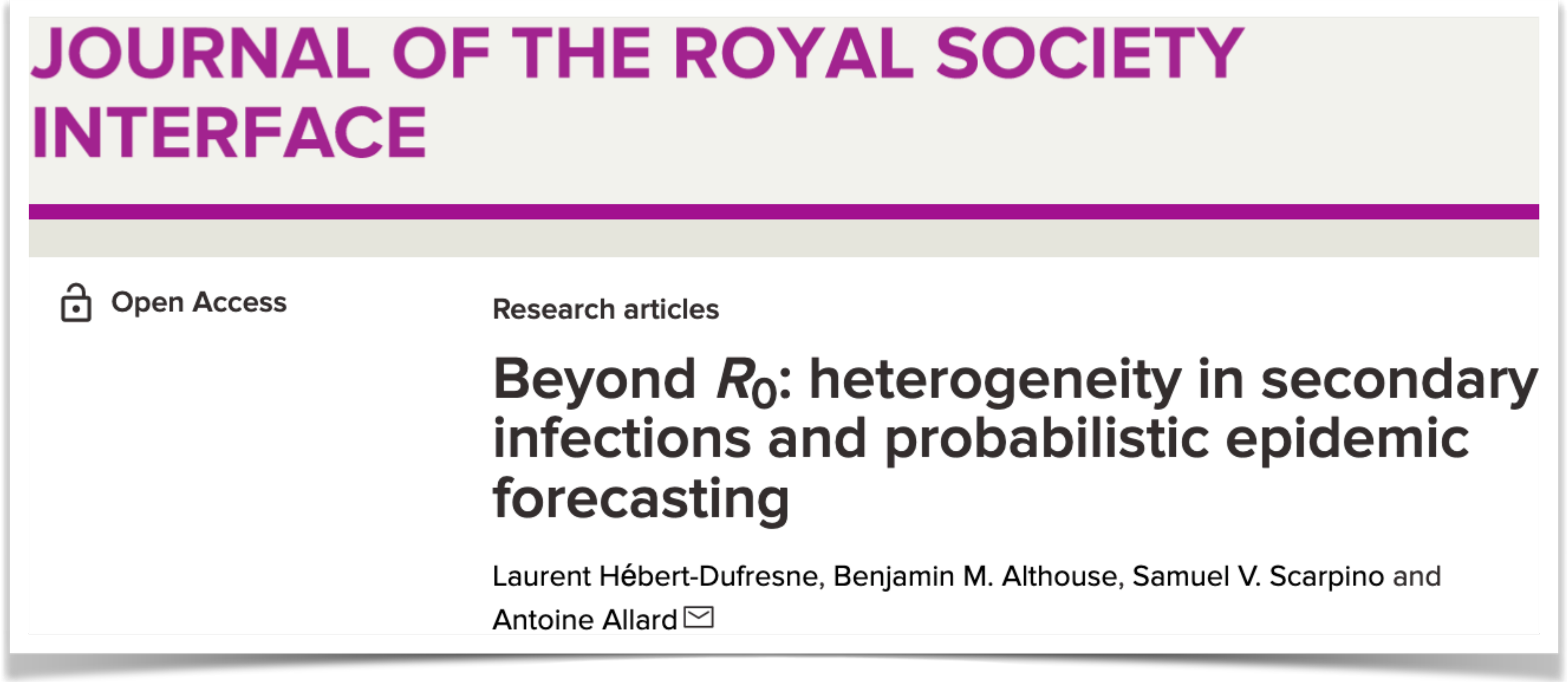

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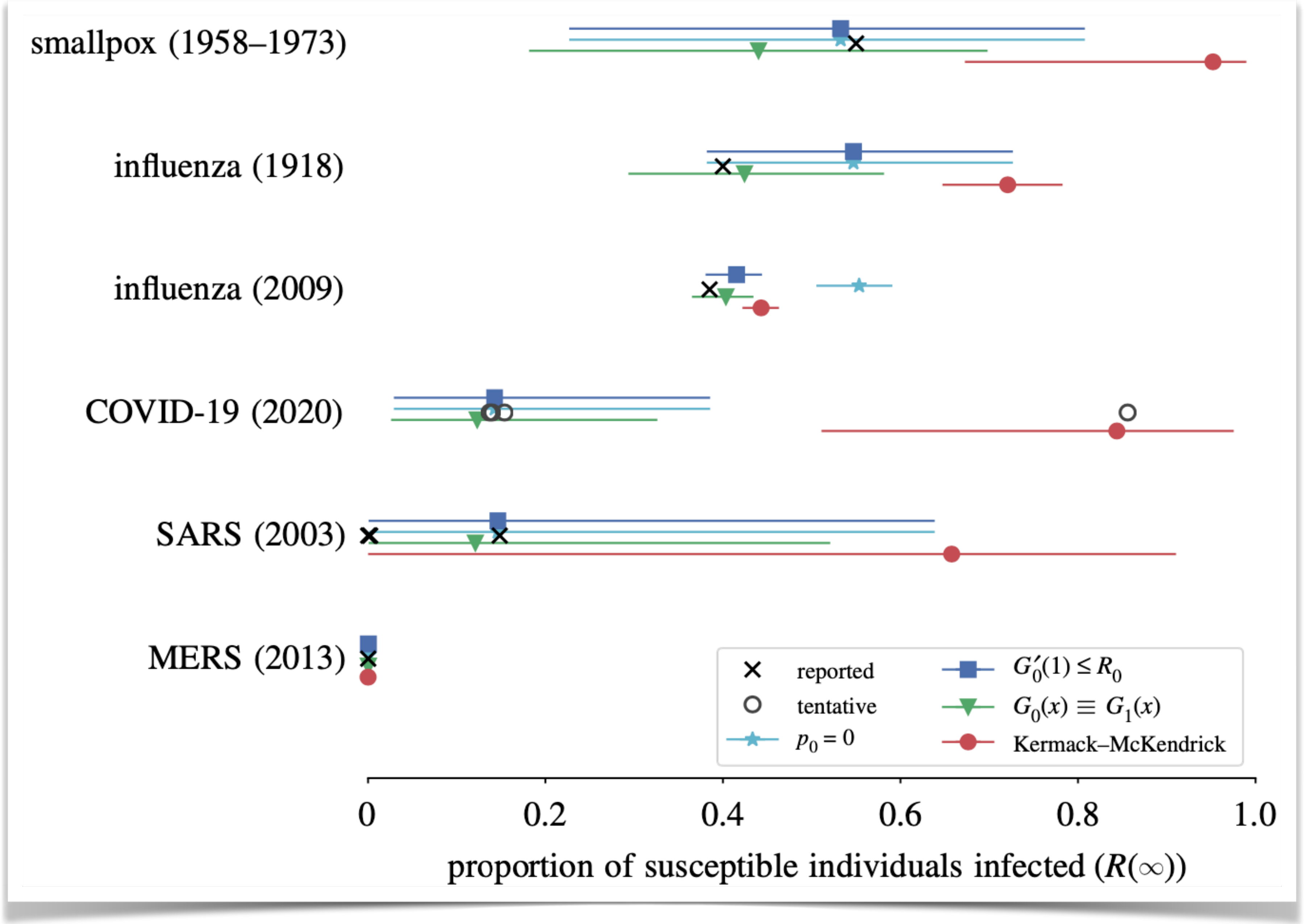
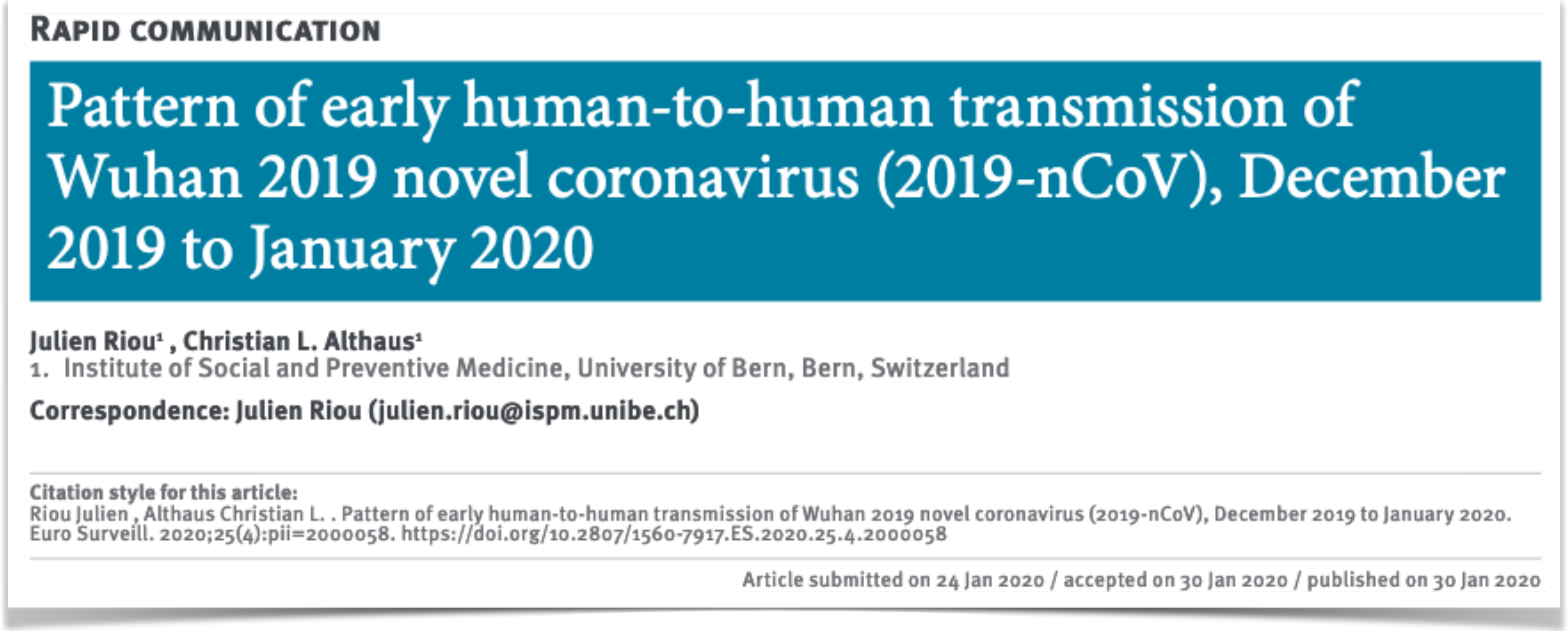
Message #4 : COVID-19 is particularly overdispersed

— plans prepared with pandemic Influenza in mind might fall short to contain the spread of COVID-19



And then came an email…

[…] As you can see, the stochastic simulations reach the same size as predicted from the classic final size equation. k doesn't seem to play a role at all. […]



Rapid communication

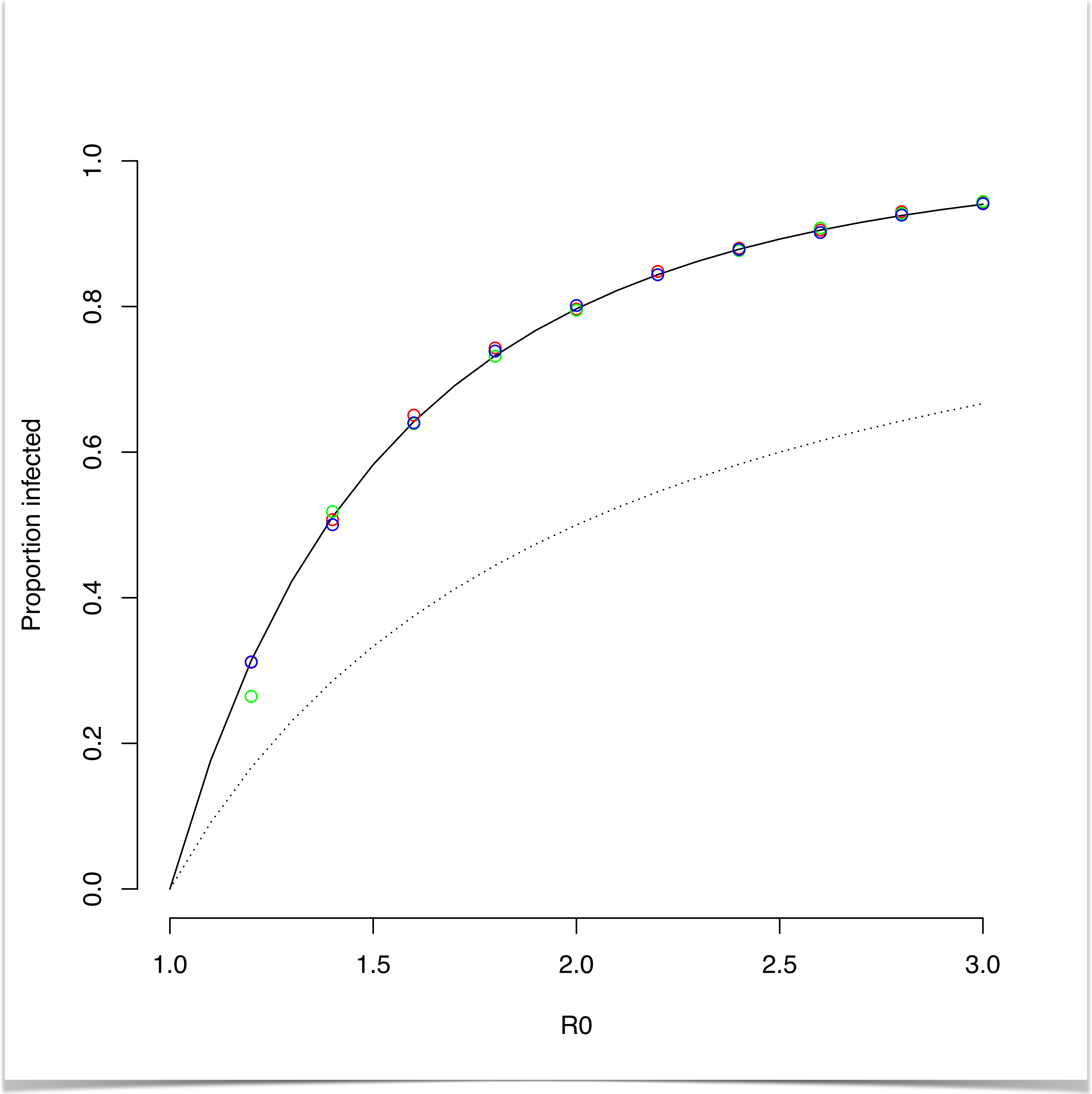
Pattern of early human-to-human transmission of Wuhan 2019 novel coronavirus (2019-nCoV), December 2019 to January 2020

Julien Riou[1], Christian L. Althaus[1]
1. Institute of Social and Preventive Medicine, University of Bern, Bern, Switzerland

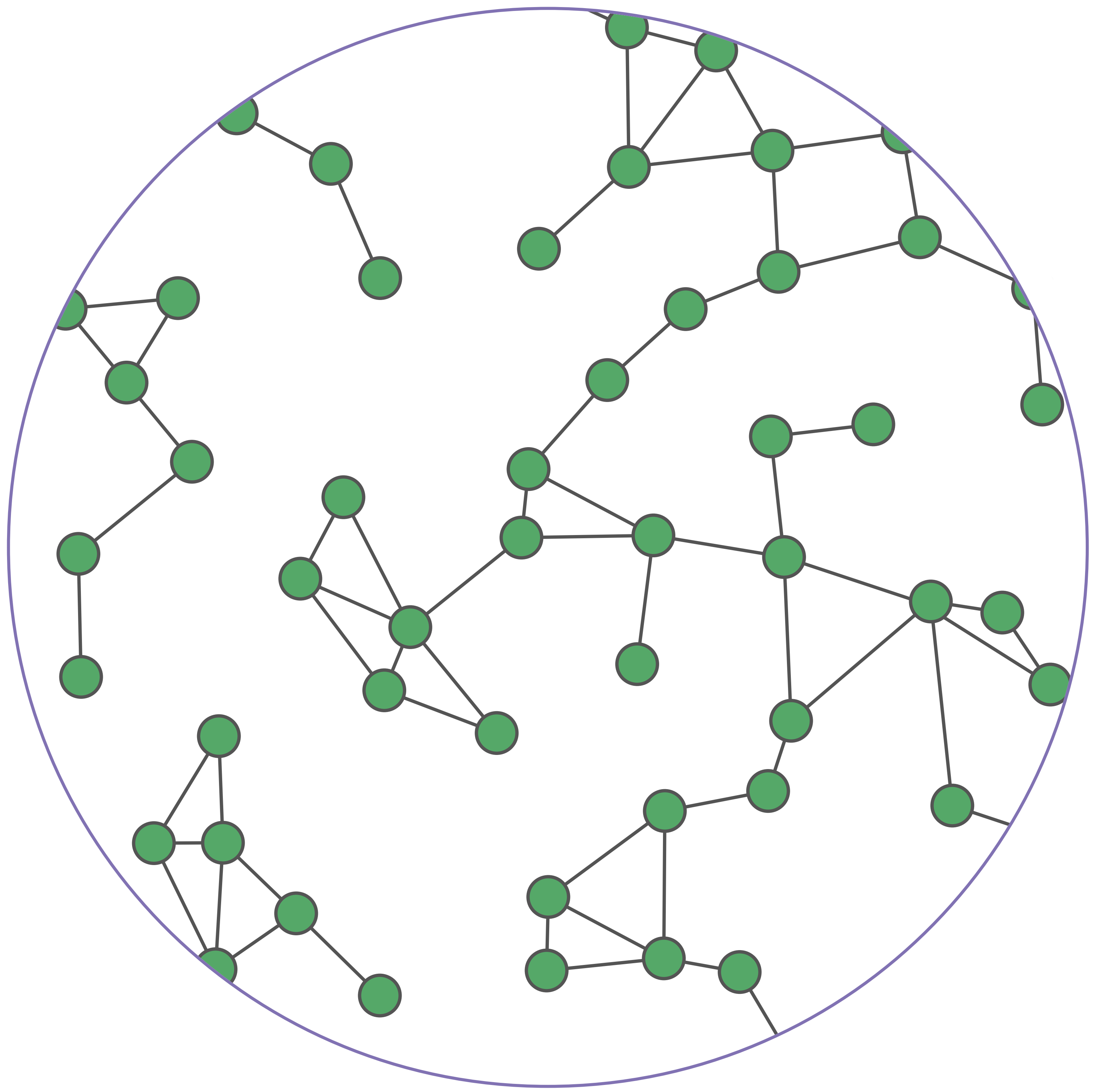
Correspondence: Julien Riou (julien.riou@ispm.unibe.ch)

Citation style for this article:
Riou Julien, Althaus Christian L.. Pattern of early human-to-human transmission of Wuhan 2019 novel coronavirus (2019-nCoV), December 2019 to January 2020. Euro Surveill. 2020;25(4):pii=2000058. https://doi.org/10.2807/1560-7917.ES.2020.25.4.2000058

Article submitted on 24 Jan 2020 / accepted on 30 Jan 2020 / published on 30 Jan 2020



Answer in the form of a question : How correlated are the in- and out-degrees ?



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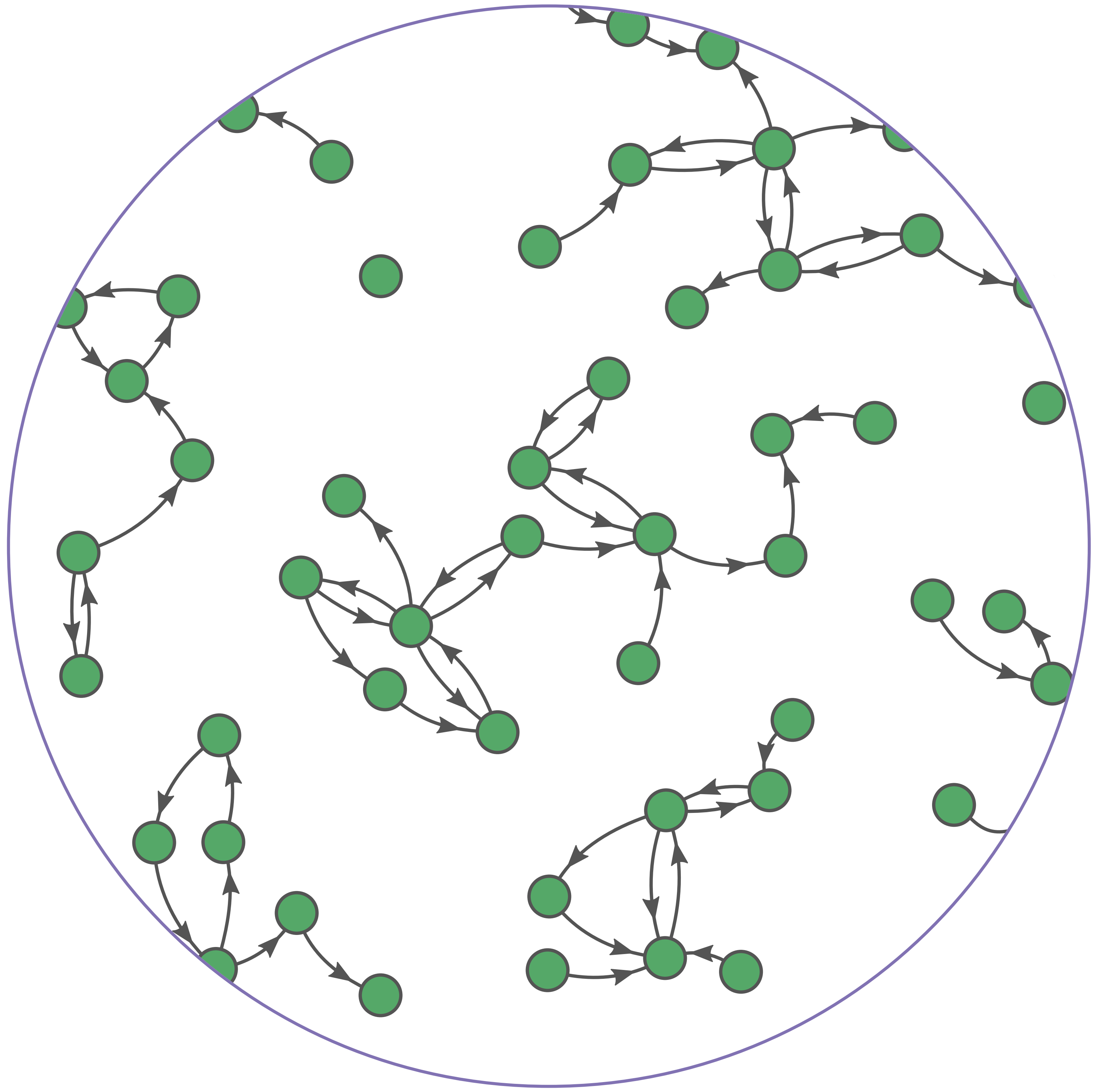

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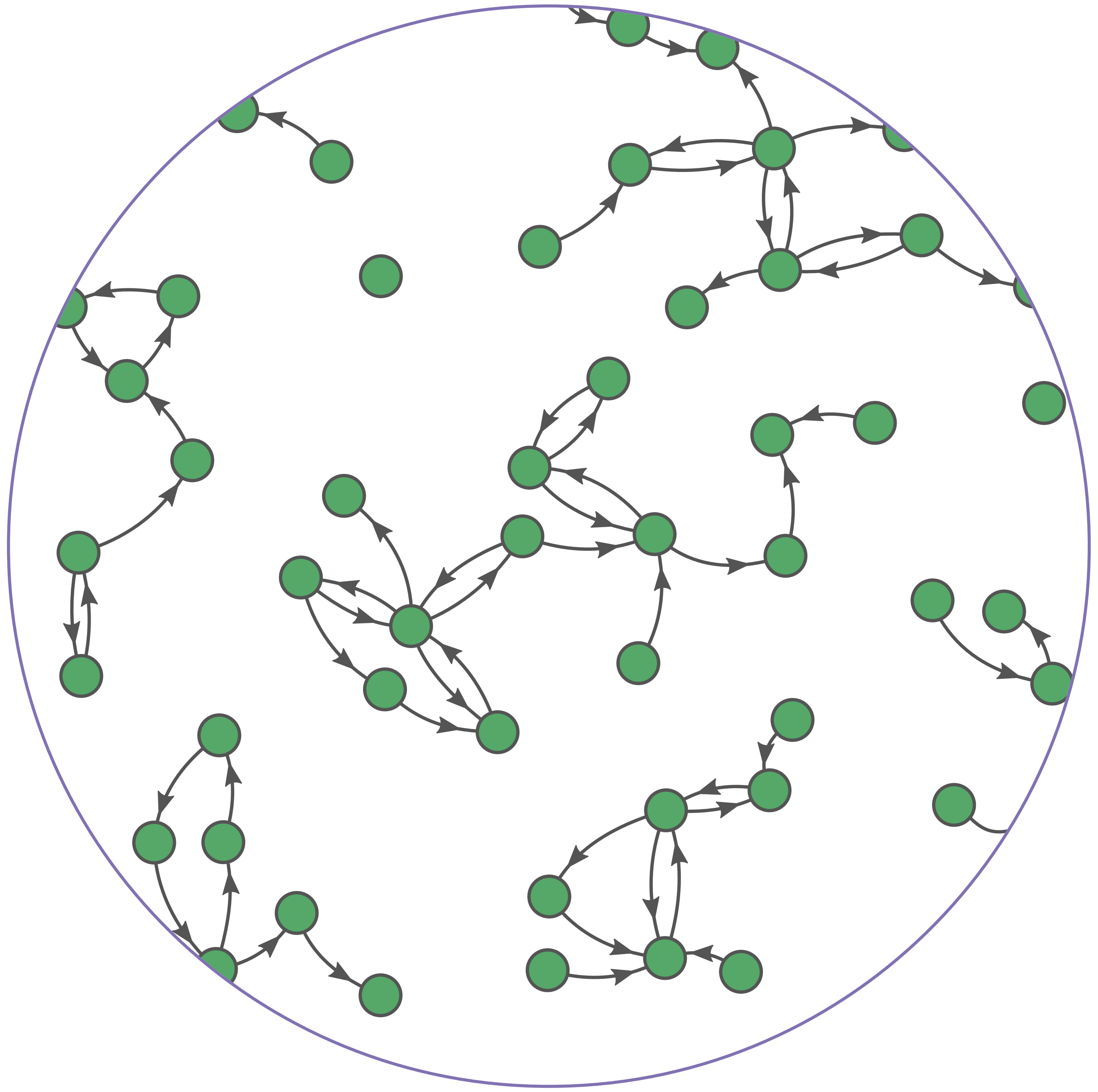

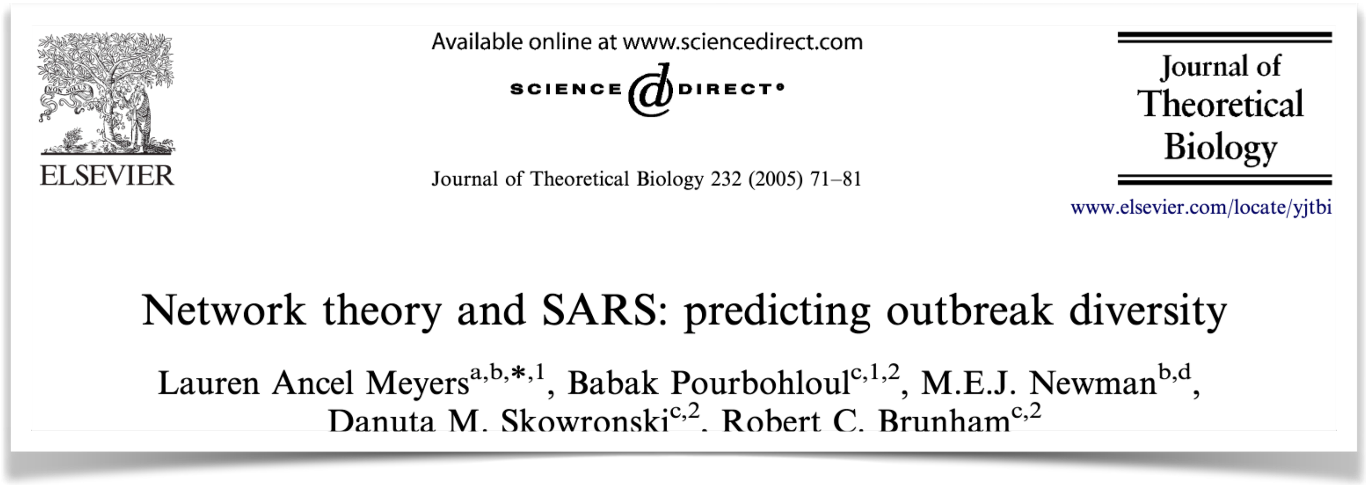

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Journal of Theoretical Biology 232 (2005) 71–81

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Network theory and SARS: predicting outbreak diversity

Lauren Ancel Meyers[a,b,*,1], Babak Pourbohloul[c,1,2], M.E.J. Newman[b,d], Danuta M. Skowronski[c,2], Robert C. Brunham[c,2]

1. R_0 depends on the correlation between in-and out-degrees

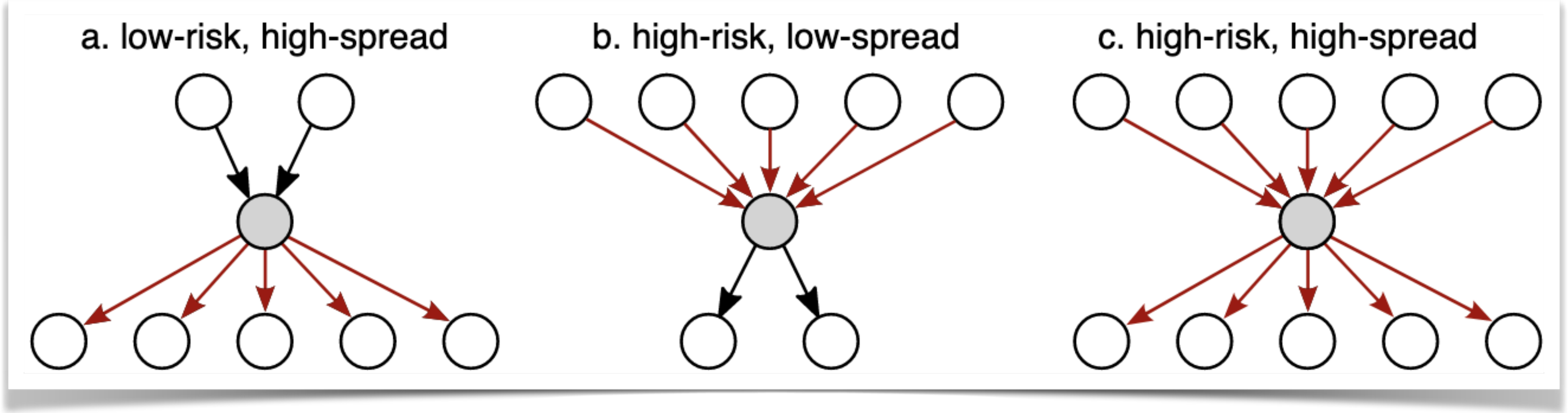
$$R_0 = \frac{\langle k_{\text{in}} k_{\text{out}} \rangle}{\langle k_{\text{in}} \rangle}$$

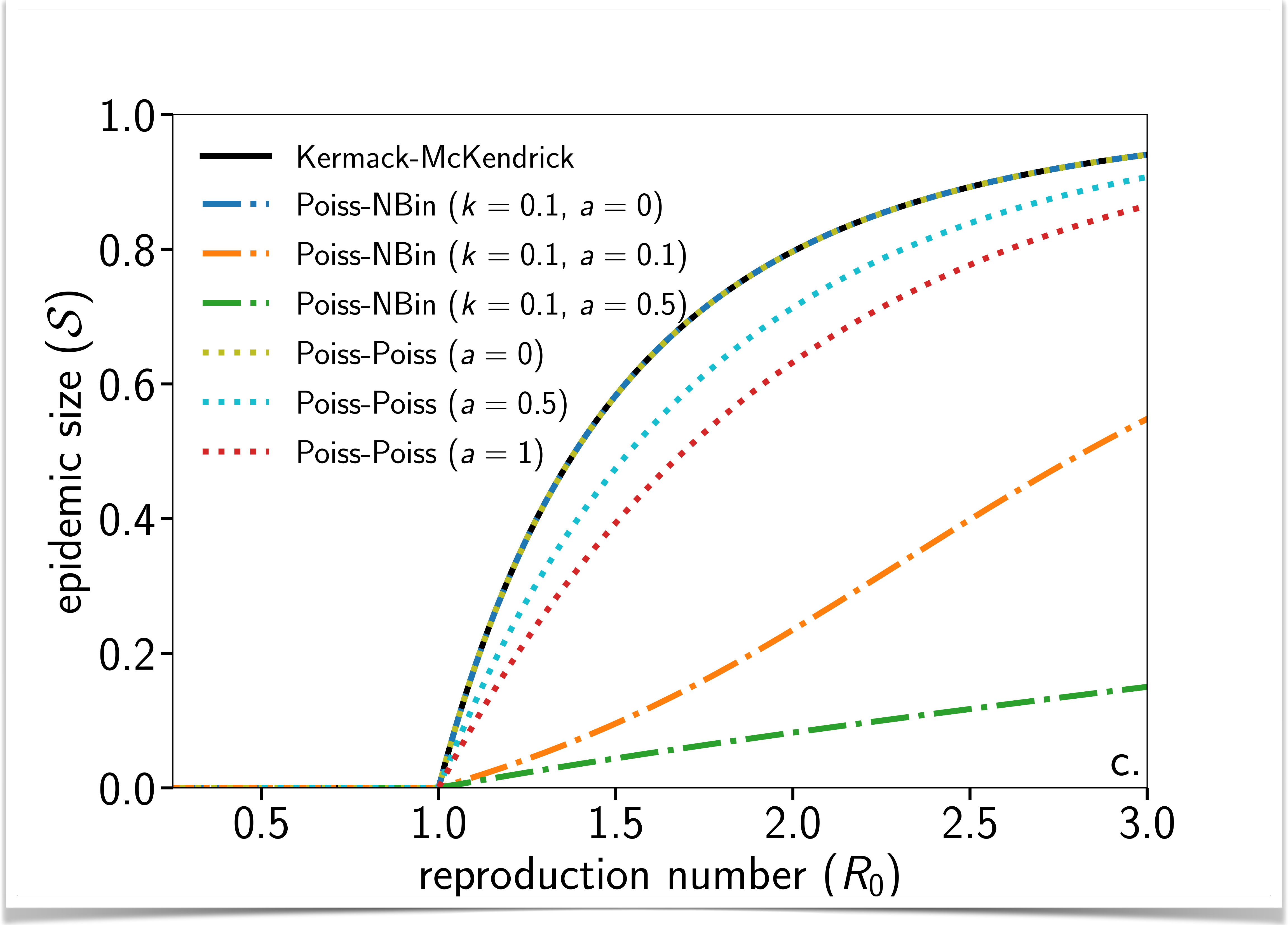
2. Expected probability of an epidemic is mainly governed by the *forward* friendship paradox (out-degrees)

3. Expected outbreak size is mainly governed by the *backward* friendship paradox (in-degrees)

Message #1 : distinction between “risk” and “spread”

- risk : contacts through which an individual can become infected (in-degree)
- spread : number of potential secondary infections if infected (out-degree)
- correlation between risk and spread greatly affects the likelihood of an epidemic as well as its size





Message #2 : *backward* contact tracing

— following links in the network in their opposite direction over-samples individuals that will cause a larger number of secondary cases

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https://doi.org/10.1038/s41567-021-01187-2

nature physics

Check for updates

The effectiveness of backward contact tracing in networks

Sadamori Kojaku[1], Laurent Hébert-Dufresne[2,3], Enys Mones[4], Sune Lehmann[4,5] and Yong-Yeol Ahn[1,6,7]

Message #3 : connection with structured differential equation models

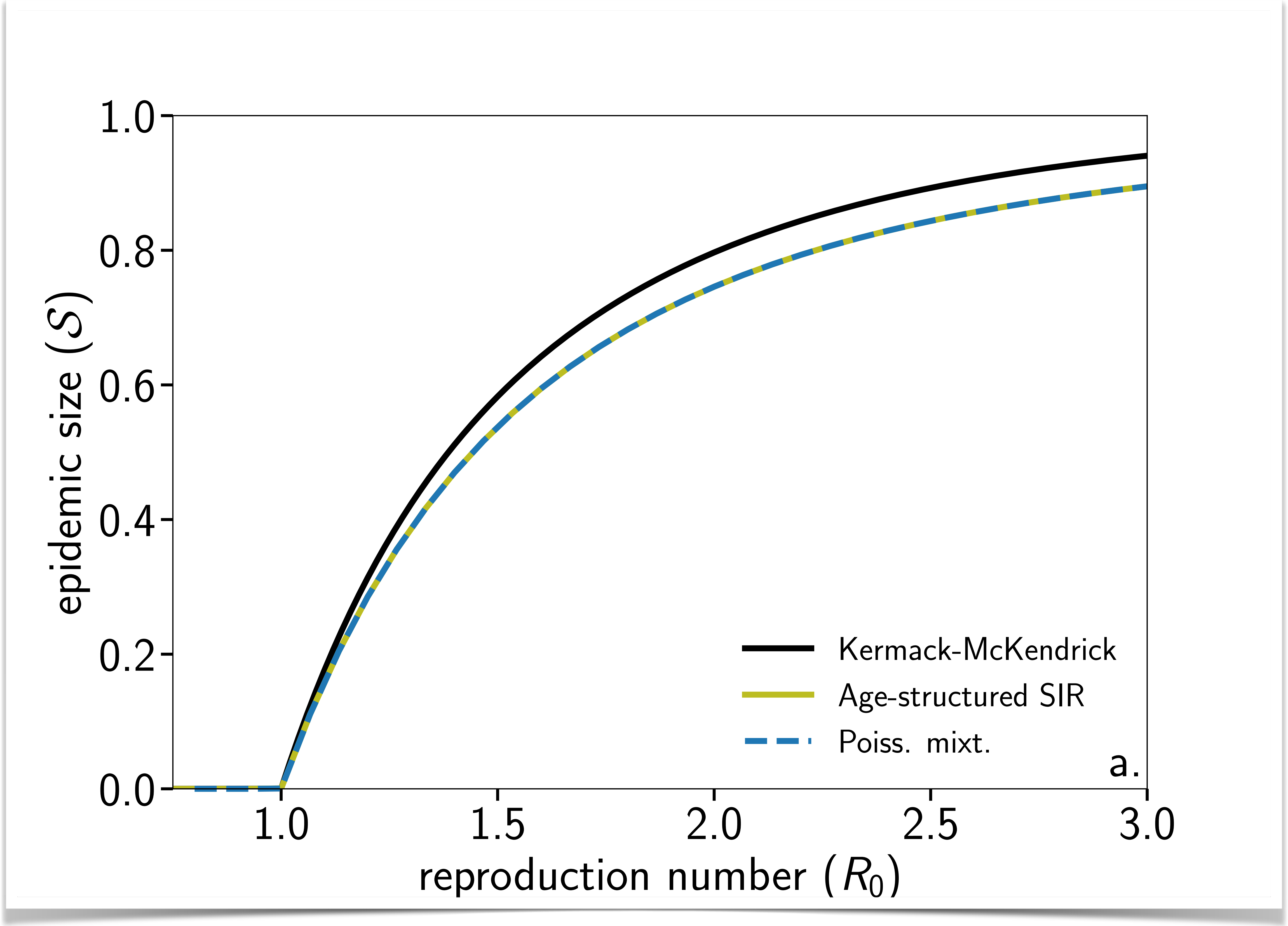
- mass-action assumes the risk for individuals to become infected is uniformly distributed (i.e. in-degree in the network is distributed according to a Poisson distribution) and is independent of spread
- the final epidemic size can be mapped to a mixture of Poisson in-degree distribution

$$\dot{S}_i(t) = -\beta\sigma_i \sum_j M_{ij} \frac{I_j}{N} S_i \, ,$$

$$\dot{I}_i(t) = \beta\sigma_i \sum_j M_{ij} \frac{I_j}{N} S_i - \gamma I_i \, ,$$

$$\dot{R}_i(t) = \gamma I_i \, ,$$

Science 368, 1481–1486 (2020)



One-sentence conclusion : Embracing networks is an important paradigm shift, but overlooking asymmetric interactions can hide important phenomena.

Laurent Hébert-Dufresne (University of Vermont)

Samuel V. Scarpino (Northeastern University)

Cristopher Moore (Santa Fe Institute)

Benjamin M. Althouse (Truveta)

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