Network Epidemiology

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SANTA FE
INSTITUTE

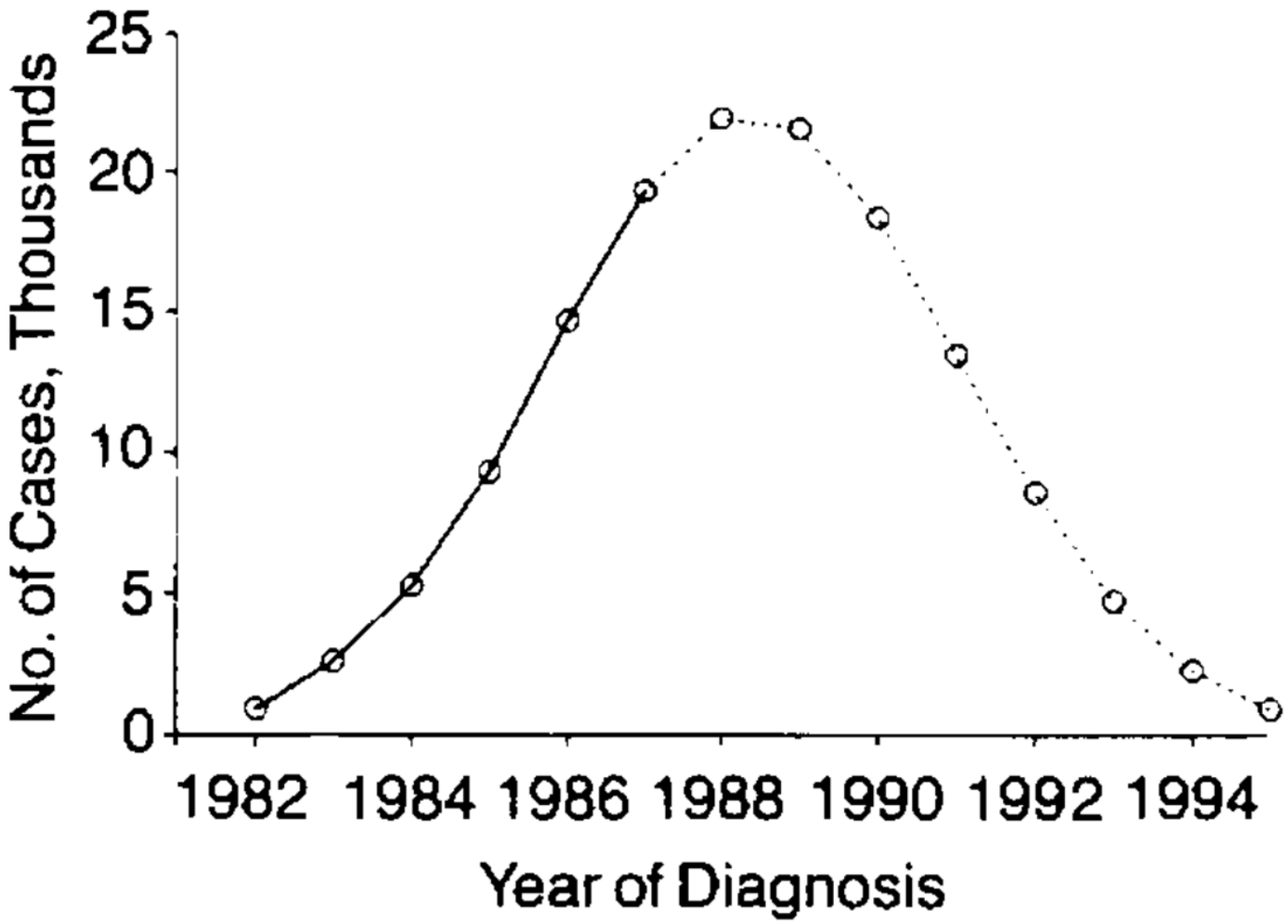
We can’t stop pandemics without using real-time, high-resolution mobility data.

Farr's Law

Epidemics appear to be generated at intervals in unhealthy places, spread, and go through a regular course, and decline; but of the cause of their evolutions no more is known than of the periodical paroxysms of ague. . . . If the latent cause of epidemics cannot be discovered, the mode by which it operates may be investigated. The laws of its action may be determined by observation.

Farr's Law Applied to AIDS Projections

Dennis J. Bregman, PhD, Alexander D. Langmuir, MD, MPH



Darakjy *et al. Injury Epidemiology* 2014, **1**:31
http://www.injepijournal.com/content/1/1/31

Injury Epidemiology
a SpringerOpen Journal

SHORT REPORT Open Access

Applying Farr's Law to project the drug overdose mortality epidemic in the United States

Salima Darakjy[1], Joanne E Brady[1,2,3], Charles J DiMaggio[1,2,3] and Guohua Li[1,2,3*]

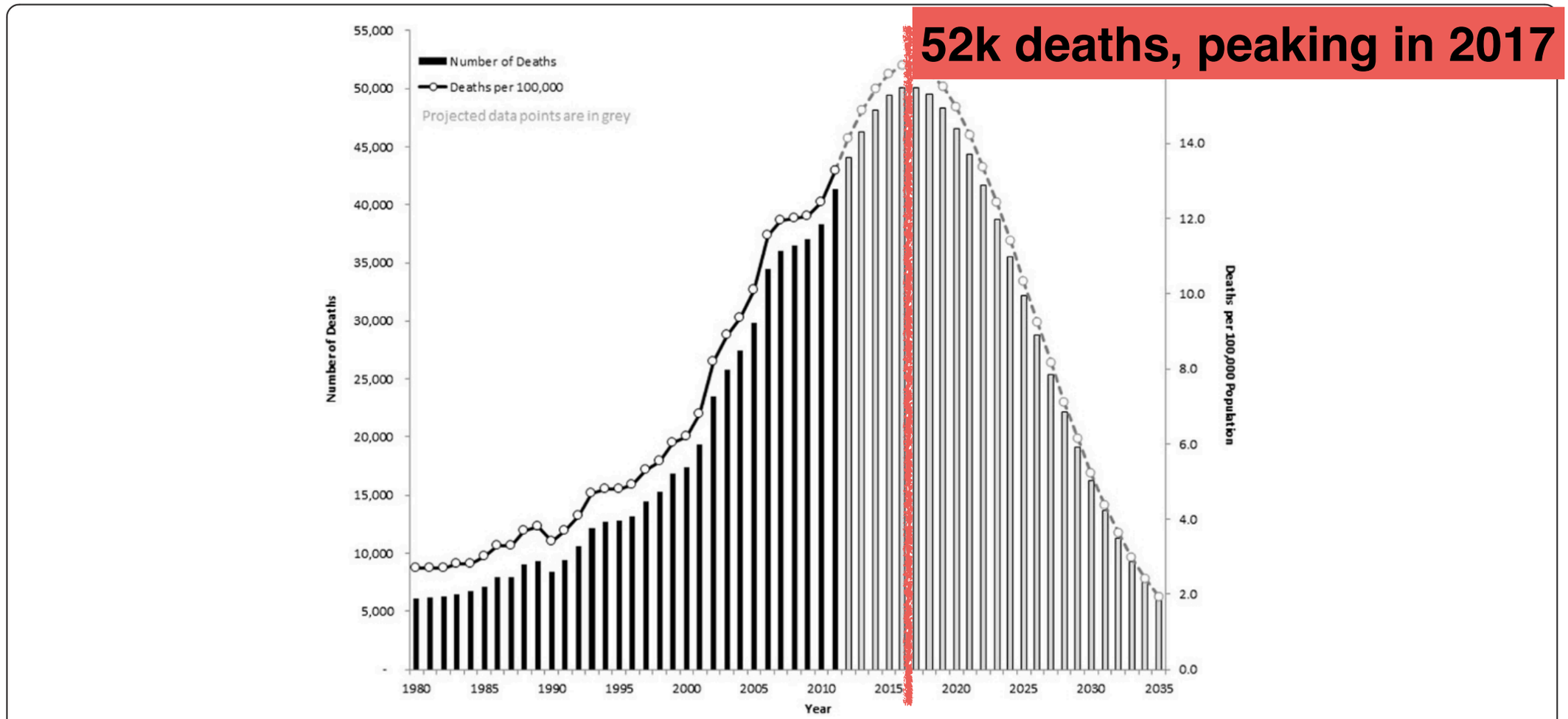


Figure 1 Annual mortality from drug overdose in the United States 1980–2011, with projections through 2035 based on Farr's Law (grey data points).

Centers for Disease Control and Prevention
CDC 24/7: Saving Lives, Protecting People™

National Center for Health Statistics

NCHS Pressroom

Weekly COVID-19 Mortality Overview

2022 Release Schedule

Upcoming

Publications Archives

Drug Overdose Deaths in the U.S. Top 100,000 Annually

For Immediate Release: November 17, 2021

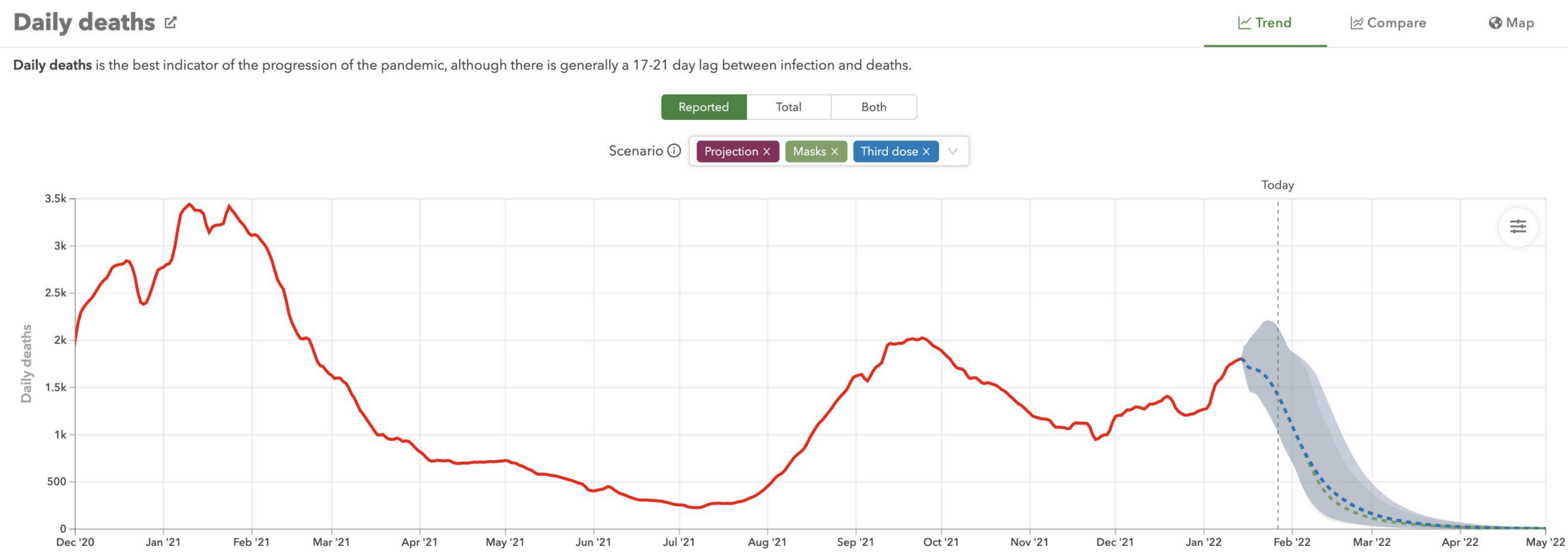
Contact: CDC, National Center for Health Statistics, Office of Communication (301) 458-4800
E-mail: paoquery@cdc.gov

Figure 1 Annual mortality from drug overdose in the United States 1980–2011, with projections through 2035 based on Farr's Law (grey data points).

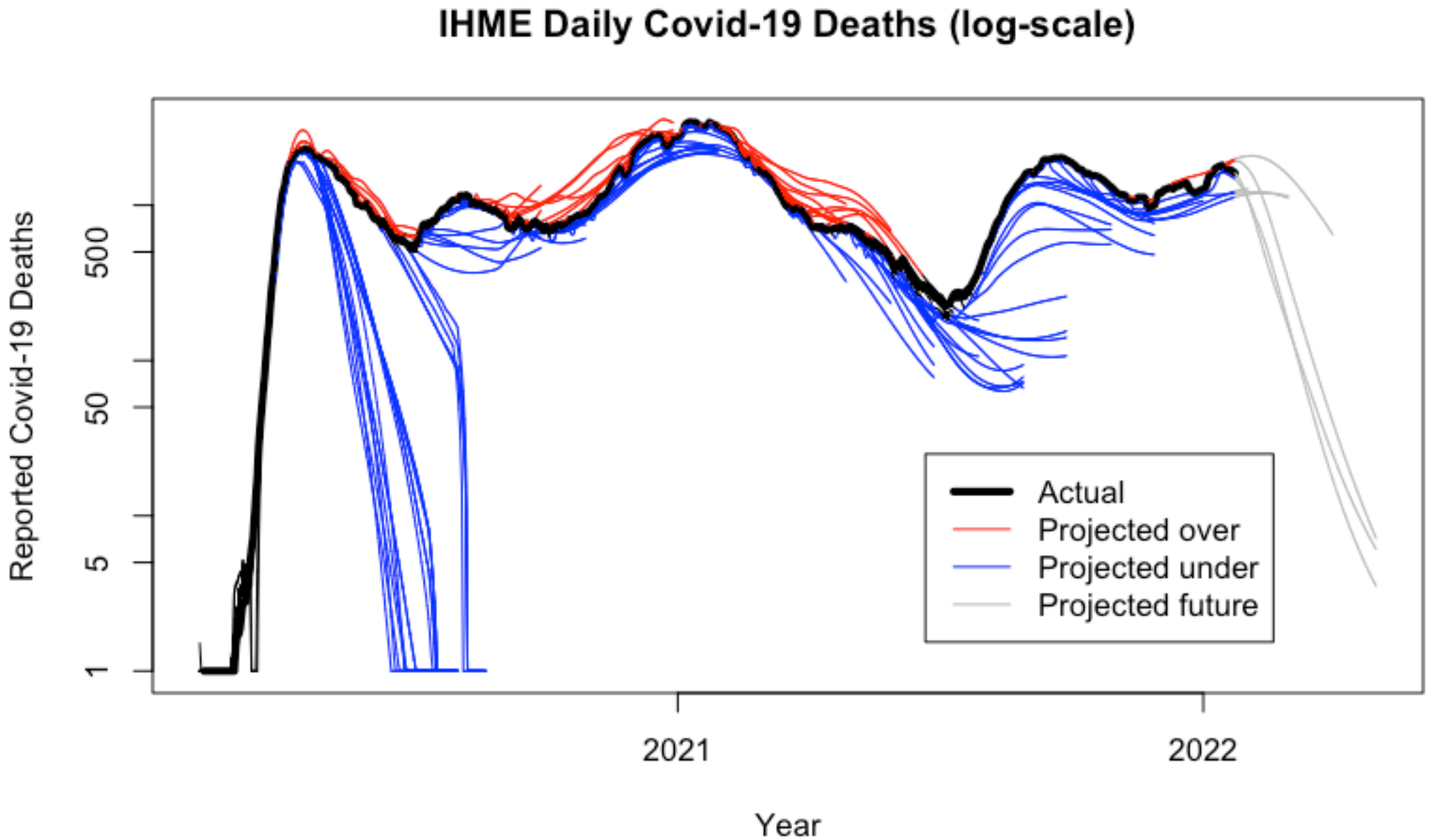
https://www.cdc.gov/nchs/pressroom/nchs_press_releases/2021/20211117.htm

Farr's Law* Applied to COVID Projections

Institute for Health Metrics and Evaluation (IHME)

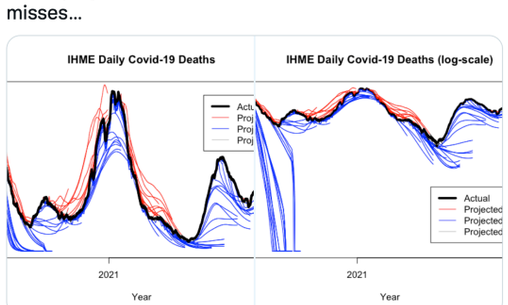


*IHME moved to slightly more realistic model in mid-2020

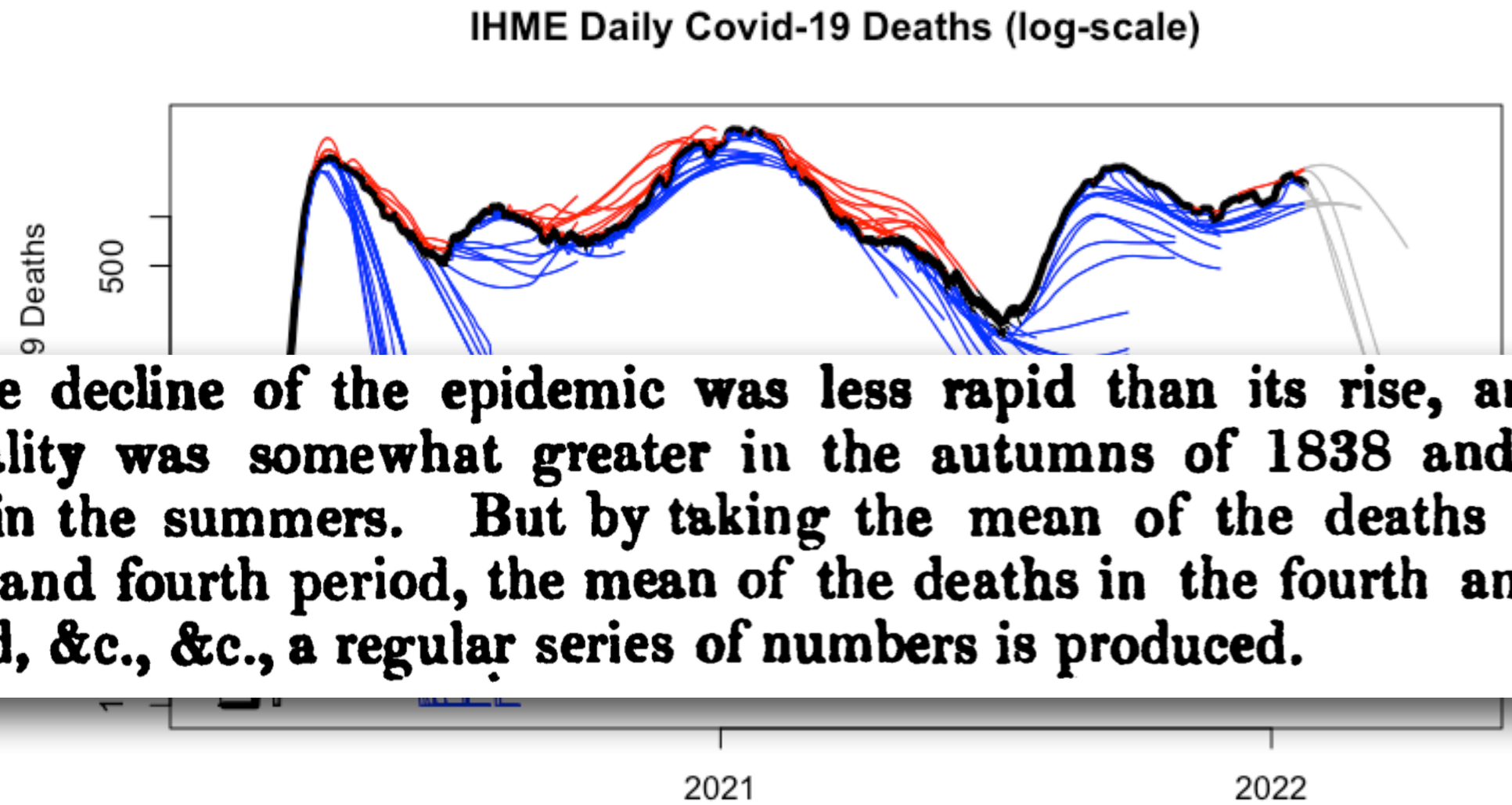


Eric F. Lock
@Doc__Lock

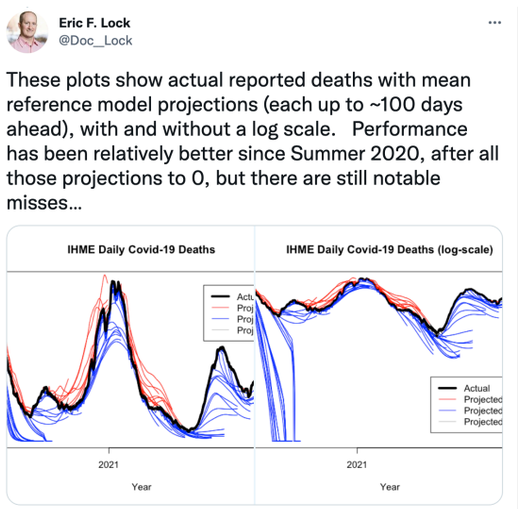
These plots show actual reported deaths with mean reference model projections (each up to ~100 days ahead), with and without a log scale. Performance has been relatively better since Summer 2020, after all those projections to 0, but there are still notable misses...



https://twitter.com/Doc__Lock/status/1487073555208622081?s=20&t=WJfKGQRUjp2R-I0lqEjUag



The decline of the epidemic was less rapid than its rise, and the mortality was somewhat greater in the autumns of 1838 and 1839 than in the summers. But by taking the mean of the deaths in the third and fourth period, the mean of the deaths in the fourth and fifth period, &c., &c., a regular series of numbers is produced.



https://twitter.com/Doc__Lock/status/1487073555208622081?s=20&t=WJfKGQRUjp2R-I0lqEjUag

We* keep using models we** know are wrong

SARS

H1N1

Ebola

Zika

SARS-CoV-2

*I'm not saying who "we" includes
**This "we" might not be the same subset

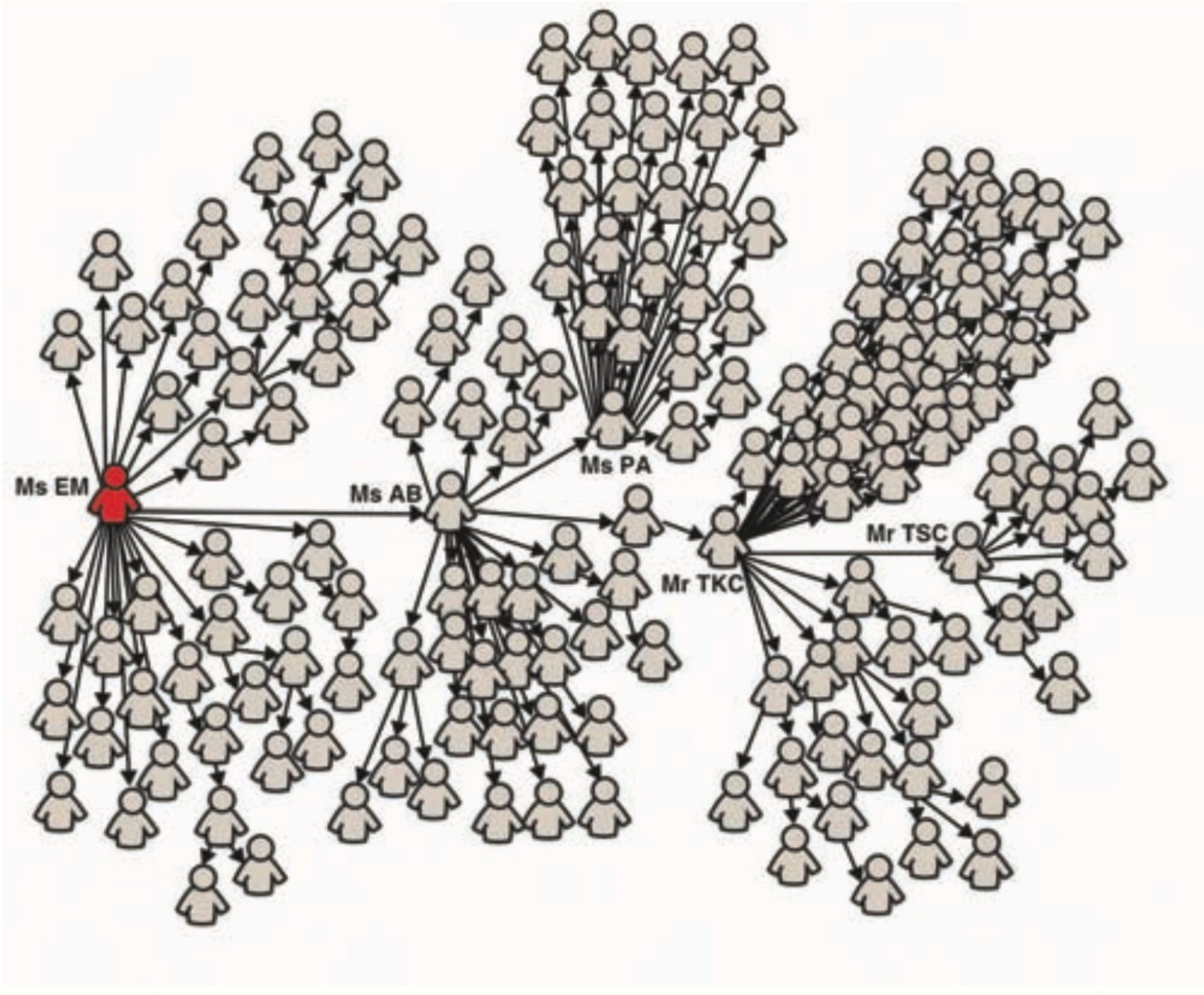
The SARS Scare

// A cautionary tale of emerging disease caught in the act

by Jonathan Shaw

At the height of the epidemic, one Canadian infectious-disease expert who had come down with SARS herself predicted that the virus would spread around the globe: "If we don't have a vaccine—yes, we are all going to get it," she told Canadian television. Her opinion was shared by many that spring.

WORLD HEALTH ORGANIZATION REGIONAL OFFICE FOR THE WESTERN PACIFIC 2005



This diagram detailing SARS transmission in Singapore shows the important role of "super-spreaders" in transmitting the disease. Five people caused more than half of the 205 cases there.

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]

[a]*Section of Integrative Biology and Institute for Cellular and Molecular Biology, University of Texas at Austin, 1 University Station C0930, Austin, TX 78712, USA*

[b]*Santa Fe Institute, 1399 Hyde Park Road, Santa Fe, NM 87501, USA*

[c]*University of British Columbia Centre for Disease Control, 655 West 12th Avenue, Vancouver, British Columbia, Canada V5Z 4R4*

[d]*Center for the Study of Complex Systems, University of Michigan, Randall Laboratory, 500 E. University Ave., Ann Arbor, MI 48109-1120, USA*

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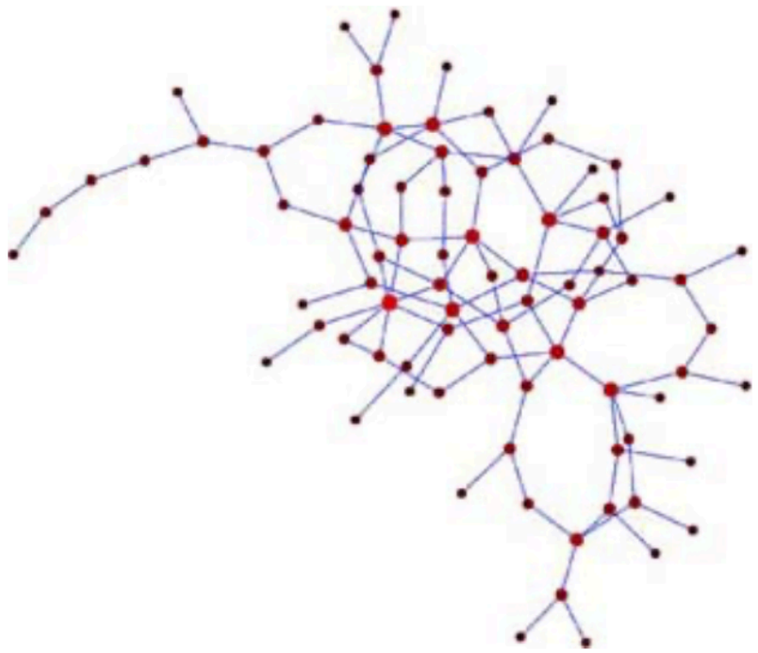
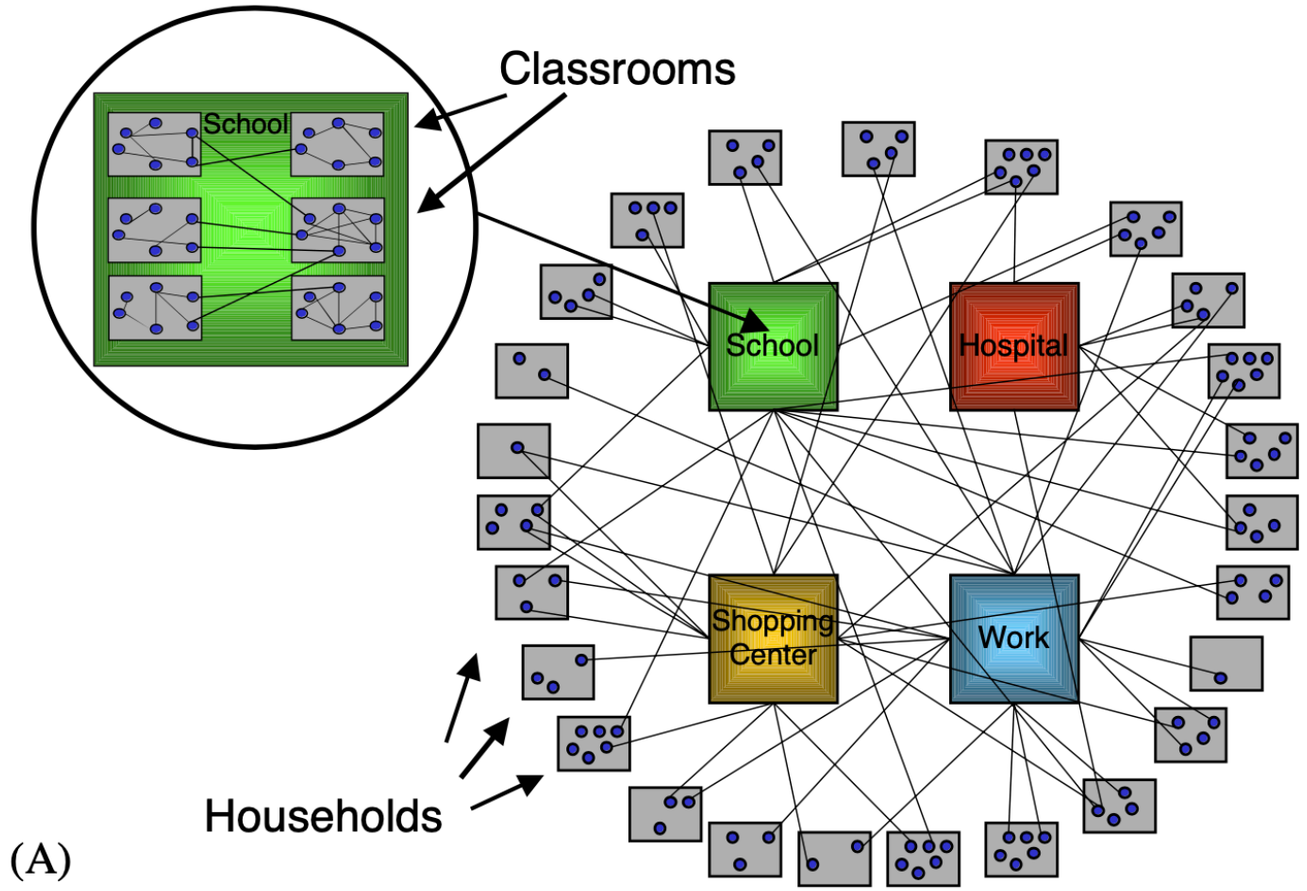
Available online 23 September 2004

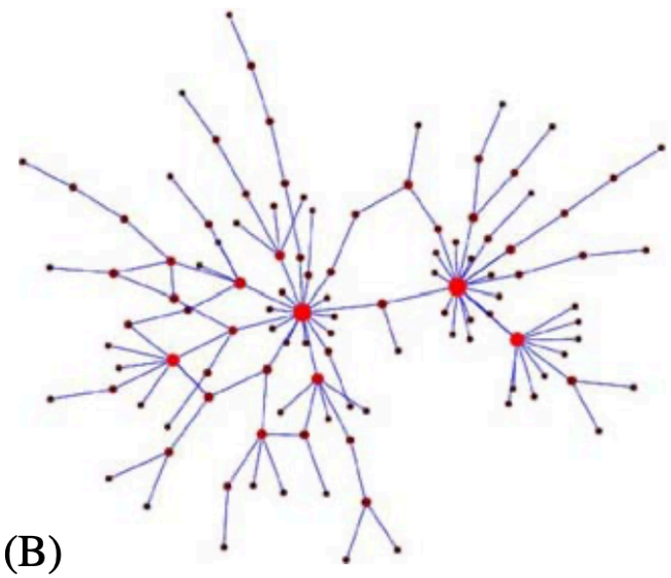
Poisson social contact network

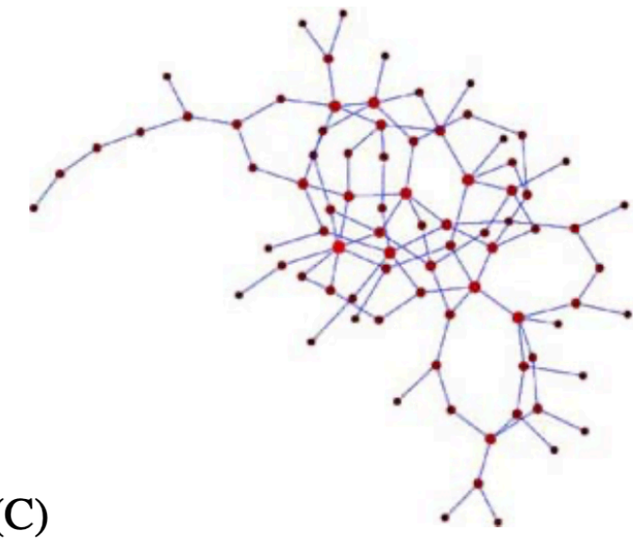


Meyers et al. 2004

Real-world social contact networks







Meyers et al. 2004

Same R0, very different stories

1918 influenza
R0 ~ 2
500,000,000 infected

2013-16 Ebola
R0 ~ 2
30,000 infected

Vol 438|17 November 2005|**doi:10.1038/nature04153**

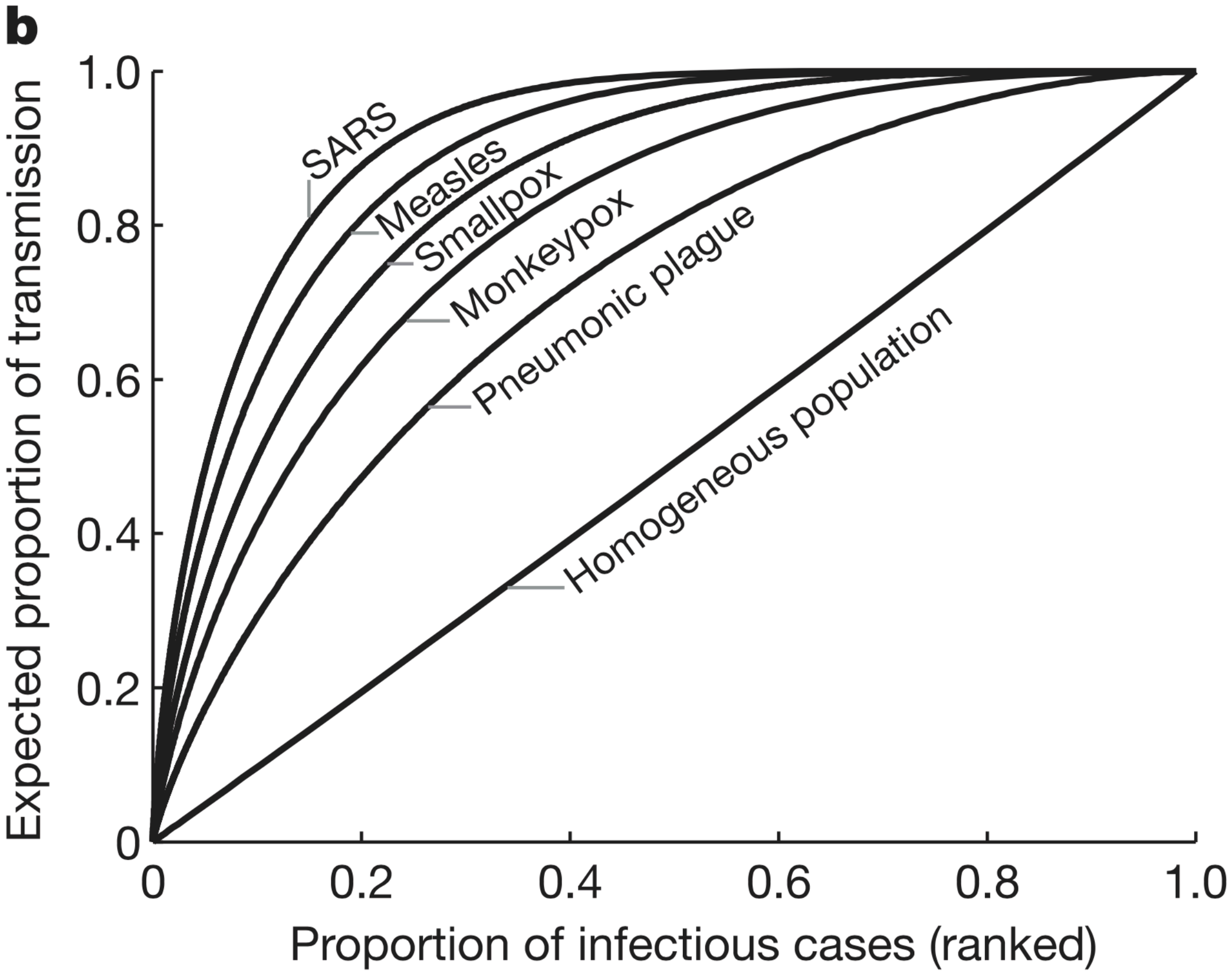
nature

LETTERS

Superspreading and the effect of individual variation on disease emergence

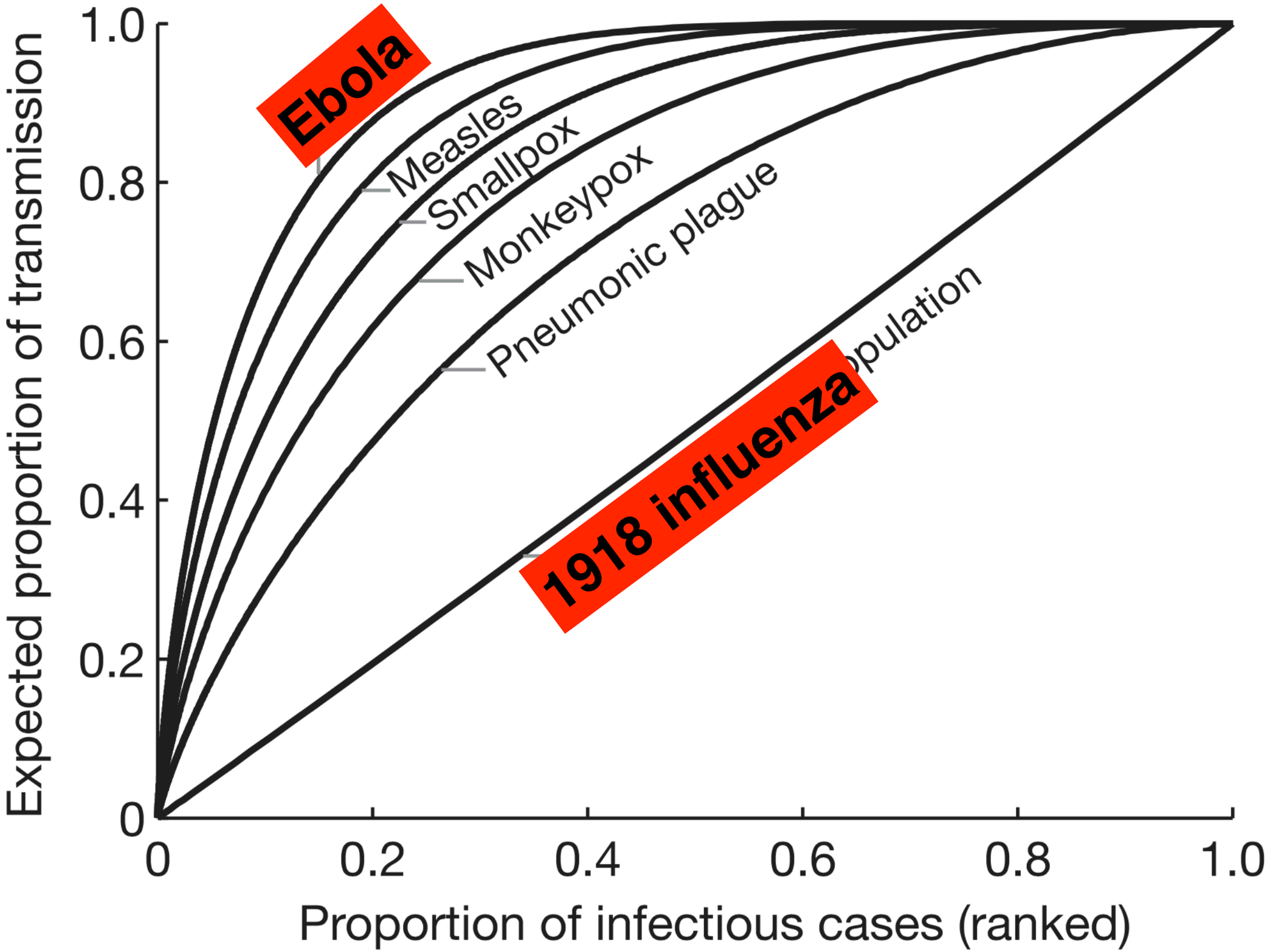
J. O. Lloyd-Smith[1,2], S. J. Schreiber[3], P. E. Kopp[4] & W. M. Getz[1]

b



Lloyd-smith et al. 2005

b



Lloyd-smith et al. 2005

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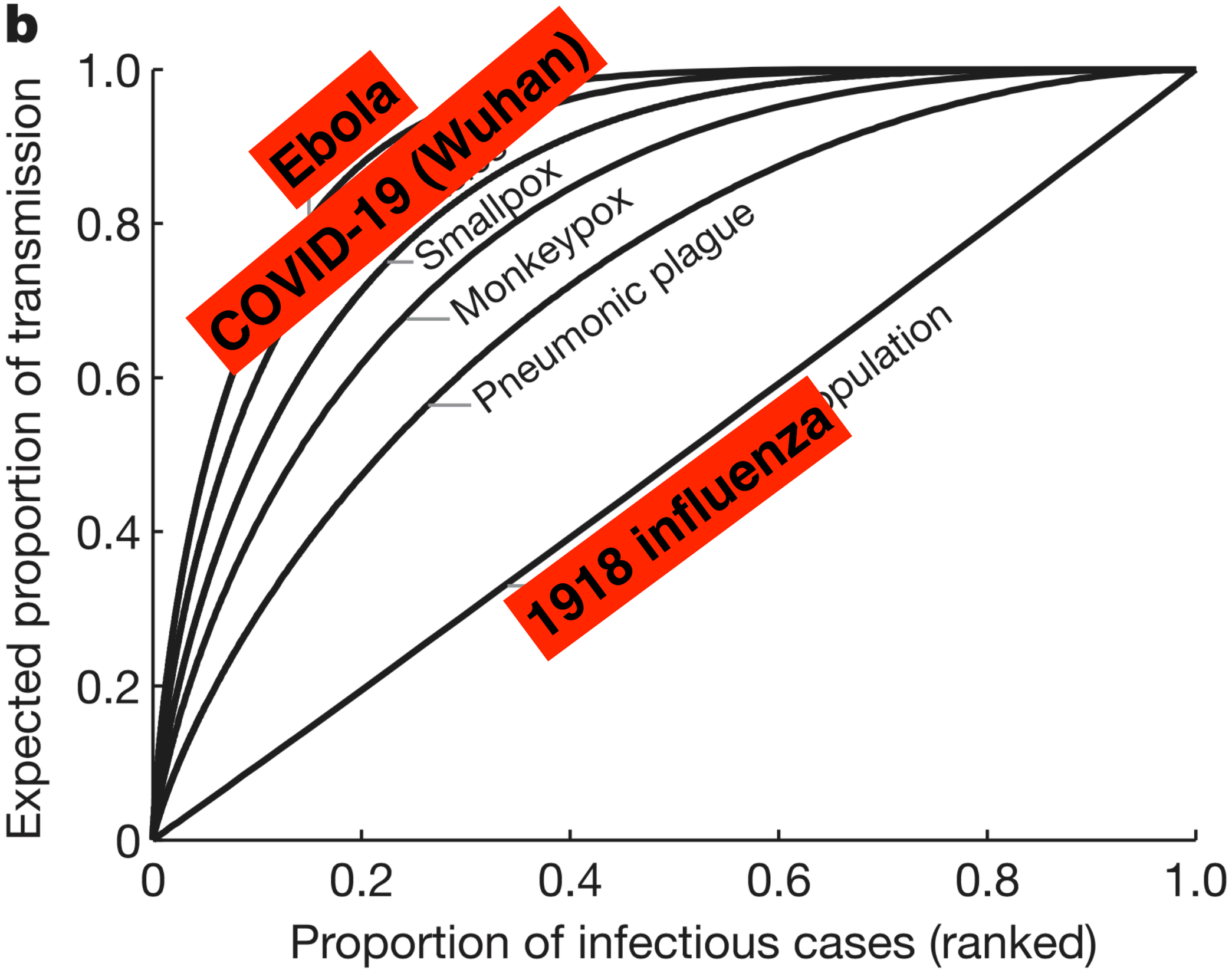


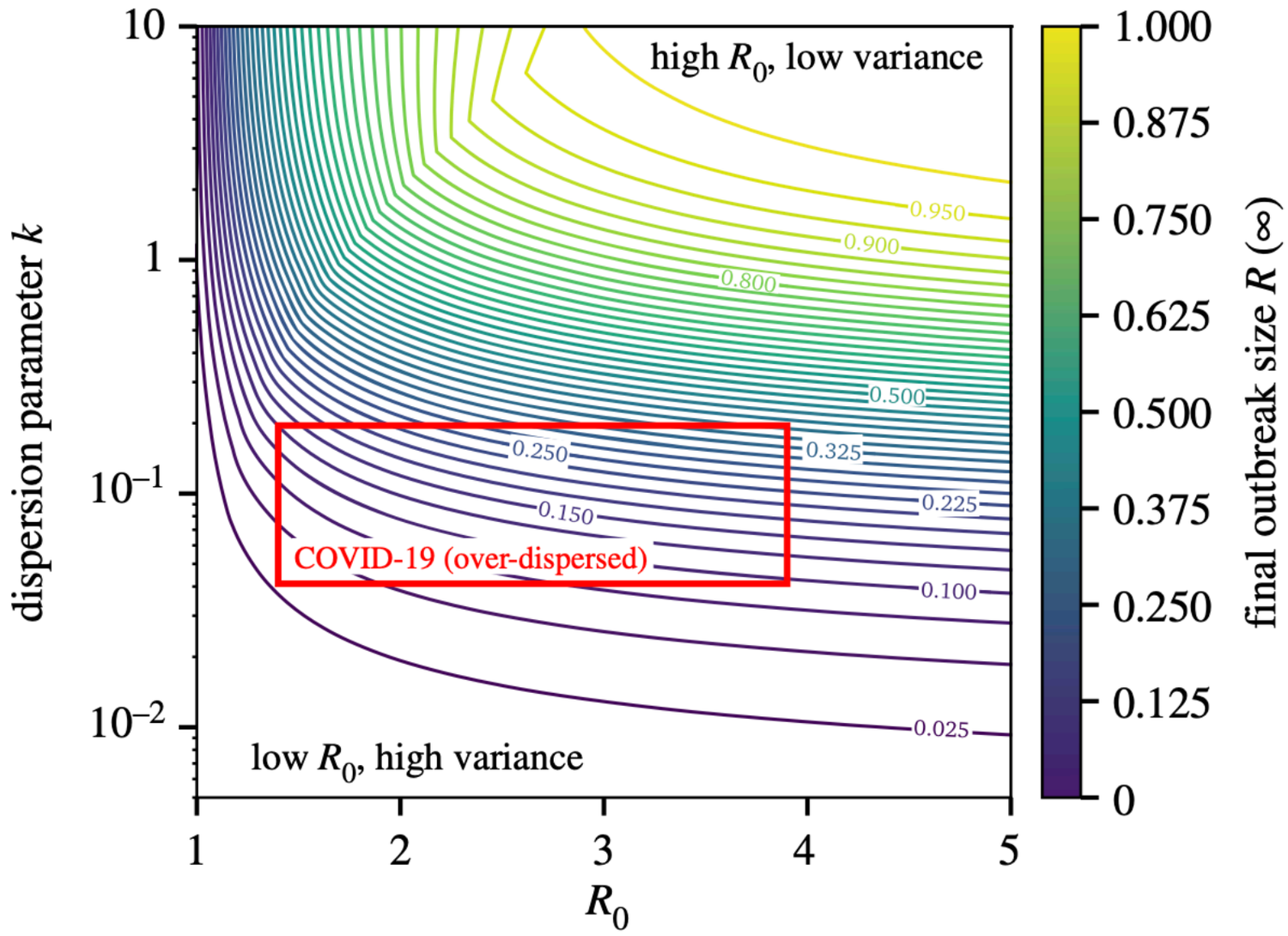
Lloyd-smith et al. 2005

Can we get a more “realistic” estimate of size?

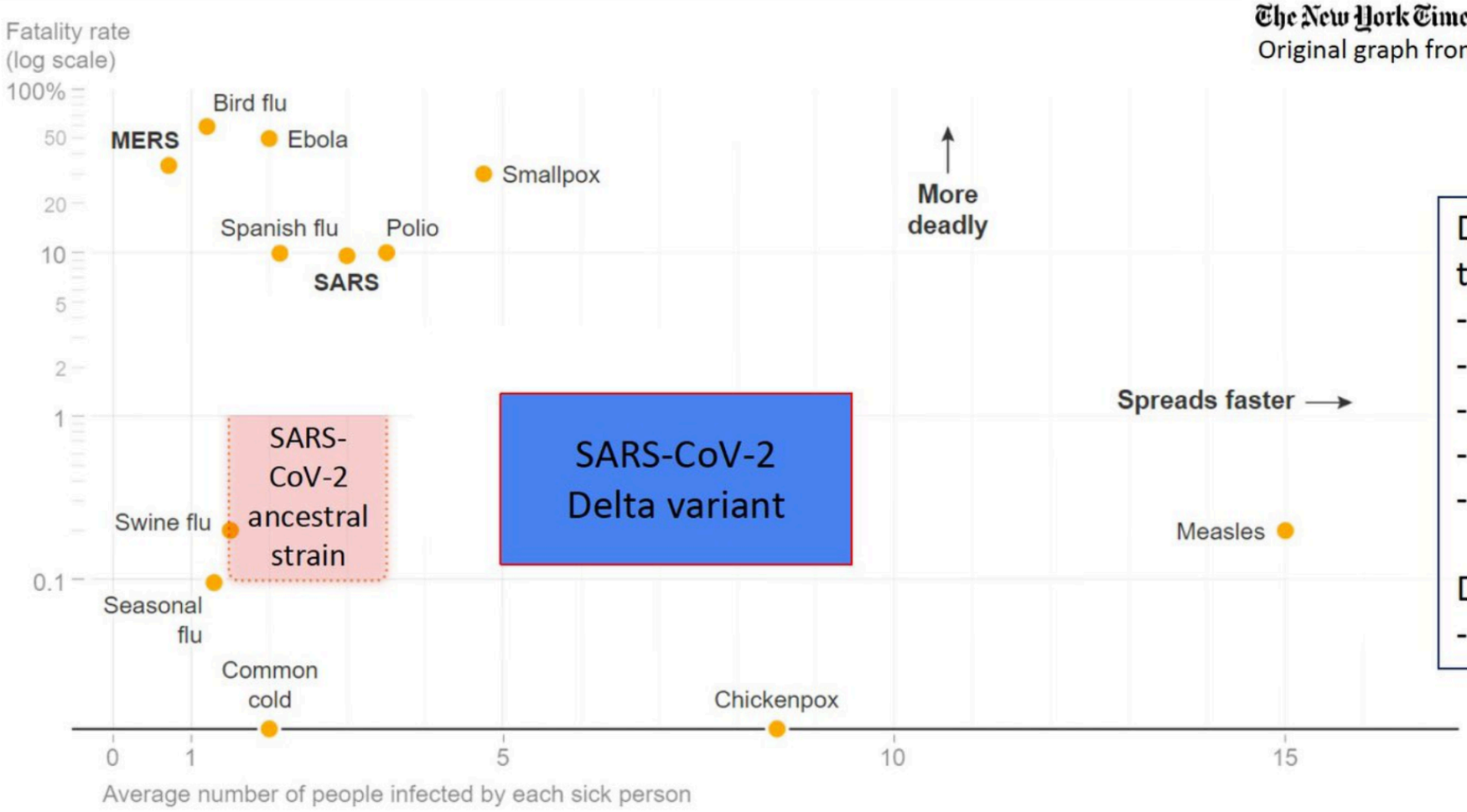
1. the disease results either in complete immunity or death,
2. the disease is transmitted in a closed population,
3. all individuals are equally susceptible,
4. contacts occur according to the law of mass-action,
5. and a deterministic analysis is appropriate.

Beyond R_0: heterogeneity in secondary infections and probabilistic epidemic forecasting

Laurent Hébert-Dufresne[1,2,3], Benjamin M. Althouse[4,5,6], Samuel V. Scarpino[7,8,9,10,11,12] and Antoine Allard[3,13]



Transmission of Delta variant vs. ancestral strain and other infectious diseases



Note: Average case-fatality rates and transmission numbers are shown. Estimates of case-fatality rates can vary, and numbers for the new coronavirus are preliminary estimates.

The New York Times
Original graph from 2/28/2020.

Delta variant is **more** transmissible than:
- MERS & SARS
- Ebola
- Common cold
- Seasonal flu & 1918 (“Spanish”) flu
- Smallpox

Delta variant is **as** transmissible as:
- Chicken Pox

There's a *potential* benefit to super spreading

PLOS BIOLOGY

ESSAY

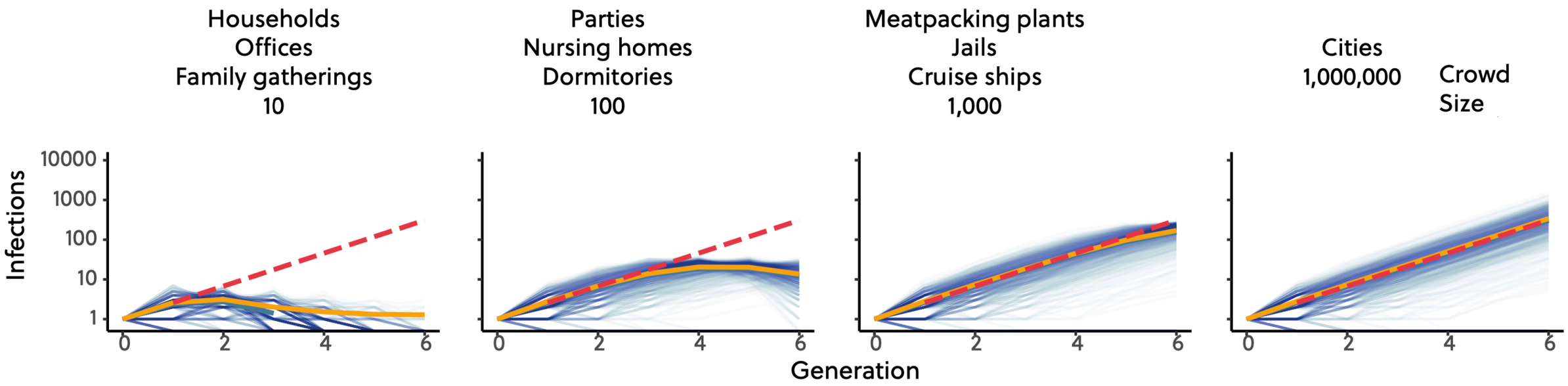
Superspreading events in the transmission dynamics of SARS-CoV-2: Opportunities for interventions and control

Benjamin M. Althouse[1,2,3]*, Edward A. Wenger[1], Joel C. Miller[4], Samuel V. Scarpino[5,6,7,8,9,10], Antoine Allard[11,12], Laurent Hébert-Dufresne[11,13,14], Hao Hu[15]

Althouse et al. 2020 PLoS Biology

There's a *potential* benefit to super spreading

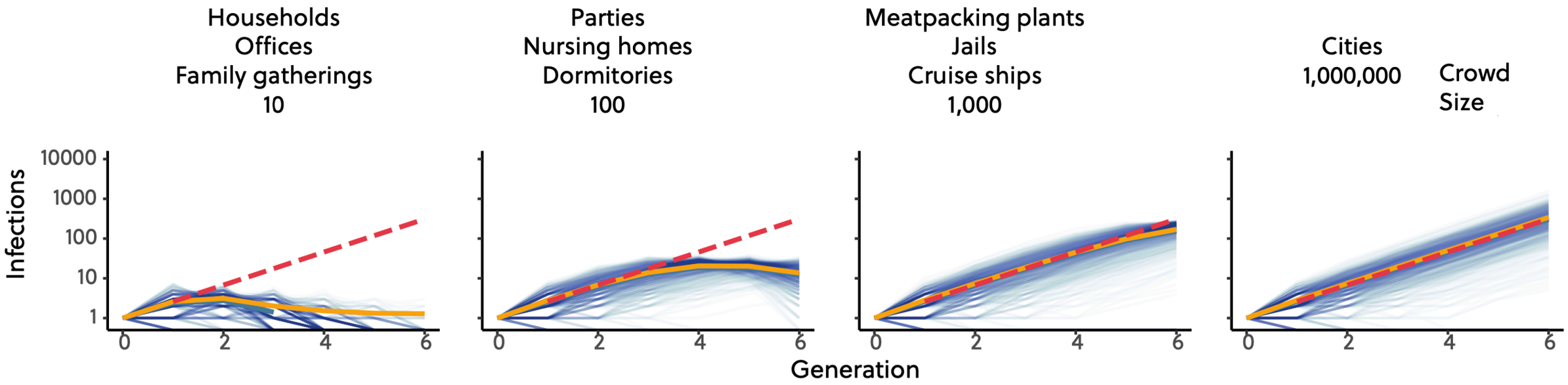
No super-spreading, R0 = 2.6



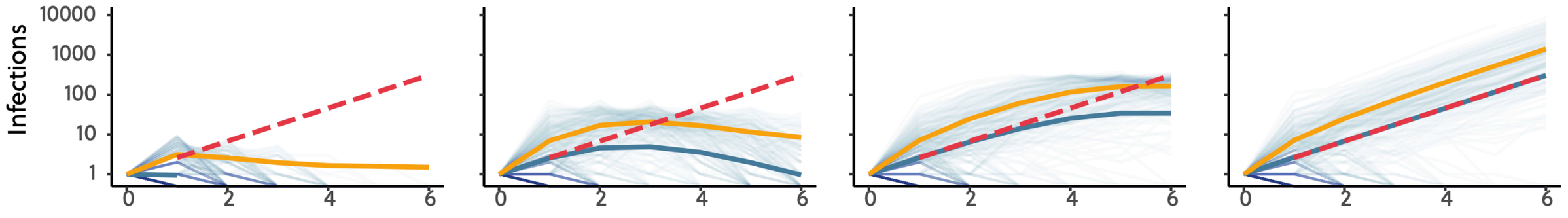
Althouse et al. *pre print*

There's a *potential* benefit to super spreading

No super-spreading, R0 = 2.6



Super-spreading, R0 = 2.6, k = 0.16



Althouse et al. *pre print*

Impact of human mobility on the emergence of dengue epidemics in Pakistan

Amy Wesolowski[a,b], Taimur Qureshi[c], Maciej F. Boni[d,e], Pål Roe Sundsøy[c], Michael A. Johansson[b,f], Syed Basit Rasheed[g], Kenth Engø-Monsen[c], and Caroline O. Buckee[a,b,1]

[a]Department of Epidemiology, Harvard T. H. Chan School of Public Health, Boston, MA 02115; [b]Center for Communicable Disease Dynamics, Harvard T. H. Chan School of Public Health, Boston, MA 02115; [c]Telenor Research, Telenor Group, N-1360 Fornebu, Norway; [d]Oxford University Clinical Research Unit, Wellcome Trust Major Overseas Programme, Ho Chi Minh City, Vietnam; [e]Centre for Tropical Medicine, Nuffield Department of Clinical Medicine, University of Oxford, Oxford OX3 7FZ, United Kingdom; [f]Division of Vector-Borne Diseases, Centers for Disease Control, San Juan, Puerto Rico 00920; and [g]Department of Zoology, University of Peshawar, Peshawar 25120, Pakistan

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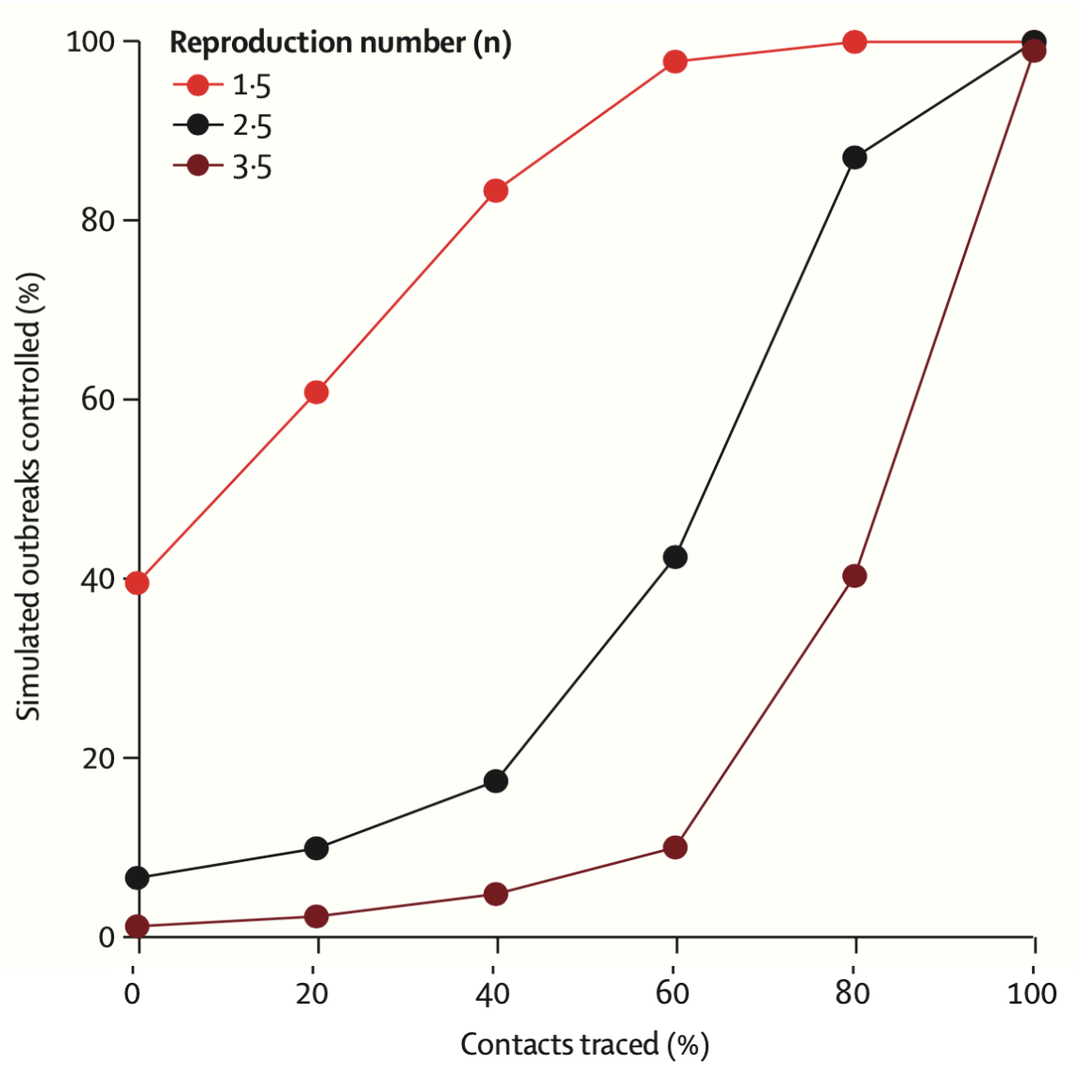
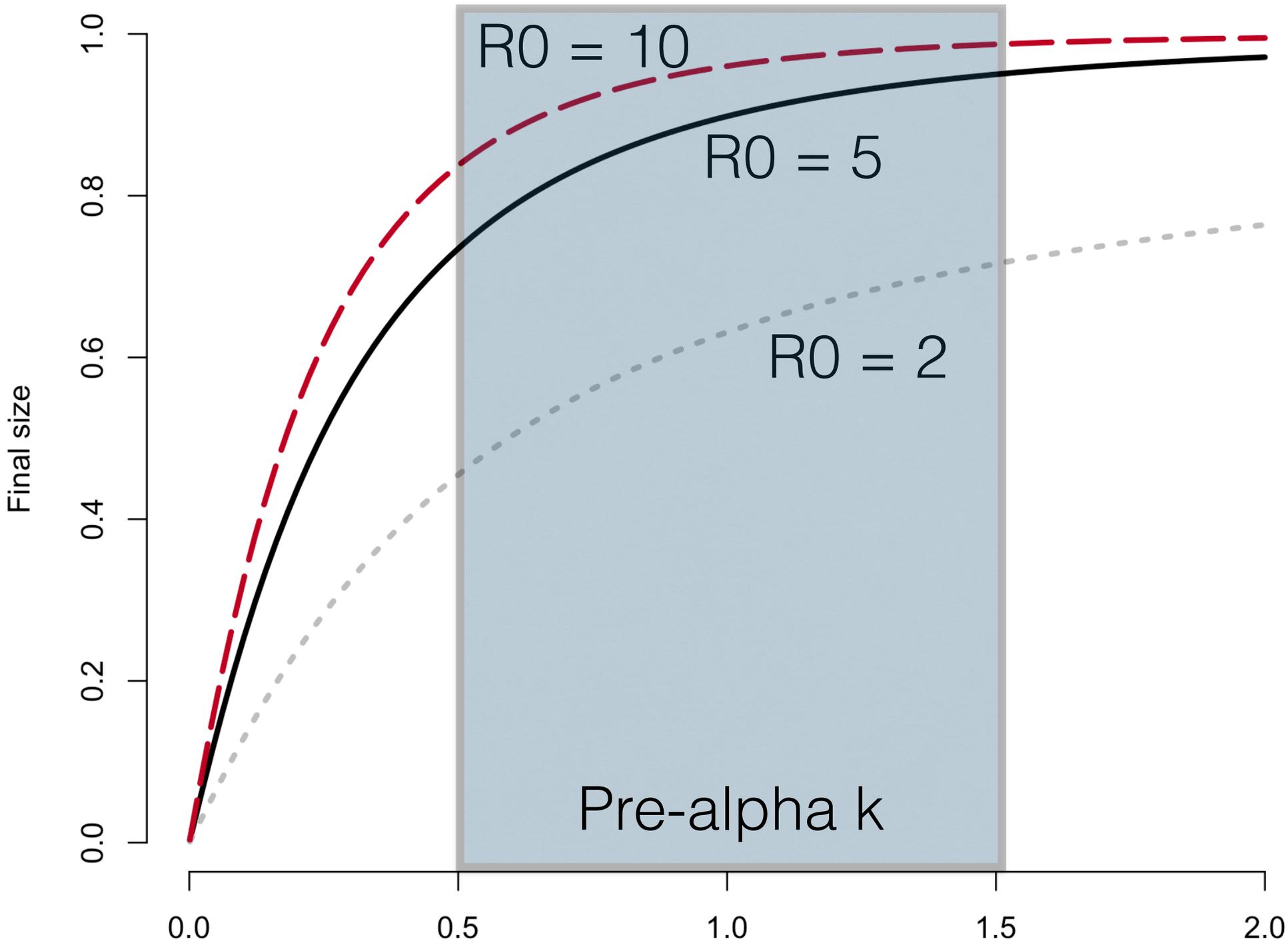
Feasibility of controlling COVID-19 outbreaks by isolation of cases and contacts

Joel Hellewell, Sam Abbott, Amy Gimma*, Nikos I Bosse, Christopher I Jarvis, Timothy W Russell, James D Munday, Adam J Kucharski, W John Edmunds, Centre for the Mathematical Modelling of Infectious Diseases COVID-19 Working Group, Sebastian Funk†, Rosalind M Eggo†*



But, at low super-spreading (flu), k doesn't matter



Scarpino unpublished

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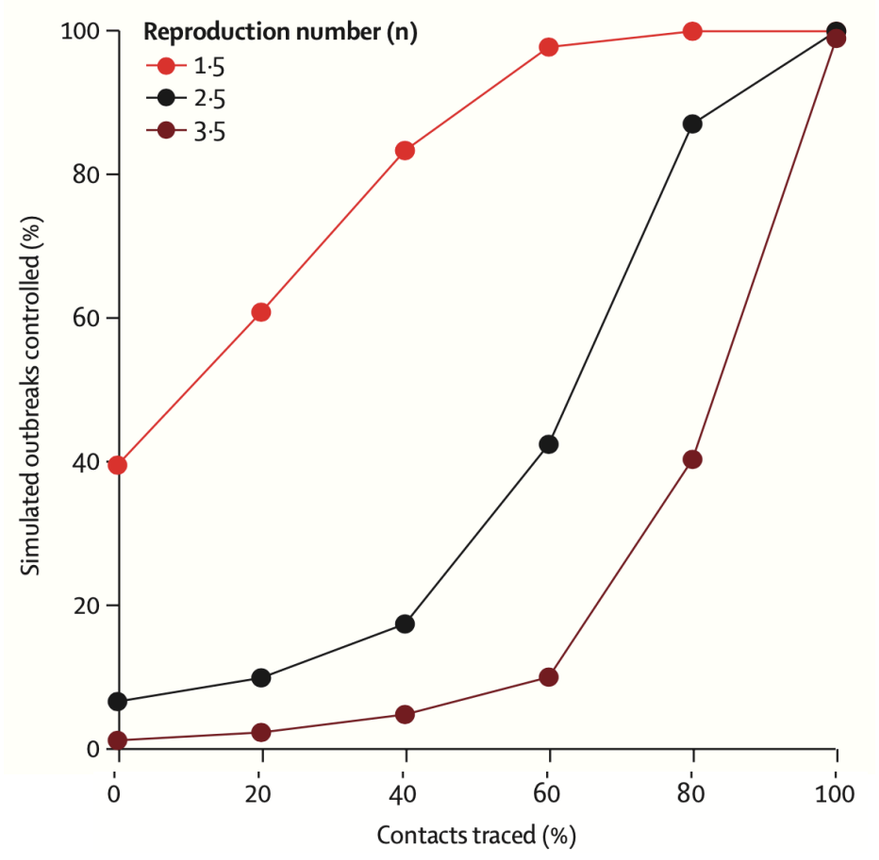

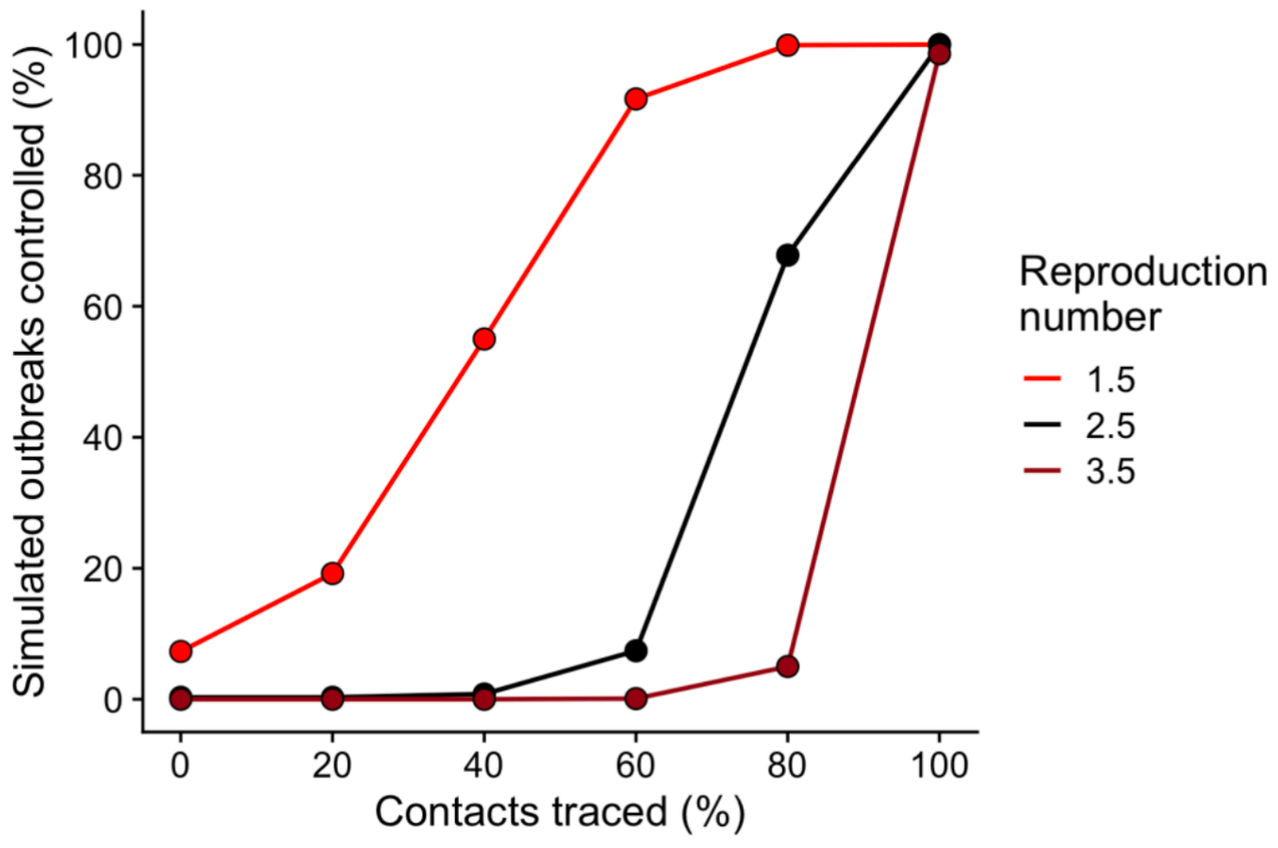

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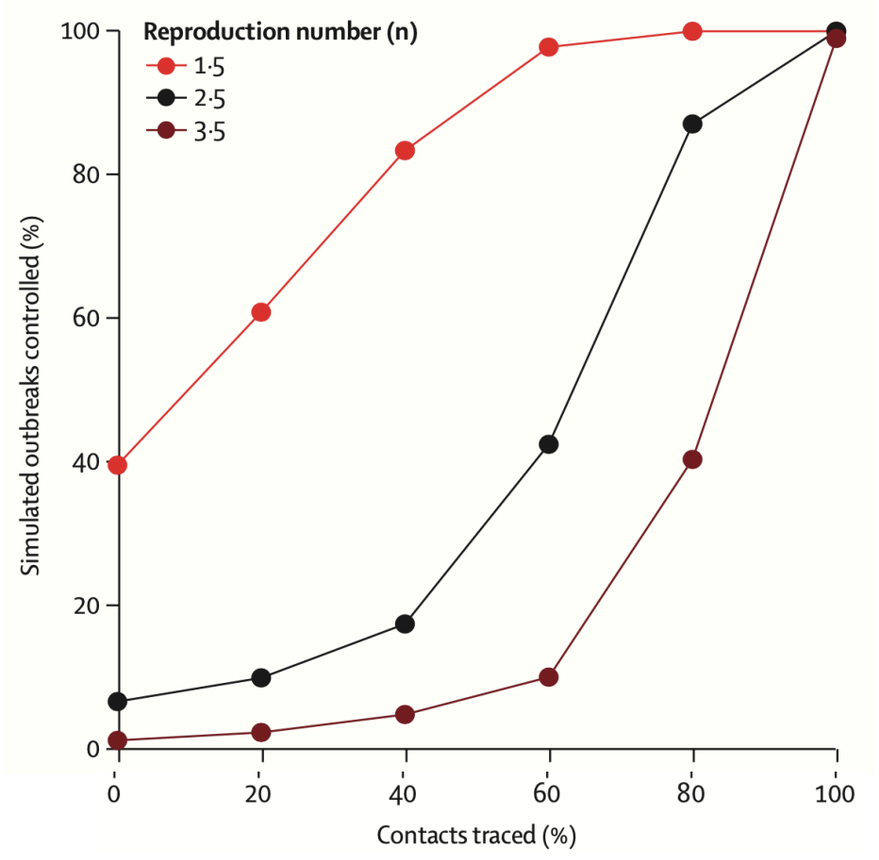
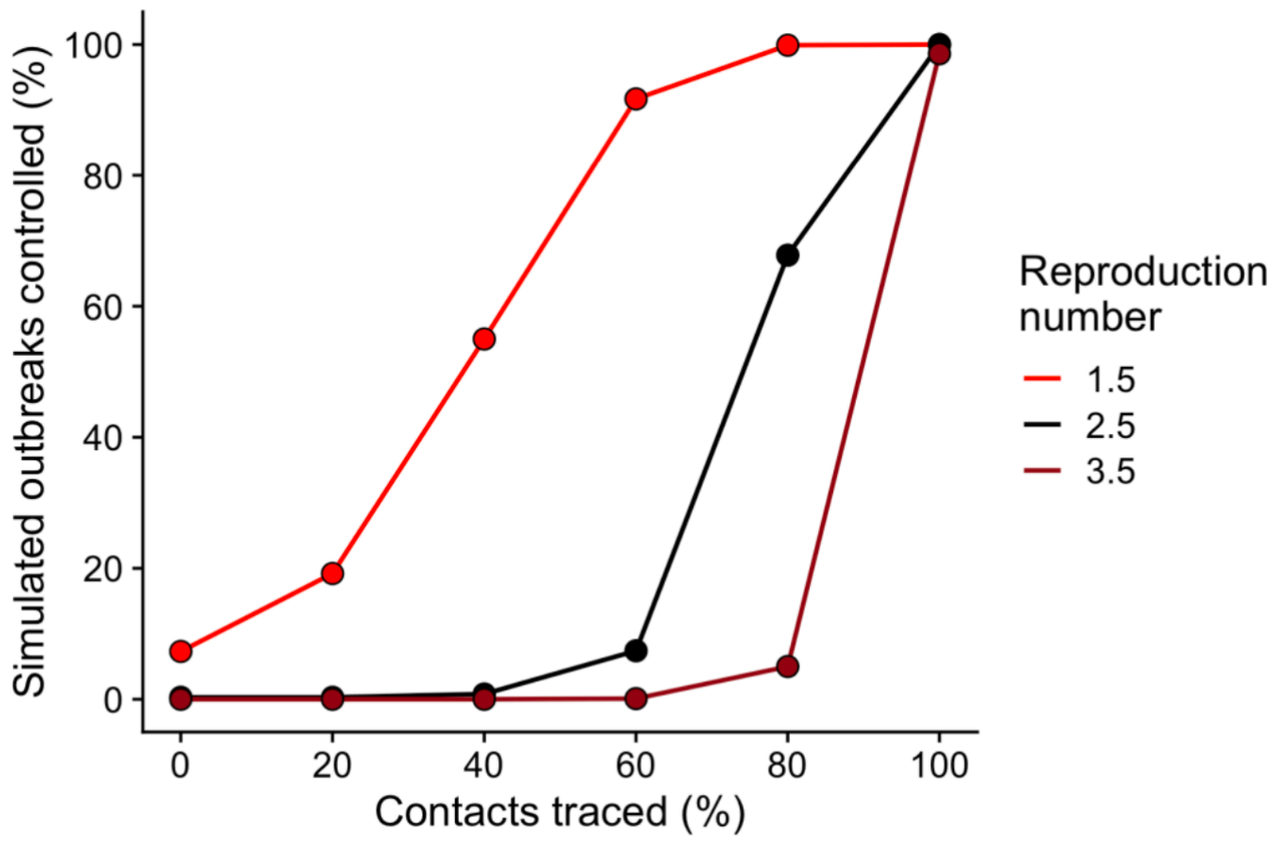
SARS-CoV-2 Wuhan



SARS-CoV-2 Omicron



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Beyond R_0: heterogeneity in secondary infections and probabilistic epidemic forecasting

Laurent Hébert-Dufresne[1,2,3], Benjamin M. Althouse[4,5,6], Samuel V. Scarpino[7,8,9,10,11,12] and Antoine Allard[3,13]

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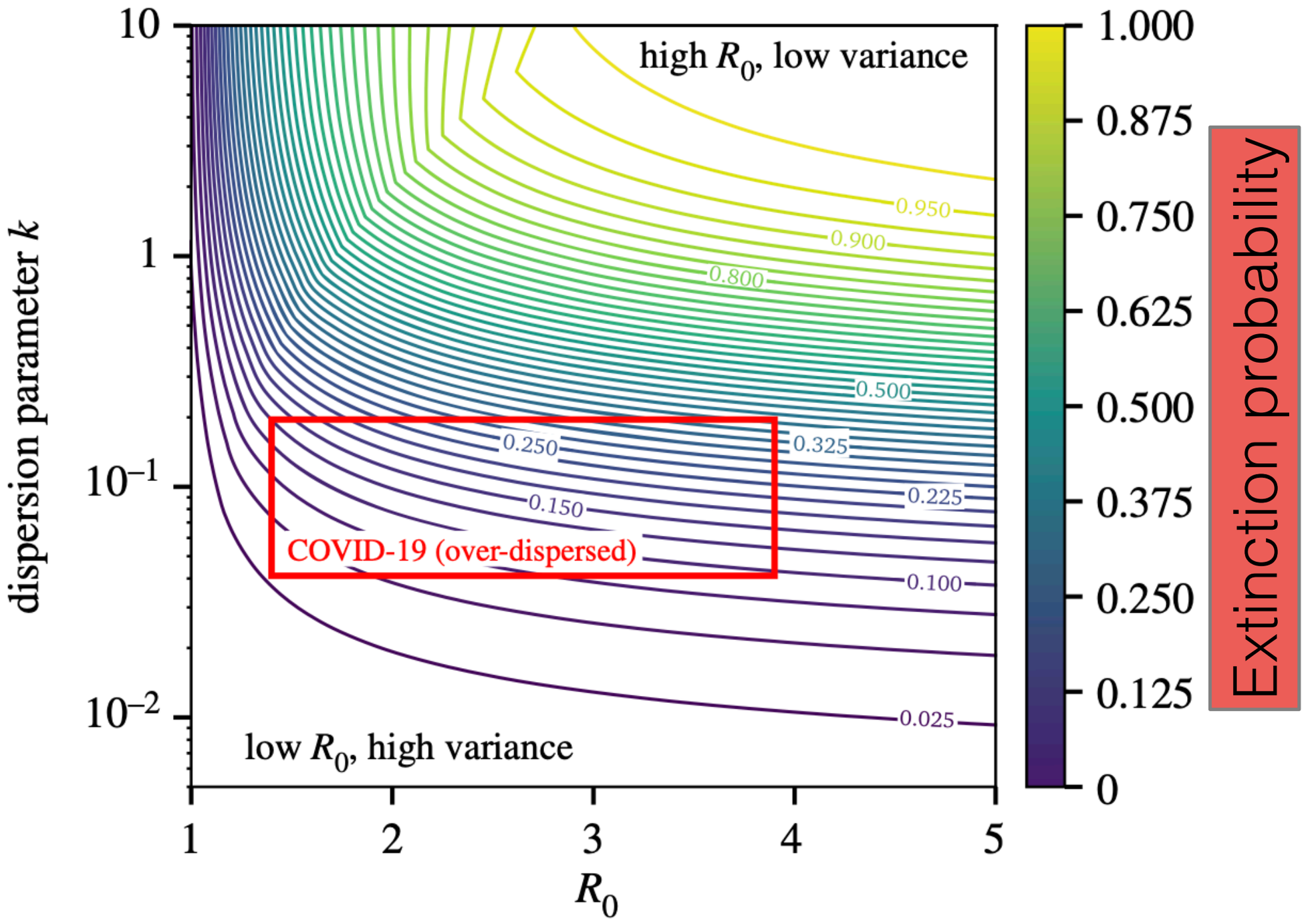
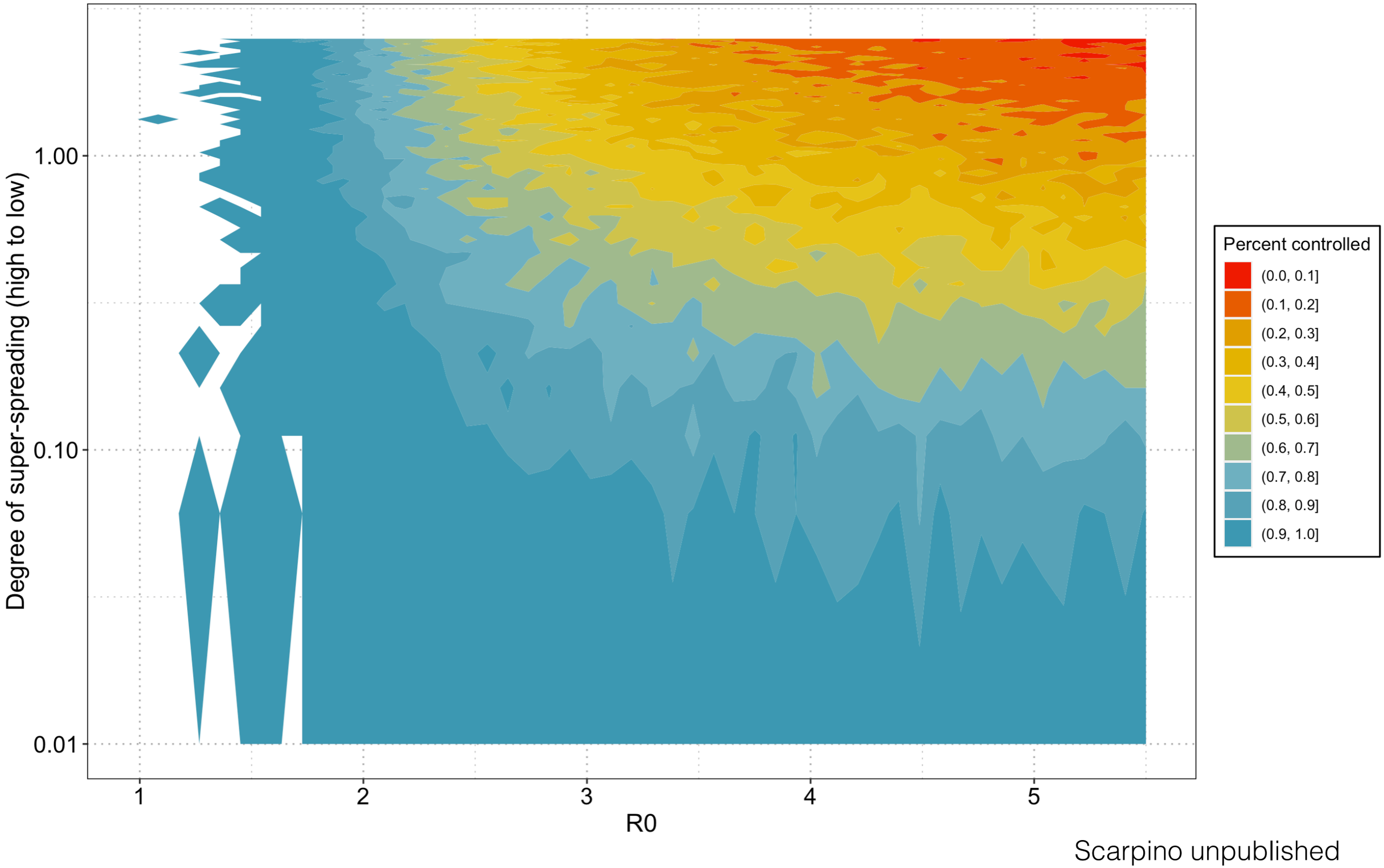
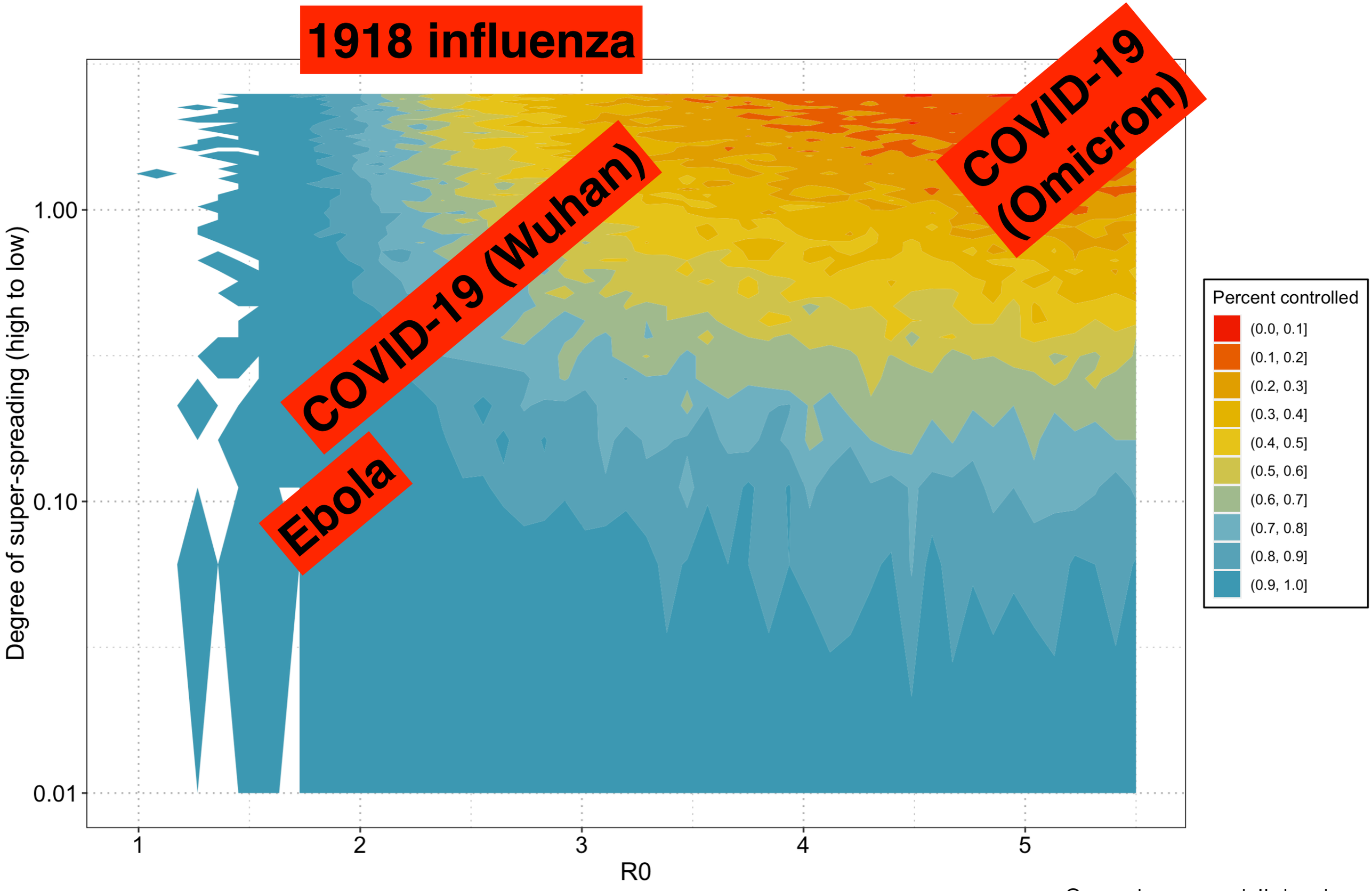
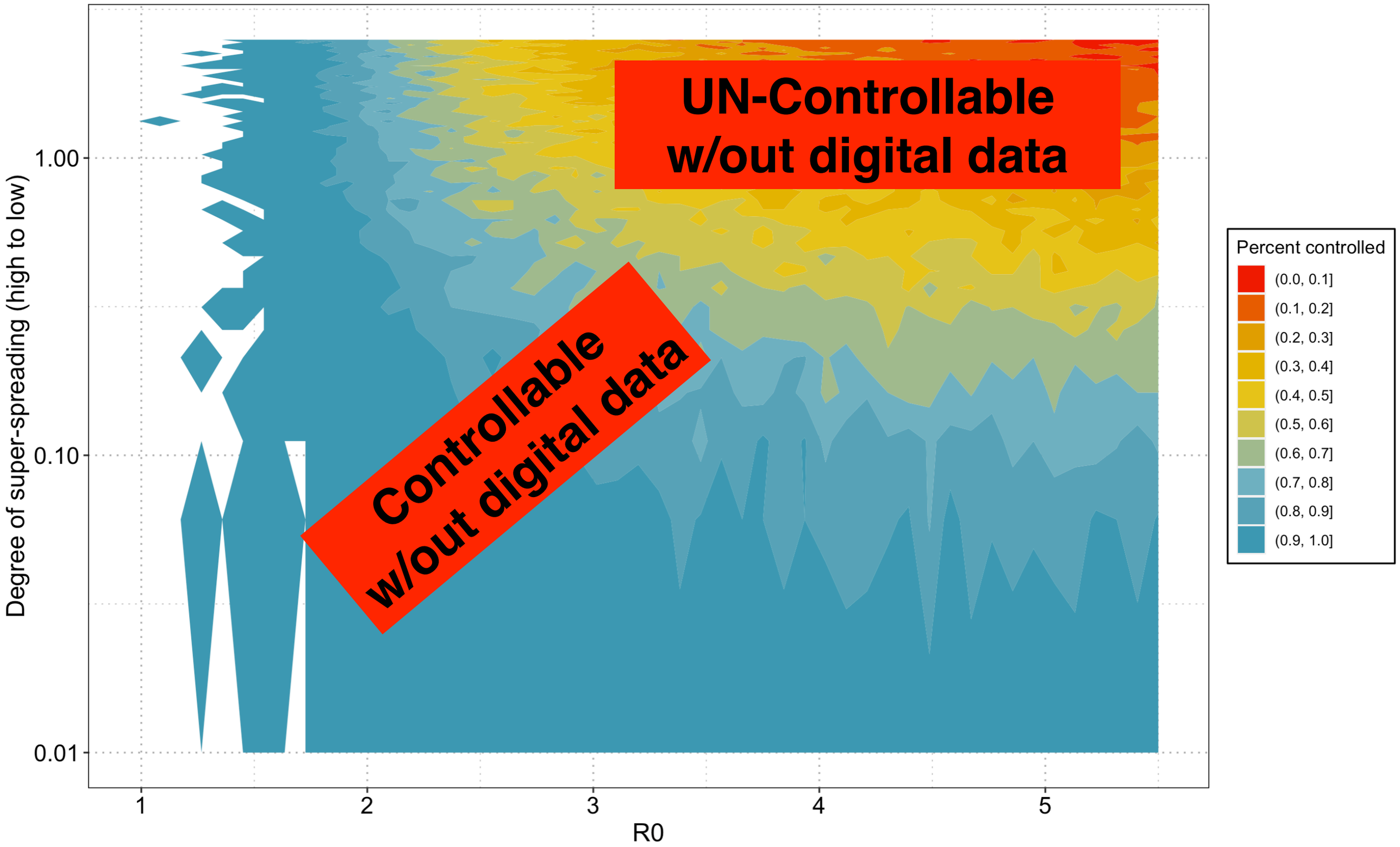




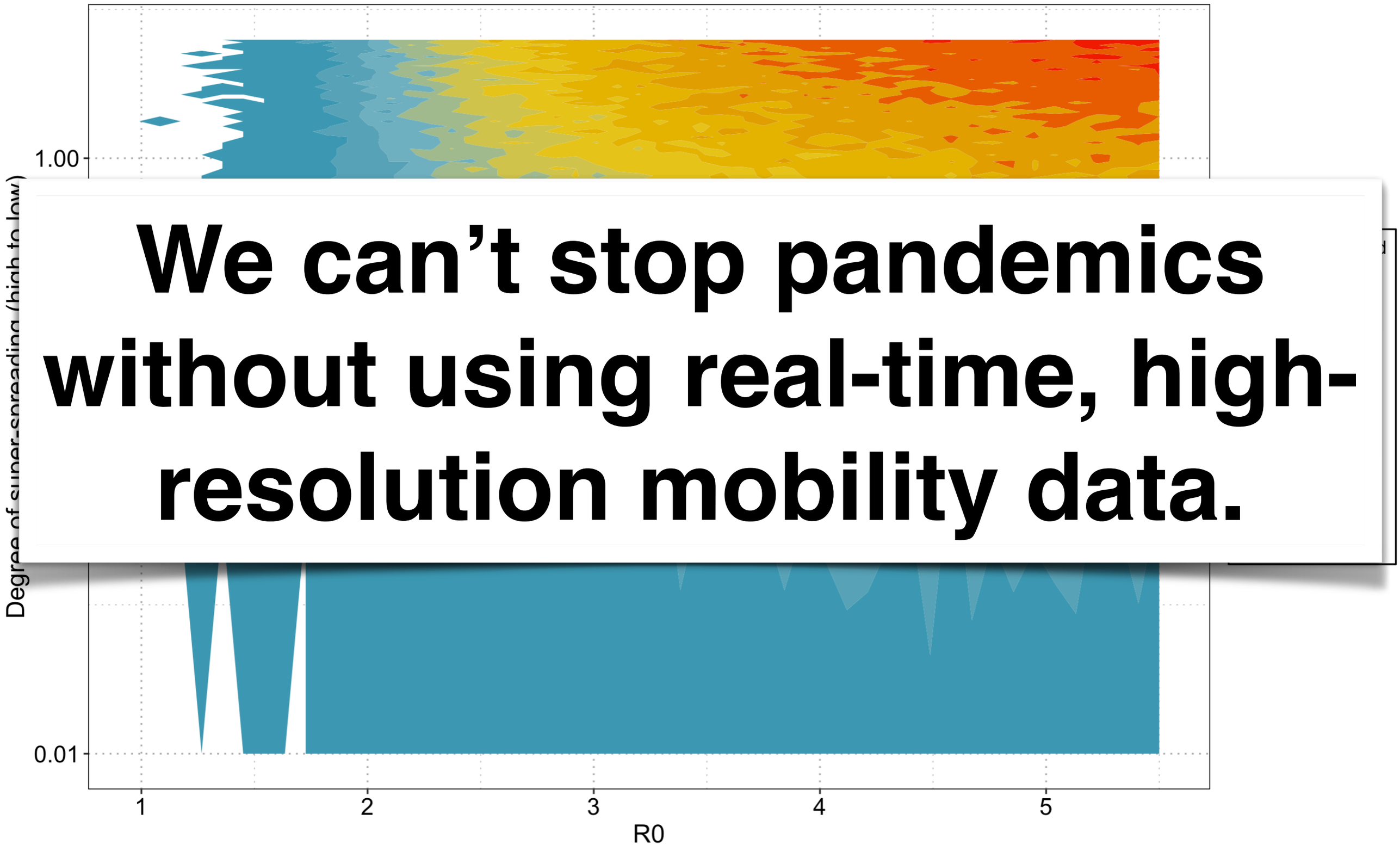
Scarpino unpublished



Scarpino unpublished



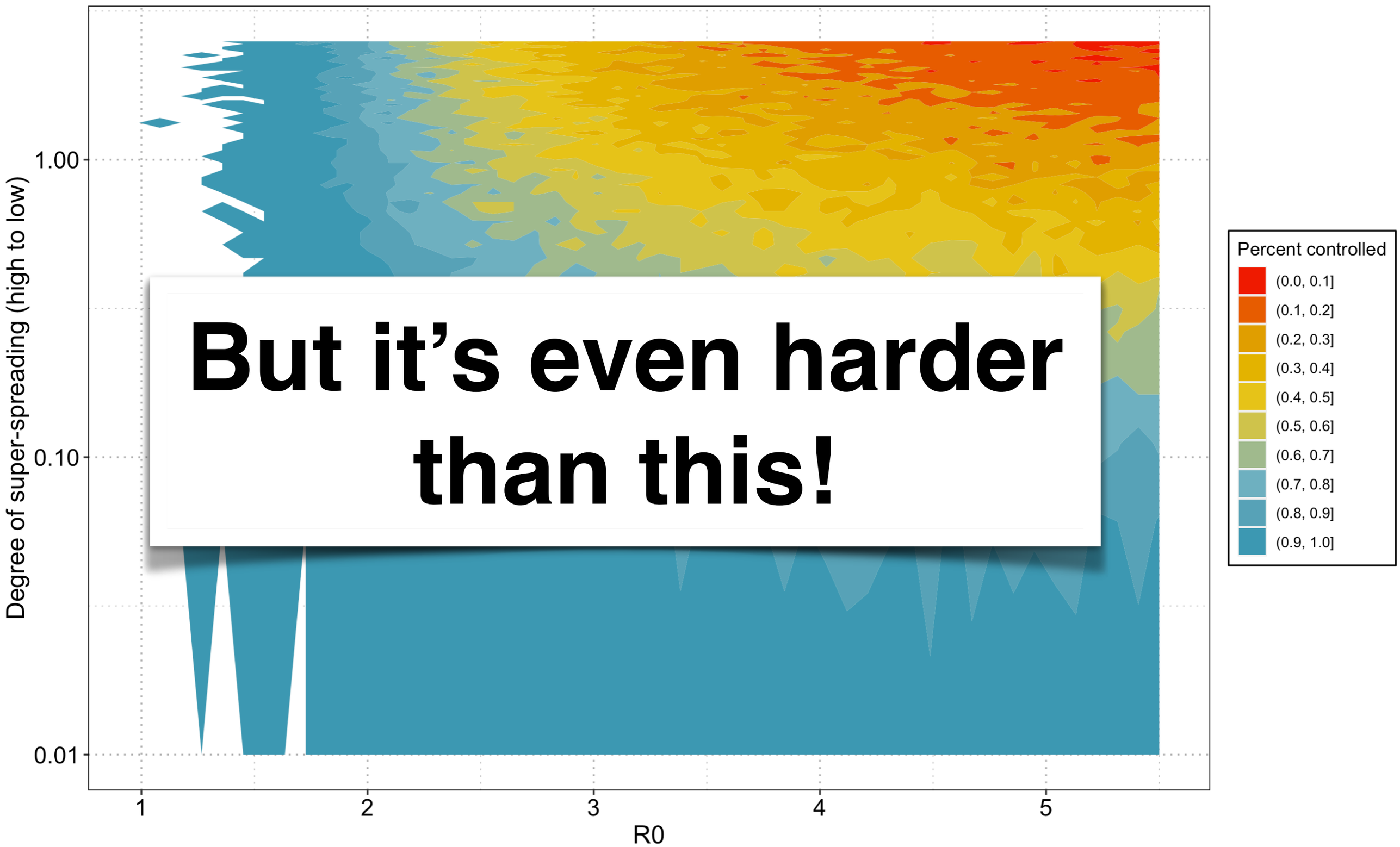
Scarpino unpublished



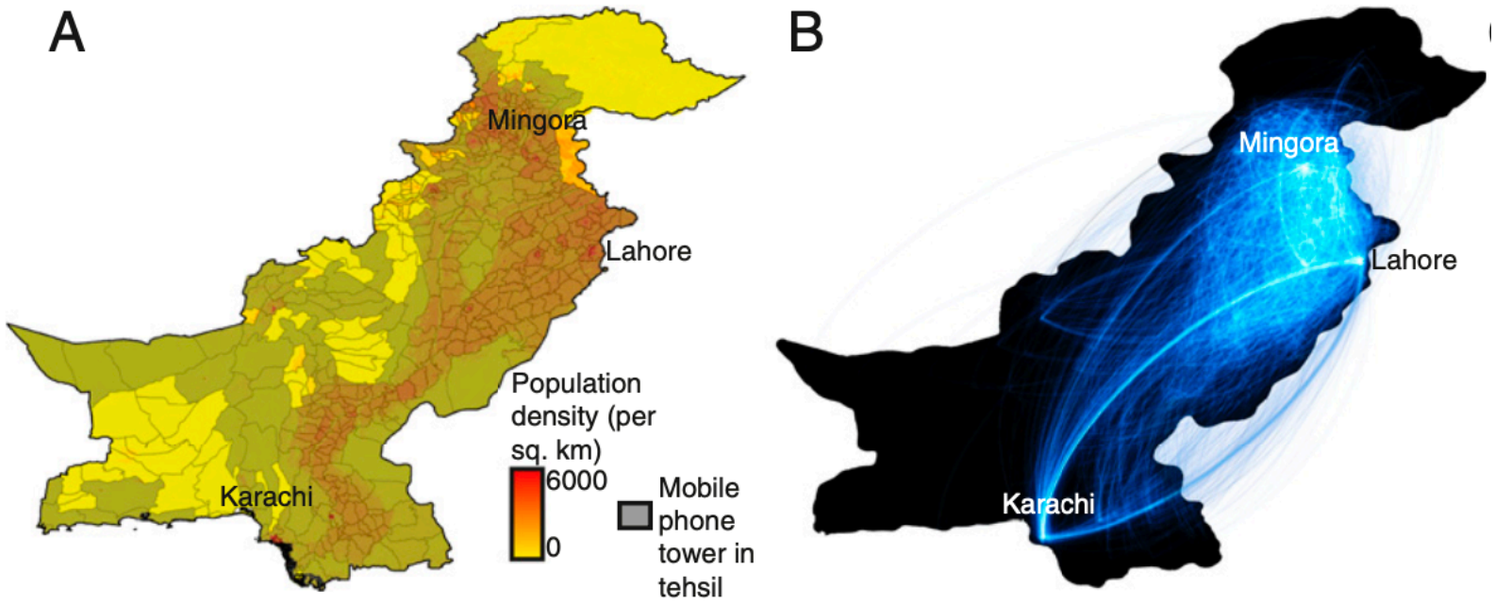
We can’t stop pandemics without using real-time, high-resolution mobility data.

Scarpino unpublished

But it’s even harder than this!



Scarpino unpublished



PNAS

Impact of human mobility on the emergence of dengue epidemics in Pakistan

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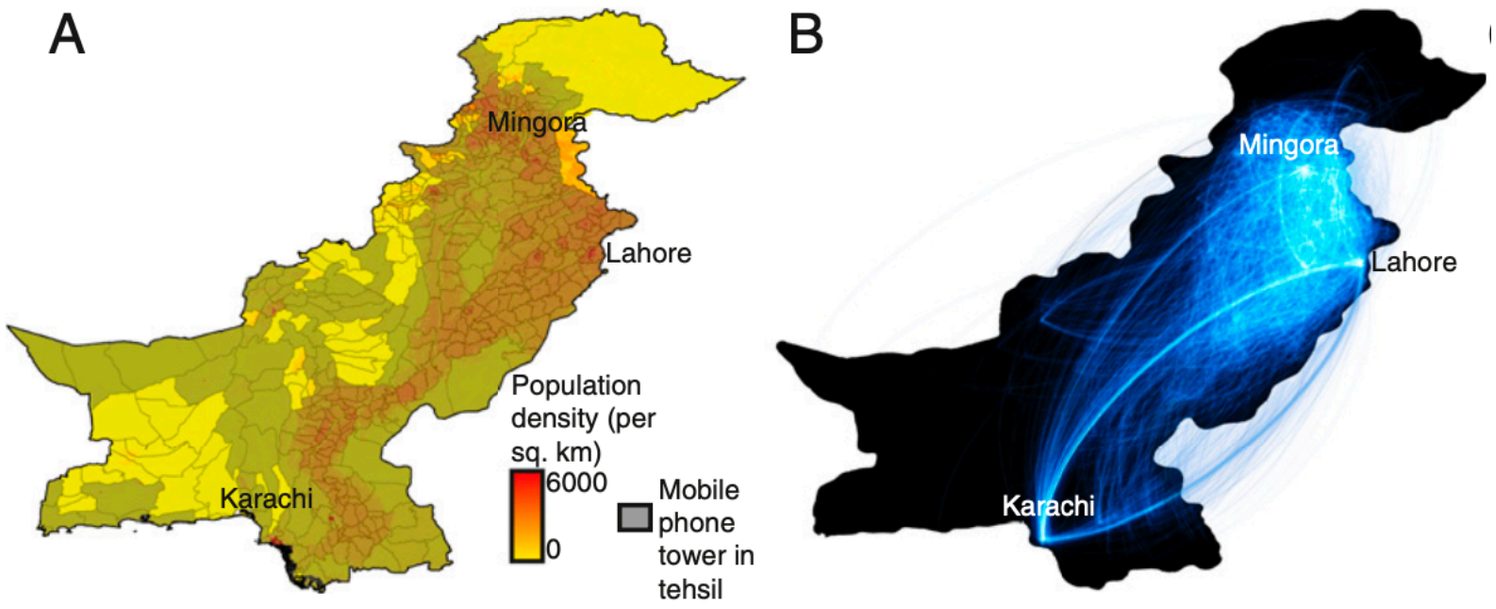
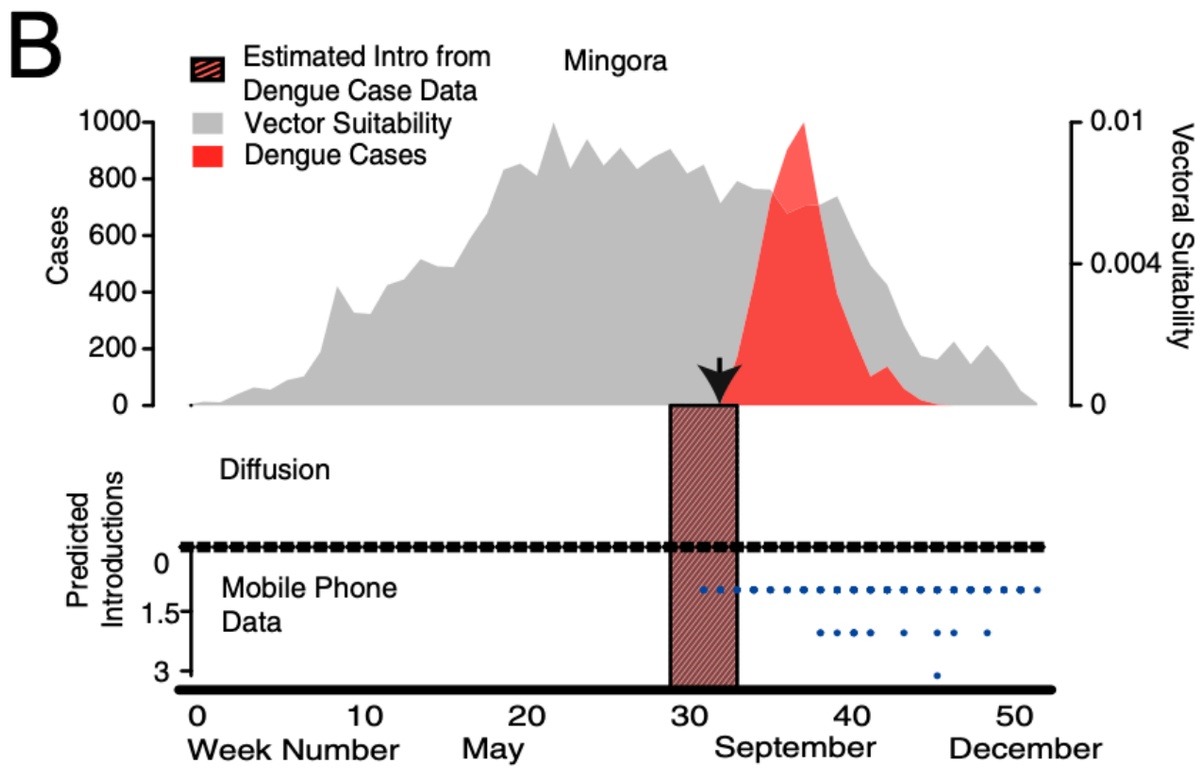
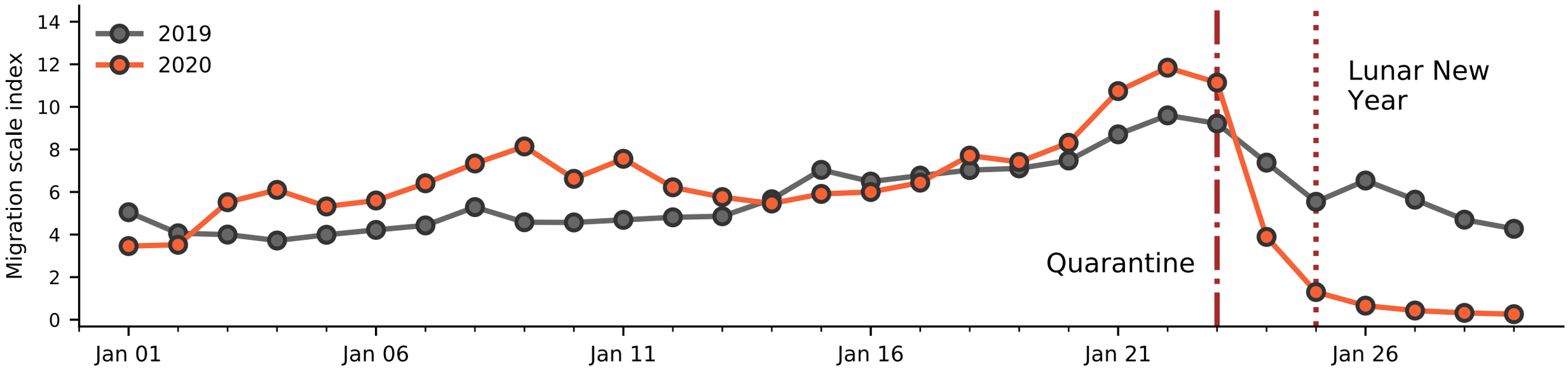
[a]Department of Epidemiology, Harvard T. H. Chan School of Public Health, Boston, MA 02115; [b]Center for Communicable Disease Dynamics, Harvard T. H. Chan School of Public Health, Boston, MA 02115; [c]Telenor Research, Telenor Group, N-1360 Fornebu, Norway; [d]Oxford University Clinical Research Unit, Wellcome Trust Major Overseas Programme, Ho Chi Minh City, Vietnam; [e]Centre for Tropical Medicine, Nuffield Department of Clinical Medicine, University of Oxford, Oxford OX3 7FZ, United Kingdom; [f]Division of Vector-Borne Diseases, Centers for Disease Control, San Juan, Puerto Rico 00920; and [g]Department of Zoology, University of Peshawar, Peshawar 25120, Pakistan


A
Mingora
Lahore
Karachi
Population density (per sq. km)
6000
0
Mobile phone tower in tehsil
B
Mingora
Lahore
Karachi


B
Estimated Intro from Dengue Case Data
Vector Suitability
Dengue Cases
Mingora
Cases
1000
800
600
400
200
0
0.01
0.004
0
Vectoral Suitability
Diffusion
Predicted Introductions
0
1.5
3
Mobile Phone Data
0
10
20
30
40
50
Week Number
May
September
December

Perhaps 5 million people left Wuhan in Jan 2020



Science

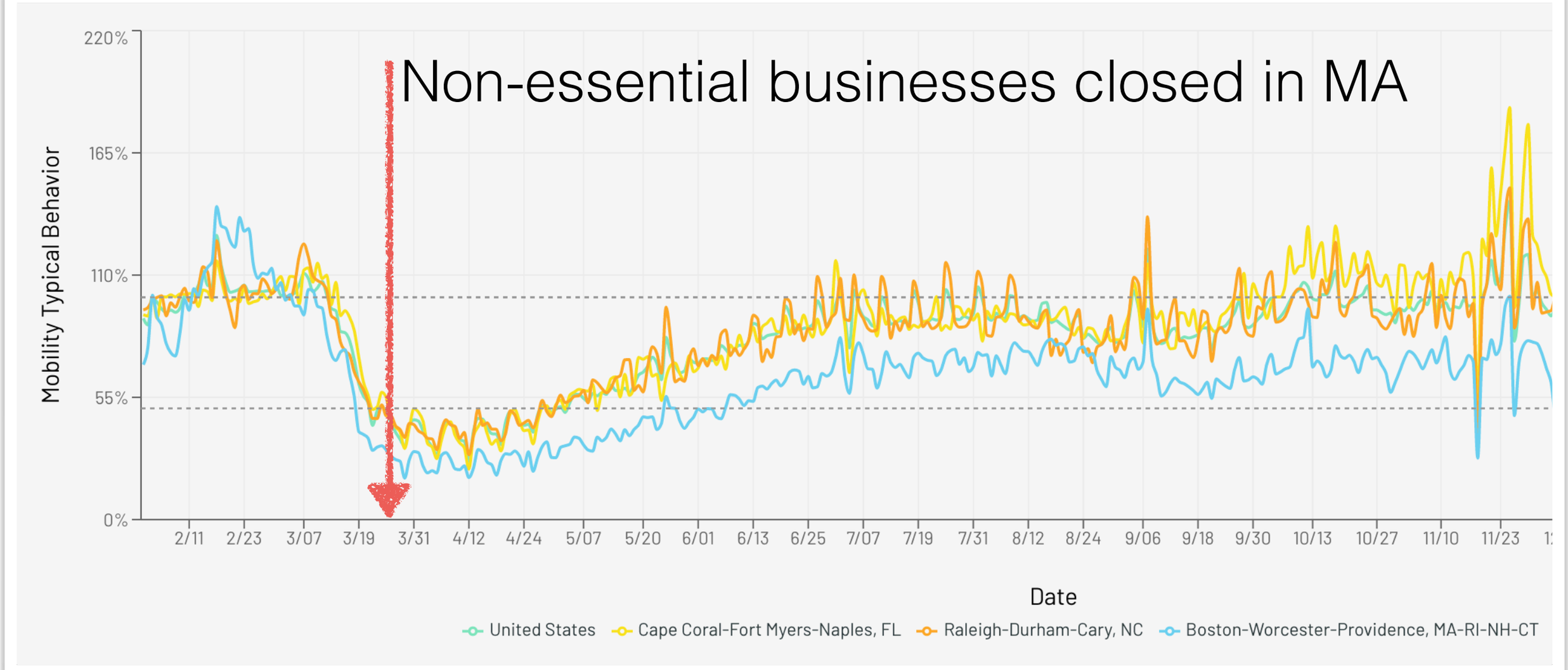
RESEARCH ARTICLES

Cite as: M. U. G. Kraemer *et al.*, *Science*
10.1126/science.abb4218 (2020).

The effect of human mobility and control measures on the COVID-19 epidemic in China

Moritz U. G. Kraemer[1,2,3]*, Chia-Hung Yang[4], Bernardo Gutierrez[1,5], Chieh-Hsi Wu[6], Brennan Klein[4], David M. Pigott[7], Open COVID-19 Data Working Group†, Louis du Plessis[1], Nuno R. Faria[1], Ruoran Li[8], William P. Hanage[8], John S. Brownstein[2,3], Maylis Layan[9,10], Alessandro Vespignani[4,11], Huaiyu Tian[12], Christopher Dye[1], Oliver G. Pybus[1,13]*, Samuel V. Scarpino[4]*

People act before measures go into place

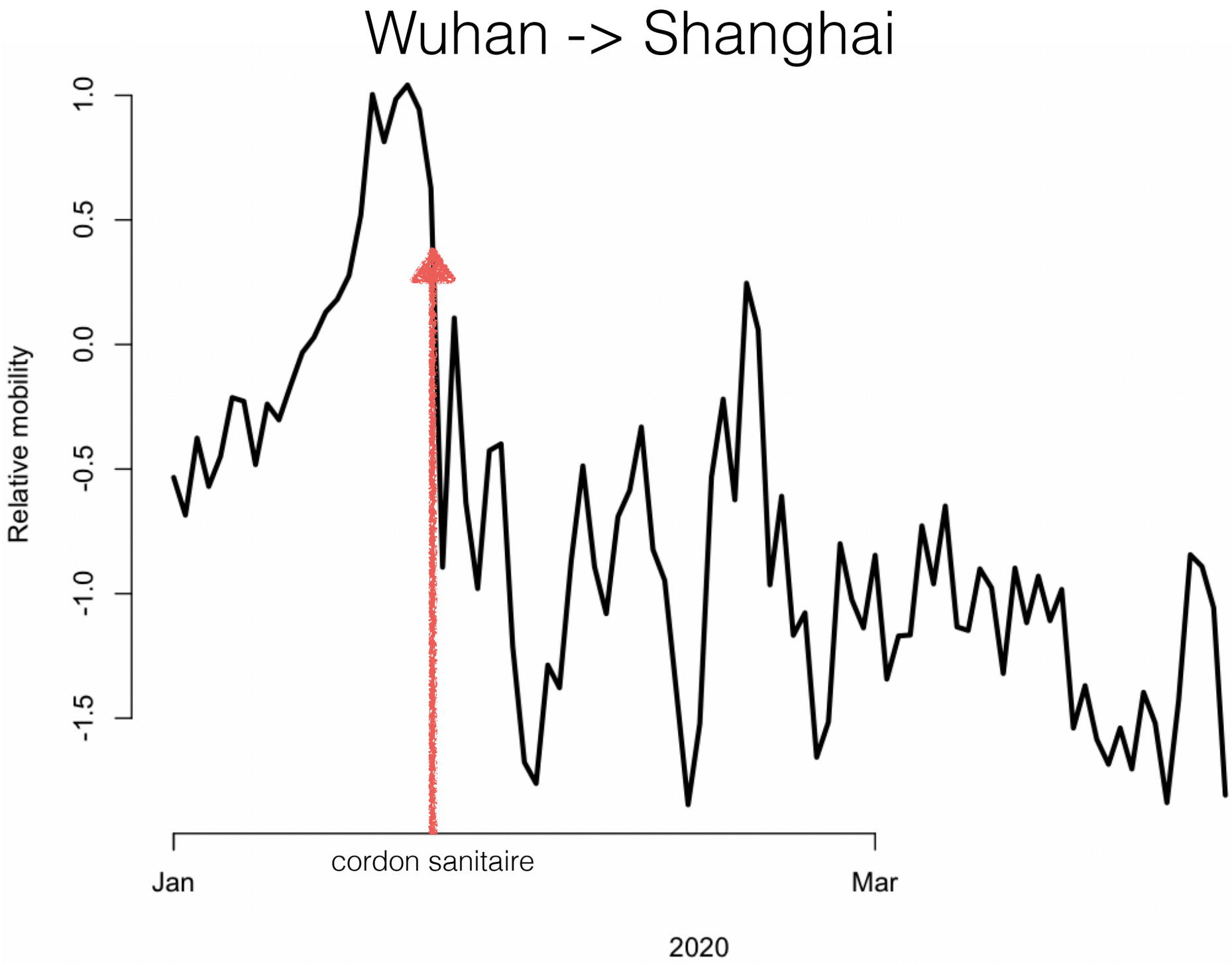


MOBS LAB

https://covid19.gleamproject.org/mobility

GLEAM PROJECT

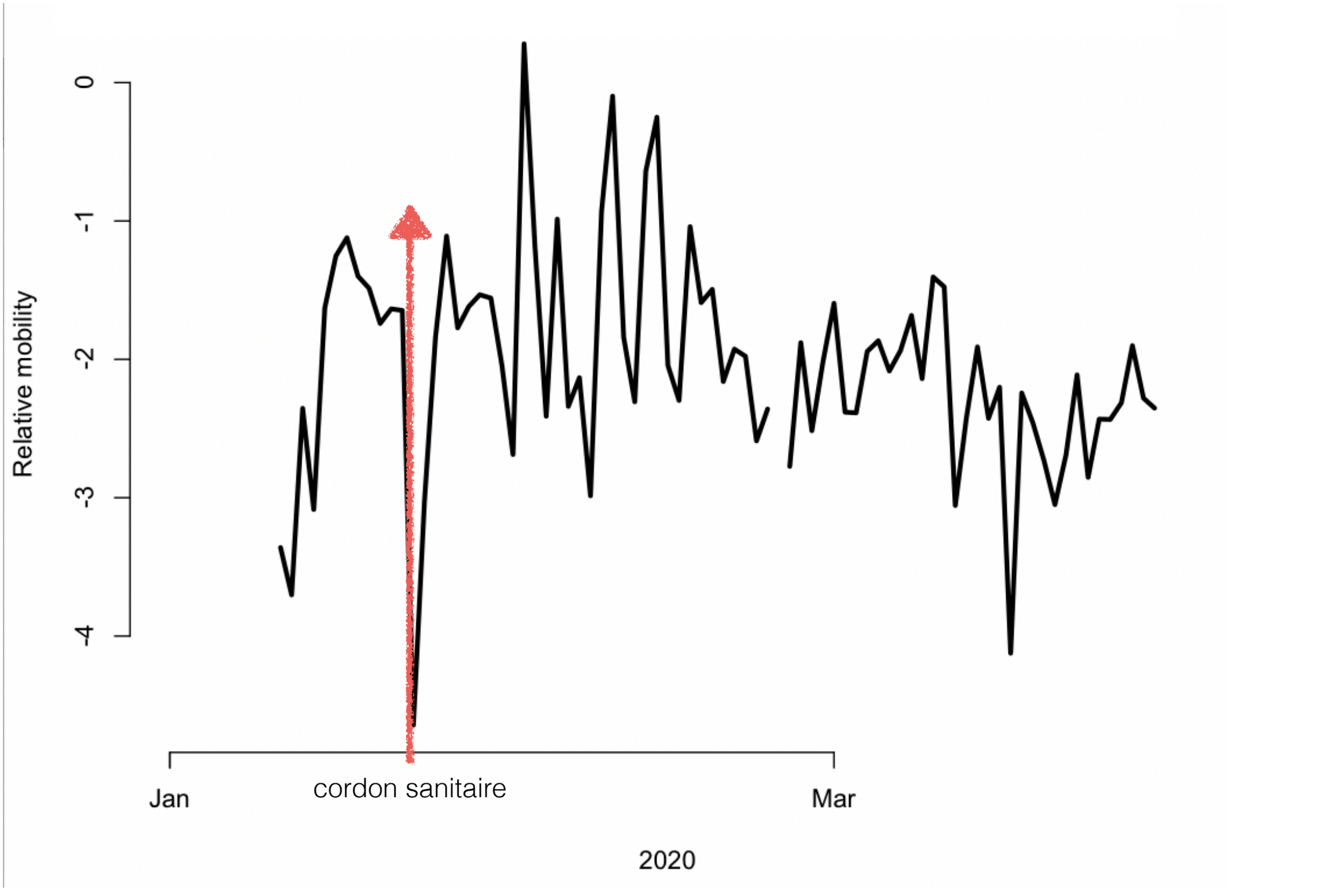
But they didn't all go to the same place



Scarpino unpublished

Or said differently, a physicist didn't just "turn up the temp" :)

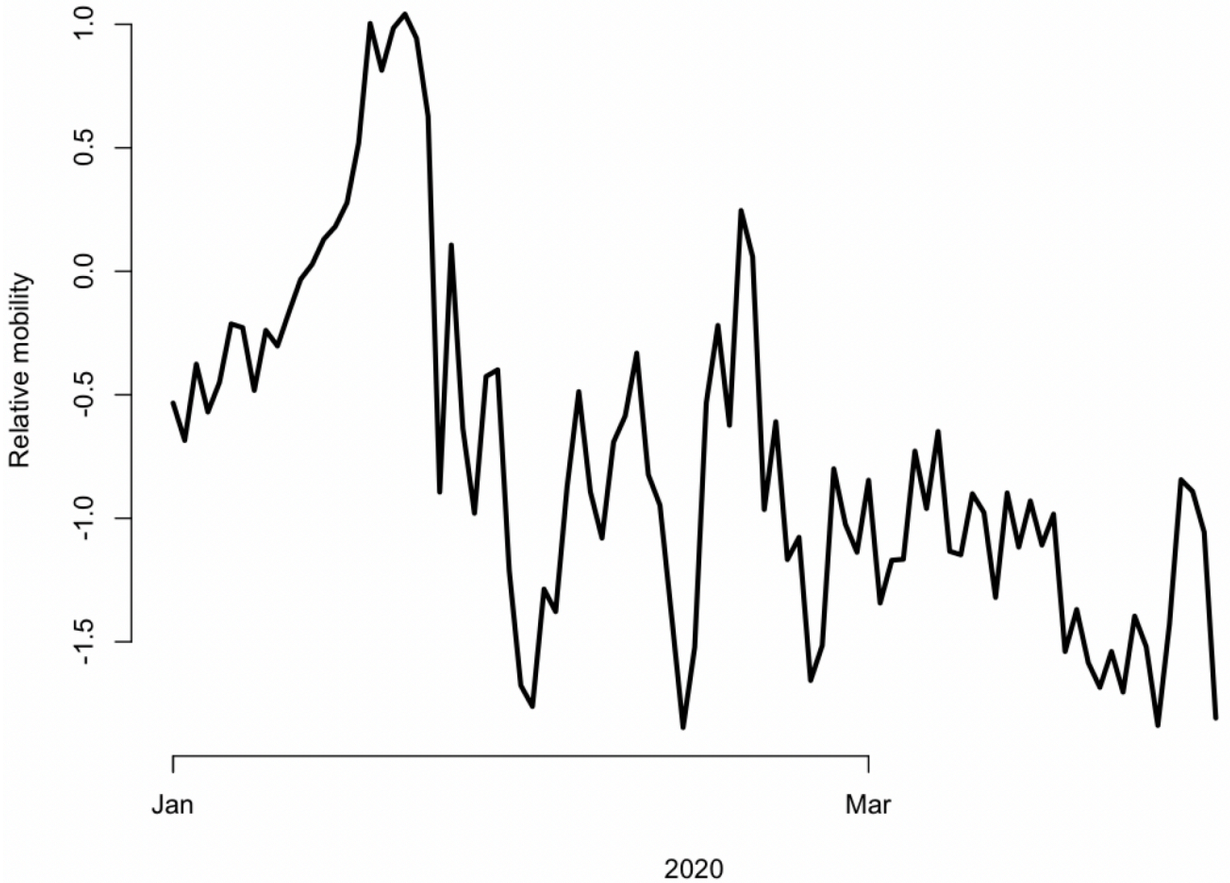
Wuhan -> Nanjing



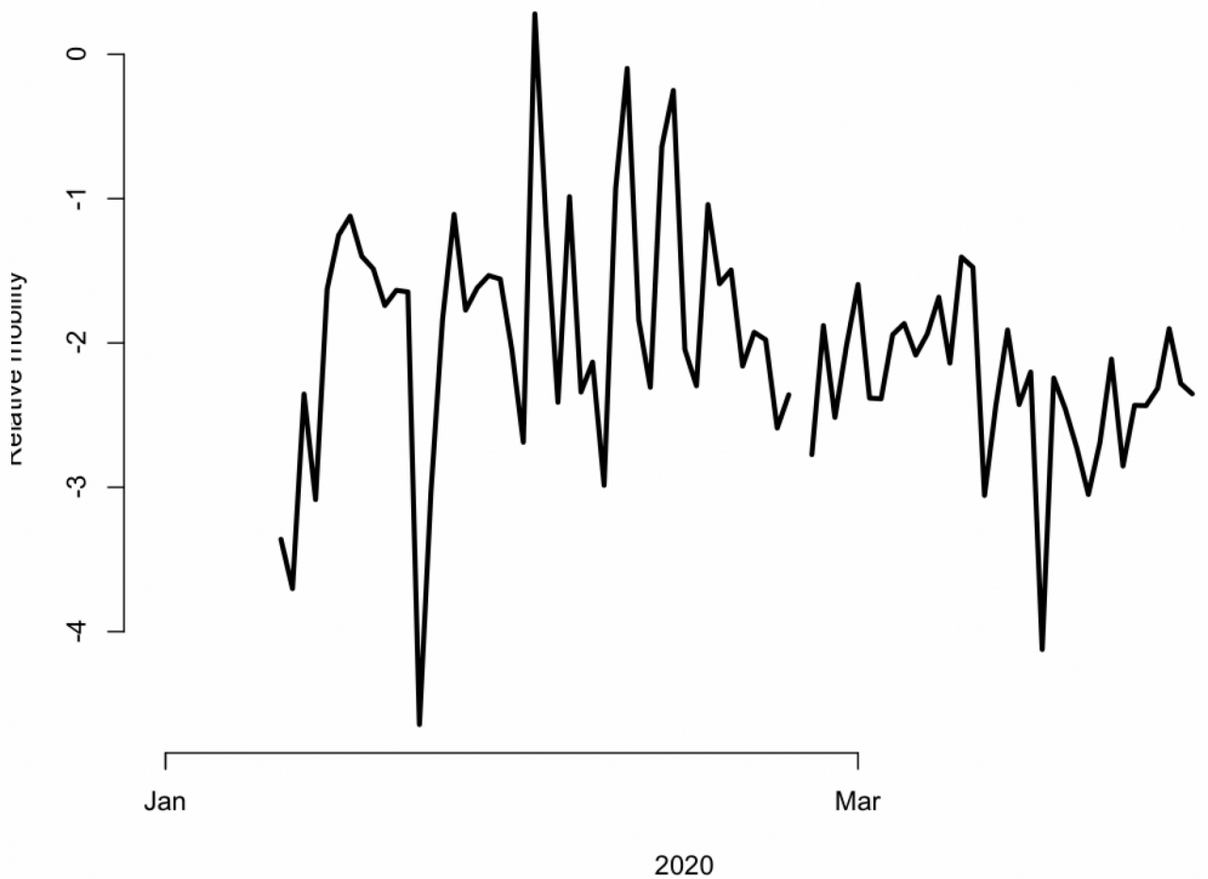
Scarpino unpublished

But they didn't all go to the same place

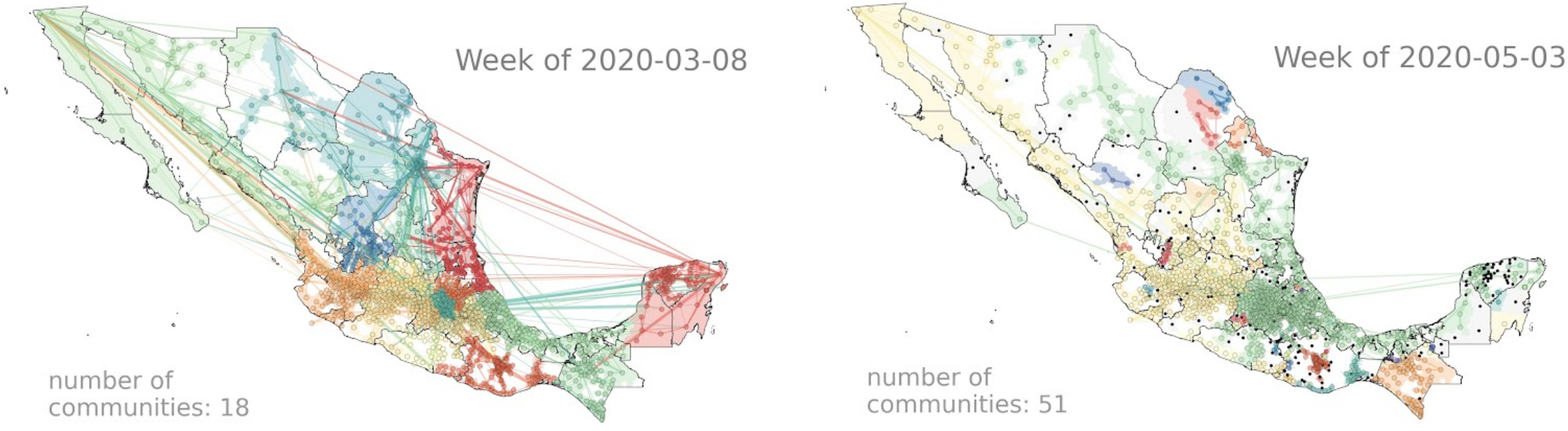
Wuhan -> Shanghai



Wuhan -> Nanjing

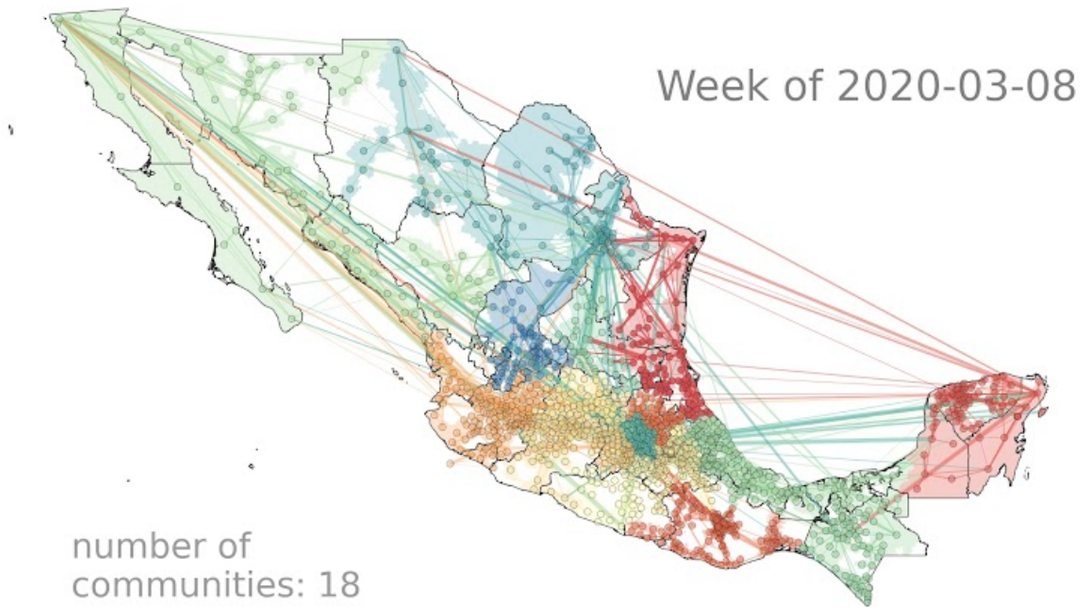


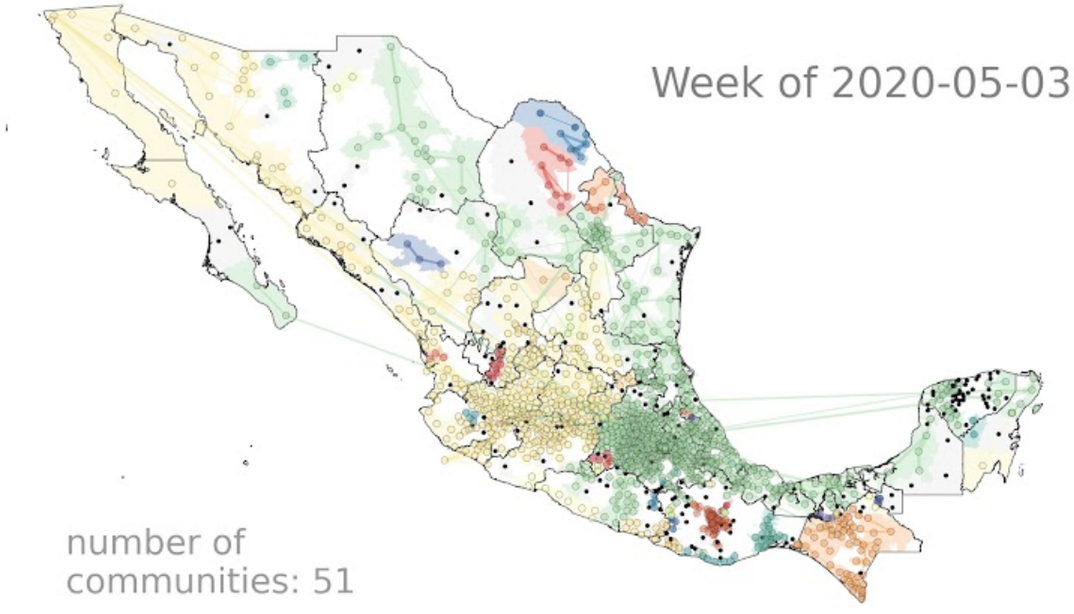
Scarpino unpublished

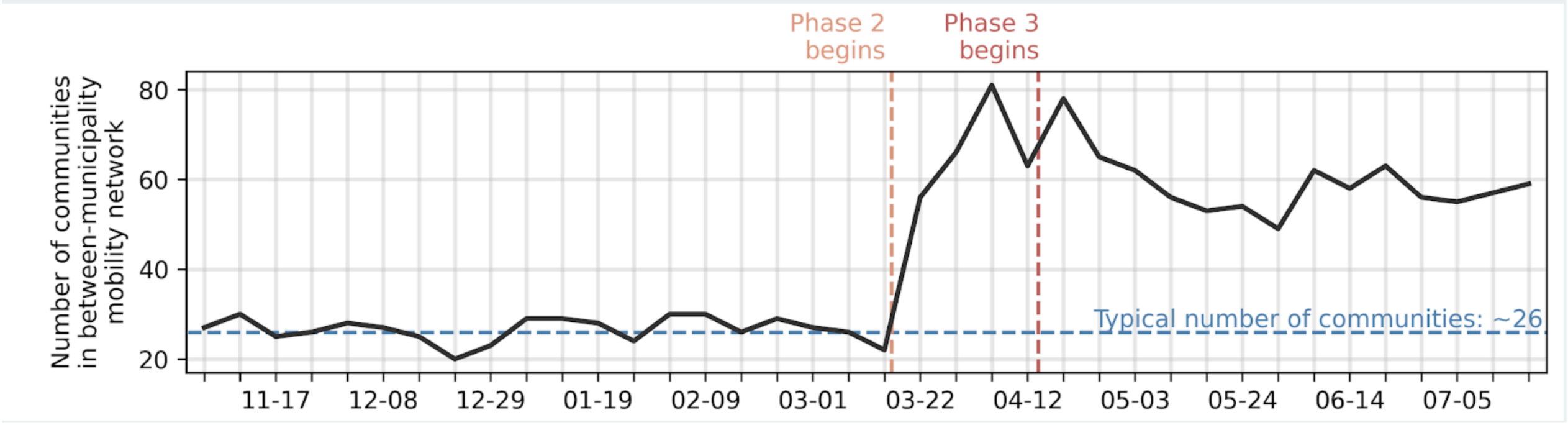


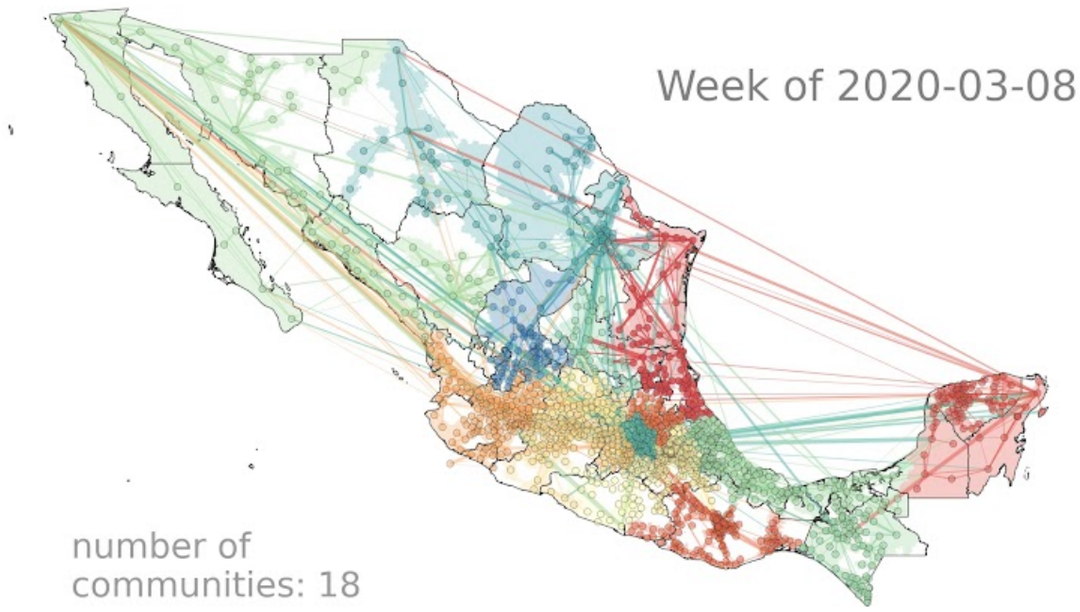
Spatial scales of COVID-19 transmission in Mexico

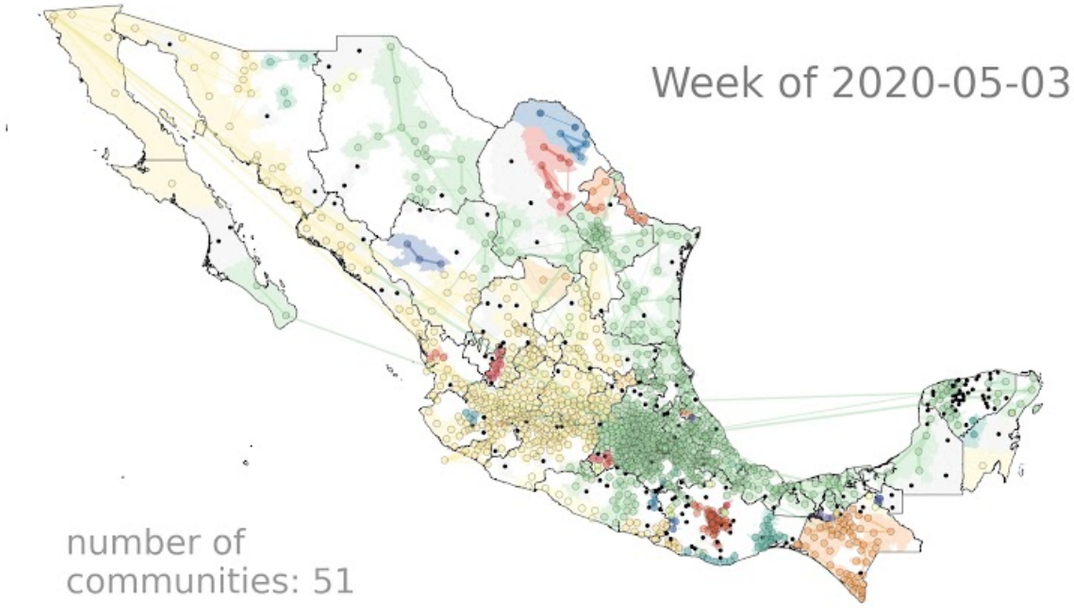
Brennan Klein*[1,2], Harrison Hartle[1], Munik Shrestha[1], Ana Cecilia Zenteno[3], David Barros Sierra Cordera[4], José R. Nicolas-Carlock[5], Ana I. Bento[6], Benjamin M. Althouse[7,8], Bernardo Gutierrez[9,10,11], Marina Escalera-Zamudio[9,11], Arturo Reyes-Sandoval[12,13], Oliver G. Pybus[9,14,18], Alessandro Vespignani[1,2], Jose Alberto Diaz-Quiñonez*†[15], Samuel V. Scarpino*‡[1,16,17], and Moritz U.G. Kraemer*§[9,18]


Week of 2020-03-08
number of
communities: 18


Week of 2020-05-03
number of
communities: 51


Phase 2
begins
Phase 3
begins
Number of communities
in between-municipality
mobility network
80
60
40
20
Typical number of communities: ~26
11-17
12-08
12-29
01-19
02-09
03-01
03-22
04-12
05-03
05-24
06-14
07-05


Week of 2020-03-08
number of
communities: 18


Week of 2020-05-03
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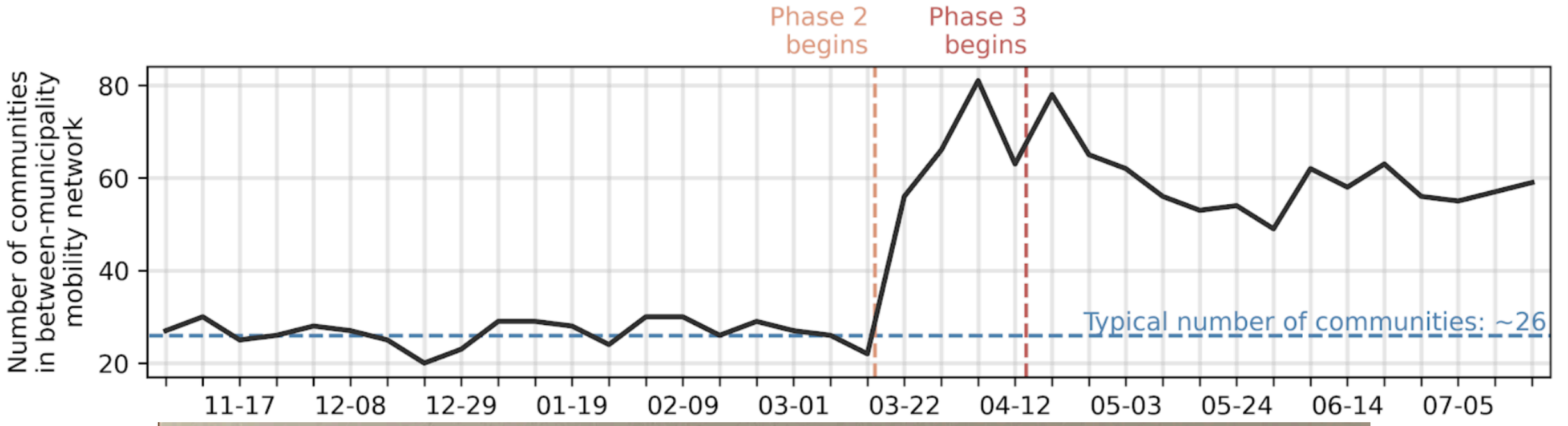
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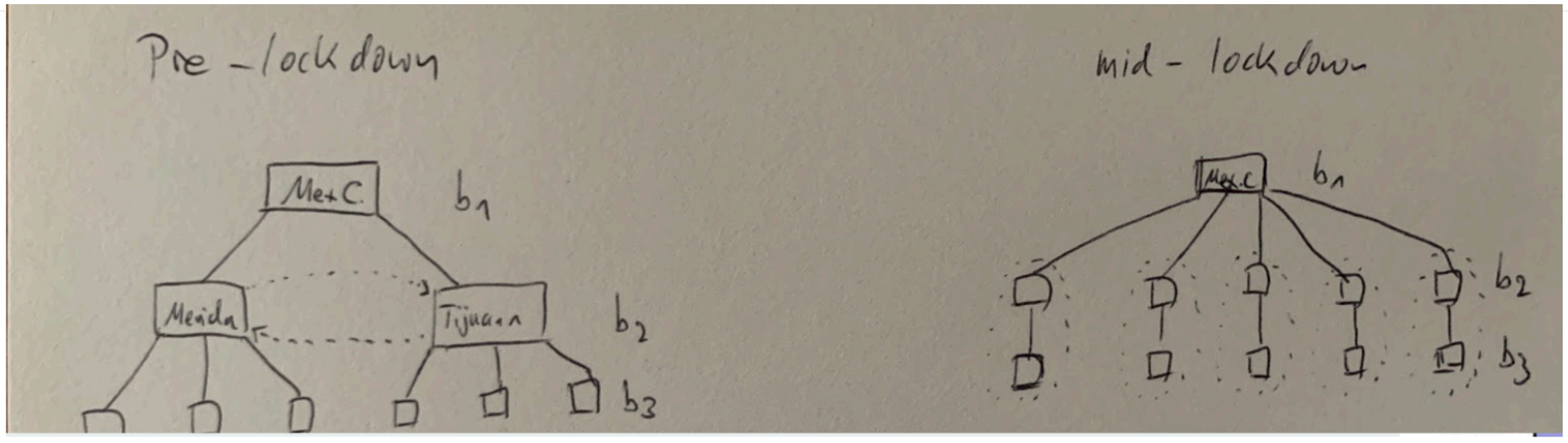
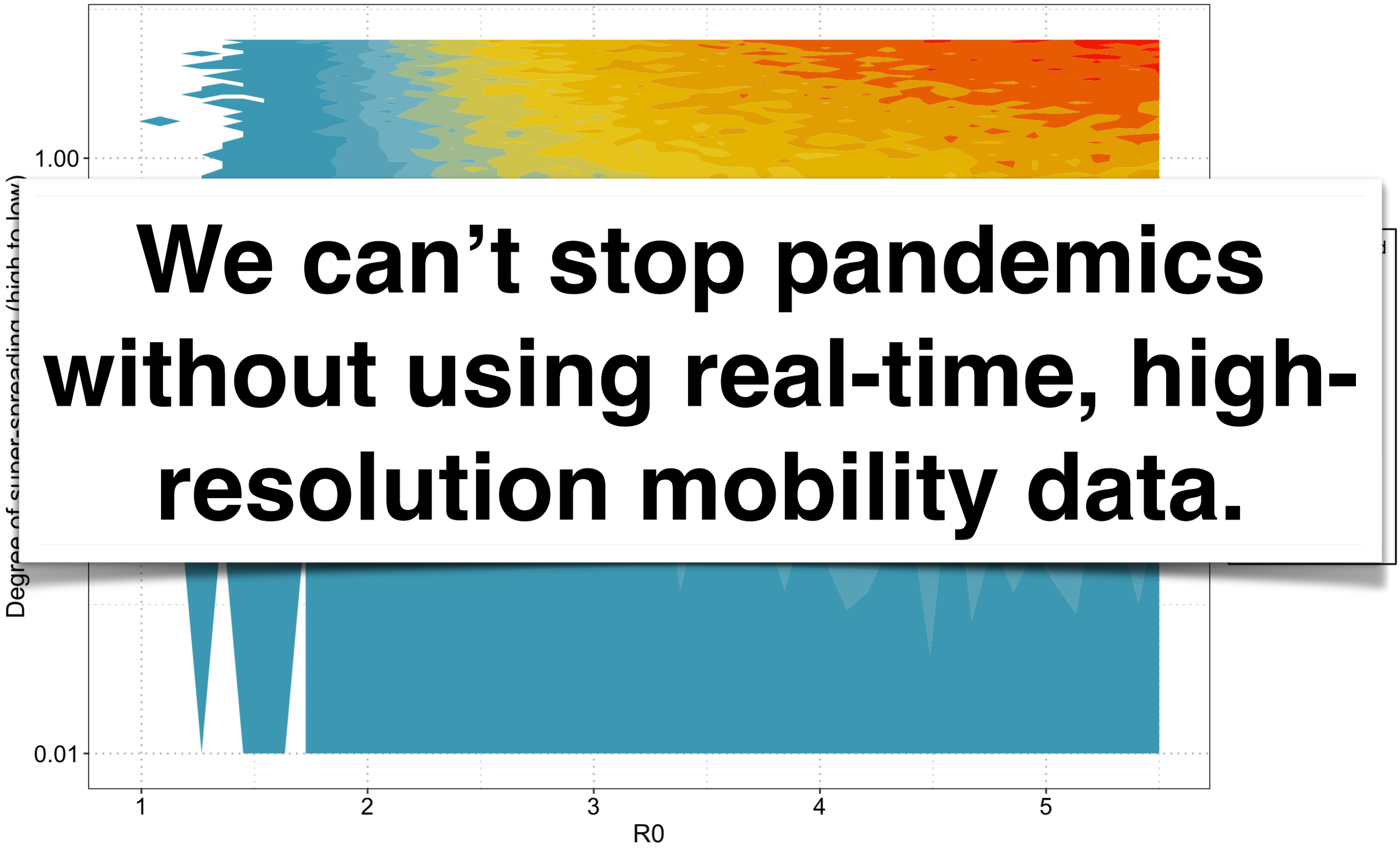

Pre - lockdown
Mex.C.
b_1
Merida
Tijuana
b_2
b_3
mid - lockdown
Mex.C
b_1
b_2
b_3

What did we learn about contagion from COVID-19?

- Everything is about meta-population dynamics.
- We need more empirical data on real-world networks.
- Super-spreading is under-appreciated for control.
- Behavior, behavior, behavior
- And the number one thing?



We can't stop pandemics without using real-time, high-resolution mobility data.

Questions?

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Professor of the Practice, Health & Computer Sciences

Northeastern University

External Faculty

Santa Fe Institute

Vermont Complex Systems Center

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