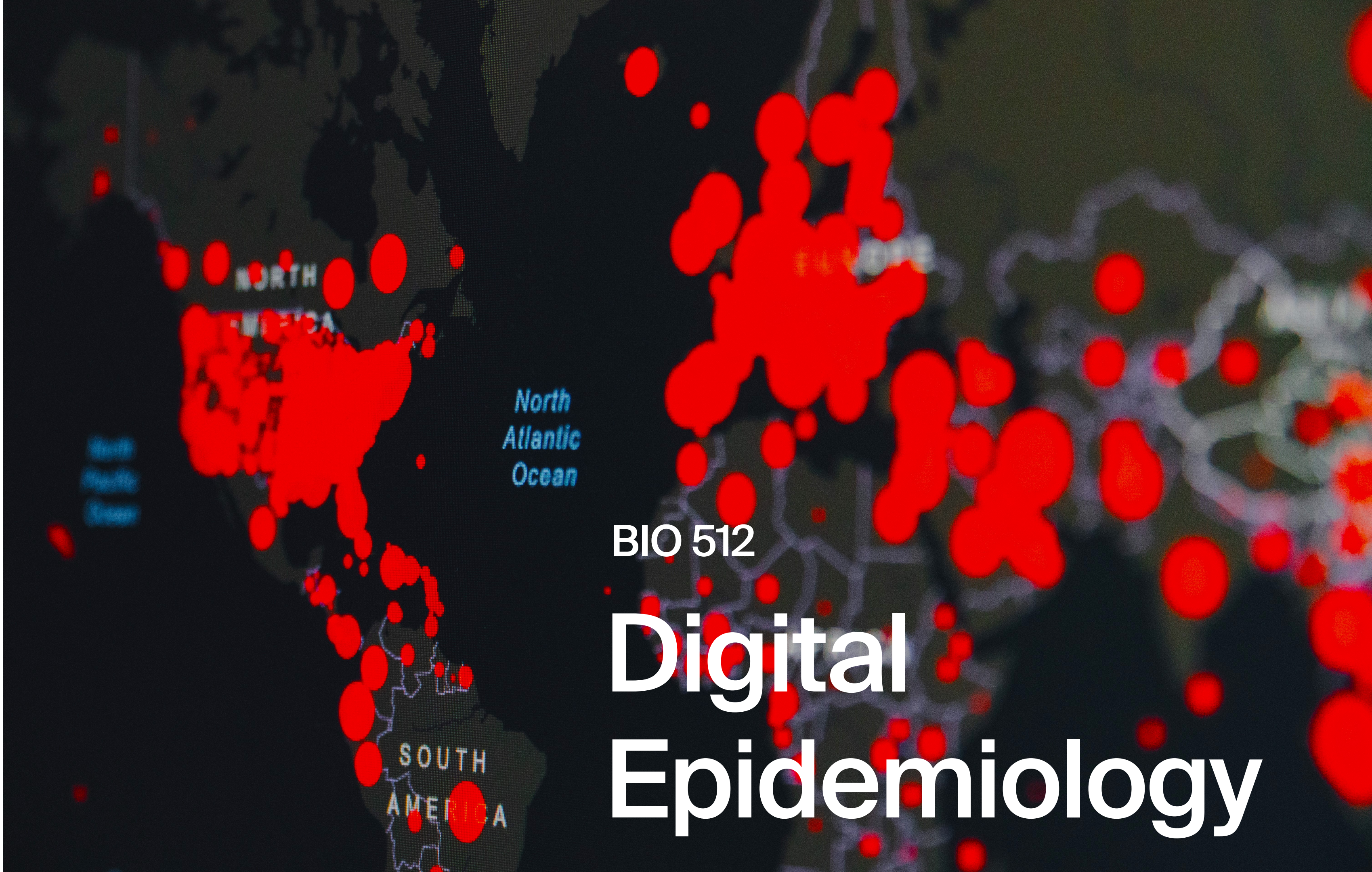
BIO 512

Digital Epidemiology

Digital Epidemiology Lab | BIO-521 | Spring semester 202



Spatial Models & Network Models
Learning Objectives

- Understand how to model space, and its effect
- Understand metapopulations
- Understand how to model network structure, and its effect

Spatial Models & Network Models
Model Complexity

- How complex should a model be?

Spatial Models & Network Models

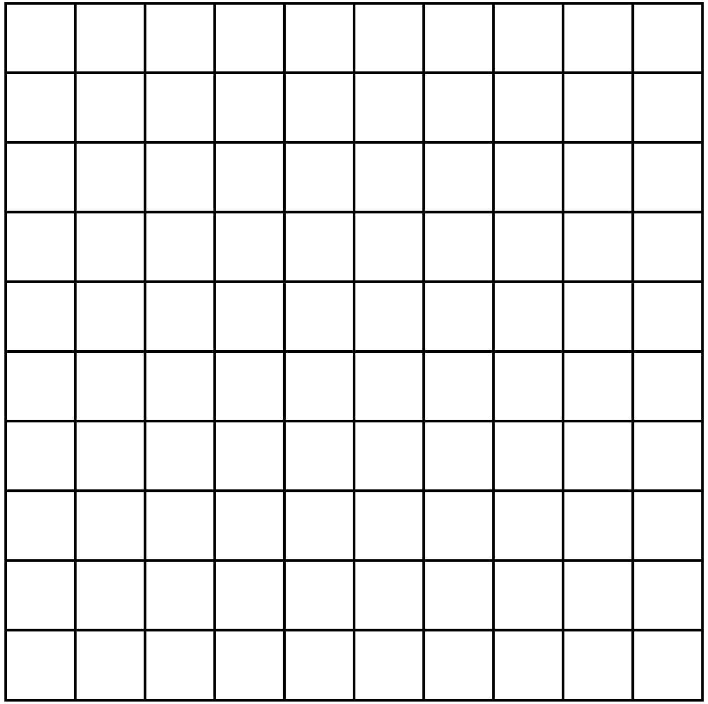
Spatial Models

- Could be deterministic -> math is rather complicated (PDEs)

- Individual-based models (agent-based models): stochastic, highly explicit models

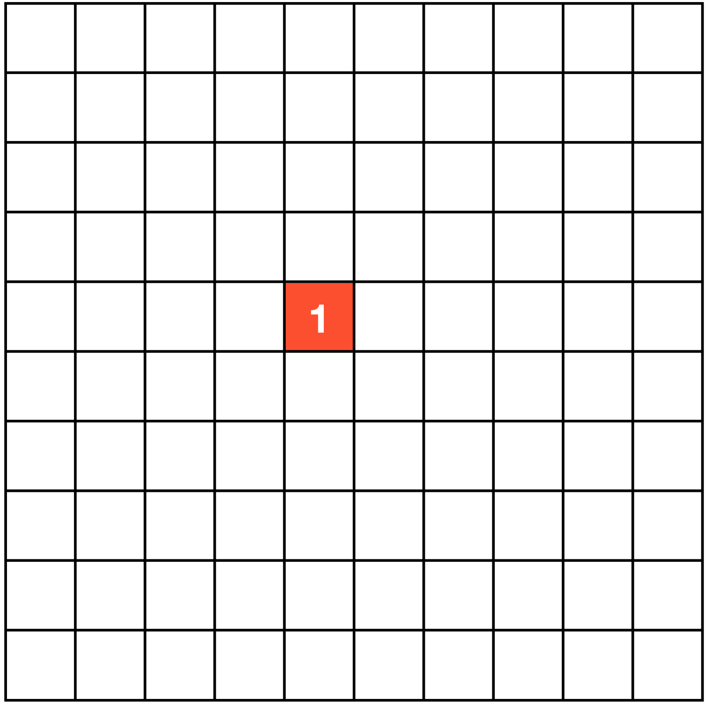
Spatial Models & Network Models

Spatial Models



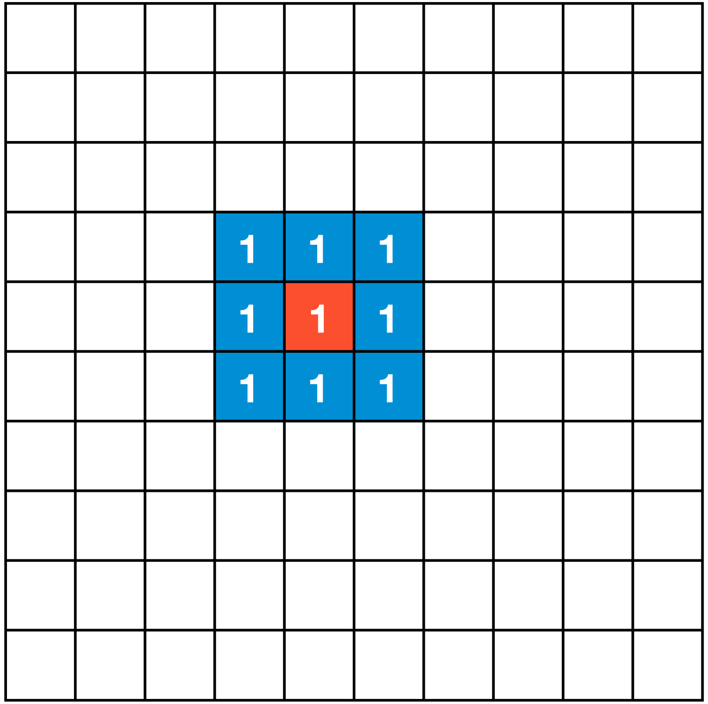
Spatial Models & Network Models

Spatial Models



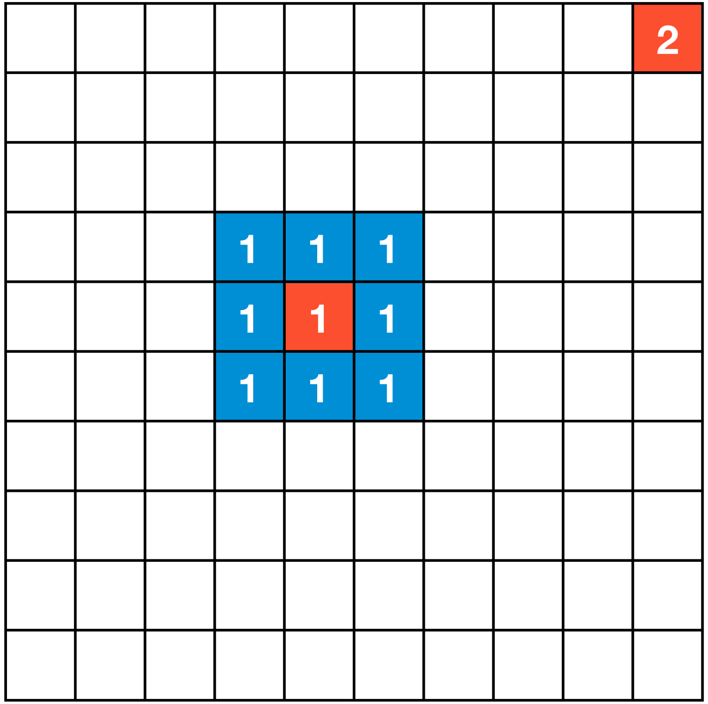
Spatial Models & Network Models

Spatial Models



Spatial Models & Network Models

Spatial Models



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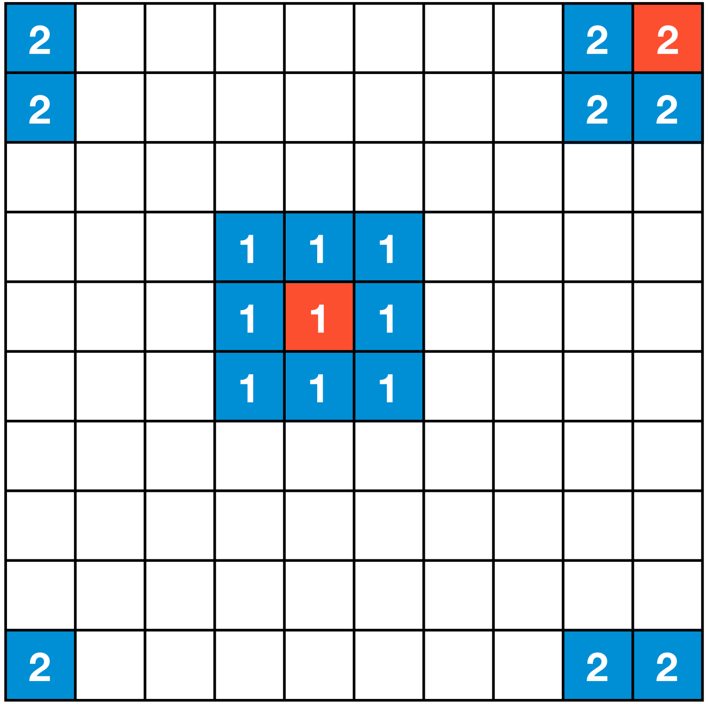
Spatial Models & Network Models

Spatial Models



Spatial Models & Network Models

Spatial Models

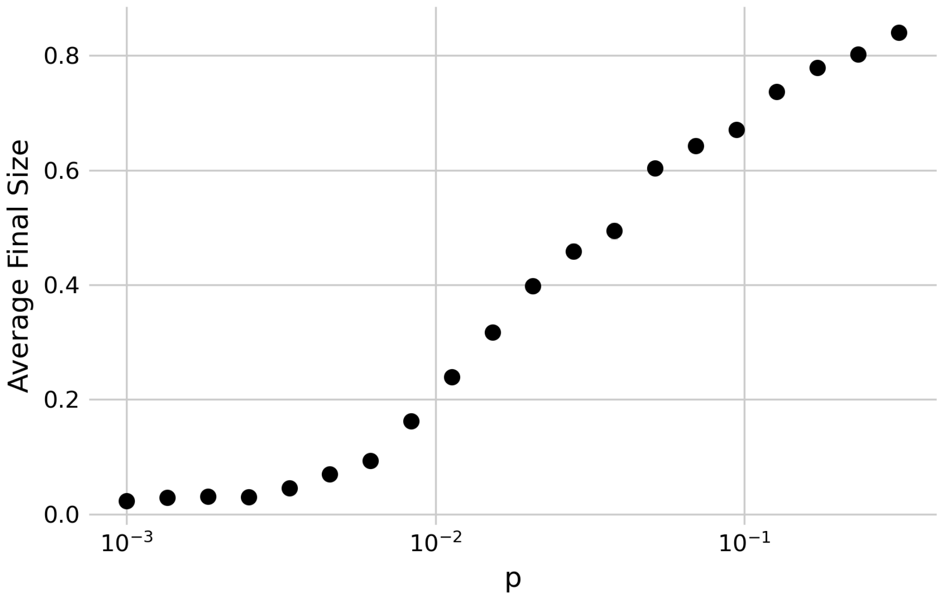
- Implementing a spatially explicit IBM

Spatial Models & Network Models

Random Connections

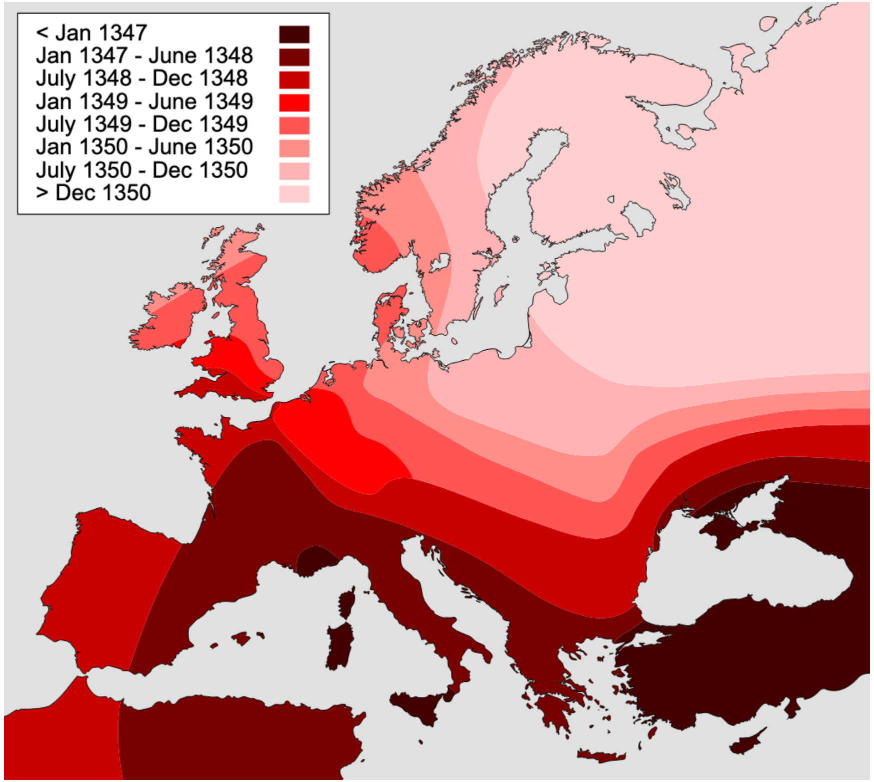
- Implement a probability p with which random connections between any two grid cell occurs.

Spatial Models & Network Models
Random Connections



Spatial Models & Network Models

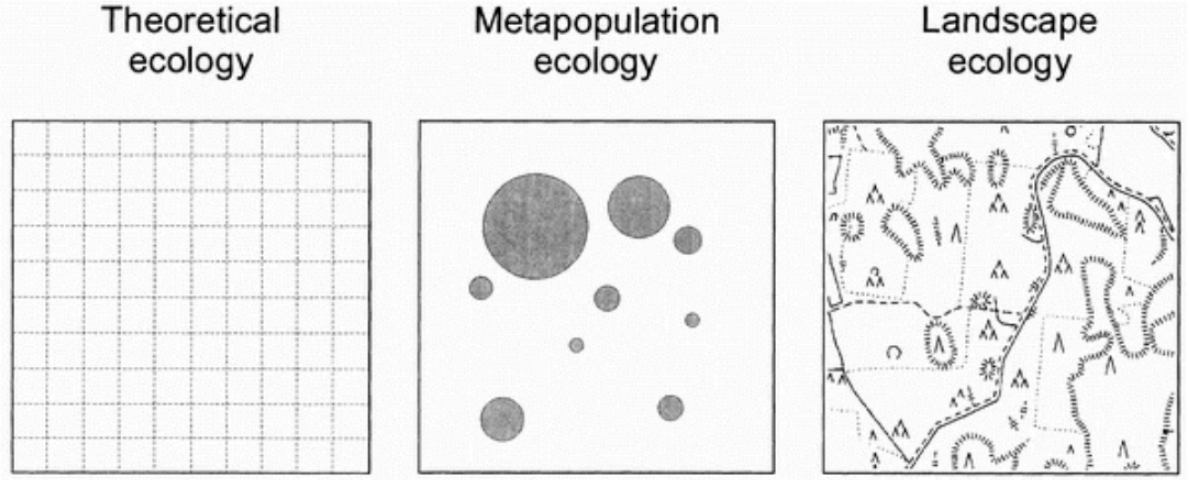
Before Global Travel



Source: Marvel et al 2013

Spatial Models & Network Models
Metapopulations

- A population of populations



Source: Hanski 1998

Article

Mobility network models of COVID-19 explain inequities and inform reopening

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Check for updates

Serina Chang[1,9], Emma Pierson[1,2,9], Pang Wei Koh[1,9], Jaline Gerardin[3], Beth Redbird[4,5], David Grusky[6,7] & Jure Leskovec[1,8] ✉

The coronavirus disease 2019 (COVID-19) pandemic markedly changed human mobility patterns, necessitating epidemiological models that can capture the effects of these changes in mobility on the spread of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)[1]. Here we introduce a metapopulation susceptible–exposed–infectious–removed (SEIR) model that integrates fine-grained, dynamic mobility networks to simulate the spread of SARS-CoV-2 in ten of the largest US metropolitan areas. Our mobility networks are derived from mobile phone data and map the hourly movements of 98 million people from neighbourhoods (or census block groups) to points of interest such as restaurants and religious establishments, connecting 56,945 census block groups to 552,758 points of interest with 5.4 billion hourly edges. We show that by integrating these networks, a relatively simple SEIR model can accurately fit the real case trajectory, despite substantial changes in the behaviour of the population over time. Our model predicts that a small minority of 'superspreader' points of interest account for a large majority of the infections, and that restricting the maximum occupancy at each point of interest is more effective than uniformly reducing mobility. Our model also correctly predicts higher infection rates among disadvantaged racial and socioeconomic groups[2–8] solely as the result of differences in mobility: we find that disadvantaged groups have not been able to reduce their mobility as sharply, and that the points of interest that they visit are more crowded and are therefore associated with higher risk. By capturing who is infected at which locations, our model supports detailed analyses that can inform more-effective and equitable policy responses to COVID-19.

Spatial Models & Network Models
Metapopulations

SCIENCE ADVANCES | RESEARCH ARTICLE

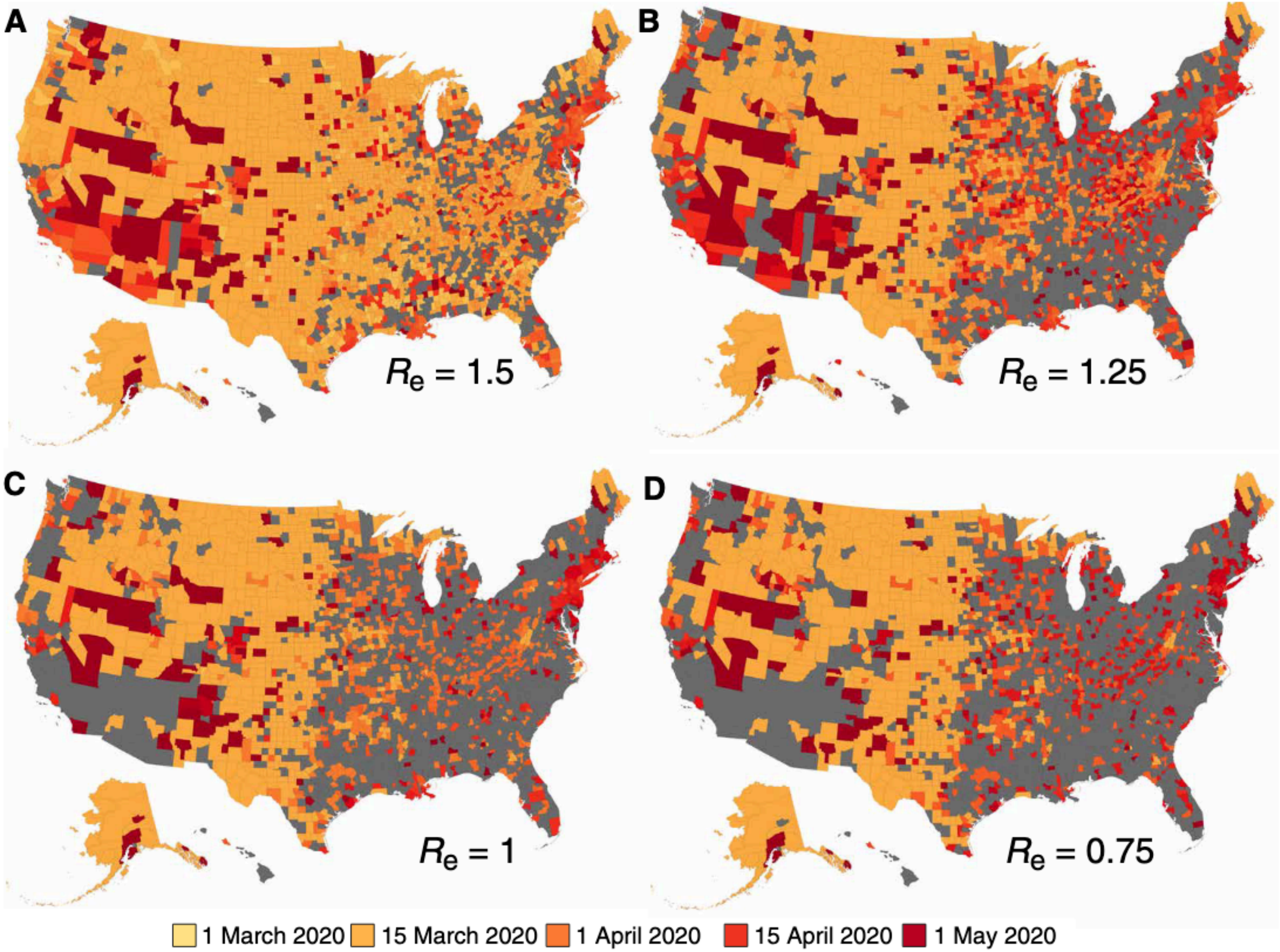
CORONAVIRUS

Differential effects of intervention timing on COVID-19 spread in the United States

Sen Pei, Sasikiran Kandula, Jeffrey Shaman*

Assessing the effects of early nonpharmaceutical interventions on coronavirus disease 2019 (COVID-19) spread is crucial for understanding and planning future control measures to combat the pandemic. We use observations of reported infections and deaths, human mobility data, and a metapopulation transmission model to quantify changes in disease transmission rates in U.S. counties from 15 March to 3 May 2020. We find that marked, asynchronous reductions of the basic reproductive number occurred throughout the United States in association with social distancing and other control measures. Counterfactual simulations indicate that, had these same measures been implemented 1 to 2 weeks earlier, substantial cases and deaths could have been averted and that delayed responses to future increased incidence will facilitate a stronger rebound of infections and death. Our findings underscore the importance of early intervention and aggressive control in combatting the COVID-19 pandemic.

EPFL

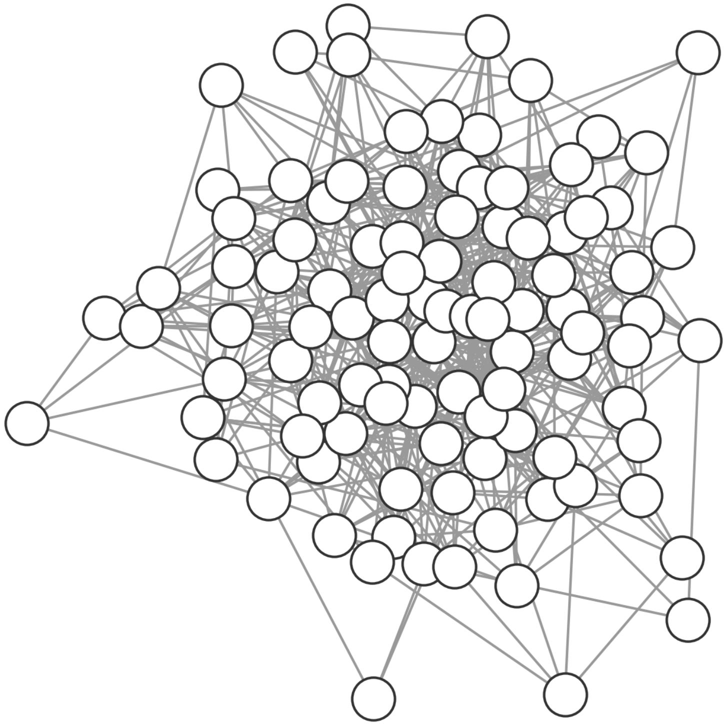

A
$R_e = 1.5$
B
$R_e = 1.25$
C
$R_e = 1$
D
$R_e = 0.75$
1 March 2020
15 March 2020
1 April 2020
15 April 2020
1 May 2020

Spatial Models & Network Models
Contact Network Models

- Graph
- Nodes
- Edges
- Degree
- Path Length
- Shortest Path
- Average Path Length

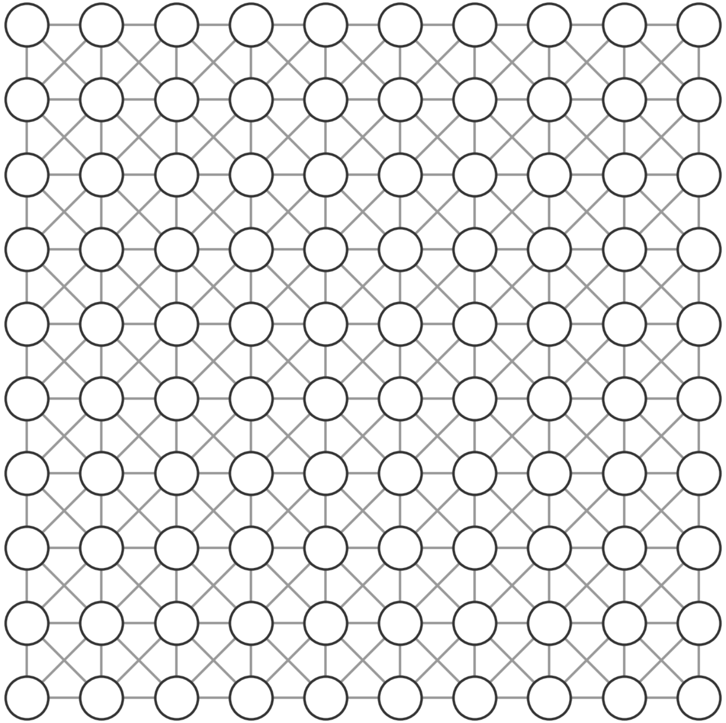
Spatial Models & Network Models

Random Networks



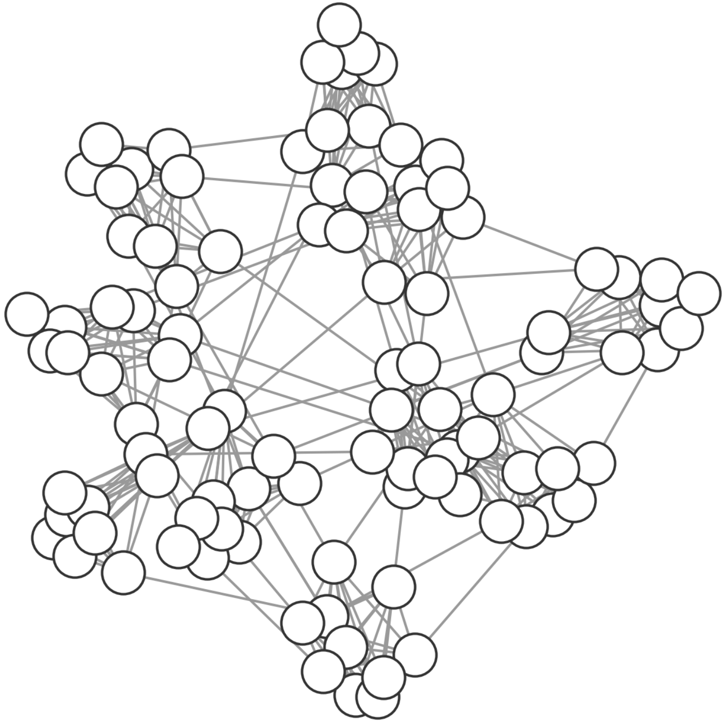
Spatial Models & Network Models

Lattice / Grid / Spatial Networks



Spatial Models & Network Models

Social Network

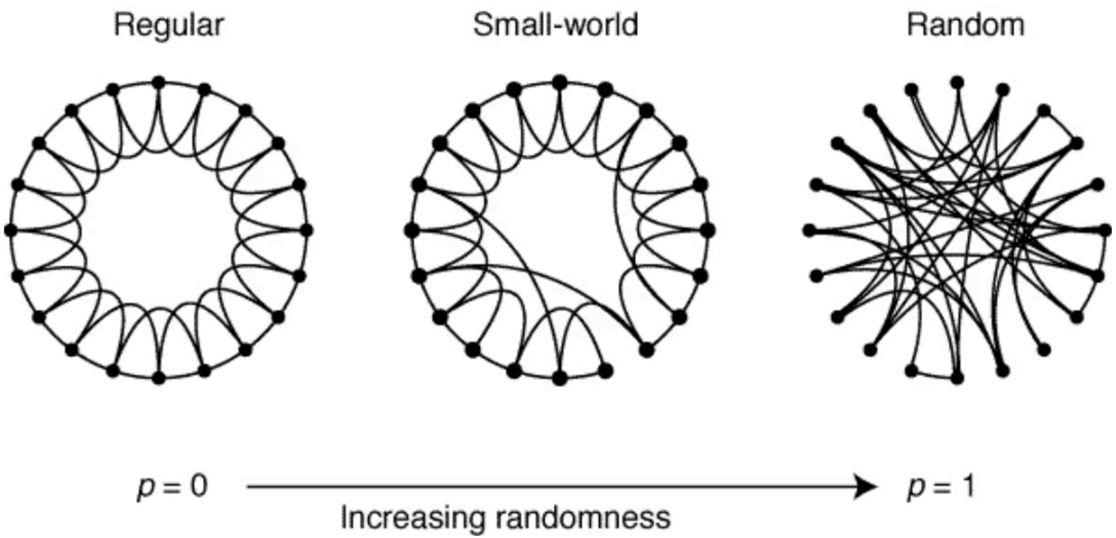


Spatial Models & Network Models
Small World

- Milgram: send letter to target person in Boston. If you don’t know target person, send letter to another person who might.
- “Sig degrees of separation”, “It’s a small world”

Spatial Models & Network Models
Small World

- Ring network, each node connected to k neighbors. Randomly rewire with probability p.



Source: Watts & Strogatz 1998

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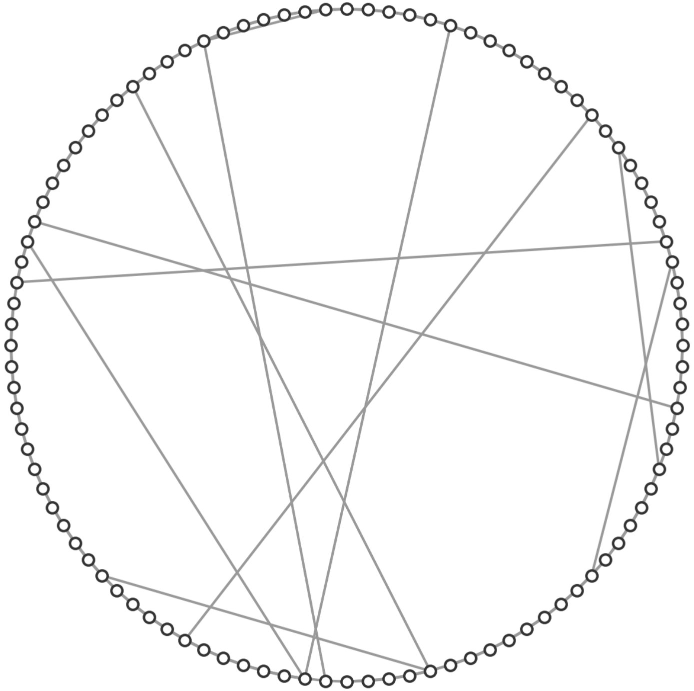
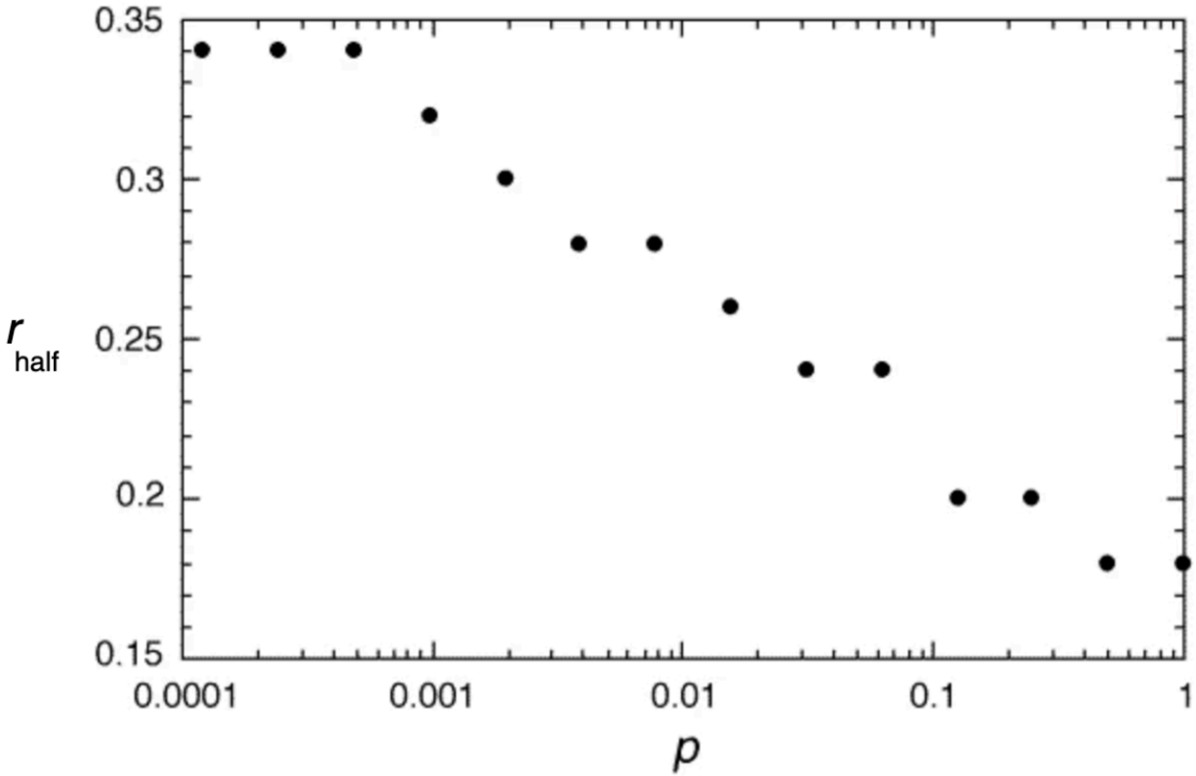
Spatial Models & Network Models

Small World

- N = 100
- k = 4
- p = 0.05



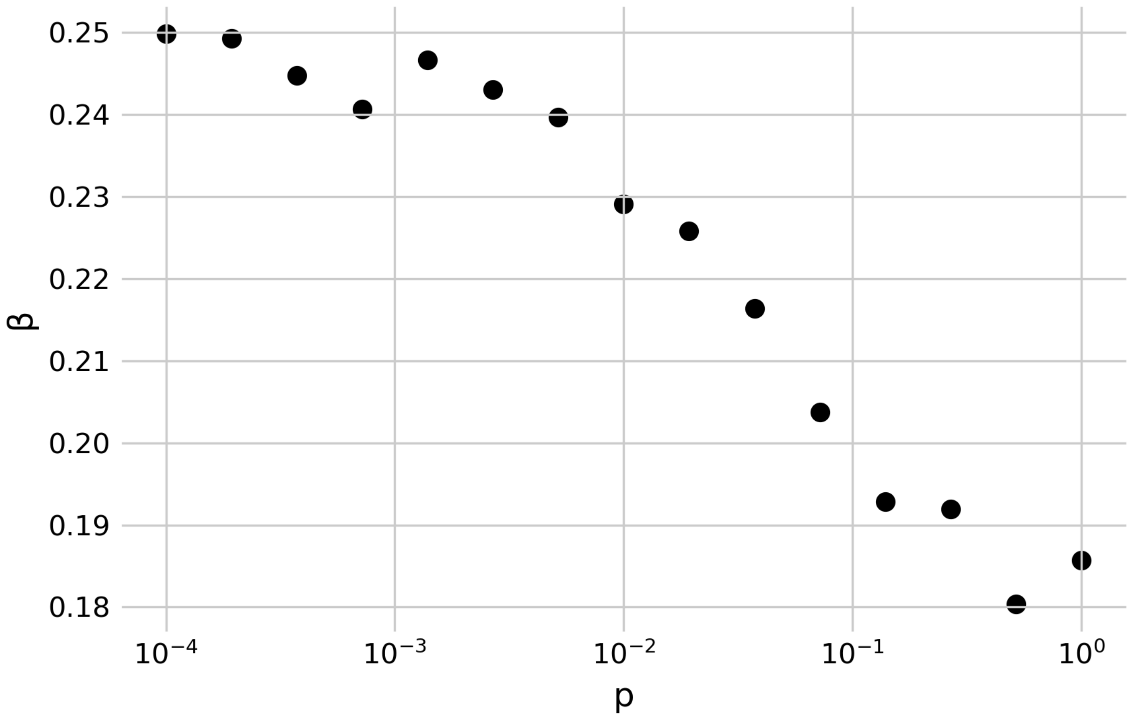
Spatial Models & Network Models
Small World



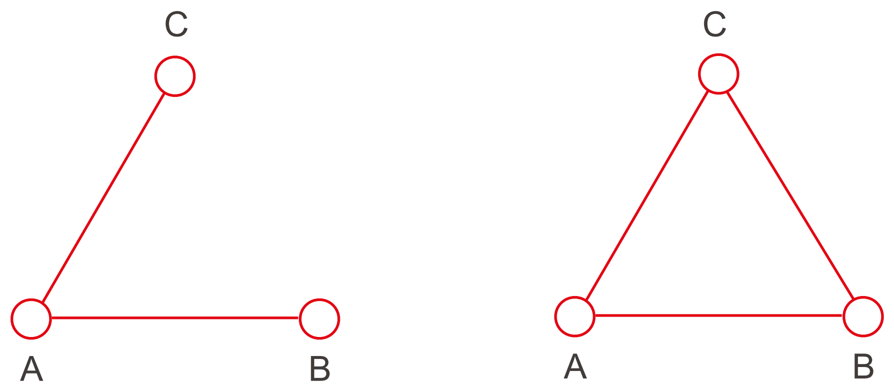
Source: Watts & Strogatz 1998

Spatial Models & Network Models

Small World

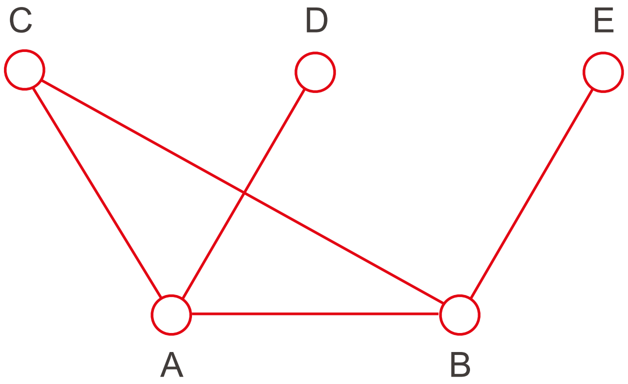


Spatial Models & Network Models
Small World

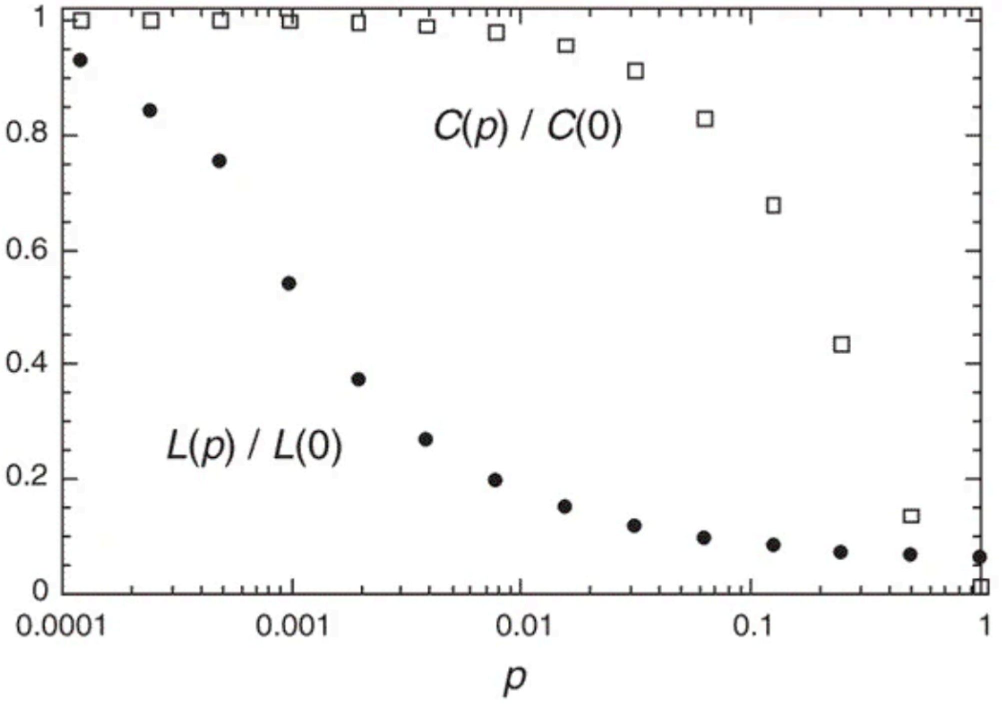


Spatial Models & Network Models

Small World



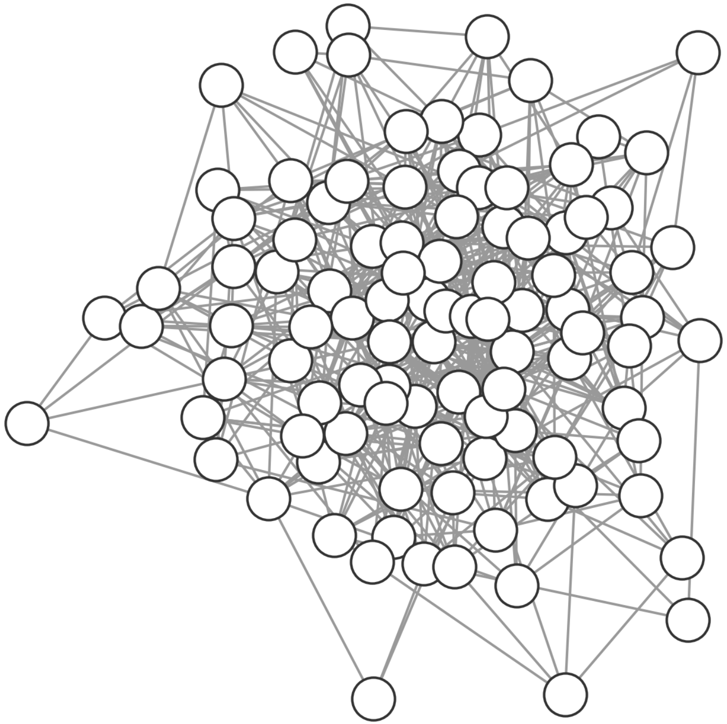
Spatial Models & Network Models
Small World



Source: Watts & Strogatz 1998

Spatial Models & Network Models

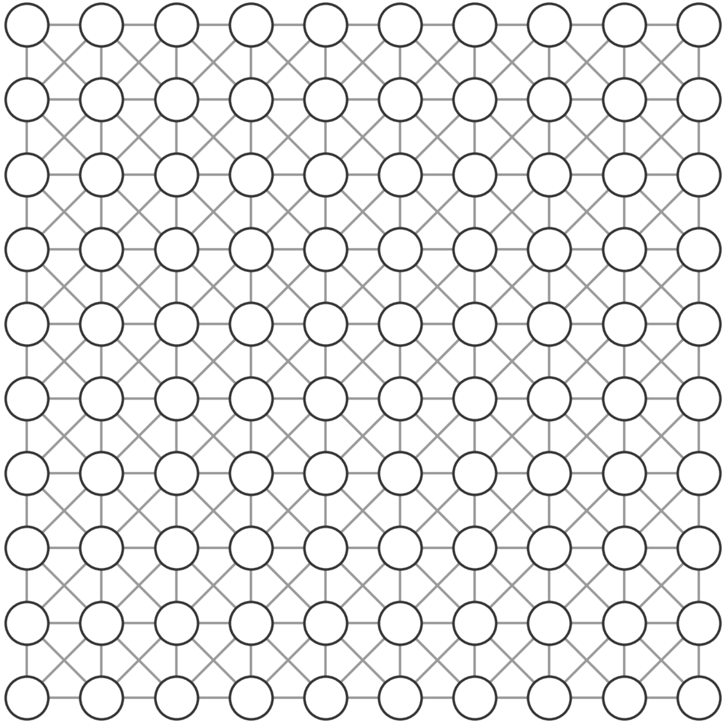
Random Networks



C = 0.11

Spatial Models & Network Models

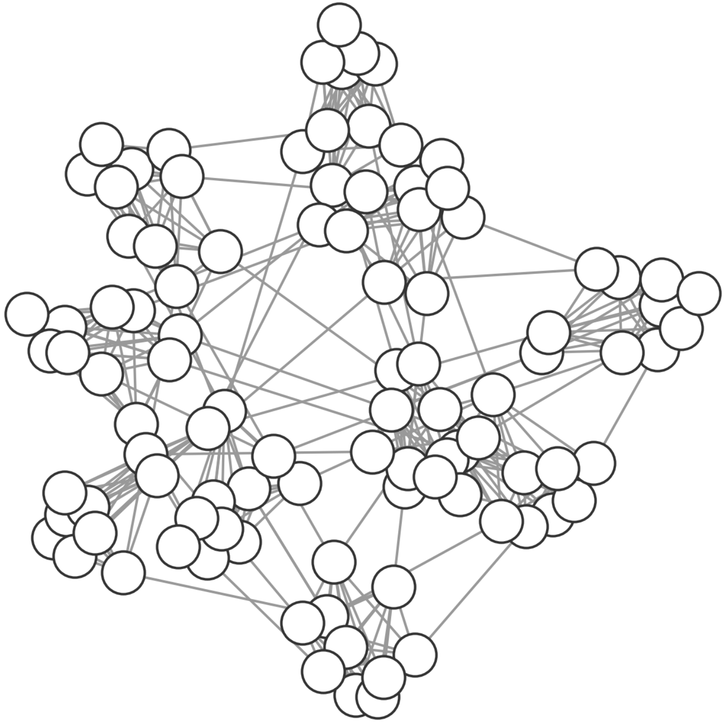
Lattice / Grid / Spatial Networks



C = 0.51

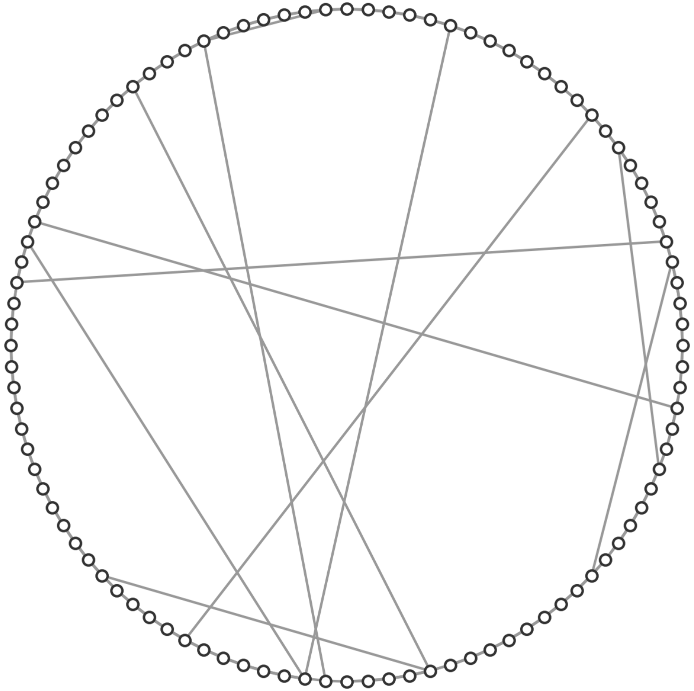
Spatial Models & Network Models

Social Network



C = 0.73

Spatial Models & Network Models
Small World

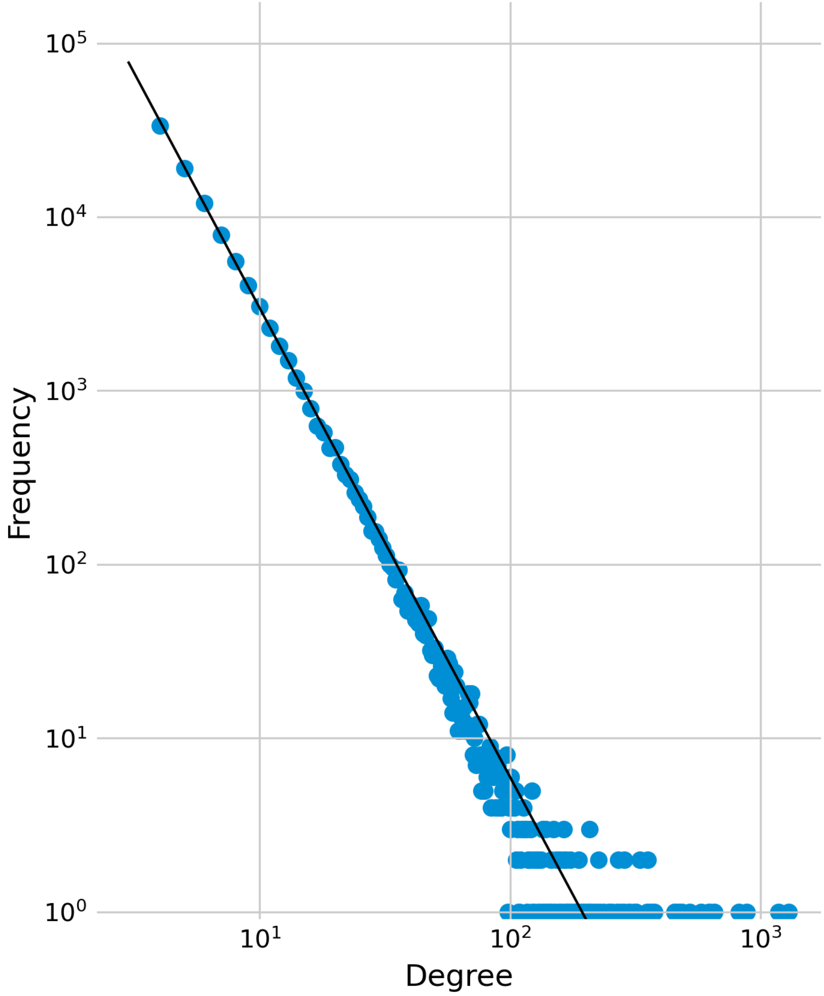


C = 0.44

Spatial Models & Network Models
Fat-tailed networks

- Barabasi-Albert: Scale-free networks

  “the probability P(k) that a vertex in the network interacts with k other vertices decays as a power law, following $P(k) \sim k^{-\gamma}$”,



- 33.4% of nodes have minimum degree of 4
- most connected node has degree of 1295
- γ = -2.7

MONKEYPOX

Heavy-tailed sexual contact networks and monkeypox epidemiology in the global outbreak, 2022

Akira Endo[1,2,3]*, Hiroaki Murayama[4], Sam Abbott[1,2], Ruwan Ratnayake[1,2], Carl A. B. Pearson[1,2,5], W. John Edmunds[1,2], Elizabeth Fearon[2,6]†, Sebastian Funk[1,2]†

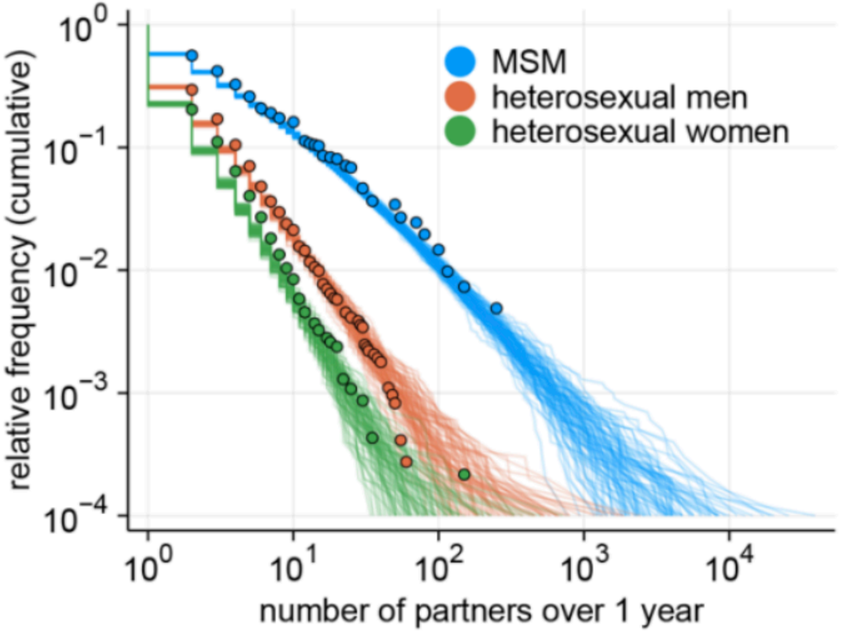
The outbreak of monkeypox across non-endemic regions confirmed in May 2022 shows epidemiological features distinct from previously imported outbreaks, most notably its observed growth and predominance amongst men who have sex with men (MSM). We use a transmission model fitted to empirical sexual partnership data to show that the heavy-tailed sexual partnership distribution, in which a handful of individuals have disproportionately many partners, can explain the sustained growth of monkeypox among MSM despite the absence of such patterns previously. We suggest that the basic reproduction number (R_0) for monkeypox over the MSM sexual network may be substantially above 1, which poses challenges to outbreak containment. Ensuring support and tailored messaging to facilitate prevention and early detection among MSM with high numbers of partners is warranted.

In May 2022 multiple countries in Europe, North America, and elsewhere reported clusters of monkeypox cases (*1–4*). As of 31 May 2022 (time of analysis) a total of 728 confirmed and suspected cases have been reported in more than 25 countries from outbreaks in Central and West Africa identified a relatively limited proportion of cases of human-to-human transmission, with at most seven generations observed (*8*, *9*, *11*, *12*), and previous estimates of the basic reproduction number (R_0) for monkeypox have been be- importation events documented in non-endemic settings starting in 2003 (*13–17*).

We show that transmission over a sexual contact network empirically characterized by a heavy-tailed partnership distribution can reasonably explain the rapid growth of human-to-human transmission in the current monkeypox outbreak despite the absence of such patterns of spread in the past. Specifically, it is plausible that monkeypox has had a substantial transmission potential in the MSM sexual contact network but because of the small cumulative number of imported cases in non-endemic settings, it had not reached members of this network with high numbers of contacts from whom onward transmission was most probable. The main analysis of this study was conducted using only information available as of 31 May 2022, a few weeks after the outbreak had been first recognized, and the original version was submitted on 12 June 2022 [available from (*22*)] to provide key insights from the earliest data available. We retain this original context of the analysis in this paper to highlight that the findings were obtainable in the earliest phase of the outbreak and discuss them in retrospect given the up-

Spatial Models & Network Models

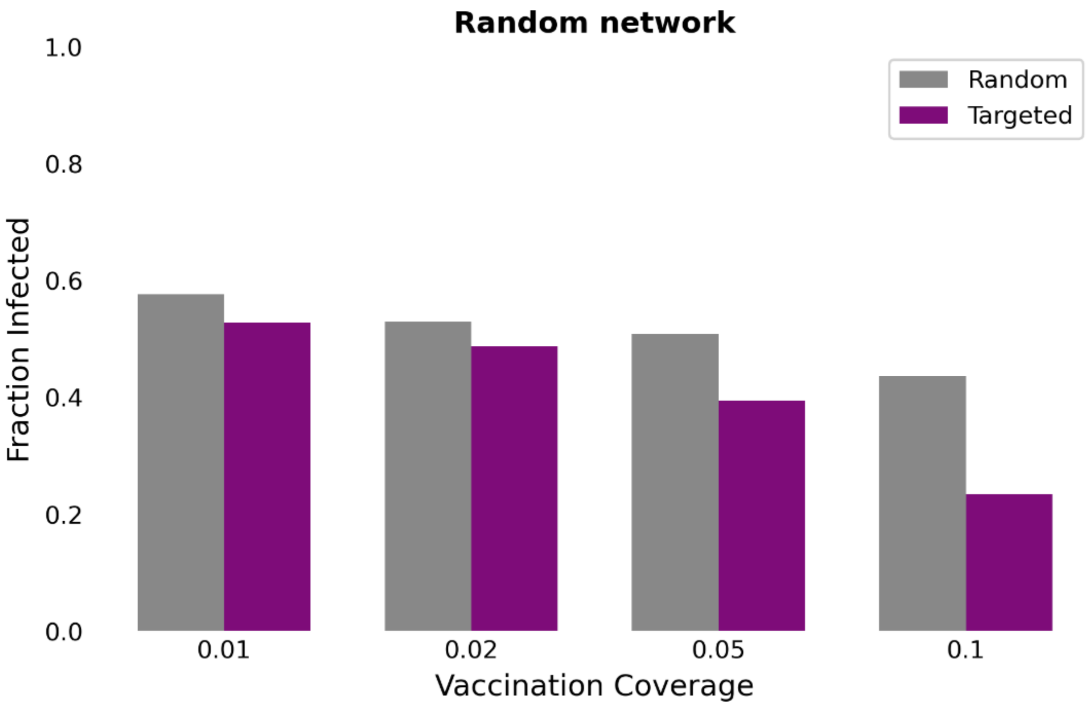
Fat-tailed networks



Spatial Models & Network Models
Fat-tailed networks

- Highly connected nodes pose a problem, but also a solution: targeted protection
- Fat-tailed networks are error tolerant, but prone to attack - we can use this for control!

Spatial Models & Network Models
Fat-tailed networks



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Spatial Models & Network Models
Fat-tailed networks