

Graphe poissonnier, un oxymore?

UNE JOURNÉE POUR Poisson

Antoine Allard

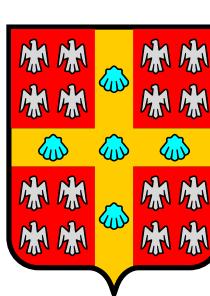
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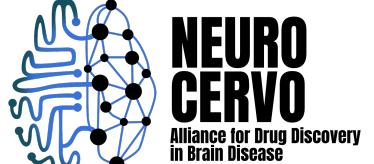
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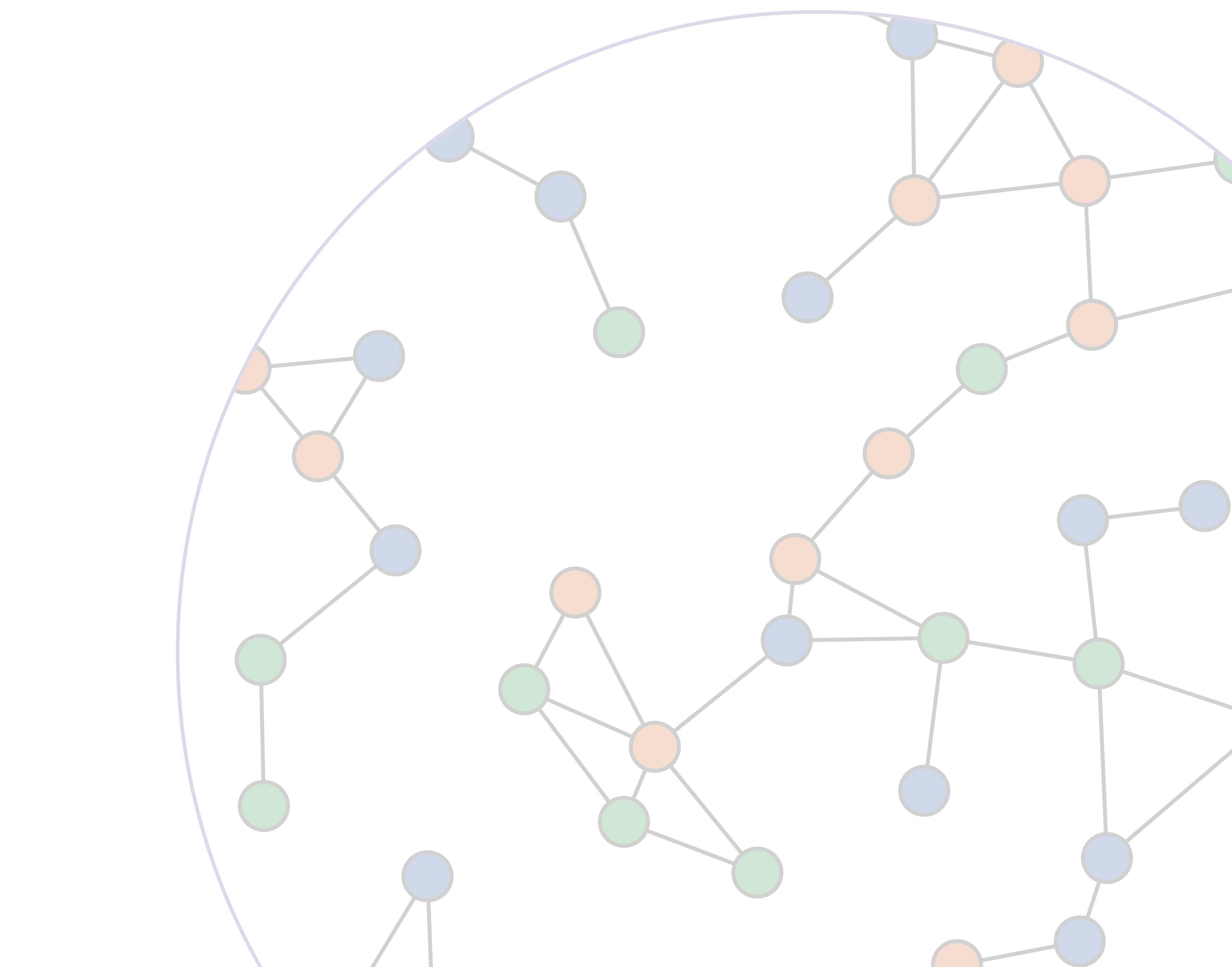
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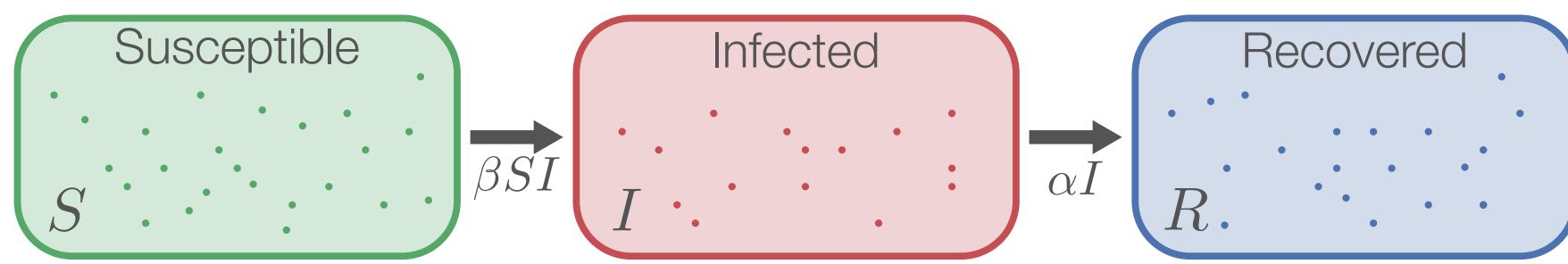
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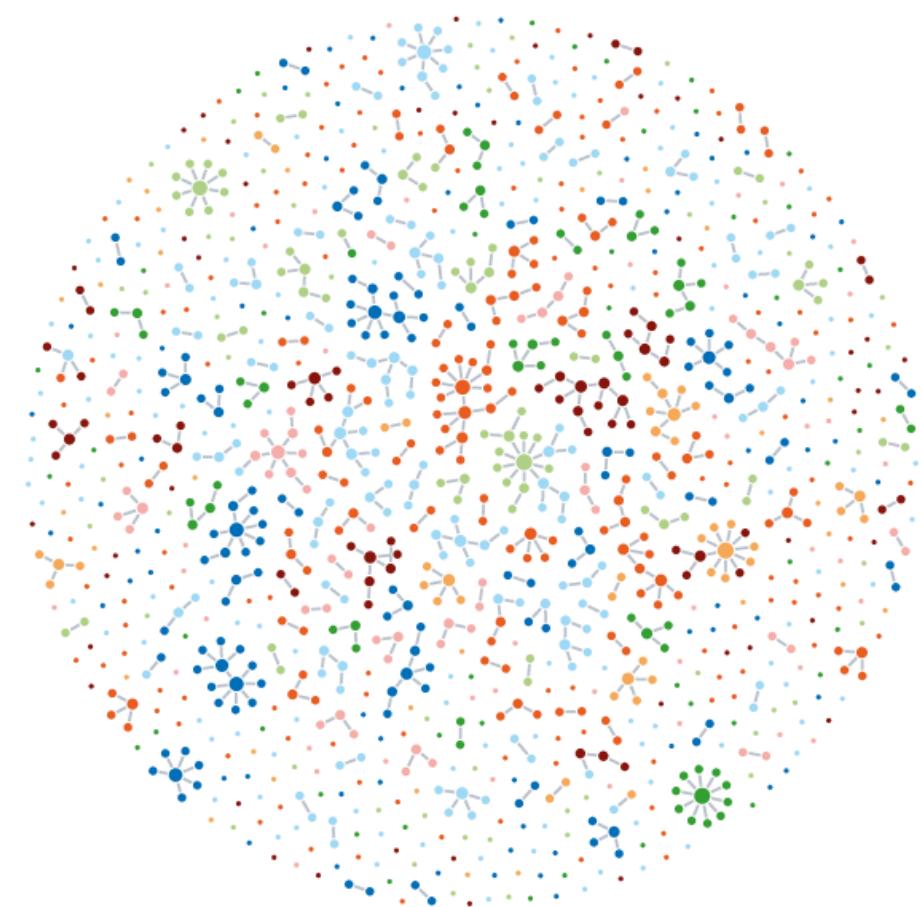
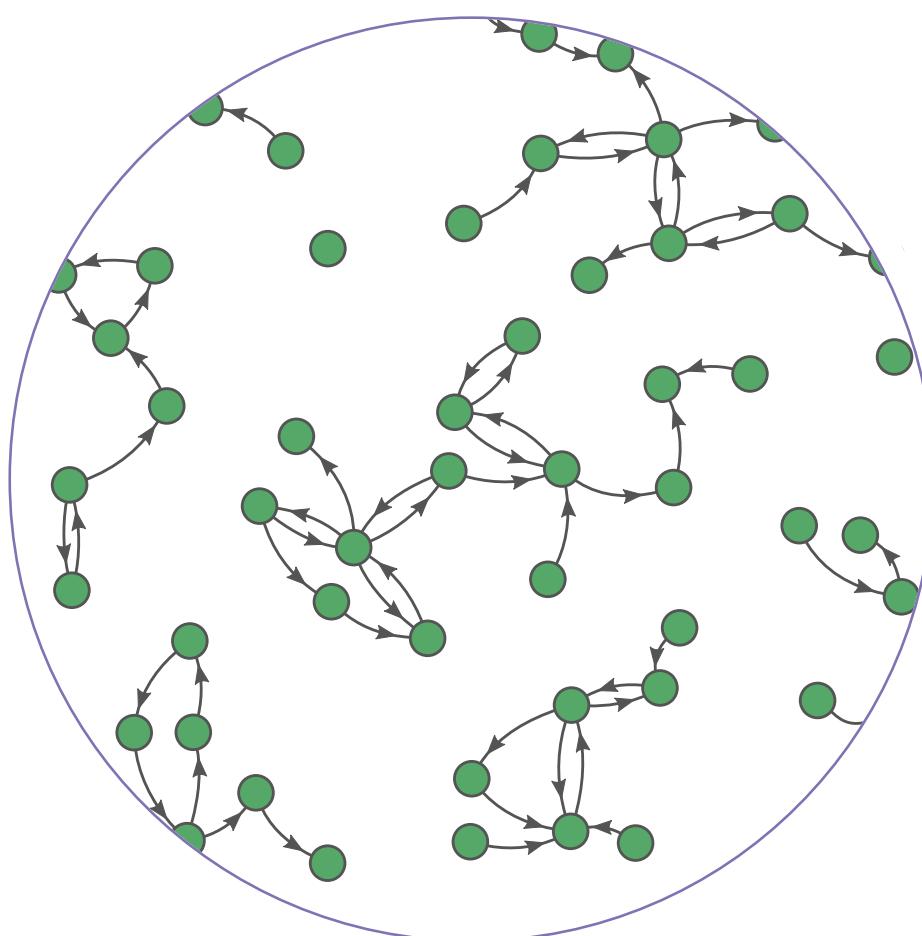
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Outline :

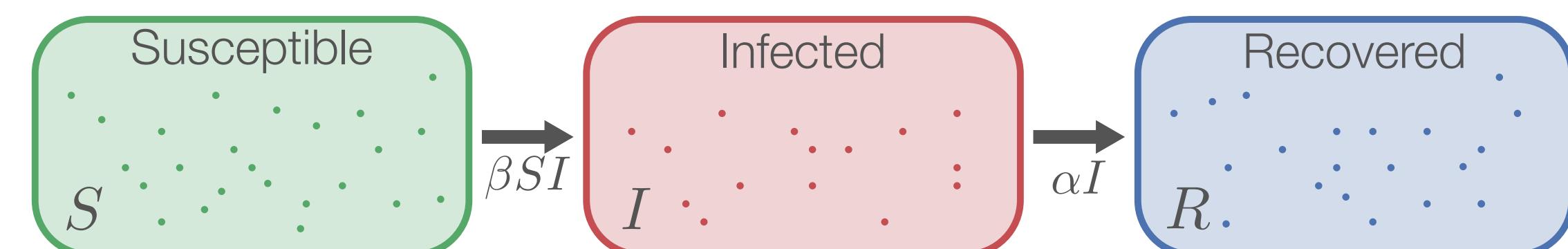
1. Basic epidemiological model
2. How infectious diseases challenge some assumptions made by “traditional” models
3. Contact network epidemiology
4. A random graph model in the sparse limit
5. Poisson graph : a fish out of water?



Basic epidemiological model

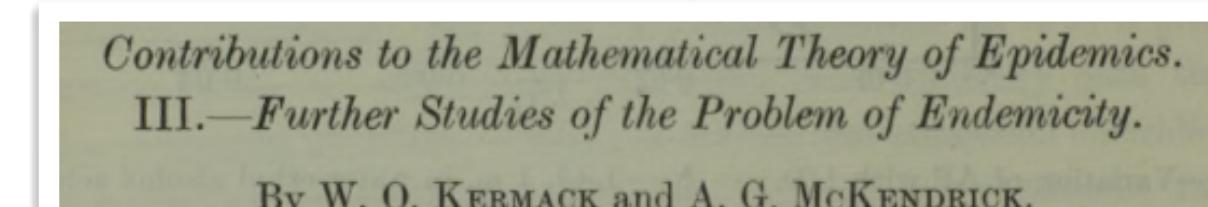
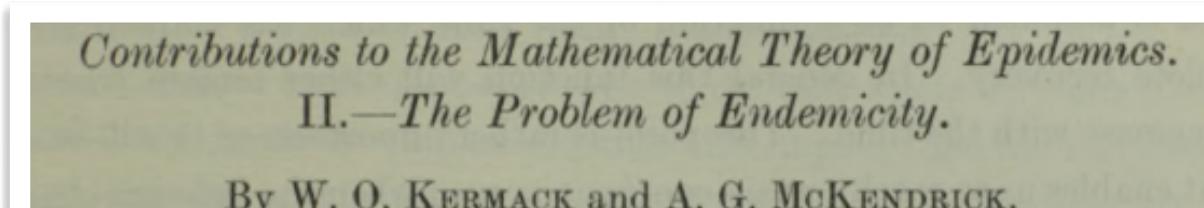
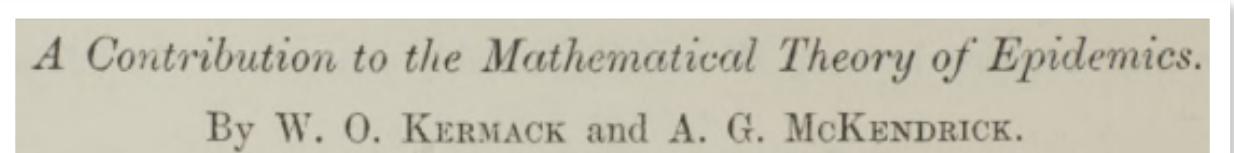
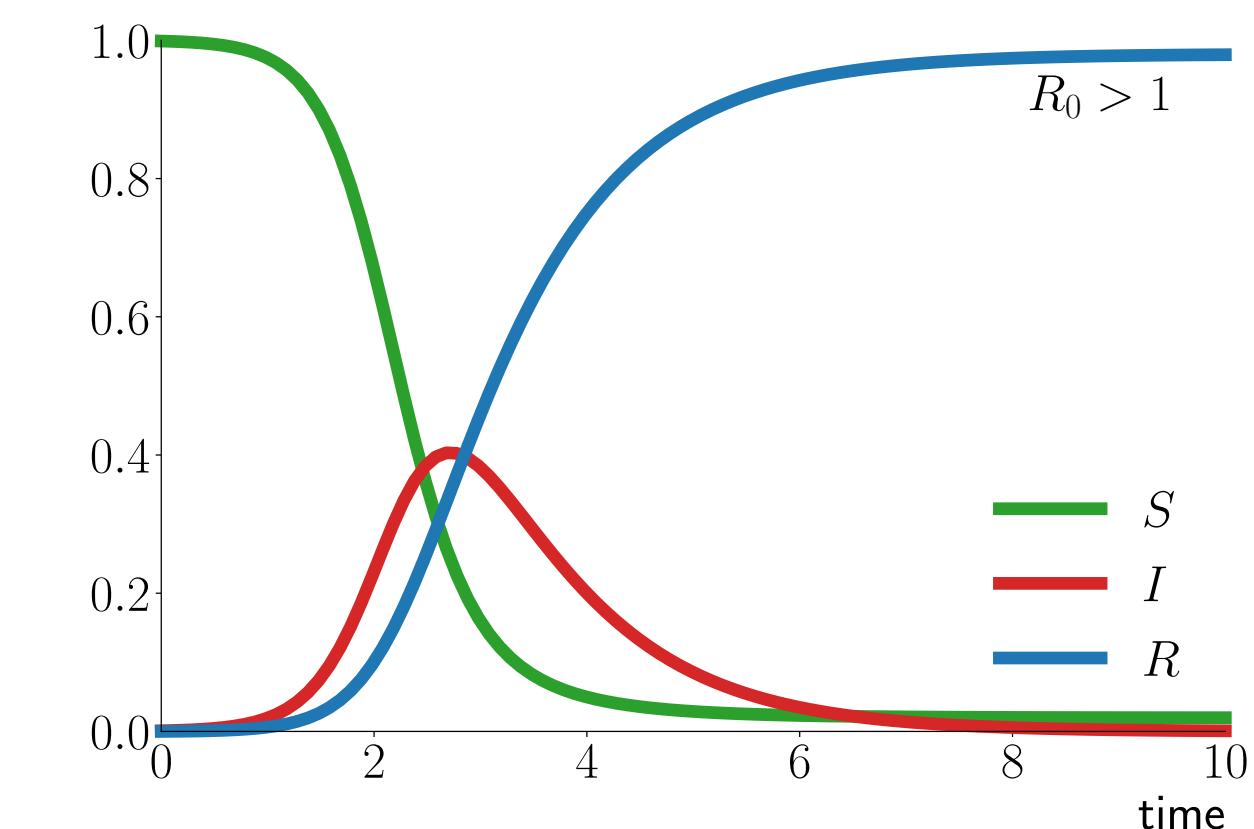
Main epidemiological assumptions

- the disease results either in complete immunity or death
- all individuals are equally susceptible



Main structural assumptions

- the disease is transmitted in a closed population
- contacts occur according to the law of mass-action
- the population is large enough to justify a deterministic analysis



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The Mathematics of Infectious Diseases*

Herbert W. Hethcote[†]

Basic epidemiological model

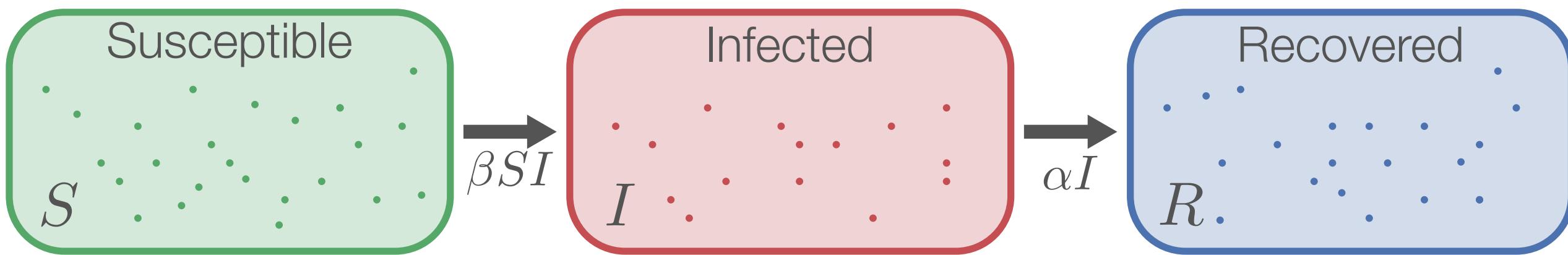
Susceptible-Infected-Recovered (SIR) dynamics

- the disease results either in complete immunity or death
- S : fraction of the pop. susceptible to the disease
- I : fraction of the pop. infected by the disease
- R : fraction of the pop. having recovered from the disease
- susceptible and infected individuals come into contact at a rate $\propto SI$ (mass-action assumption)

$$\frac{dS}{dt} = -\beta SI$$

$$\frac{dI}{dt} = \beta SI - \alpha I$$

$$\frac{dR}{dt} = \alpha I$$

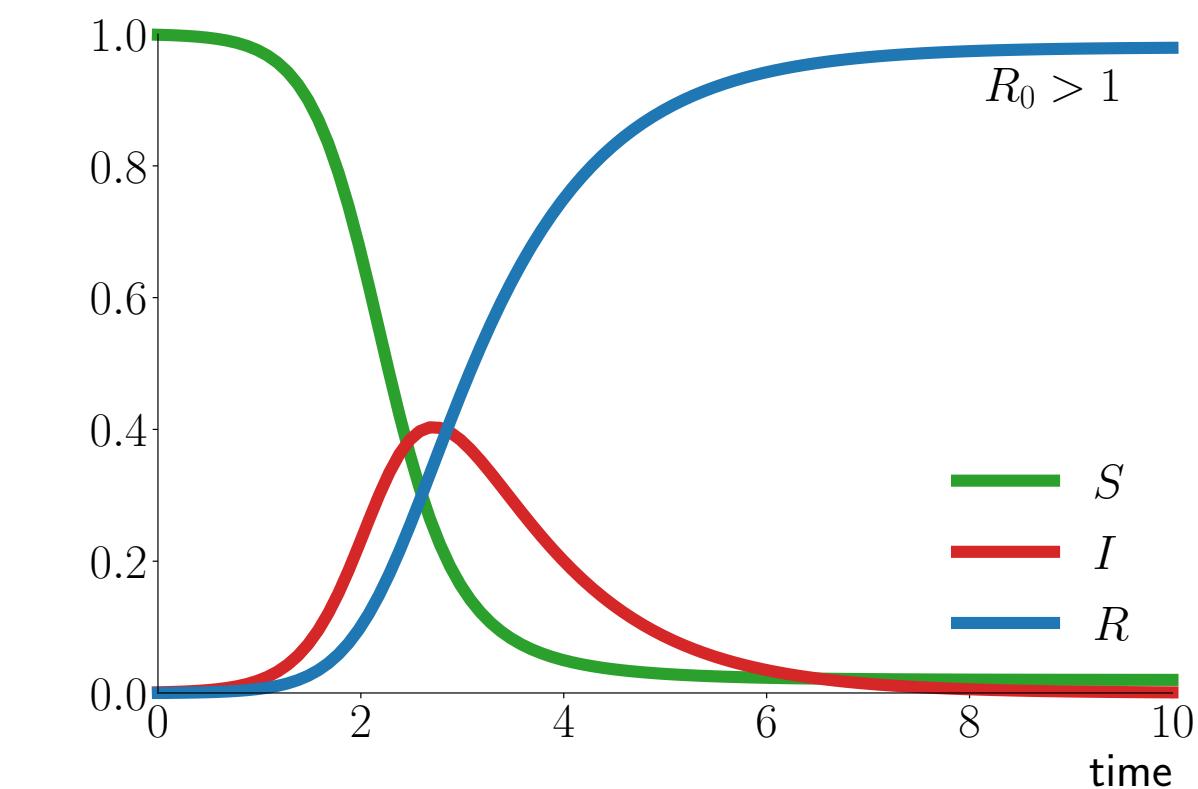
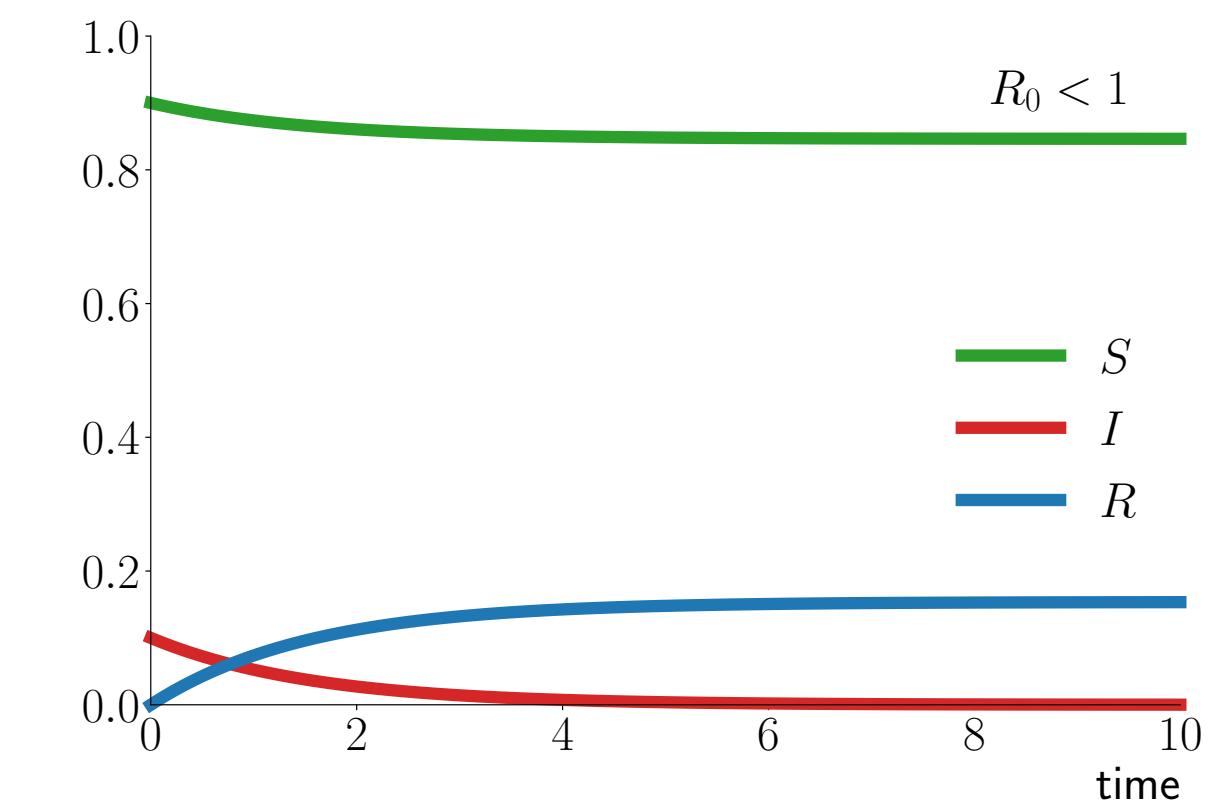


- the fraction of the population who will be infected by the disease eventually is a solution of

$$R(\infty) = 1 - S(0)e^{-R_0(R(\infty)-R(0))} \simeq 1 - e^{-R_0 R(\infty)}$$

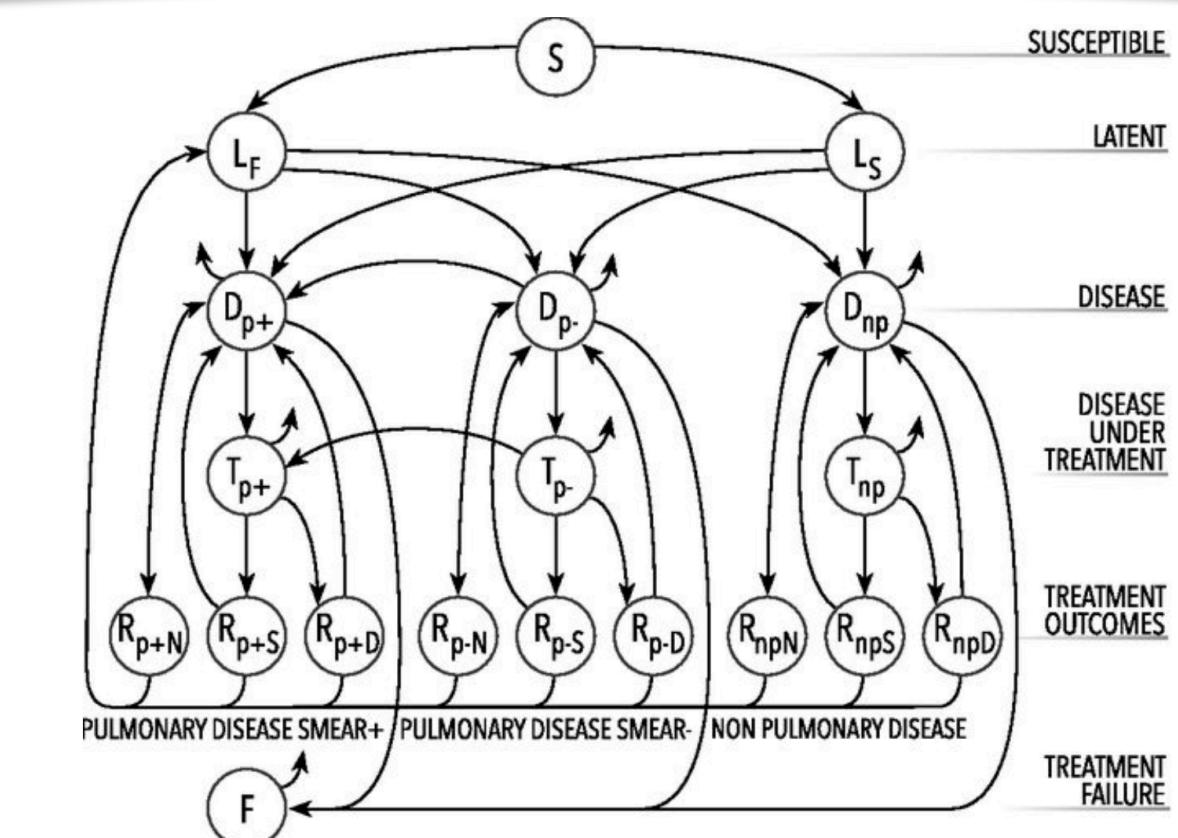
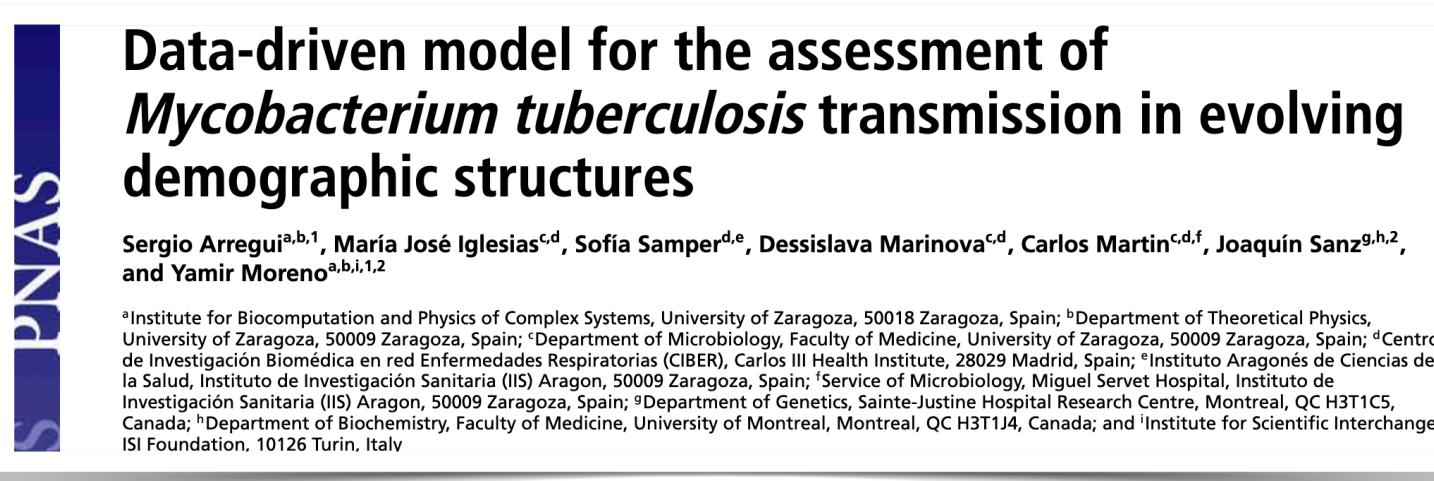
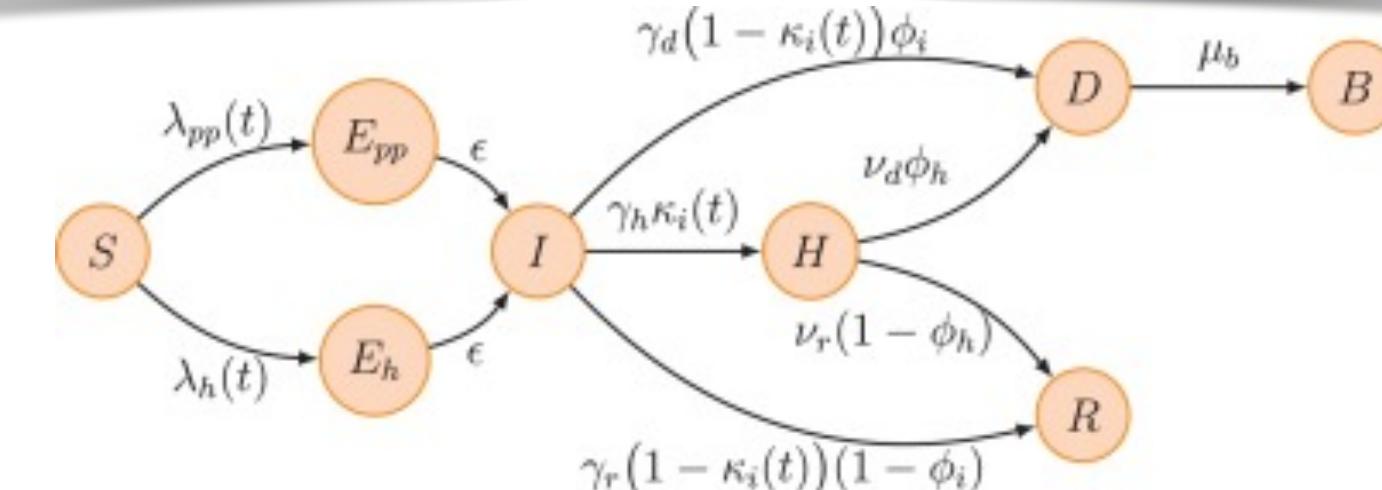
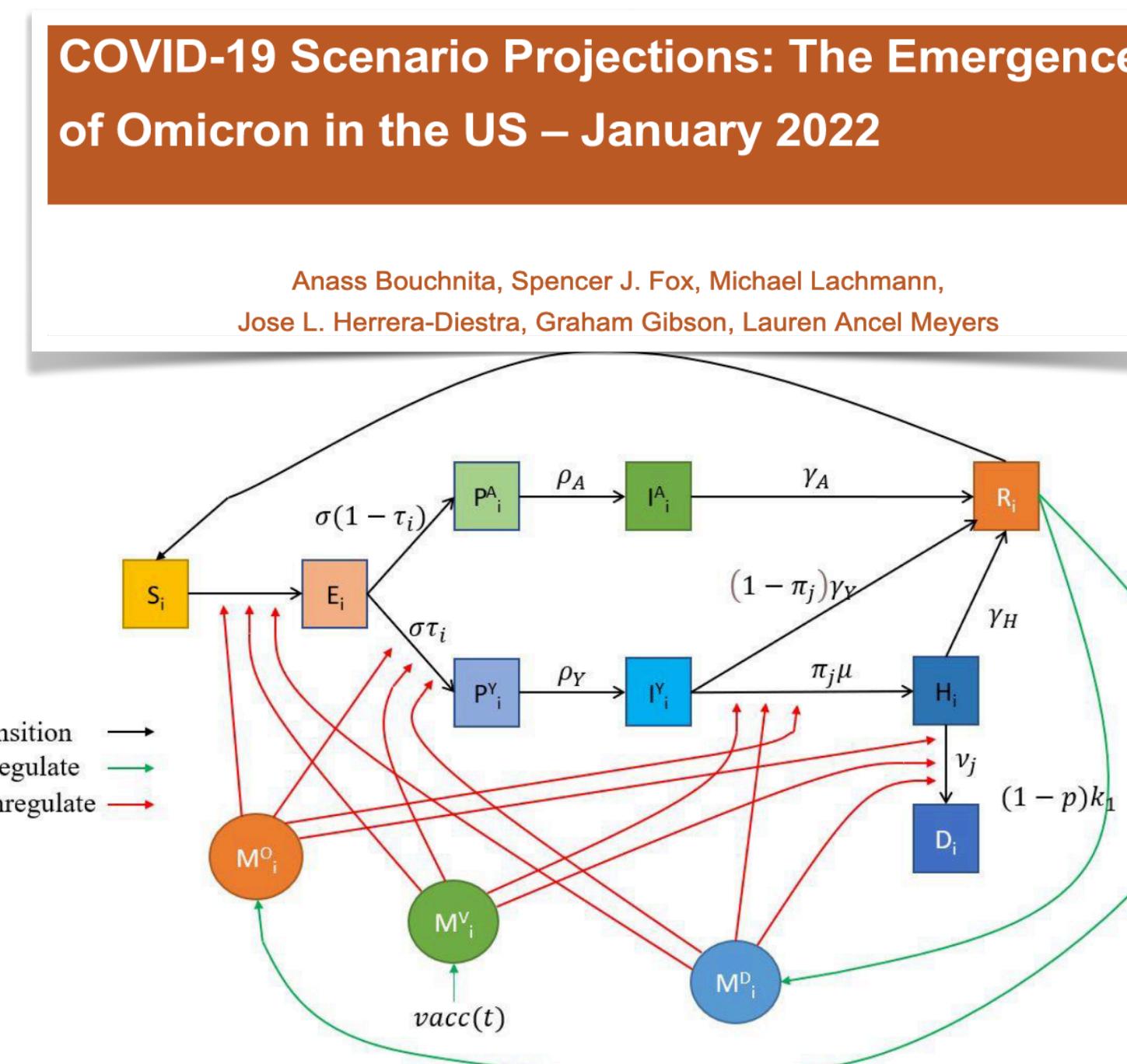
with $R_0 = \beta/\alpha$ being the *basic reproduction number*

- there will be an epidemic wave if $R_0 > 1$, otherwise the outbreak will die out
- there is herd immunity if a fraction $R(0) = 1 - 1/R_0$ of the population is already immune



Basic epidemiological model

Models used in more realistic settings are more complex, but the basic ingredients remain largely the same.



Assumptions challenged by some infectious diseases

Main epidemiological assumptions

- the disease results either in complete immunity or death
- all individuals are equally susceptible

Main *structural* assumptions

- the disease is transmitted in a closed population
- contacts occur according to the law of mass-action
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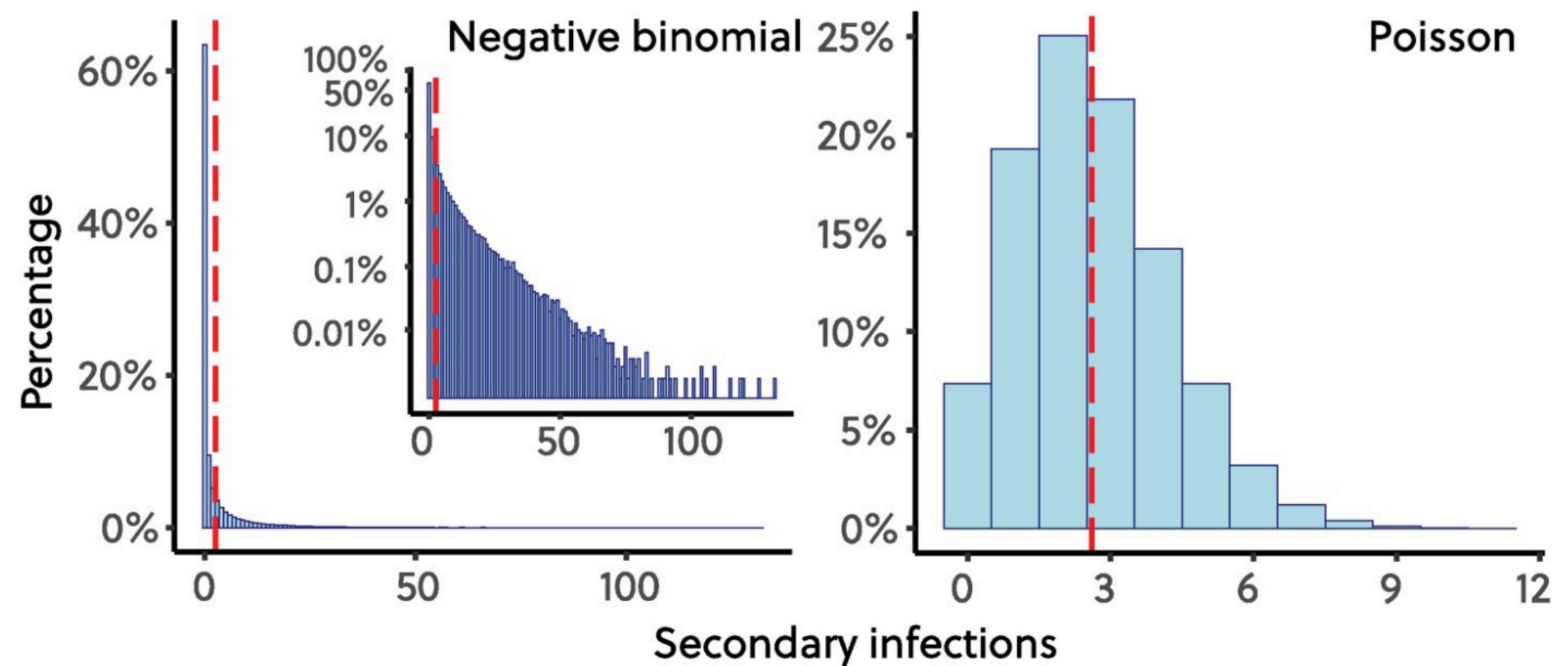
Assumptions challenged by some infectious diseases

Challenged assumption #1 : contacts occur according to the law of mass-action

- ★ many outbreaks are not shaped by the “average” individuals but rather by a minority of superspreading events

Challenged assumption #2 : the population is large enough to justify a deterministic analysis

- ★ at the early stage, the outcome of an outbreak depends on stochastic events



LETTERS

Superspreading and the effect of individual variation on disease emergence

J. O. Lloyd-Smith^{1,2}, S. J. Schreiber³, P. E. Kopp⁴ & W. M. Getz¹



Spatial and temporal dynamics of superspreading events in the 2014–2015 West Africa Ebola epidemic

Max S. Y. Lau^{a,1}, Benjamin Douglas Dalziel^{b,c}, Sebastian Funk^d, Amanda McClelland^e, Amanda Tiffany^f, Steven Riley^g, C. Jessica E. Metcalf^a, and Bryan T. Grenfell^{a,h}

^aDepartment of Ecology and Evolutionary Biology, Princeton University, Princeton, NJ 08544; ^bDepartment of Integrative Biology, Oregon State University, Corvallis, OR 97331; ^cDepartment of Mathematics, Oregon State University, Corvallis, OR 97331; ^dCentre for the Mathematical Modelling of Infectious Diseases, London School of Hygiene and Tropical Medicine, London WC1E 7HT, United Kingdom; ^eInternational Federation of Red Cross and Red Crescent Societies, CH-1211 Geneva 19, Switzerland; ^fEpicentre, CH-1211 Geneva 6, Switzerland; ^gMedical Research Council Centre for Outbreak Analysis and Modelling, Department of Infectious Disease Epidemiology, Imperial College London, London SW7 2AZ, United Kingdom; and ^hFogarty International Center, National Institutes of Health, Bethesda, MD 20892

THE LANCET

CORRESPONDENCE | VOLUME 395, ISSUE 10227, E47, MARCH 14, 2020

Secondary attack rate and superspreading events for SARS-CoV-2

Yang Liu • Rosalind M Eggo • Adam J Kucharski

THE LANCET Infectious Diseases

COMMENT | VOLUME 21, ISSUE 9, P1203-1204, SEPTEMBER 01, 2021

Understanding why superspreading drives the COVID-19 pandemic but not the H1N1 pandemic

Paul Z Chen • Marion Koopmans • David N Fisman • Frank X Gu

SCIENTIFIC AMERICAN

How ‘Superspreading’ Events Drive Most COVID-19 Spread

As few as 10 percent of infected people may drive a whopping 80 percent of cases in specific types of situations

By Christie Aschwanden on June 23, 2020



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Biology

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 Pourbohlou^{c,1,2}, M.E.J. Newman^{b,d}, Danuta M. Skowronski^{c,2}, Robert C. Brunham^{c,2}

Contact network epidemiology

Modelling disease outbreaks in realistic urban social networks

Stephen Eubank , Hasan Guclu, V. S. Anil Kumar, Madhav V. Marathe, Aravind Srinivasan, Zoltán Toroczkai & Nan Wang

Nature 429, 180–184 (2004)

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Article electronically published on October 17, 2006

CONTACT NETWORK EPIDEMIOLOGY: BOND PERCOLATION
APPLIED TO INFECTIOUS DISEASE PREDICTION AND
CONTROL

LAUREN ANCEL MEYERS

Main ideas :

- takes into account the contact network between individuals
- infectious disease transmitted from an infected individual to their susceptible neighbors in the contact network
- the structure of this contact network shapes the spreading dynamics

Mathematical abstraction :

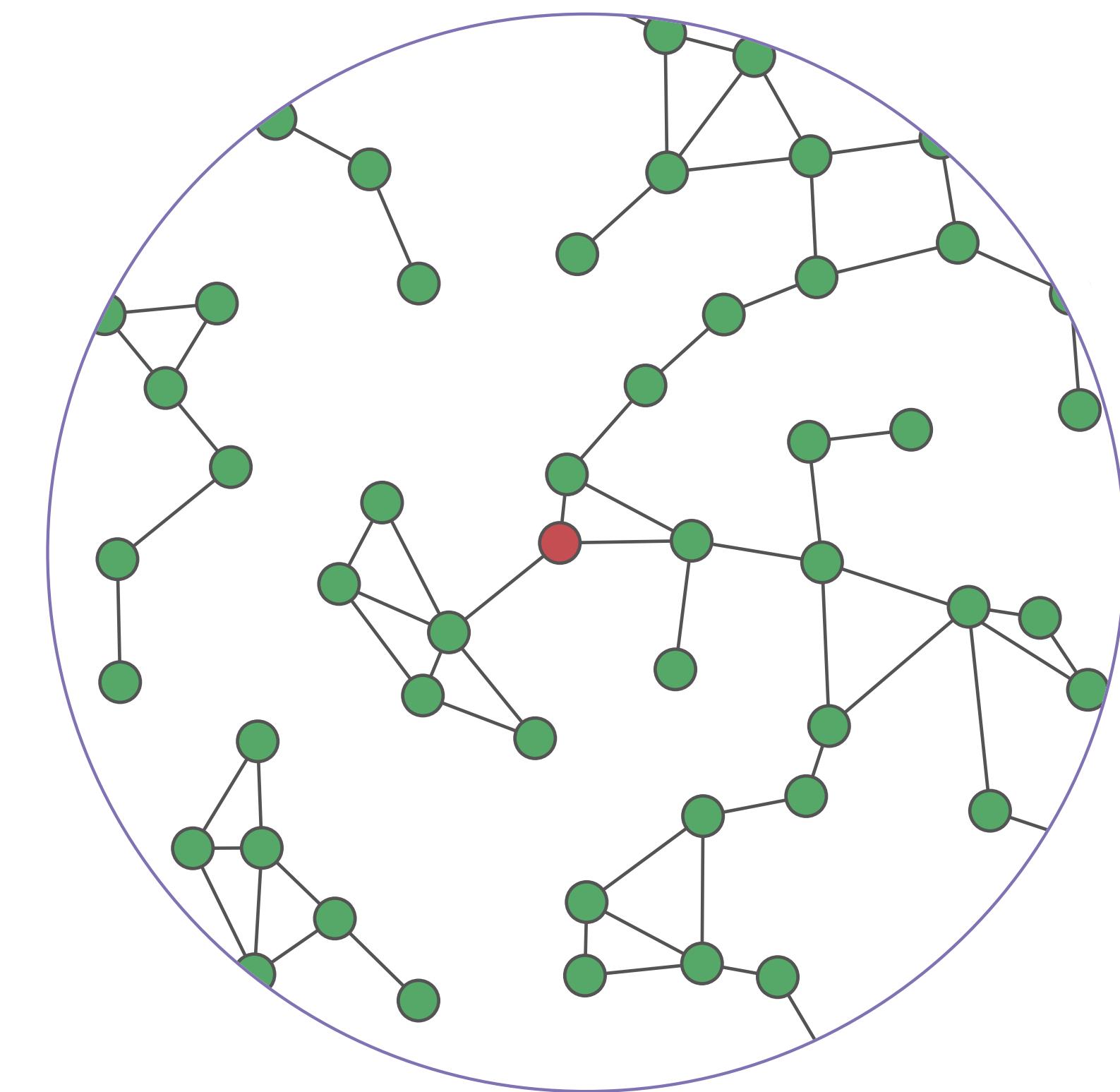
- network (graph) : contact network of a population
- nodes (vertices) : individuals
- links (edges) : (potential) disease-causing contacts between two individuals



Interdisciplinary Perspectives on Infectious Diseases
Volume 2011, Article ID 284909, 28 pages
doi:10.1155/2011/284909

Review Article
Networks and the Epidemiology of Infectious Disease

Leon Danon,¹ Ashley P. Ford,² Thomas House,³ Chris P. Jewell,² Matt J. Keeling,^{1,3}
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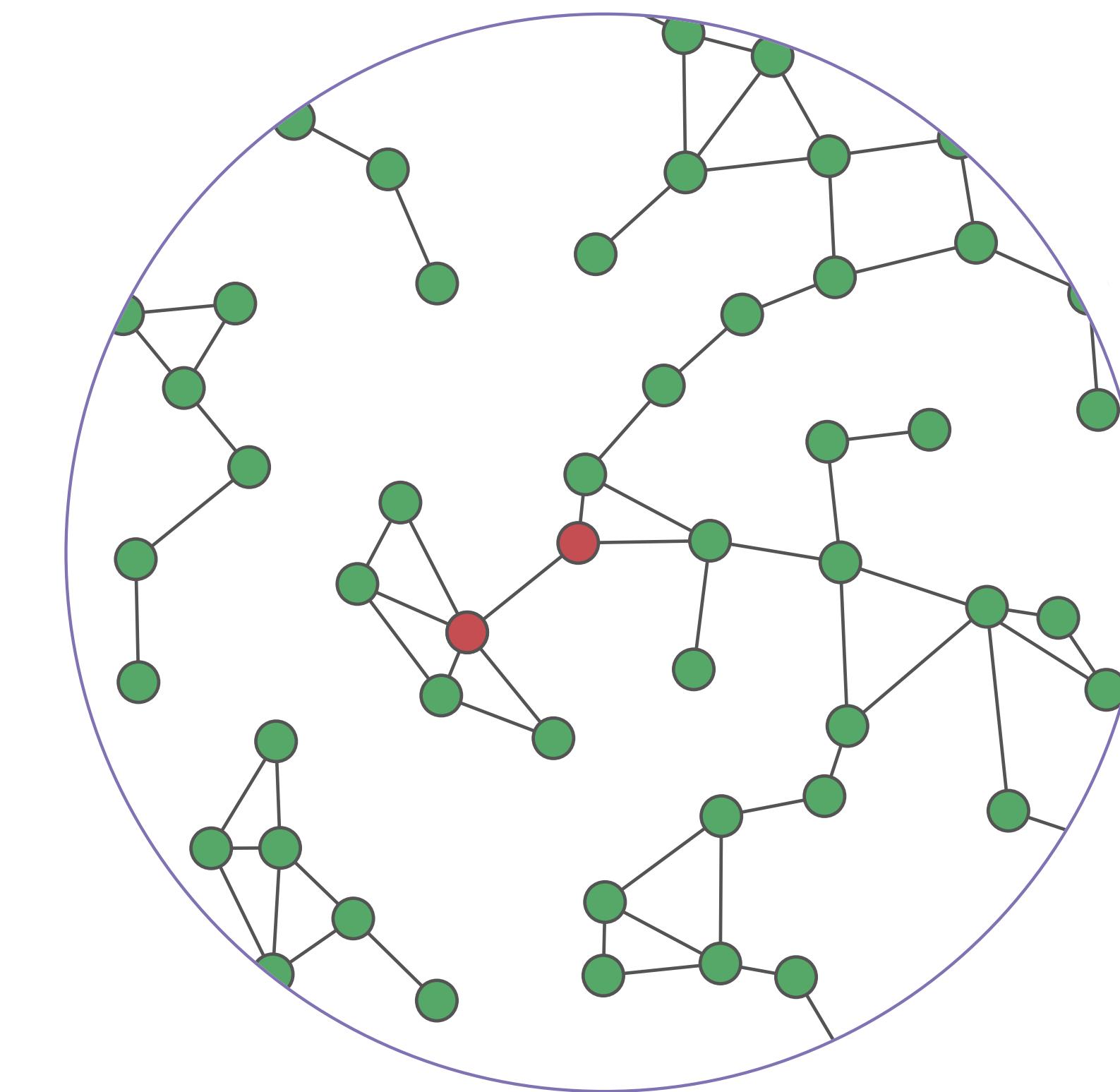
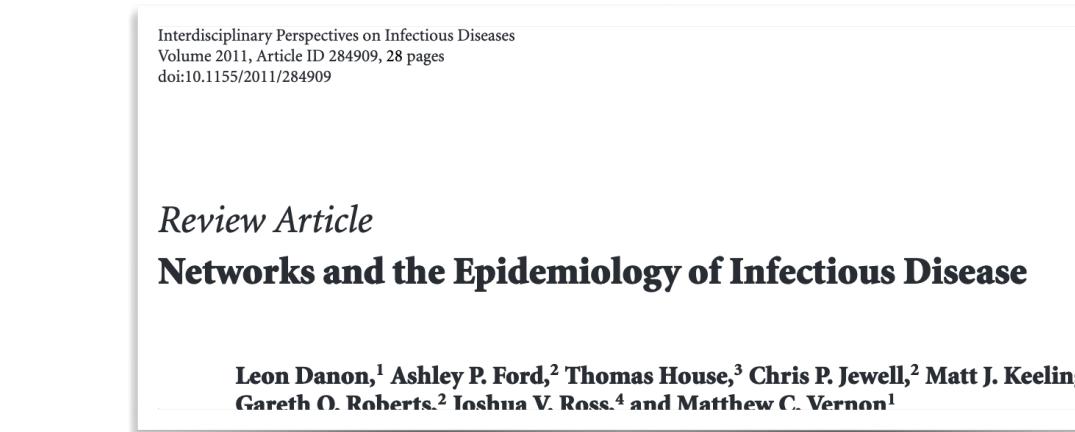
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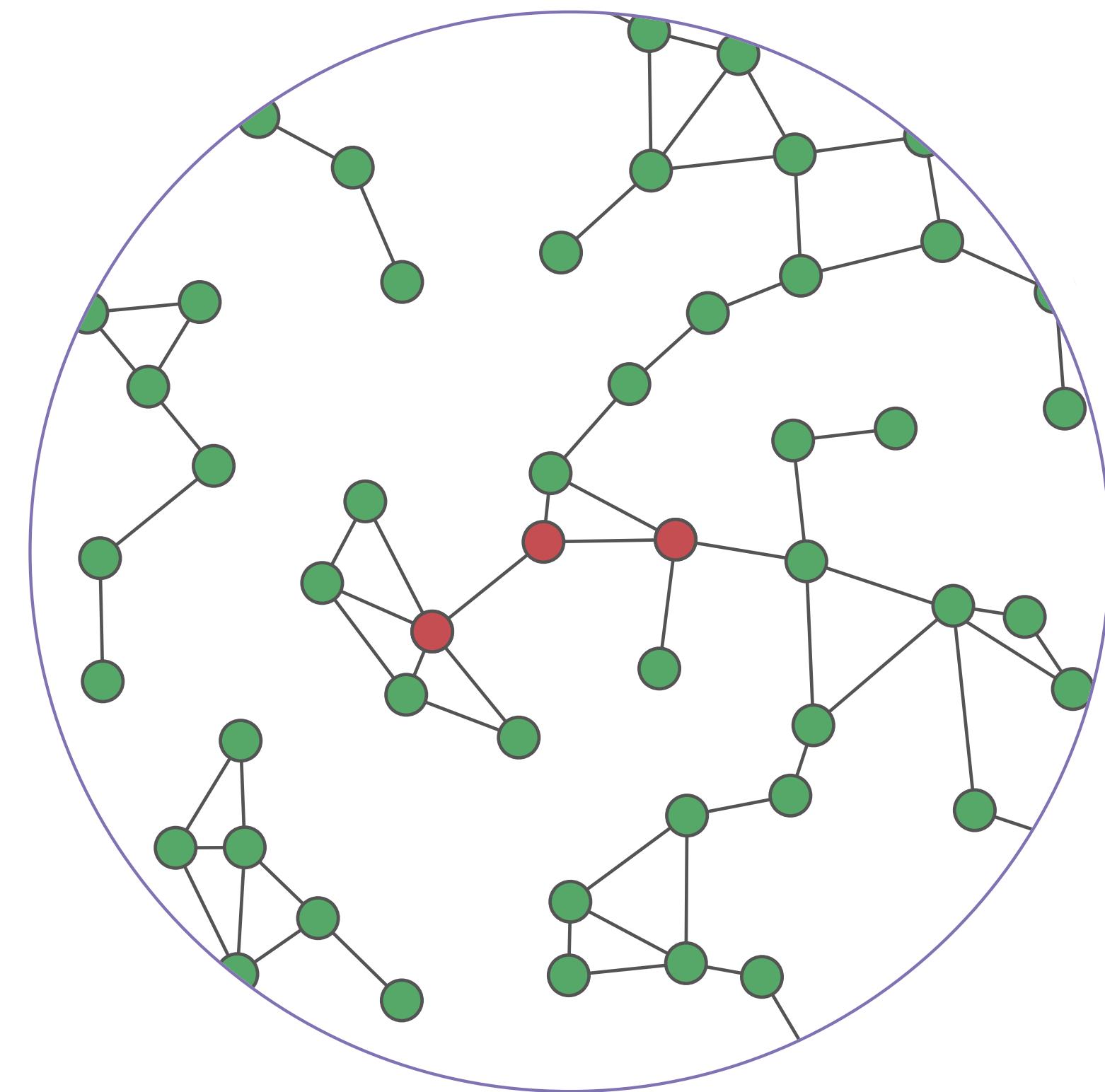
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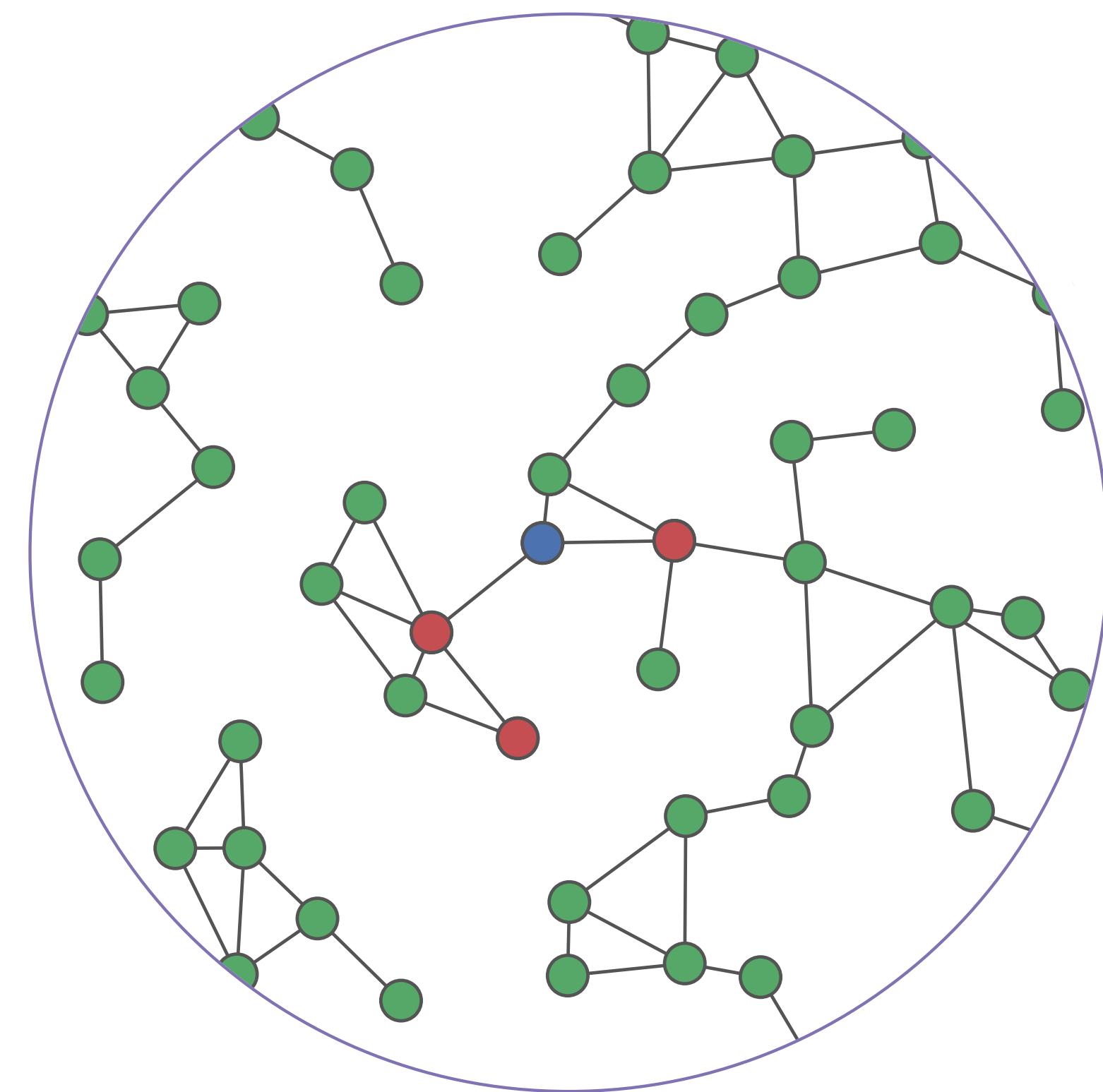
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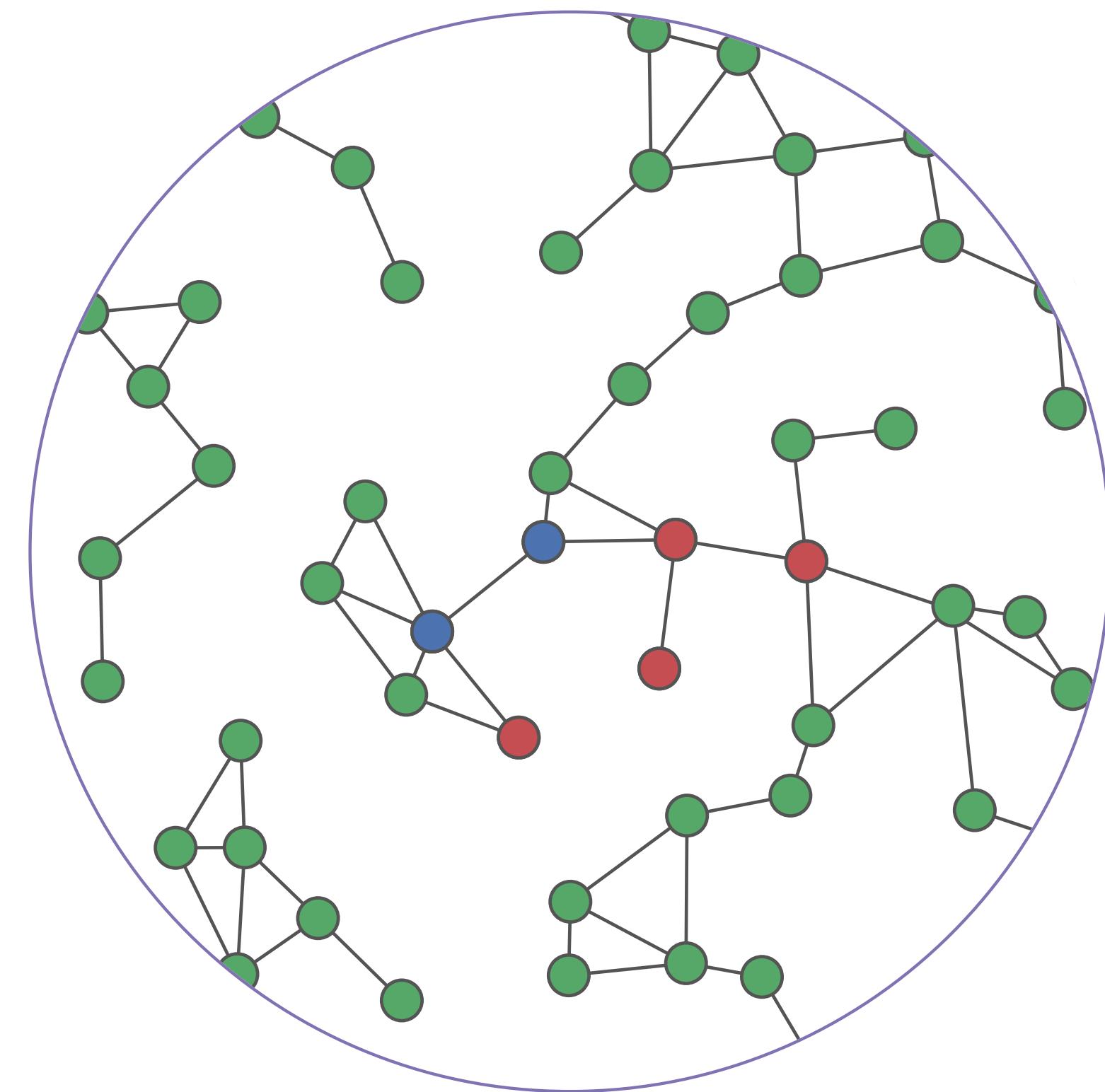
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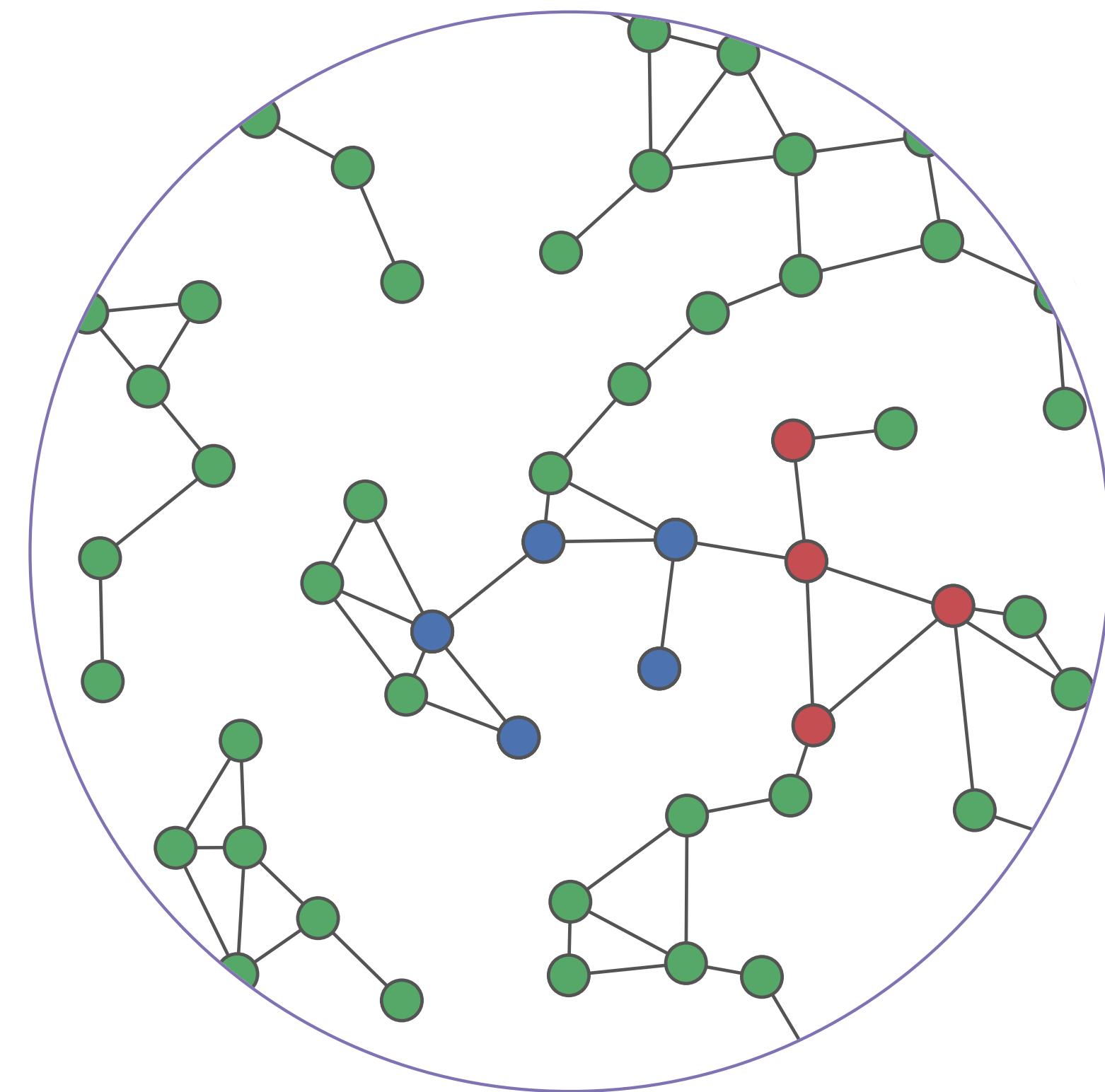
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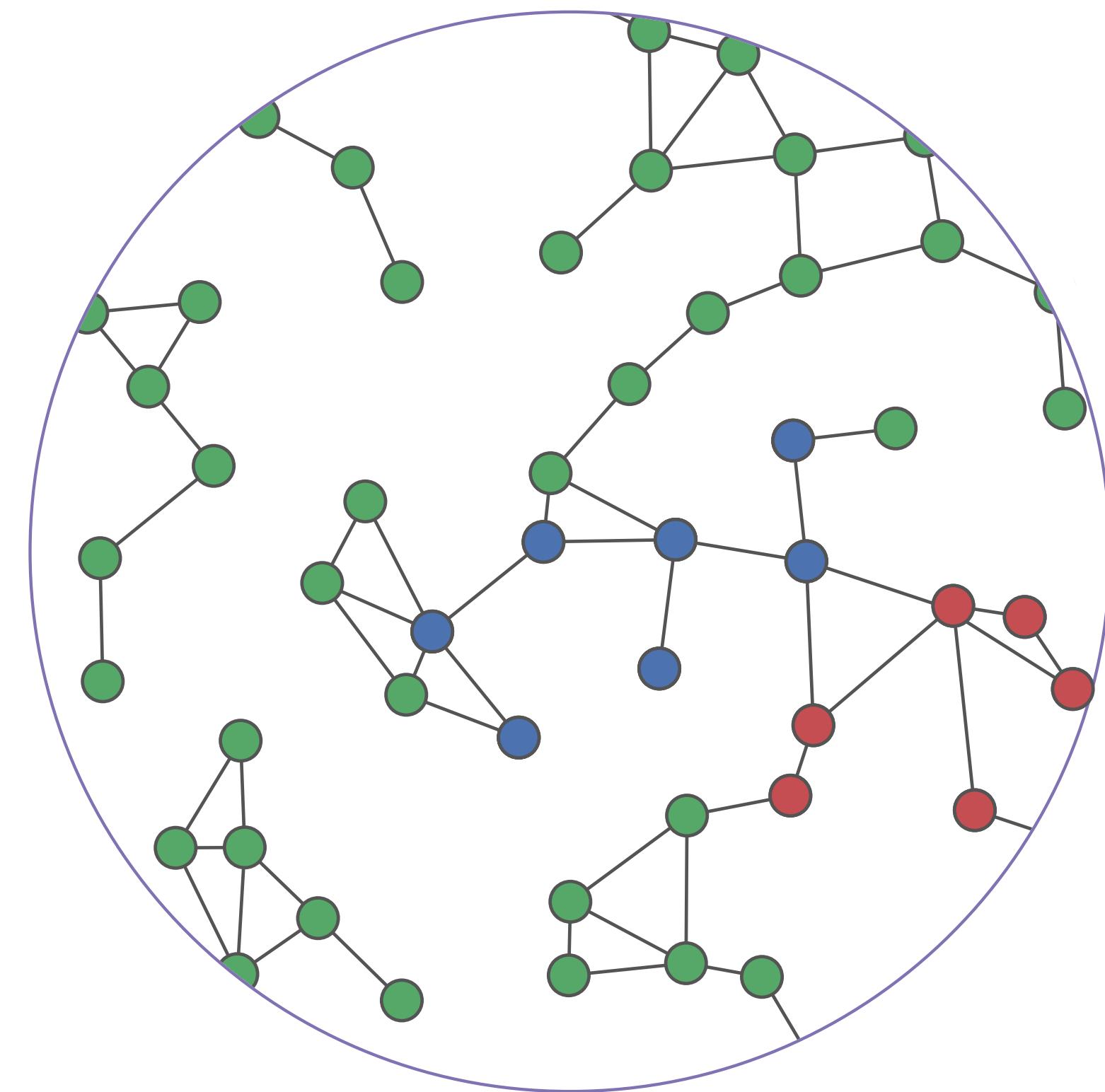
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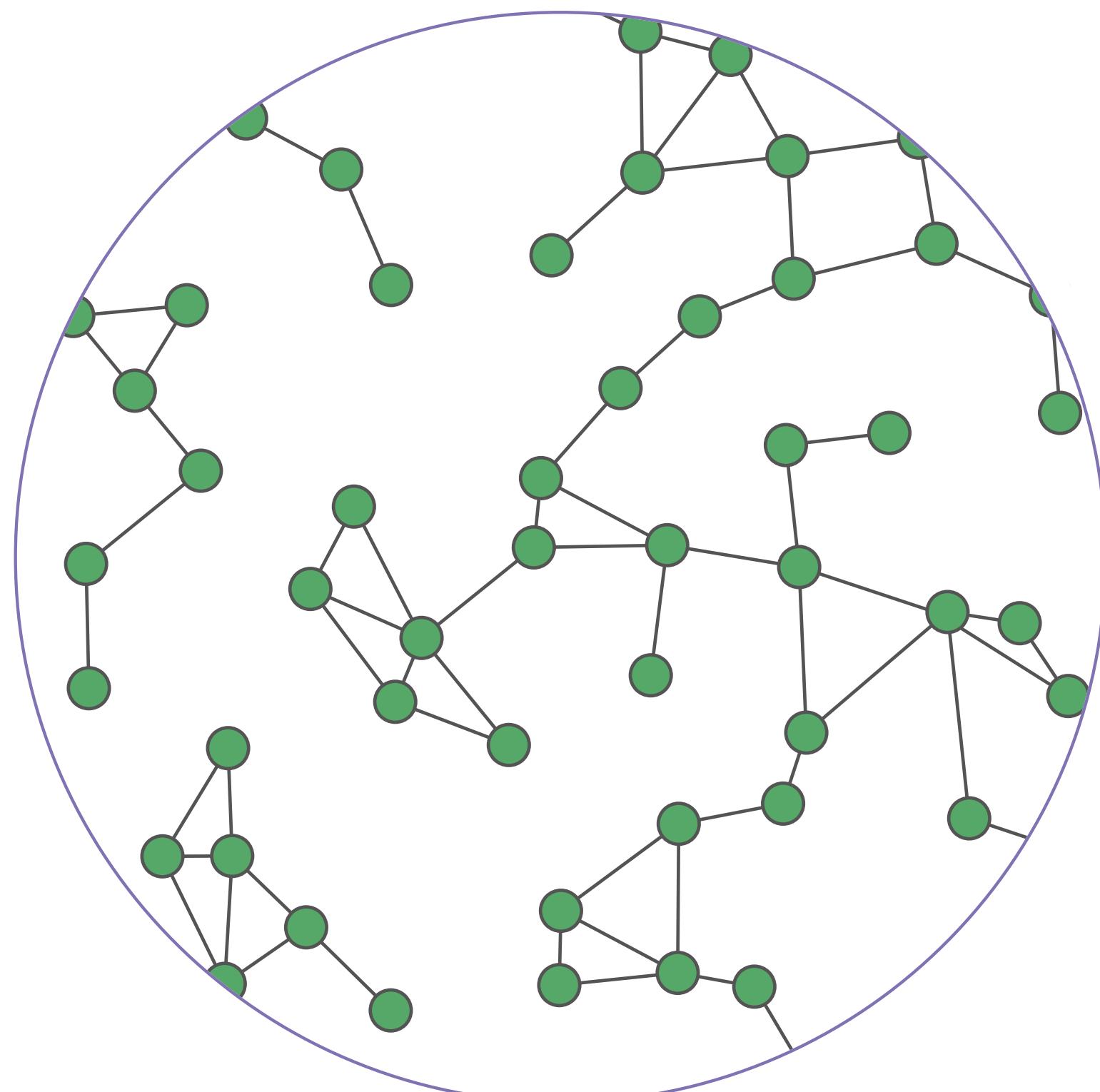
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Contact network epidemiology

Epidemic percolation networks (EPN) :

- previous slide : stochastic process is taking place on the contact network to produce an outcome
 - EPN : consider an ensemble of random networks encoding all possible outcomes
 - links indicate contacts that *will* transmit the disease
- ⇒ studying the EPN random network ensemble becomes equivalent to studying the spreading dynamics



Interdisciplinary Perspectives on Infectious Diseases
Volume 2011, Article ID 543520, 13 pages
doi:10.1155/2011/543520

Research Article
Epidemic Percolation Networks, Epidemic Outcomes, and Interventions

Eben Kenah¹ and Joel C. Miller^{2,3}

PHYSICAL REVIEW E 76, 036113 (2007)

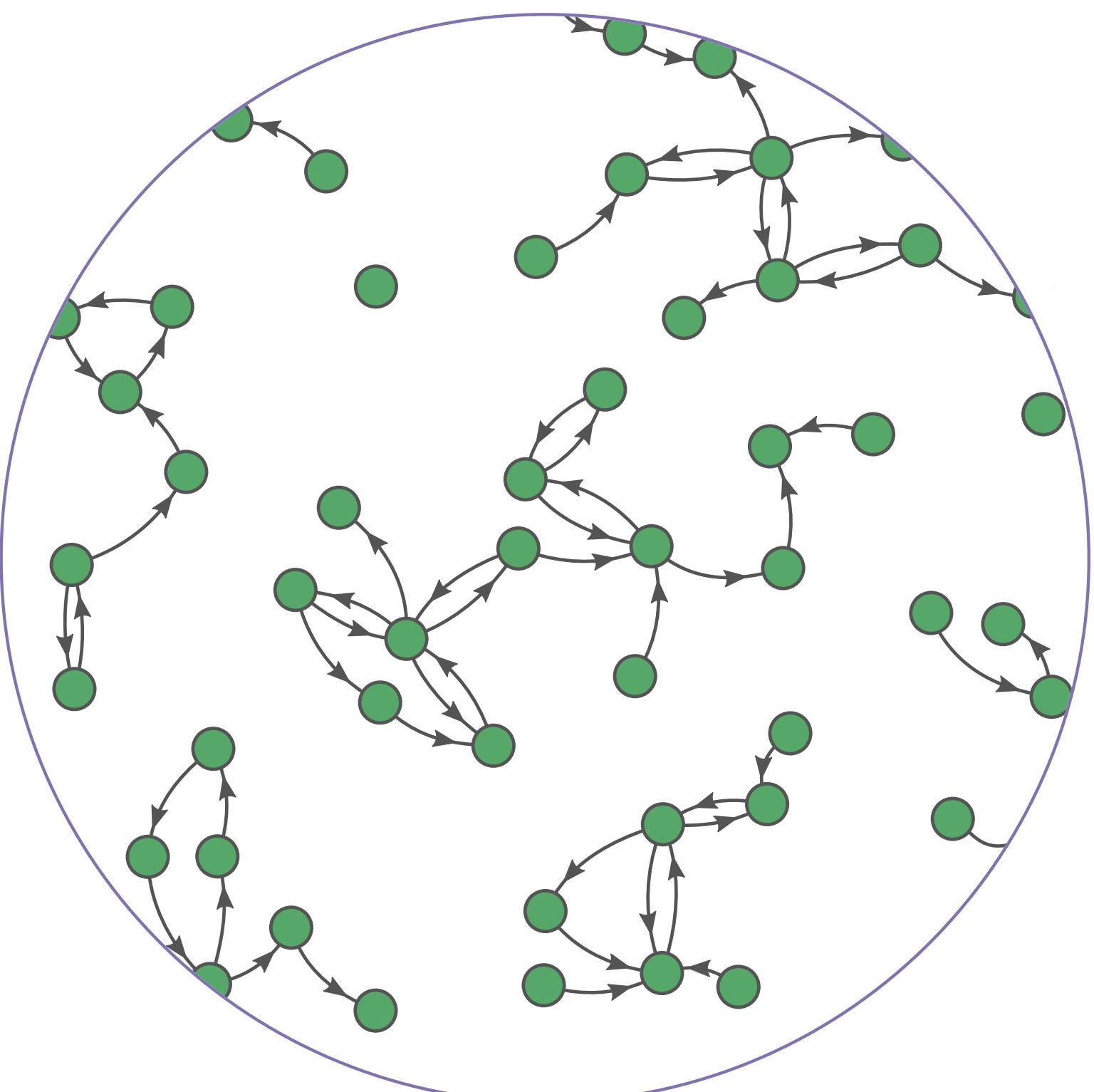
Second look at the spread of epidemics on networks

Eben Kenah* and James M. Robins

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Contact network epidemiology

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

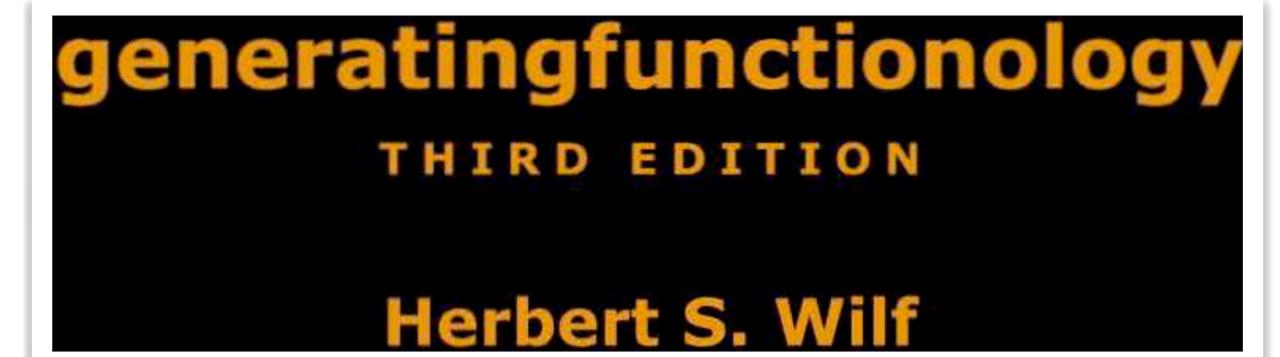
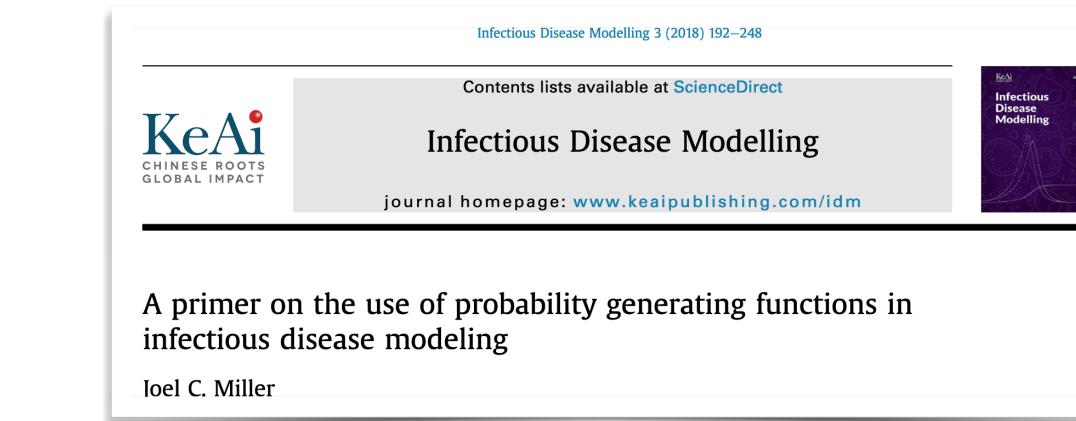
$$A(1) = \sum_{n \geq 0}^{\infty} a_n = 1 ; \quad \langle n \rangle = \sum_{n \geq 0}^{\infty} n a_n = \frac{dA(x)}{dx} \Big|_{x=1} = A'(1) ; \quad \langle n^p \rangle = \sum_{n \geq 0}^{\infty} n^p a_n = \left(x \frac{d}{dx} \right)^p A(x) \Big|_{x=1}$$

- extracting the coefficients

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

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

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



Contact network epidemiology

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 EPN)

$$G_0(x) = \bullet + \bullet x + \bullet x^2 + \bullet x^3 + \dots = \sum_{k \geq 0}^{\infty} p_k x^k ; \quad \langle k \rangle = \sum_{k \geq 0}^{\infty} k p_k = G'_0(1) ; \quad \langle k^2 \rangle = \sum_{k \geq 0}^{\infty} k^2 p_k$$

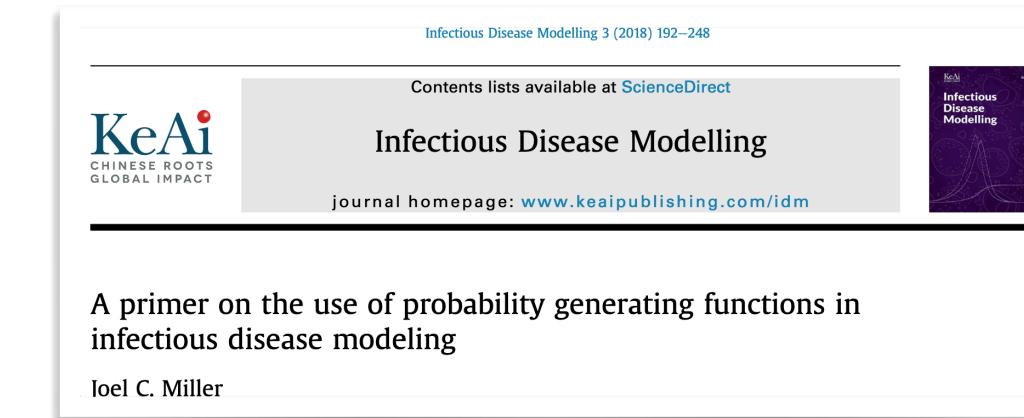
- a newly infected individual causes k new infections with probability $(k+1)p_{k+1}/\langle k \rangle$ (excess degree distribution of the EPN)

$$G_1(x) = \bullet + \bullet x + \bullet x^2 + \bullet x^3 + \dots = \sum_{k \geq 0}^{\infty} \frac{(k+1)p_{k+1}}{\langle k \rangle} x^k = \frac{G'_0(x)}{G'_0(1)}$$

- 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 $R_0 > 1$



PHYSICAL REVIEW E 66, 016128 (2002)

Spread of epidemic disease on networks

M. E. J. Newman

Contact network epidemiology

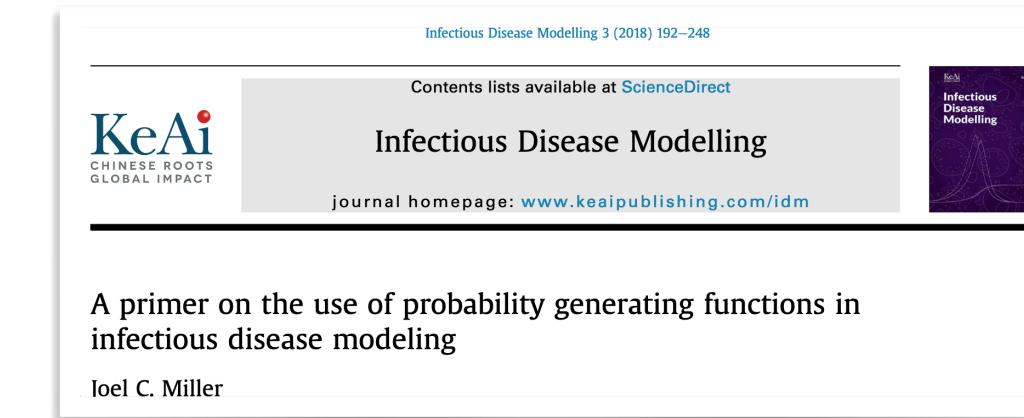
Probability generating functions (PGFs) formalism

- probability u that an infection tree eventually dies out (without causing an epidemic wave)

$$u = \text{[graph]} = \bullet + \text{[graph]} + \text{[graph]} + \text{[graph]} + \dots = \sum_{k \geq 0} \frac{(k+1)p_{k+1}}{\langle k \rangle} u^k = G_1(u)$$

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

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



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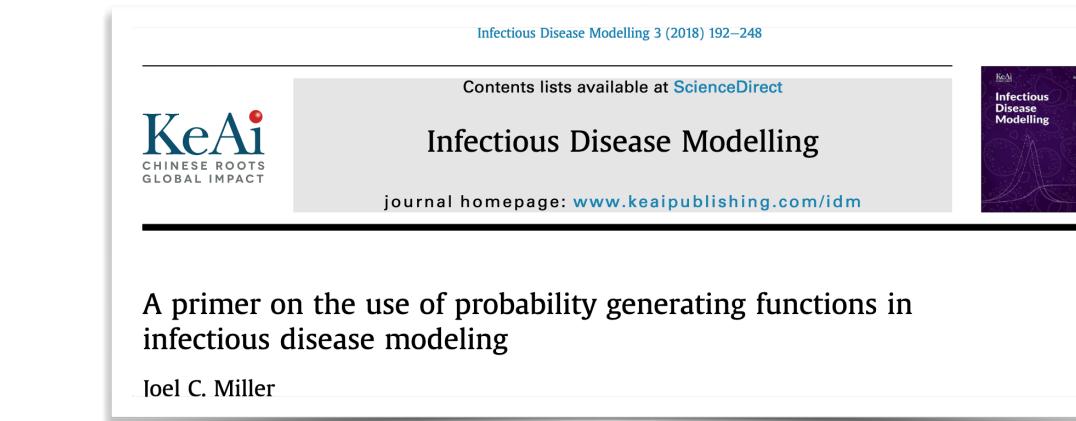
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Remark : the friendship paradox

- on average, your friends have more friends than you do
 - a random individual has k friends with probability p_k (generated by $G_0(x)$)
 - however, their friends have k friends with probability $\propto kp_k$ (generated by $G_1(x)$)
- by spreading on a contact network, the disease naturally oversamples 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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A random graph model

RANDOM GRAPHS

By E. N. GILBERT

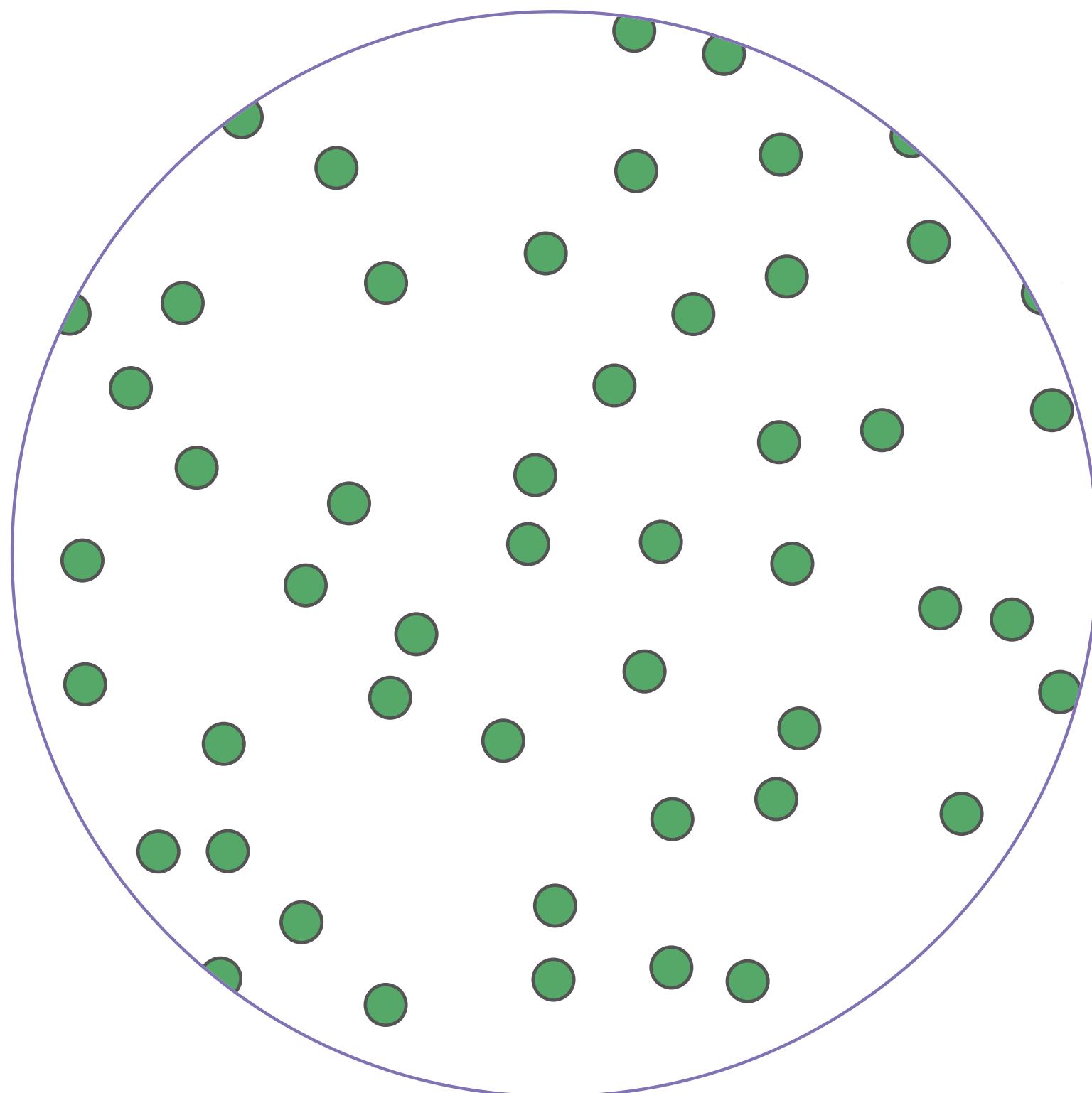
Bell Telephone Laboratories, Inc., Murray Hill, New Jersey

1. Introduction. Let N points, numbered $1, 2, \dots, N$, be given. There are $N(N - 1)/2$ lines which can be drawn joining pairs of these points. Choosing a subset of these lines to draw, one obtains a graph; there are $2^{N(N-1)/2}$ possible graphs in total. Pick one of these graphs by the following random process. For all pairs of points make random choices, independent of each other, whether or not to join the points of the pair by a line. Let the common probability of joining be p . Equivalently, one may erase lines, with common probability $q = 1 - p$ from the complete graph.

$$\text{Probability that a graph has } L \text{ edges} : P(L) = \binom{\binom{N}{2}}{L} p^L (1-p)^{\binom{N}{2} - L}$$

$$\text{Probability that a node has } k \text{ neighbors (degree)} : p_k = \binom{N-1}{k} p^k (1-p)^{N-1-k}$$

$$\text{Expected degree} : \langle k \rangle = \sum_{k=0}^{N-1} kp_k = p(N-1)$$



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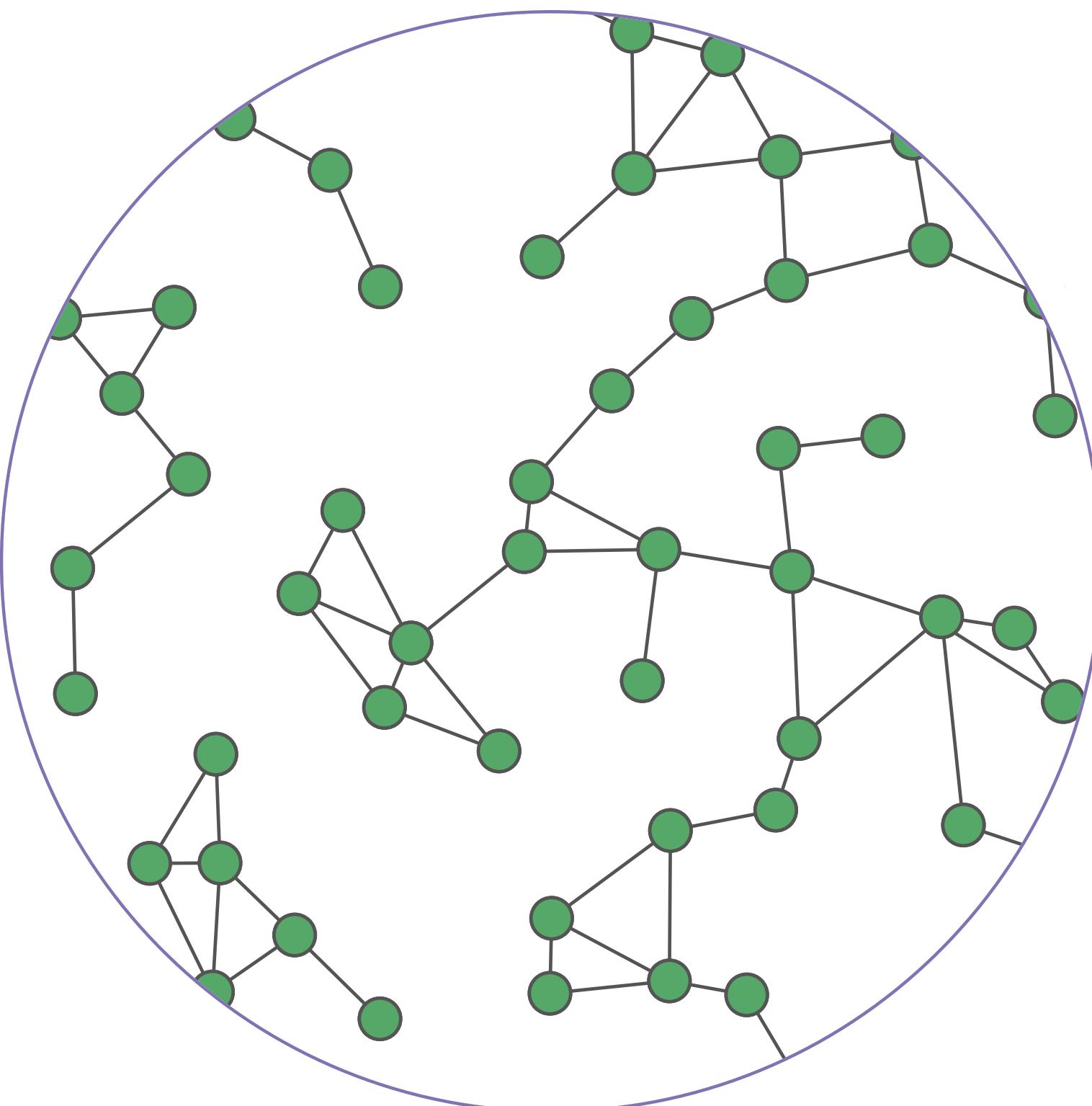
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A random graph model in the sparse limit

A sparse limit : $\langle k \rangle = \text{constant}$ with $N \rightarrow \infty$.

$$\langle k \rangle = p(N - 1) \quad \Rightarrow \quad p = \frac{\langle k \rangle}{N - 1}$$

$$\begin{aligned} G_0(x) &= \sum_{k=0}^{\infty} p_k x^k \\ &= \sum_{k=0}^{\infty} \binom{N-1}{k} (px)^k (1-p)^{N-1-k} \\ &= \left[1 + p(x-1) \right]^{N-1} \\ &= \left[1 + \frac{\langle k \rangle (x-1)}{N-1} \right]^{N-1} \\ &\stackrel{N \rightarrow \infty}{=} e^{\langle k \rangle (x-1)} \\ &= \sum_{k=0}^{\infty} \frac{\langle k \rangle^k e^{-\langle k \rangle}}{k!} x^k \end{aligned}$$

$$G_1(x) = \frac{G'_0(x)}{G'_0(1)} = e^{\langle k \rangle (x-1)} = G_0(x)$$

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Using this sparse random graph model as EPN

1. epidemic threshold : $R_0 = G'_1(1) = \langle k \rangle$

2. epidemic size :

$$R(\infty) = 1 - G_0(u) = 1 - e^{\langle k \rangle (u-1)}$$

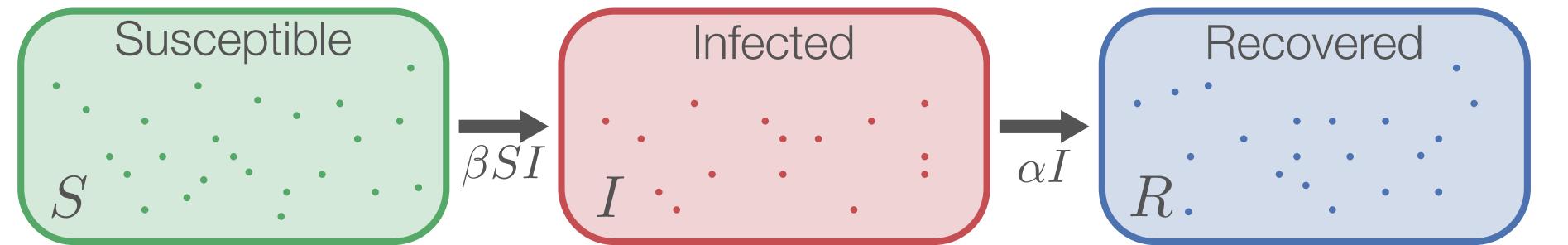
where

$$u = \text{---} = \bullet + \bullet + \bullet + \bullet + \dots = G_1(u) = e^{\langle k \rangle (u-1)}$$

which allows us to write

$$R(\infty) = 1 - u = 1 - e^{\langle k \rangle (u-1)} = 1 - e^{-R_0 R(\infty)}$$

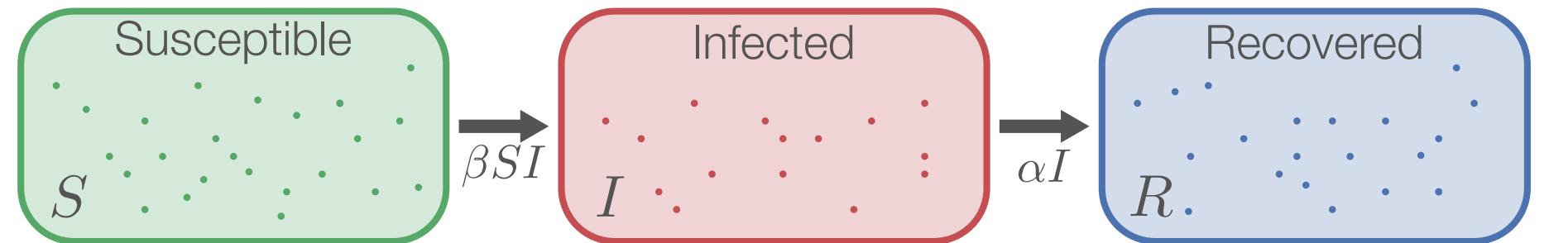
Poisson graph: a fish out of water?



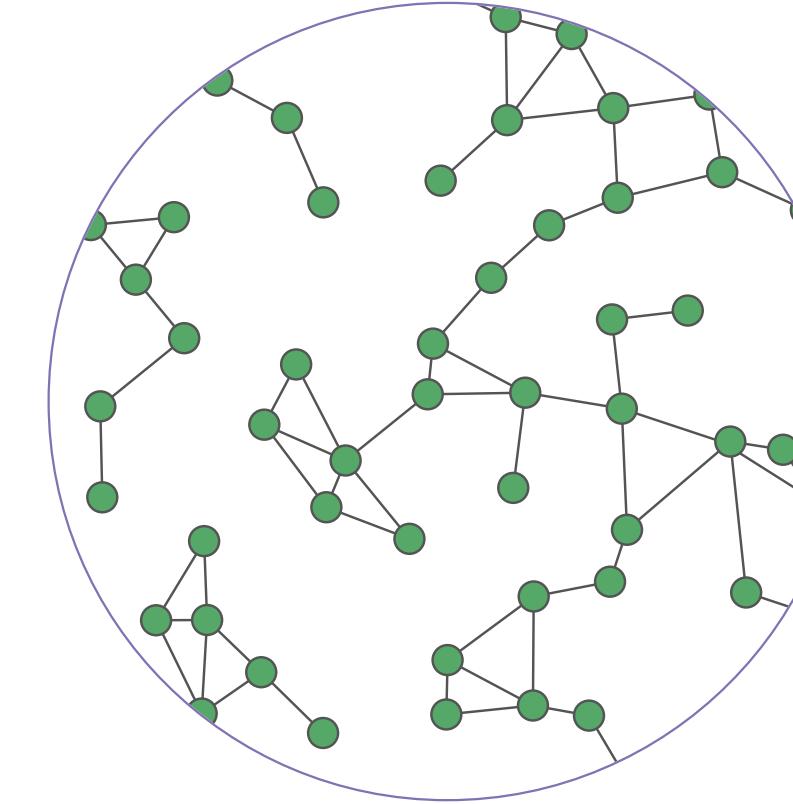
Basic epidemiological model: individuals interact randomly akin to how the molecules of a gas collide (Poisson process; mass-action assumption).

$$R(\infty) = 1 - e^{-R_0 R(\infty)}$$

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Contact network epidemiology: a graph shapes the spread of an infectious disease, notably by changing the way individuals are *sampled*.

Yet, we also find that

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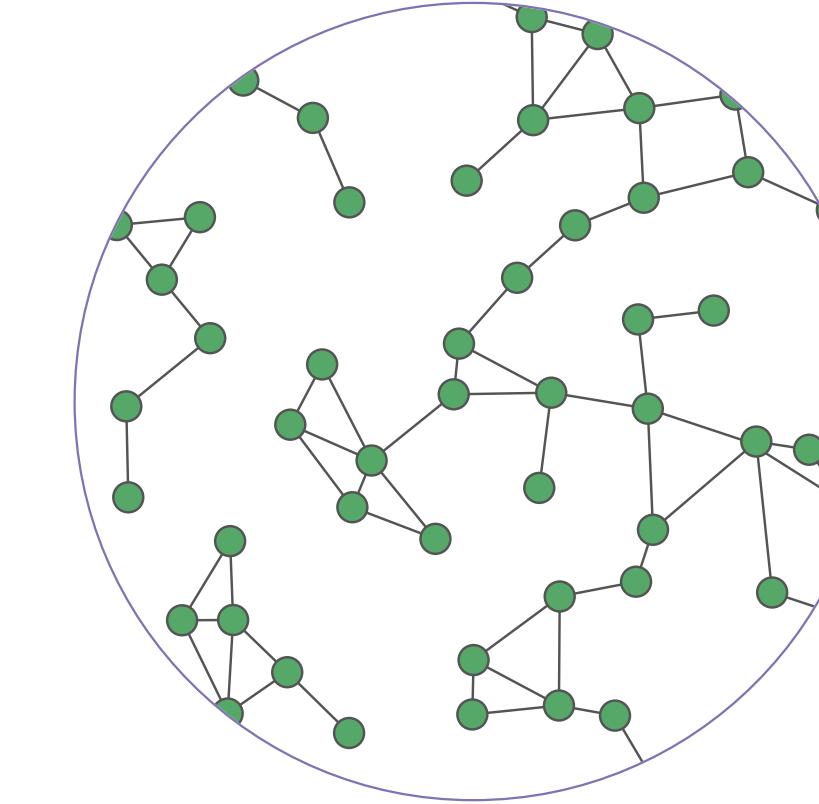
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when considering a Poisson graph.

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This begs the question : Where is the graph in a Poisson graph?

