Connecting the multiple scales of an epidemic using network epidemiology

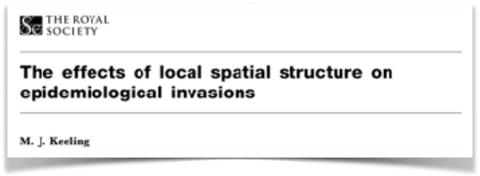
International Conference on Complex Networks (CompleNet) 2026

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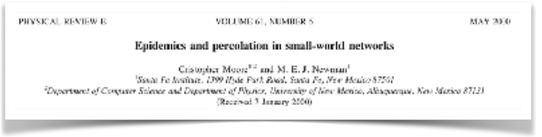
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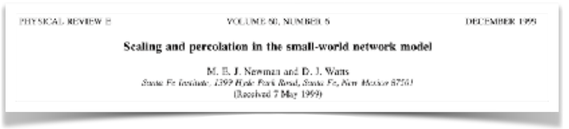
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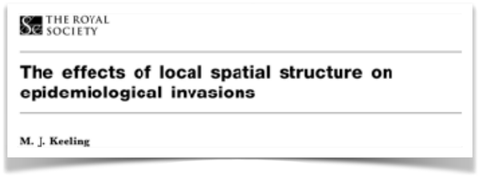
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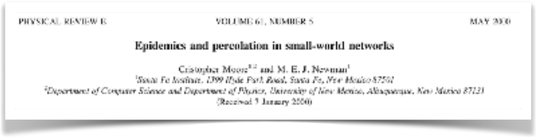
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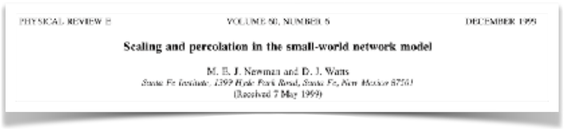
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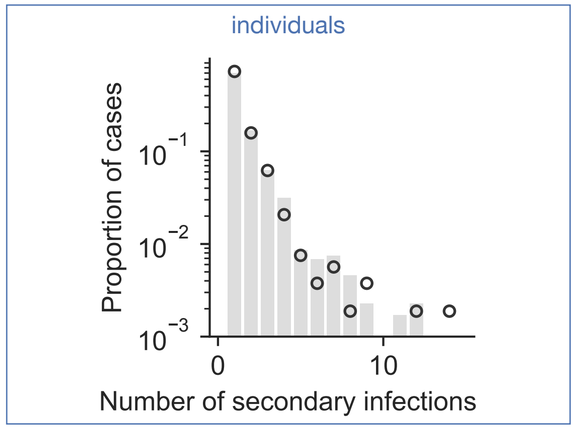
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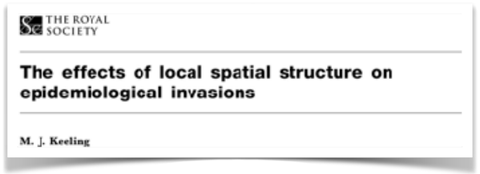
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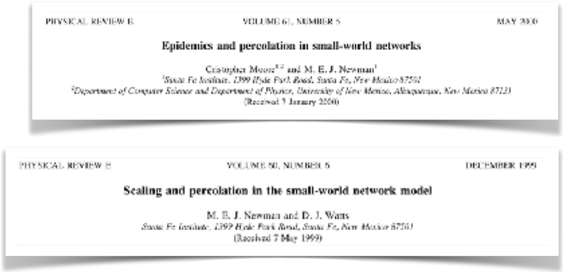


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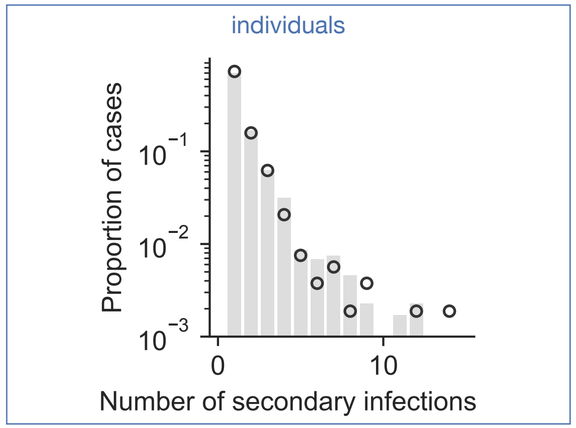
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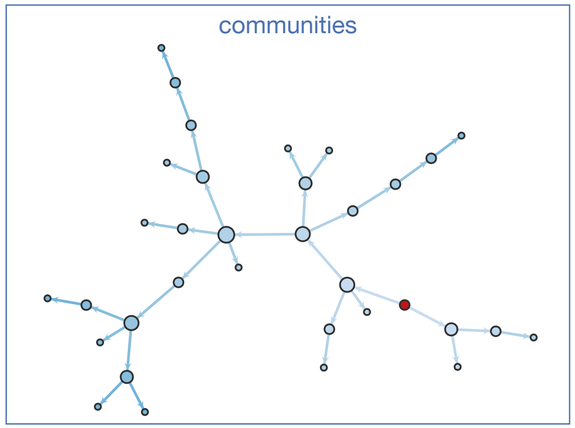
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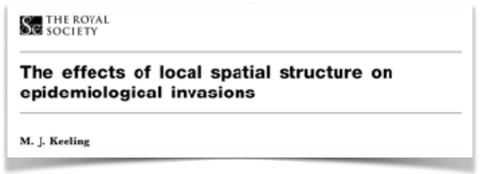
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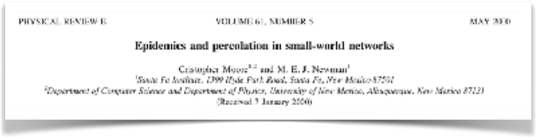


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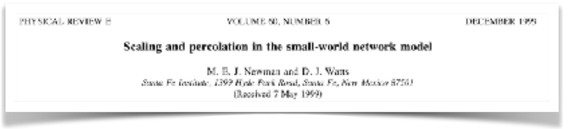
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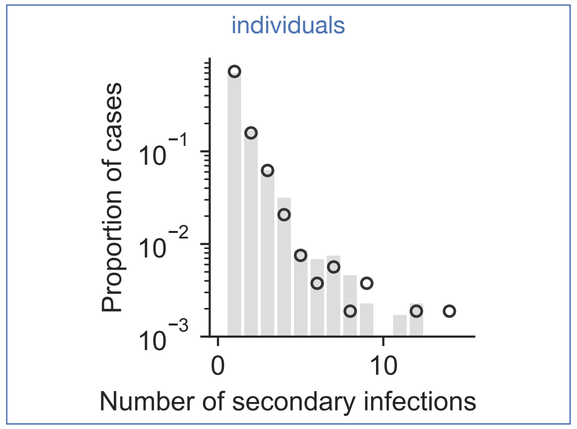
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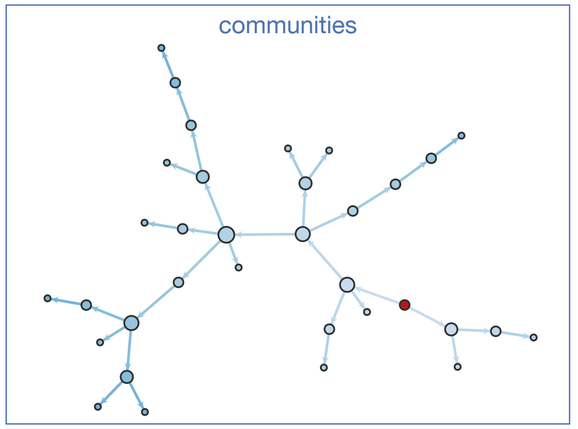
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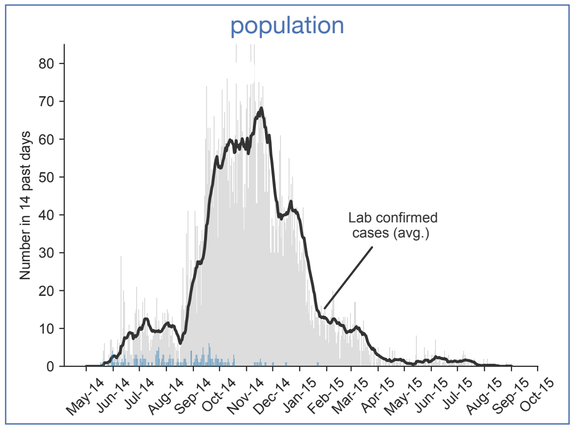
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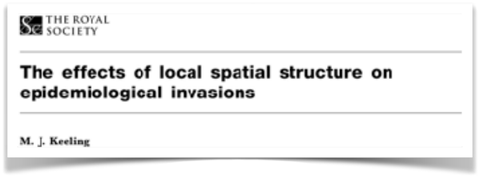
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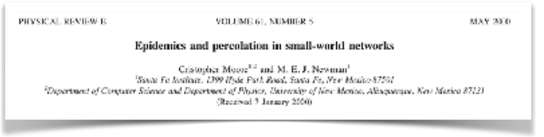


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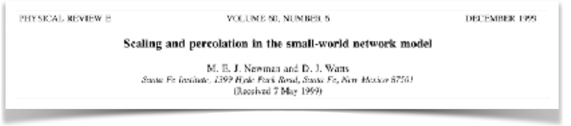
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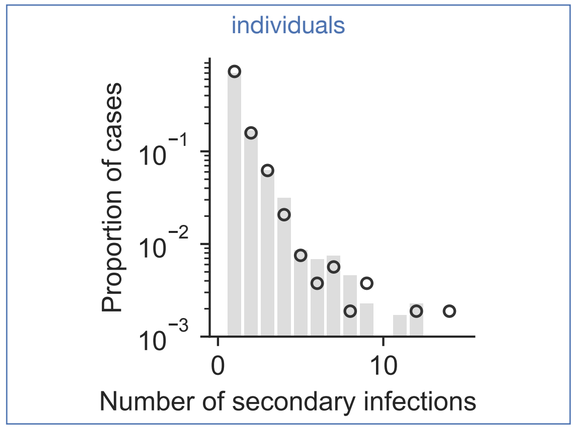
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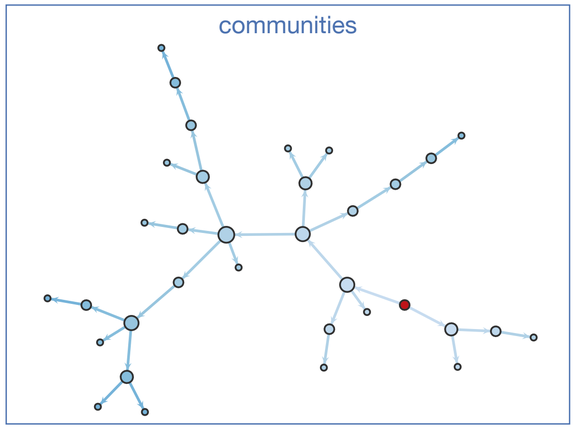
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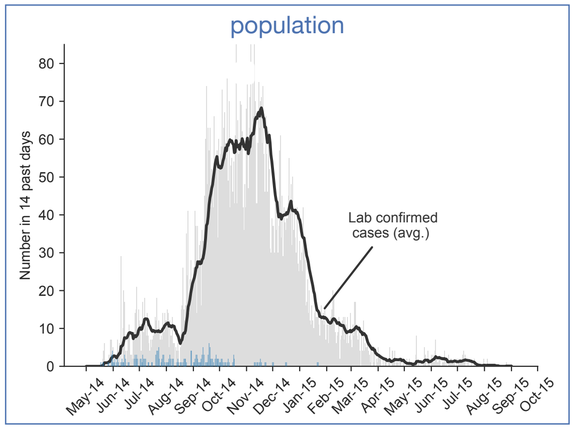
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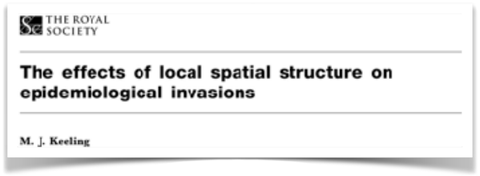
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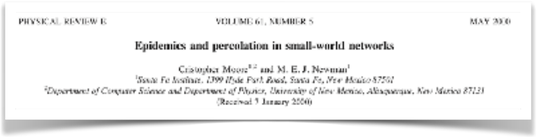


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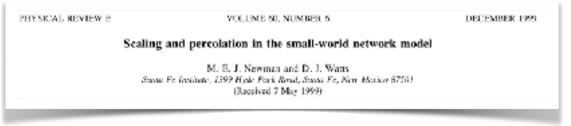
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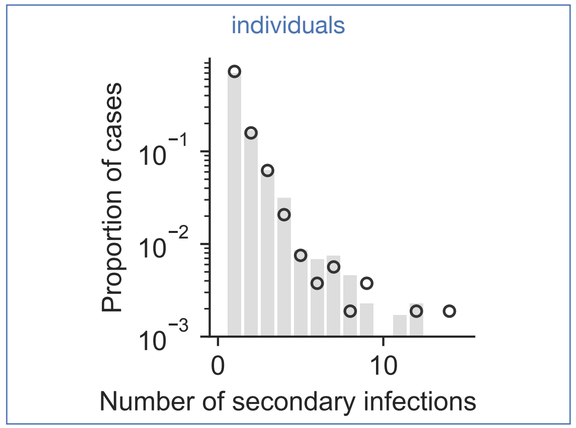
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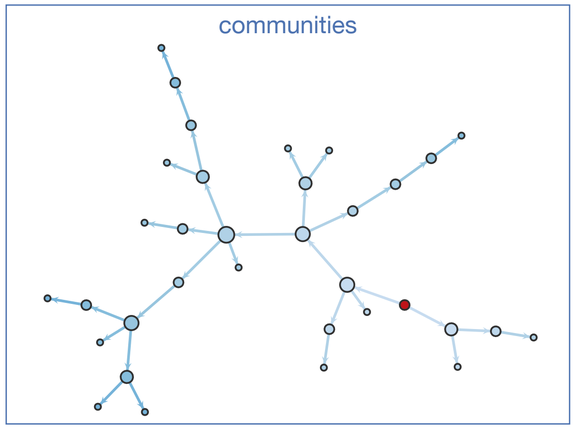
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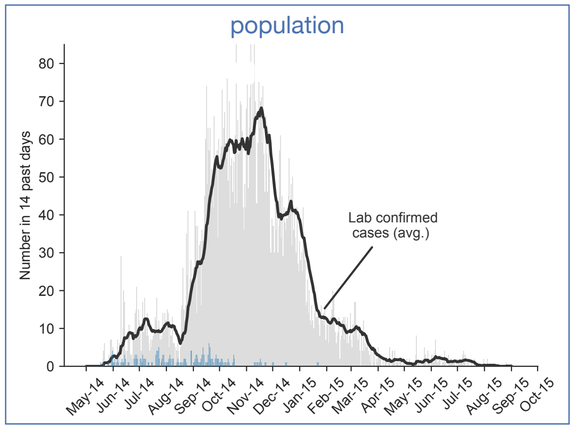
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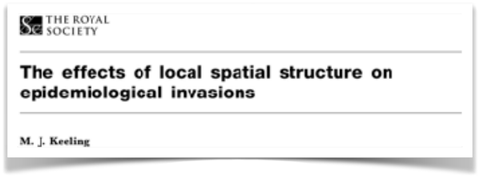
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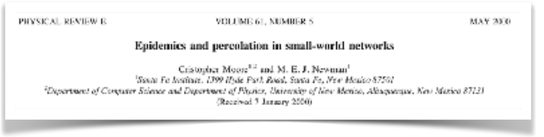


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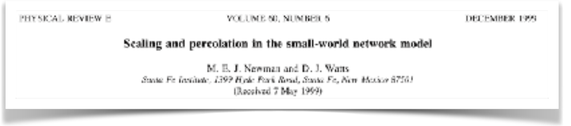
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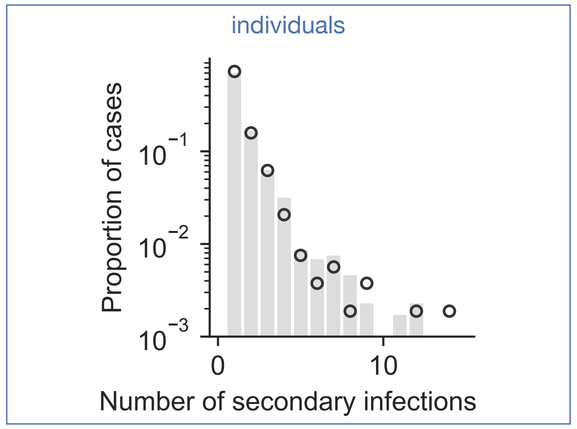
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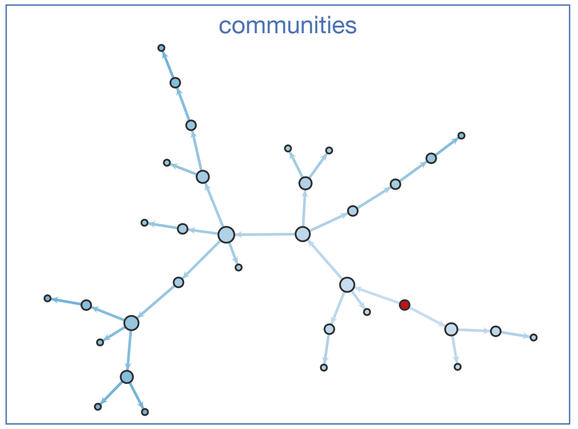
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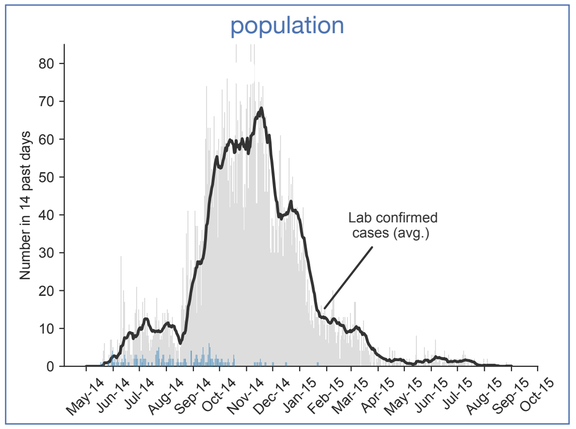
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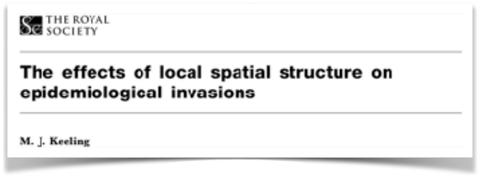
- individuals (number of secondary infections) ← where most network models live
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- communities (size of local outbreaks) ← forecasts useful to public health authorities
- population (incidence/prevalence) ← the kind of data generally accessible





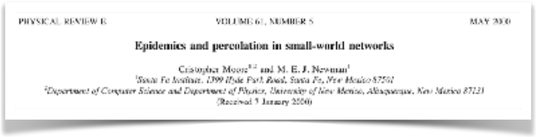


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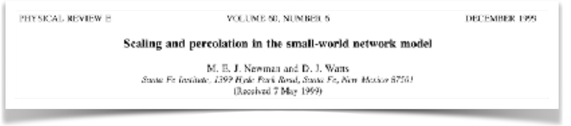
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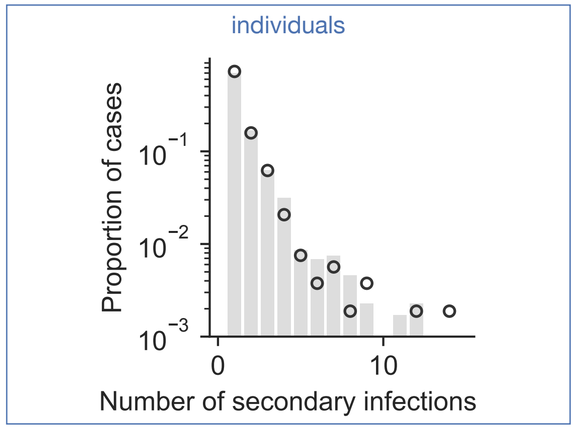
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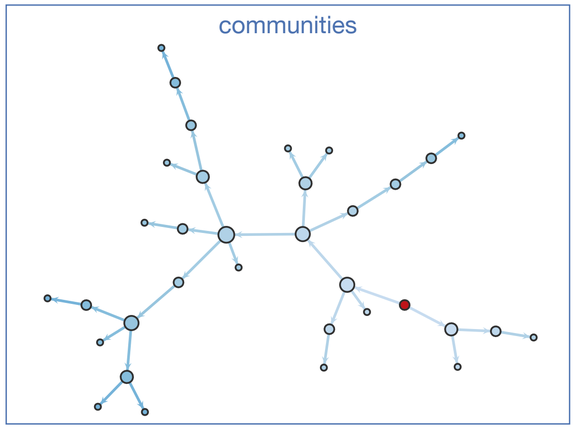
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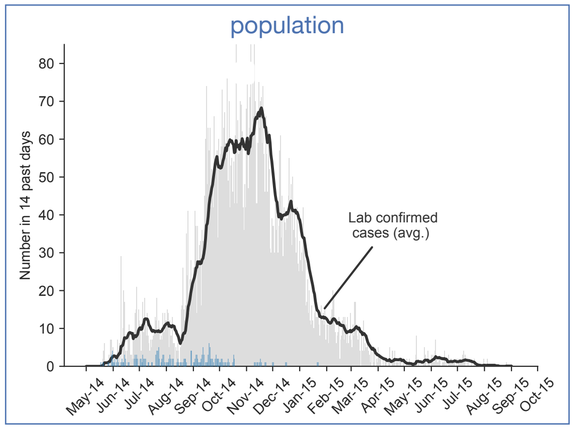
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forecasts useful to public health authorities

the kind of data generally accessible







Can network models reconcile these three scales?

The Sierra Leone Ebola Database (SLED)

The 2014-1016 EVD epidemic in West Africa

- nearly 30k cases, over 10k deaths
- widespread transmission in Guinea, Liberia and Sierra Leone
- cases in Italy, Mali, Nigeria, Senegal, Spain, UK and USA
- close to $10G in aid distribution from 70 countries
- since 2001, outbreaks were localized and never exceeded 500 cases





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Reaction of the health authorities in Sierra Leone

- focused on supportive care
- invested significantly in behavioural interventions
  - community engagement
  - traditional contact tracing
- systematically recorded information
  - 117 Call Center system and district alert phone lines
  - case investigations
  - laboratory sample testing
  - clinical management
  - safe and dignified burial records
- created the SLED
  - family reunification program
  - epidemiological research

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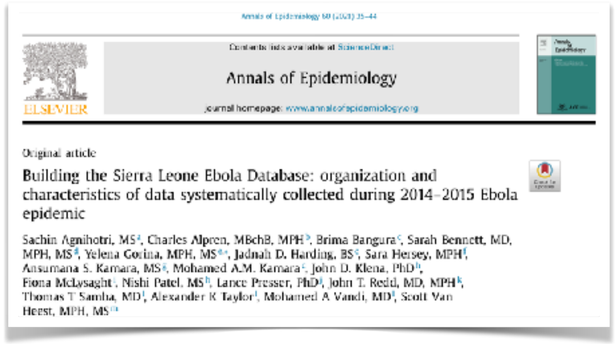


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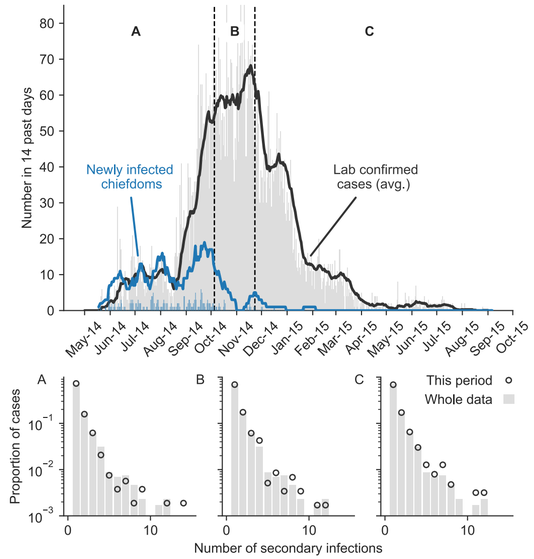
Annals of Epidemiology

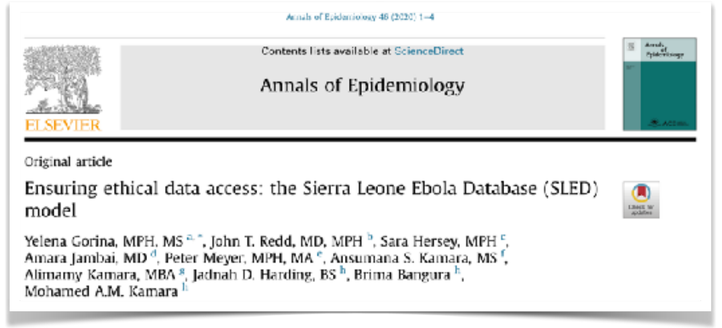
Original article

Building the Sierra Leone Ebola Database: organization and characteristics of data systematically collected during 2014–2015 Ebola epidemic

SLED is multiscale

- population: daily incidence
- communities: size of regional outbreaks (chiefdoms)
- individuals: number of secondary infections





Annals of Epidemiology

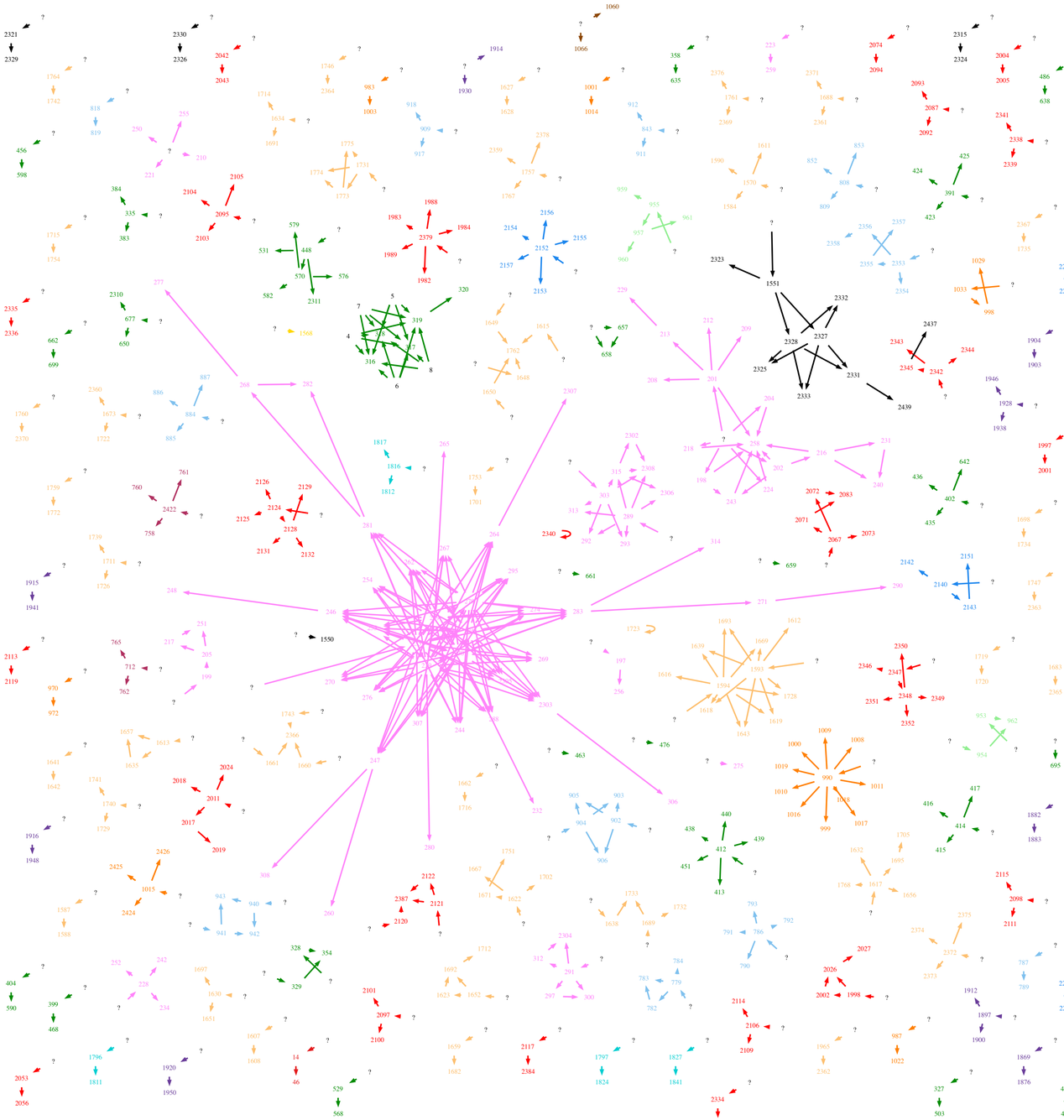
Original article

Ensuring ethical data access: the Sierra Leone Ebola Database (SLED) model

The model

We consider transmission networks (instead of contact networks)

- edges are contacts that will transmit if given the chance
- edges are infections, not just contacts
- average excess degree is R0



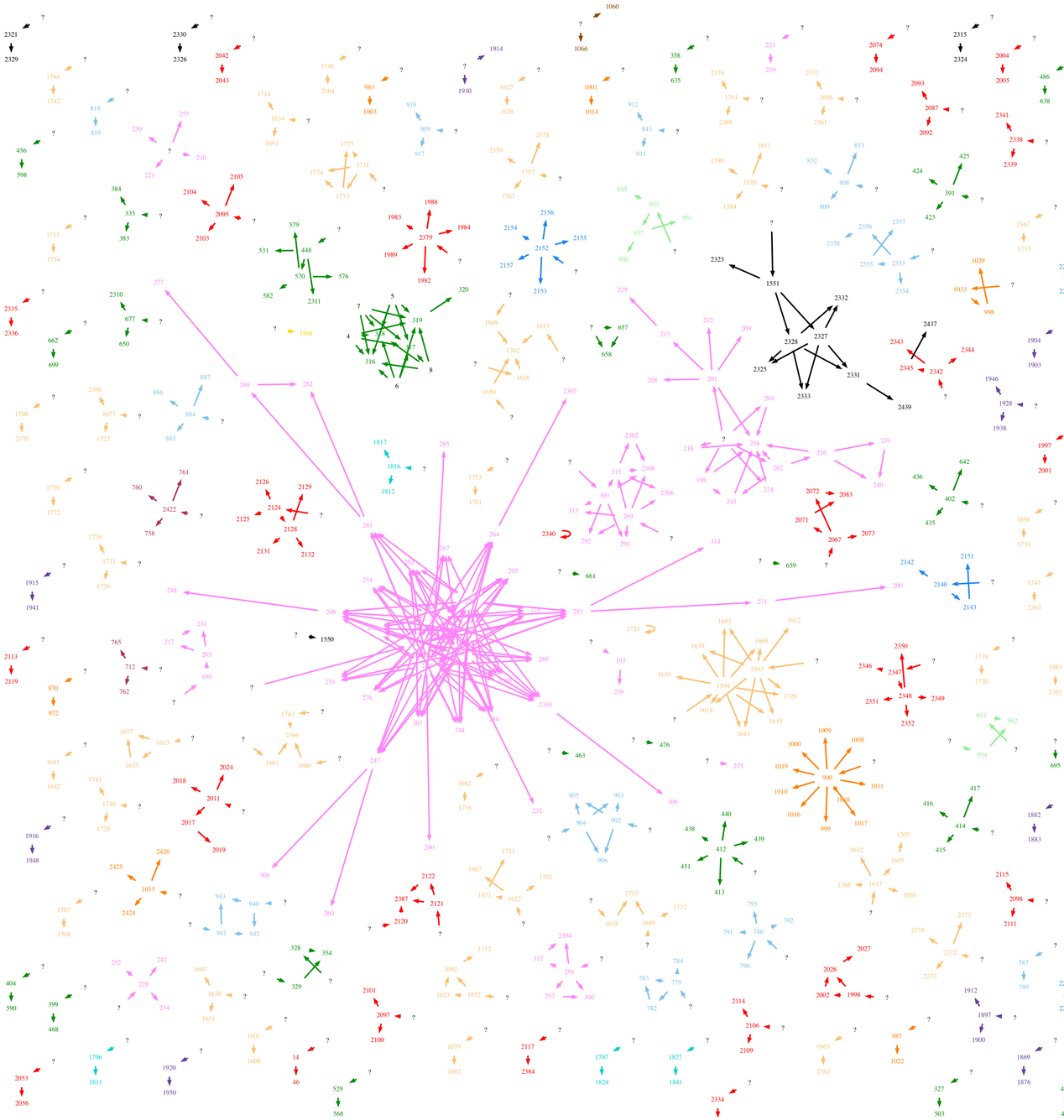
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From contact tracing data,

1. we infer the distribution secondary infections
2. we build a probabilistic model of transmission trees



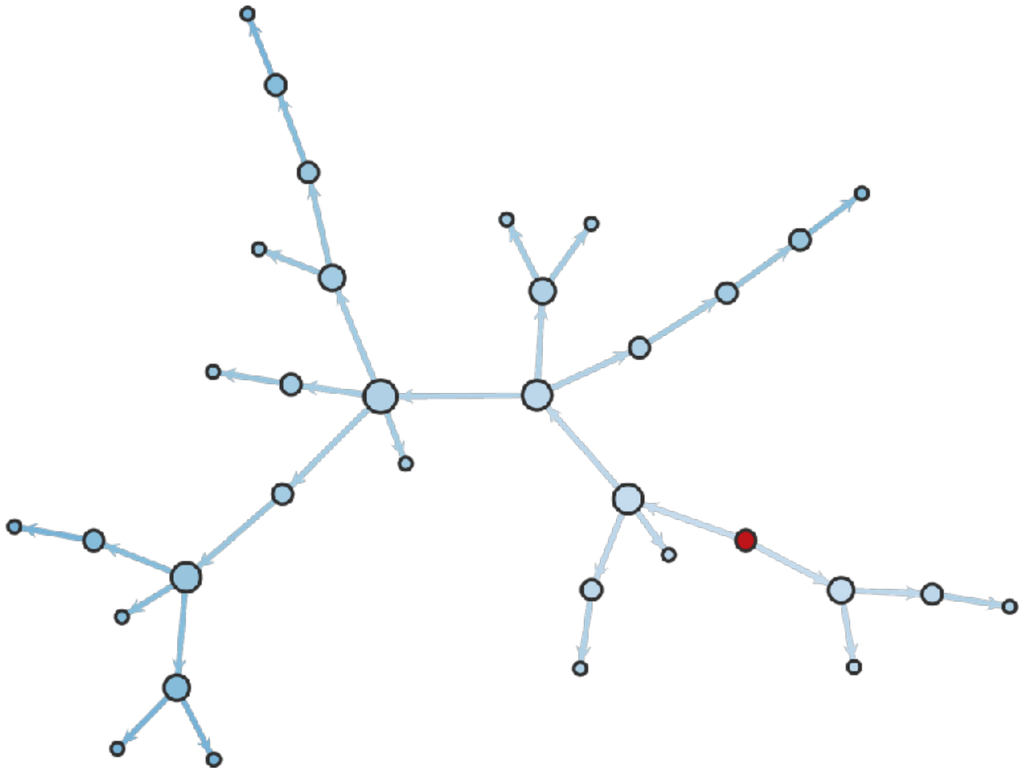
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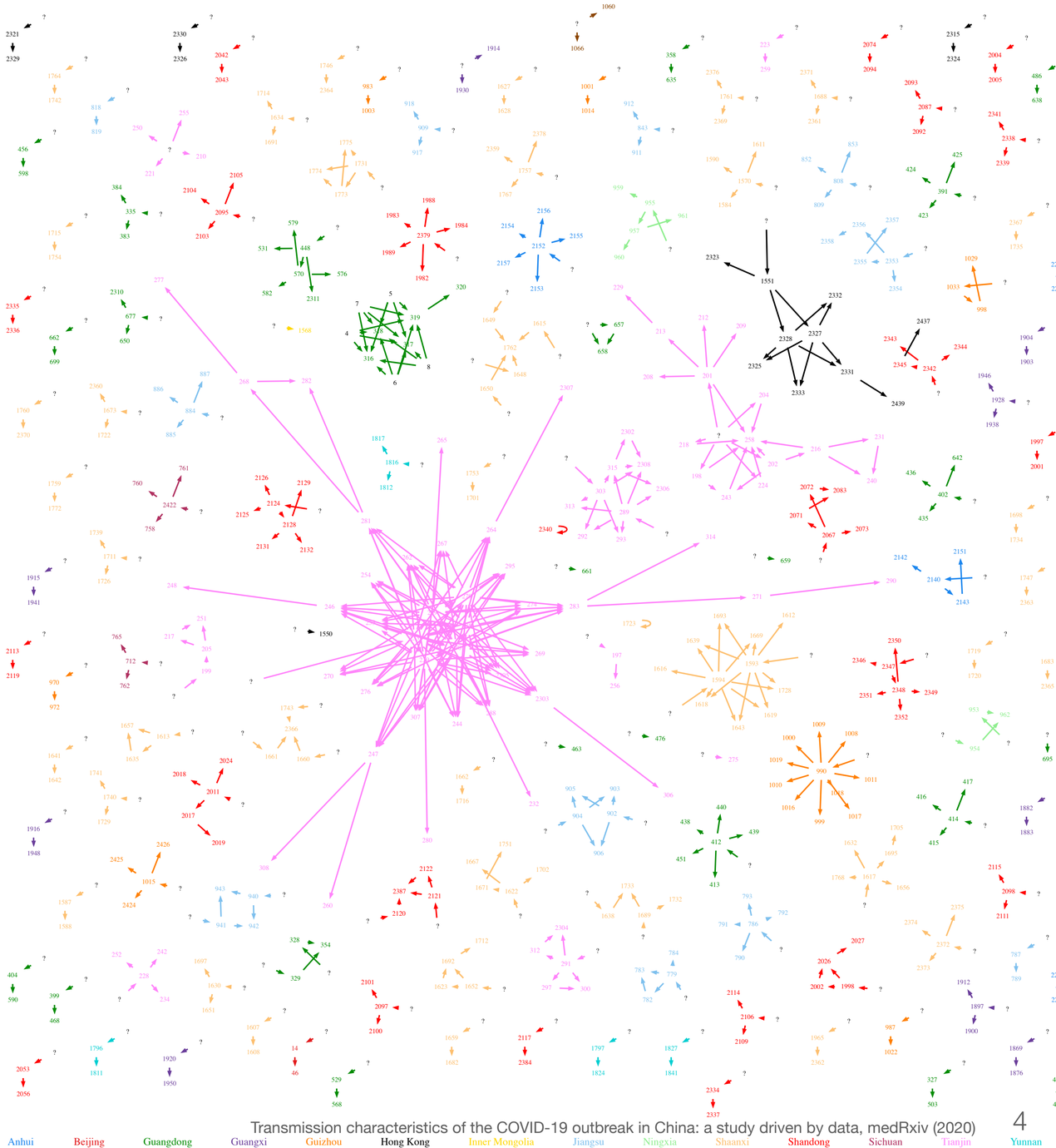
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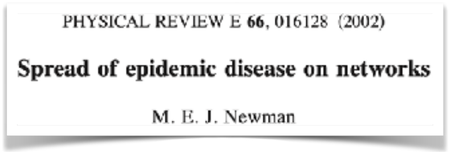
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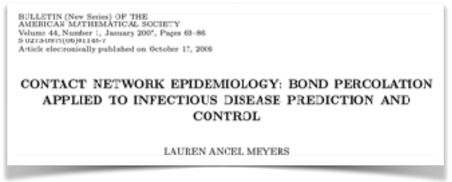
Transmission characteristics of the COVID-19 outbreak in China: a study driven by data, medRxiv (2020)

The model


PHYSICAL REVIEW E 66, 016128 (2002)

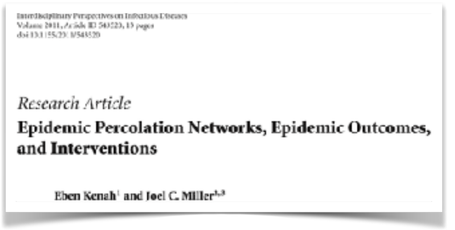
Spread of epidemic disease on networks

M. E. J. Newman


BULLETIN (New Series) OF THE AMERICAN MATHEMATICAL SOCIETY
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CONTACT NETWORK EPIDEMIOLOGY: BOND PERCOLATION APPLIED TO INFECTIOUS DISEASE PREDICTION AND CONTROL

LAUREN ANCEL MEYERS


Interdisciplinary Perspectives on Infectious Diseases
Volume 2011, Article ID 540523, 13 pages
doi:10.1155/2011/540523

Research Article

Epidemic Percolation Networks, Epidemic Outcomes, and Interventions

Eben Kenah[1] and Joel C. Miller[2,3]

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 the transmission network)

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

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

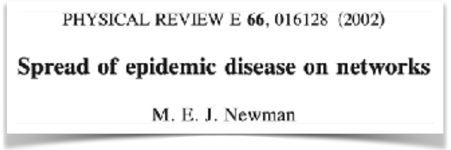
$$G_1(x) = \bullet + \bullet\, x + \bullet\, x^2 + \bullet\, x^3 + \ldots = \sum_{k\geq 0} q_k x^k = \sum_{k\geq 0} \frac{(k+1)p_{k+1}}{\langle k \rangle} x^k = \frac{G_0'(x)}{G_0'(1)}$$

- average number of secondary infections a newly infected individual causes

$$G_1'(1) = \sum_{k\geq 0} k\, q_k = \frac{\langle k^2 \rangle - \langle k \rangle}{\langle k \rangle} \equiv R_0$$

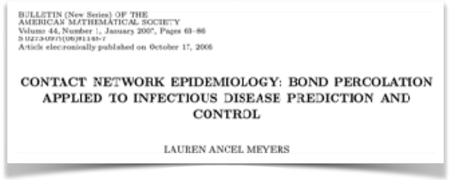
- *all* outbreaks will eventually die out when $R_0 < 1$
- *some* outbreaks will eventually die out when $R_0 > 1$

The model


PHYSICAL REVIEW E 66, 016128 (2002)

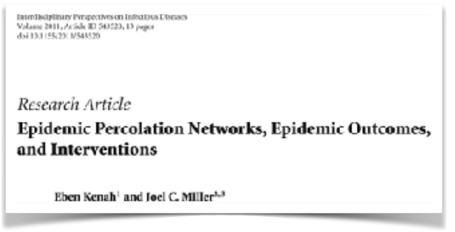
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Research Article

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Probability generating functions (PGFs) formalism

- probability u that an outbreak eventually dies out

$$u = \quad = \quad + \quad + \quad + \quad + \ldots = \sum_{k\geq 0} q_k u^k = G_1(u)$$

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

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

- probability that an outbreak will eventually die out after having s secondary infections is

$$r_s = \frac{1}{s!} \left. \frac{\mathrm{d}^s G_0\big(H_1(x)\big)}{\mathrm{d}x^s} \right|_{x=0}$$

where $H_1(x)$ is the solution of the self-consistent relation

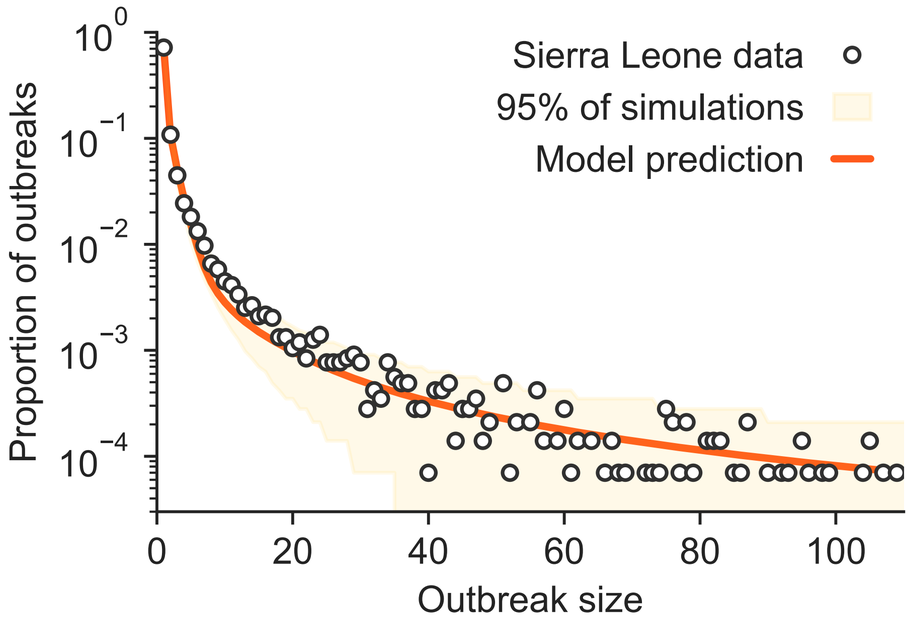
$$H_1(x) = \quad = \quad + \quad + \quad + \quad + \ldots = x \sum_{k\geq 0} q_k \left[H_1(x)\right]^k = x G_1\big(H_1(x)\big)$$

Connecting the individuals and communities scales

Forward predictions: from the distribution of the number of secondary infections ($\{q_k\}$) to the outbreak size distribution ($\{r_s\}$)

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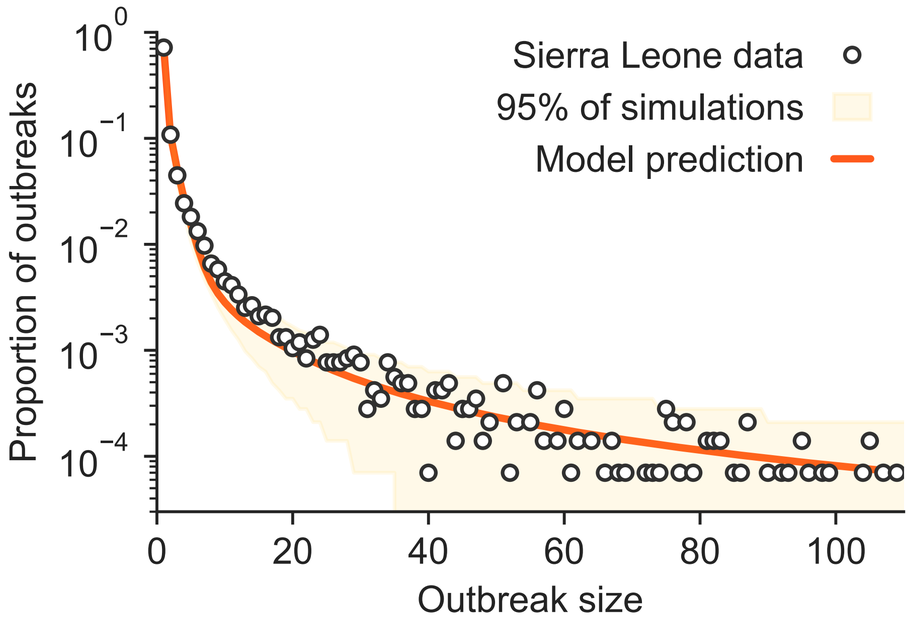
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1. cases that dit not lead to secondary infections
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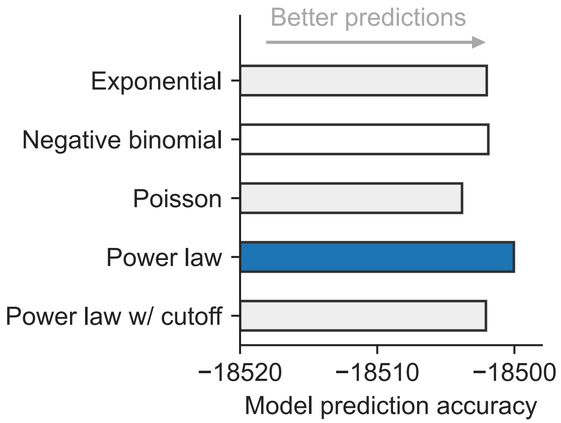
Challenge 2: estimate robustness of the distribution of secondary infections

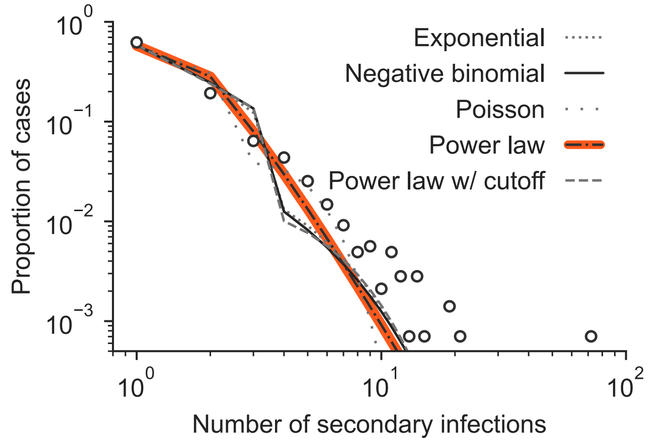
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Backward predictions: from the outbreak size distribution ($\{r_s\}$) to the distribution of the number of secondary infections ($\{q_k\}$)





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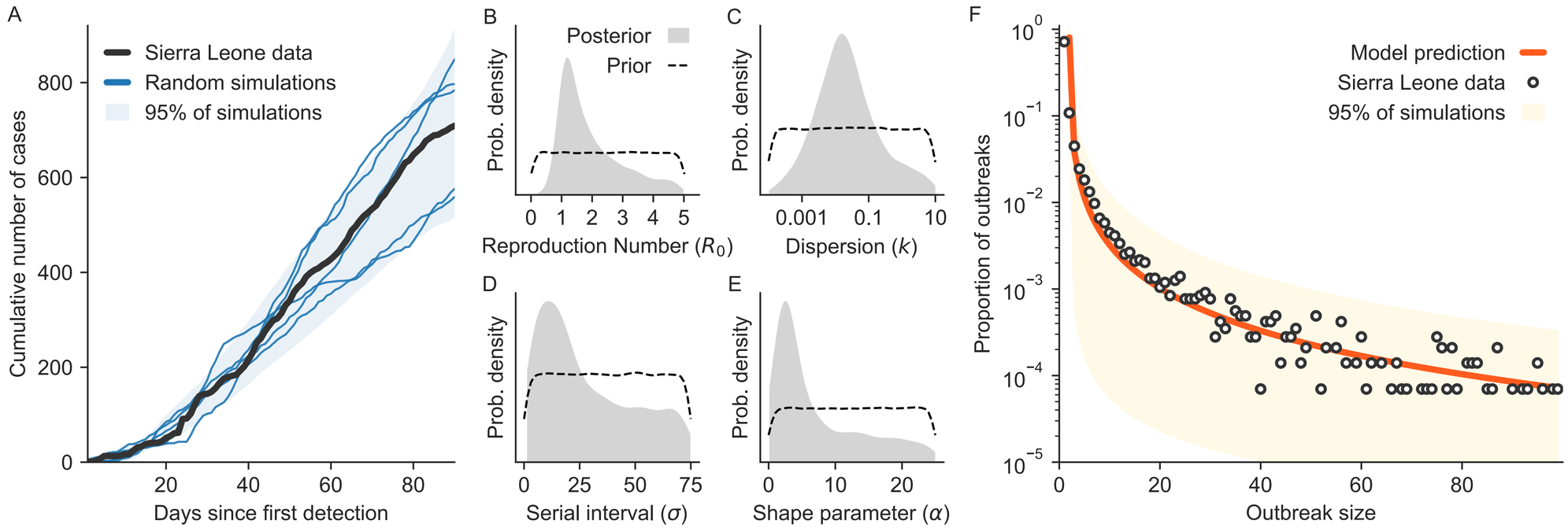
Challenge 2: estimate robustness of the distribution of secondary infections

Knowing the size of 4013 outbreaks $\{X_n\}_{n=1,\ldots,4013}$

1. choose a parametric distribution for $\{q_k\}$ with parameters θ (ex.: negative binomial)
2. sample the posterior distribution for the parameters

$$P(\theta|\{X_n\}) \propto P(\{X_n\}|\theta)P(\theta)$$
$$= P(\theta) \prod_{n=1}^{4013} r_{X_n}$$

Connecting the population and communities scales (via individuals)



Input: cumulative incidence time series over a 90-day period $\{I_t\}_{t=1,\ldots,90}$

Assumptions:

- number of secondary infections is distributed according to a negative binomial

$$q_n \equiv P(n|R_0,k) = \frac{\Gamma(n+k)}{\Gamma(n+1)\Gamma(k)}\left(\frac{R_0}{R_0+k}\right)^n\left(1-\frac{R_0}{R_0+k}\right)^k$$

  with mean $R_0 > 0$ and dispersion $k > 0$

- serial interval (i.e. time between infections) is distributed according to a Gamma

$$Q(t|\sigma,\alpha) = \frac{\alpha^\alpha}{\sigma^\alpha\Gamma(\alpha)}t^{\alpha-1}\mathrm{e}^{-\frac{\alpha t}{\sigma}}$$

  of mean $\sigma > 0$ and shape $\alpha > 0$

Approximate Bayesian Computation (ABC)

1. generate a sample for (R_0, k, α, σ) and σ from a uniform prior distribution
2. generate a sequence of cumulative incidence $\{\tilde{I}_t\}$ using (R_0, k, α, σ)
3. (R_0, k, α, σ) is added to the sample of the posterior distribution if

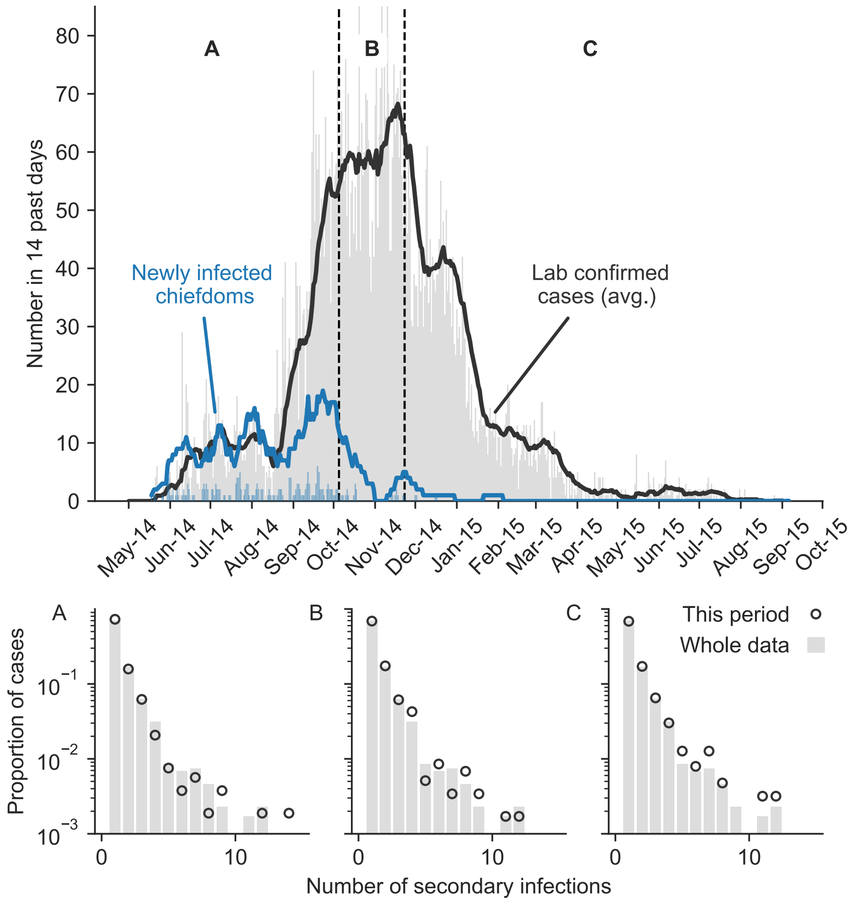
$$\varepsilon_d = \frac{|\tilde{I}_d - I_d|}{I_d} < 0.30 \quad \text{for } d = 15, 30, 45, 60, 75, 90$$

Output: distribution of outbreak size $\{r_s\}$ for each (R_0, k) in the posterior distribution

Why did this work?

Assumptions:

1. the communities (chiefdoms) were the characteristic scale of the epidemic
    - ▷ secondary infections remained confined within chiefdoms
    - ▷ each outbreak within chiefdoms was effectively an independent realization of the same stochastic process ($\{r_s\}$)
2. the distribution of secondary infections ($\{q_k\}$) did not change through time
    - ▷ very surprising given the scale of epidemic control efforts



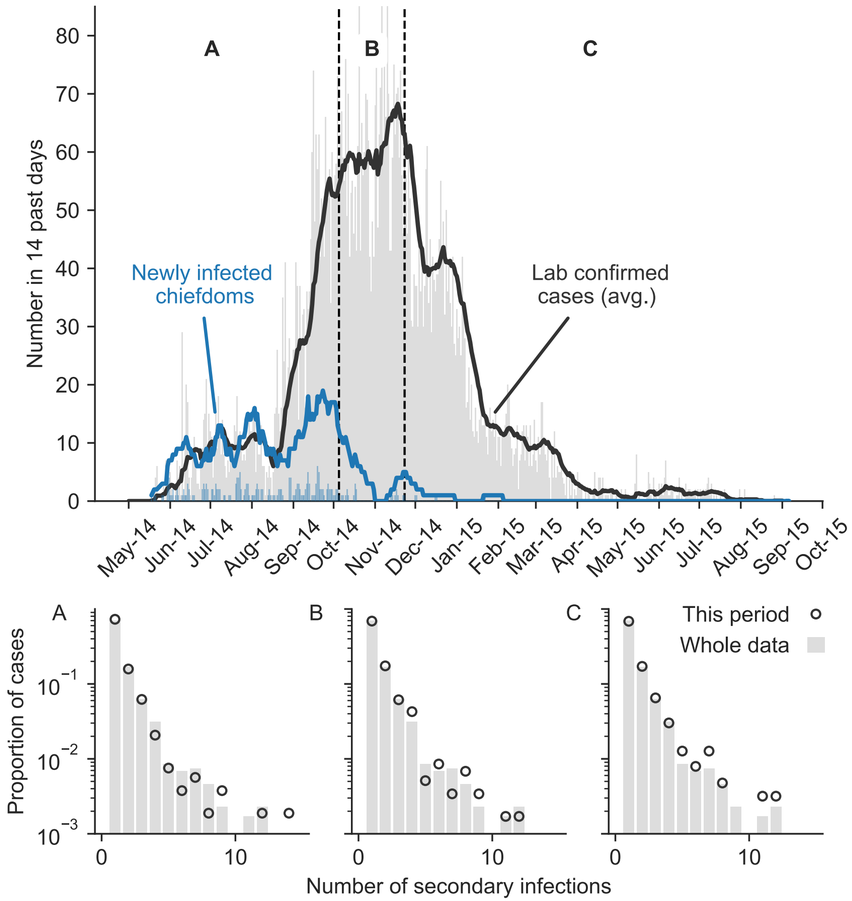
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Why did the epidemic stop?

- ▷ not because of a reduction in local transmission patterns (secondary infections), although interventions reduced the mortality rate from 75% to 40%
- ▷ but rather the reduction of introduction in new clusters (primary cases)



The network epidemiology of an Ebola epidemic

Laurent Hébert-Dufresne, Jean-Gabriel Young, Jamie Bedson, Laura A. Skrip, Danielle Pedi, Mohamed F. Jalloh, Bastian Raulier, Olivier Lapointe-Gagné, Amara Jambai, Antoine Allard, Benjamin M. Althouse

arXiv:2111.08686
(will be updated soon)



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Dynamica

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CIMMUL
Centre interdisciplinaire en modélisation mathématique de l'Université Laval

Alliance de recherche numérique du Canada

NSERC CRSNG

Fonds de recherche Québec

npj | complexity

Editorial | Open access | Published: 17 April 2024

The path of complexity

Laurent Hébert-Dufresne ✉, Antoine Allard, Joshua Garland, Elizabeth A. Hobson & Luis Zaman

npj Complexity **1**, Article number: 4 (2024)

Aims & Scopes

npj Complexity considers research that explores all aspects of complex systems at the interface of multiple fields.

The journal covers a broad range of topics including but not limited to:

- Network science, including the analysis of complex networks such as social networks, biological networks, infrastructure and information networks
- Emergent phenomena, self-organization, and scaling in complex systems
- Nonlinear dynamics, chaos theory, and dynamical systems theory
- Agent-based modeling and simulation techniques for studying complex systems
- Complex adaptive systems, such as adaptive behavior in biological, ecological, and social systems
- Multi-scale analysis techniques across different levels of organization, from micro to macro scales
- Robustness and resilience of complex systems
- Evolutionary dynamics and game theory
- Digital humanities, dynamics of information, and science of science
- Information processing and computation in complex systems and artificial intelligence
- Interdisciplinary approaches to complex problems such as epidemics, climate change, misinformation, governance, and sustainability

⌜ Preprint ⌝

⌜ Slides ⌝