

Contagion spread in clustered and unclustered small world networks

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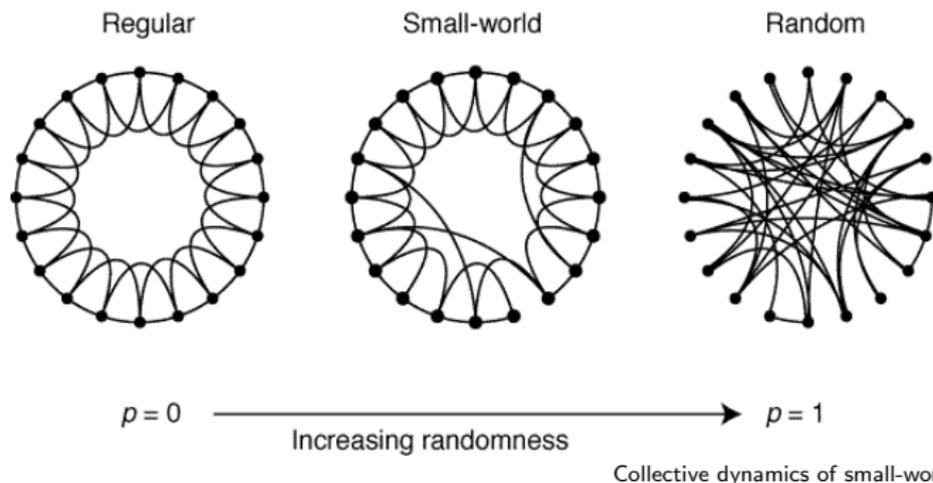
June 11, 2018

[mixture of completed and in progress work]

Outline

- ▶ Small world networks.
 - ▶ Clustered small world networks.
 - ▶ Unclustered small world networks.
- ▶ SIR disease in small-worlds and spatial networks.
- ▶ Analytic models in unclustered spatial networks.
- ▶ What constitutes a small-world?

Defining small-world networks



A “Small-world” network is typically understood to be a network with high clustering, but for which the typical shortest path length between two nodes is short (can always find shortcuts).

Properties of small-world networks

Networks, Dynamics, and the Small-World Phenomenon:

What do we mean when we say the world is “small”? In general, there is no precise answer, but in this article, “small” means that almost every element of the network is somehow “close” to almost every other element, even those that are perceived as likely to be far away.

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All four criteria are necessary for the small-world phenomenon to be remarkable . . . if the network were not clustered . . . then it follows from random-graph theory that most people would be only a few degrees of separation apart even for very large n .

Downsides of standard Small-World network models

- ▶ Homogeneous degree distribution.
- ▶ Analytically difficult (due to clustering).
- ▶ Difficult to distinguish effect of “closeness” from “clustering”.

Random Spatial Networks (RSNs)

How else can we generate networks where a node is
*close to almost every other element, even those that are
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without requiring clustering?

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- ▶ and make it **analytically tractable**?

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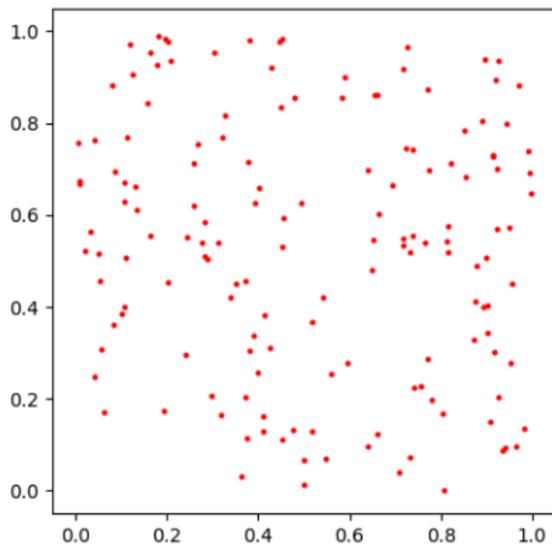
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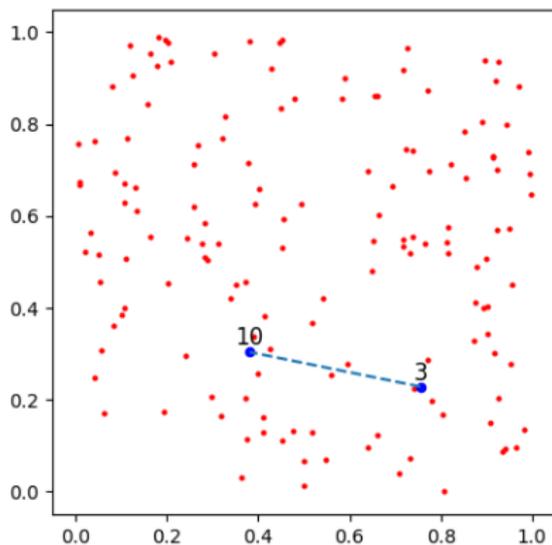
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We need some concept of **distance** where nodes are much more likely to connect to nearby nodes, perhaps with enough nearby nodes that they don't have to have triangles.

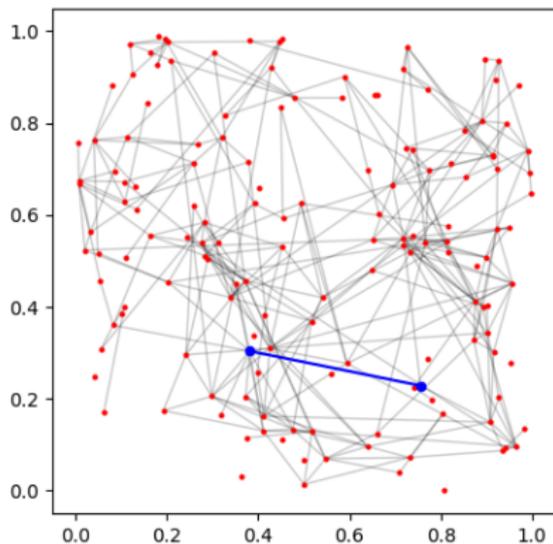


The most obvious distance is geometric distance. Place nodes in a 2D region.



We can assign weights κ to the nodes, and place an edge with probability **proportional to their weights** and some **function of their distance**. For example:

$$P(u, v) \propto \frac{3 \times 10}{3r^3 + .01}$$



In the resulting network, all edges exist independently and node u 's degree comes from a Poisson distribution with mean κ_u .

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- ▶ Place N nodes uniformly at random in some space Ω with density ρ .

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 - ▶ Controls lengths of edges. Determines frequency of shortcuts.

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$$P(u, v) = \min \left(\frac{\kappa_u \kappa_v f(d_{uv})}{\rho \langle K \rangle}, 1 \right)$$

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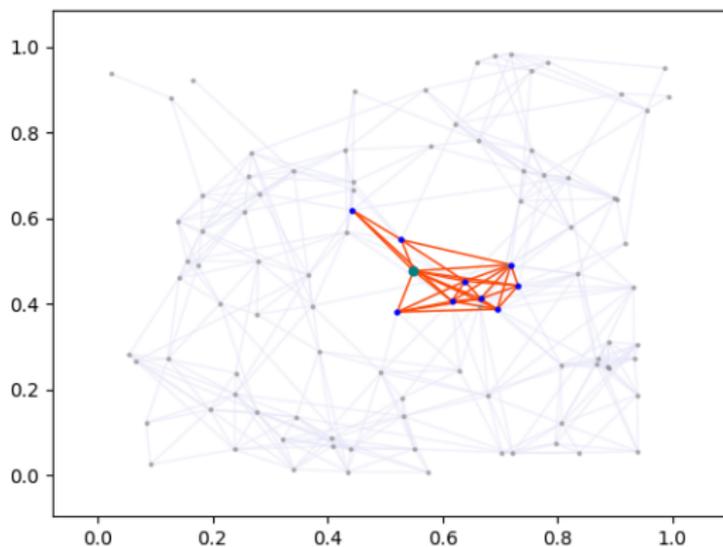
$$P(u, v) = \min \left(\frac{\kappa_u \kappa_v f(d_{uv})}{\rho \langle K \rangle}, 1 \right)$$

- ▶ There are reasonably efficient ways to do this¹, and it may be possible to make even better algorithms.

¹based on Miller & Hagberg: [Efficient Generation of Networks with Given Expected Degrees](#), 2011 

The high-density limit

As density ρ increases, clustering scales like $1/\rho$:

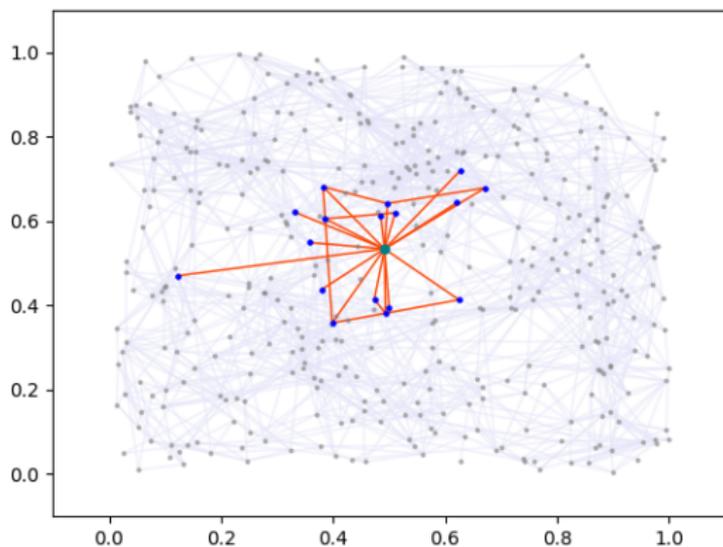


$$\rho = 100$$

$$f(d) = \frac{1}{96d^5 + 0.01}$$

The high-density limit

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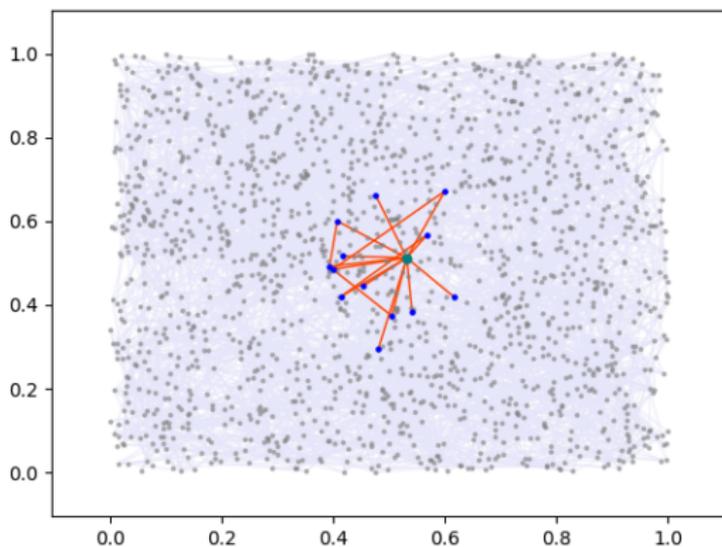


$$\rho = 400$$

$$f(d) = \frac{1}{96d^5 + 0.01}$$

The high-density limit

As density ρ increases, clustering scales like $1/\rho$:

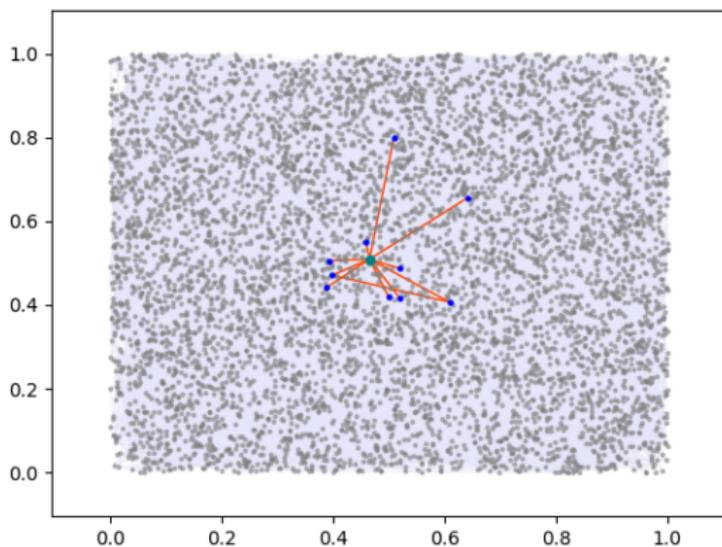


$$\rho = 1600$$

$$f(d) = \frac{1}{96d^5 + 0.01}$$

The high-density limit

As density ρ increases, clustering scales like $1/\rho$:



$$\rho = 6400$$

$$f(d) = \frac{1}{96d^5 + 0.01}$$

Small-world like behavior

Consider a 2-dimensional RSN with

$$f(d) = \begin{cases} \frac{N_0}{k} \left[1 - \epsilon \frac{1 - \pi r_0^2}{\pi r_0^2} \right] & d < r_0 \\ \frac{N_0}{k} \epsilon & d \geq r_0 \end{cases}$$

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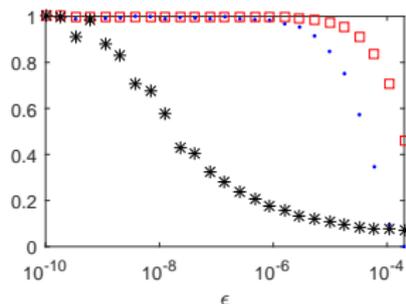
Most edges are within a small disk, but a small fraction are outside.

Small-world like behavior

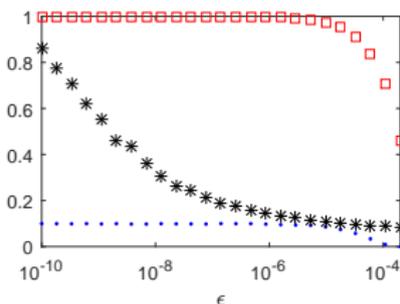
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Most edges are within a small disk, but a small fraction are outside.



$$N = N_0 = 10^5$$



$$N = 10^6 = 10N_0$$

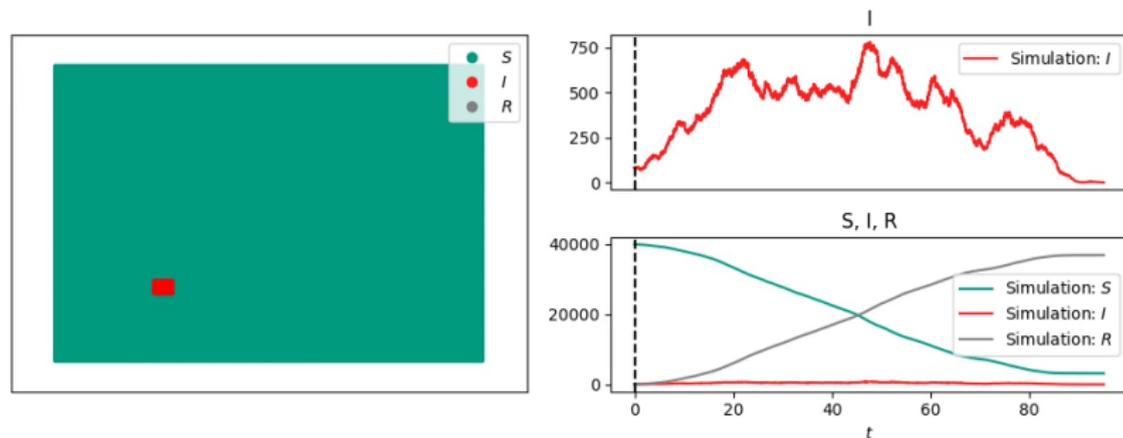
- : scaled clustering
- : scaled average "closeness" of neighbors
- *: scaled average shortest path length

Signposting

We now look at SIR disease spread in the two network types.

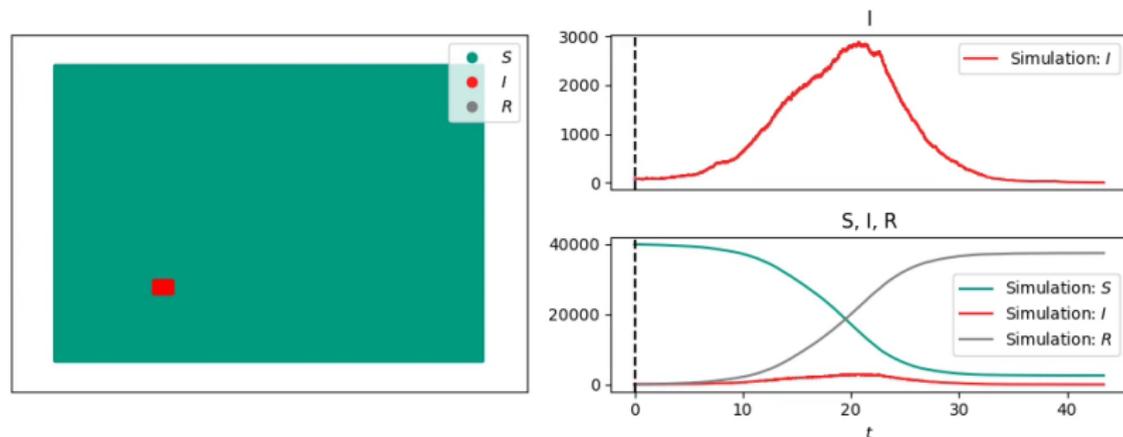
- ▶ Simulations in Watts–Strogatz-style networks with/without short cuts.
- ▶ Simulations in RSNs with/without short cuts.
- ▶ Impact of node density.
- ▶ Behavior of the front.

Disease spread in 2D Watts–Strogatz-style small-world networks



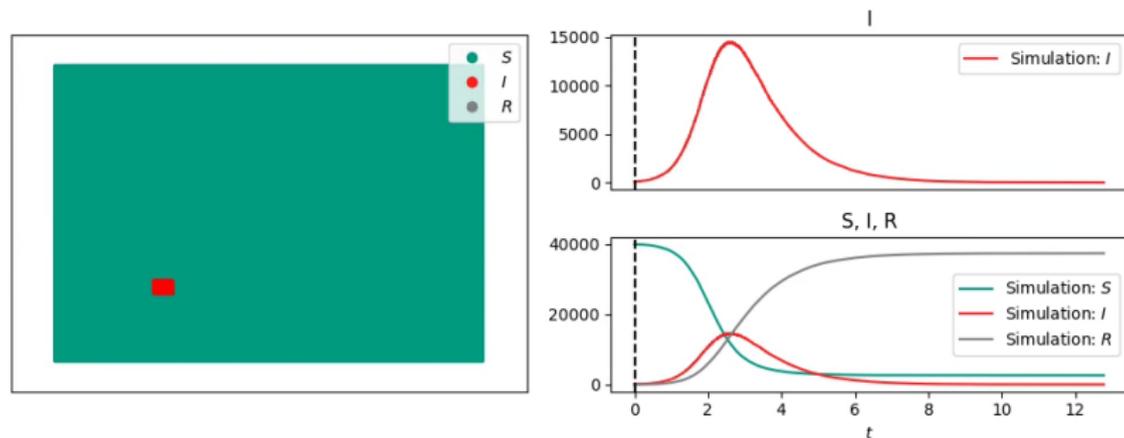
No shortcuts, clustering coefficient ≈ 0.45

Disease spread in 2D Watts–Strogatz-style small-world networks



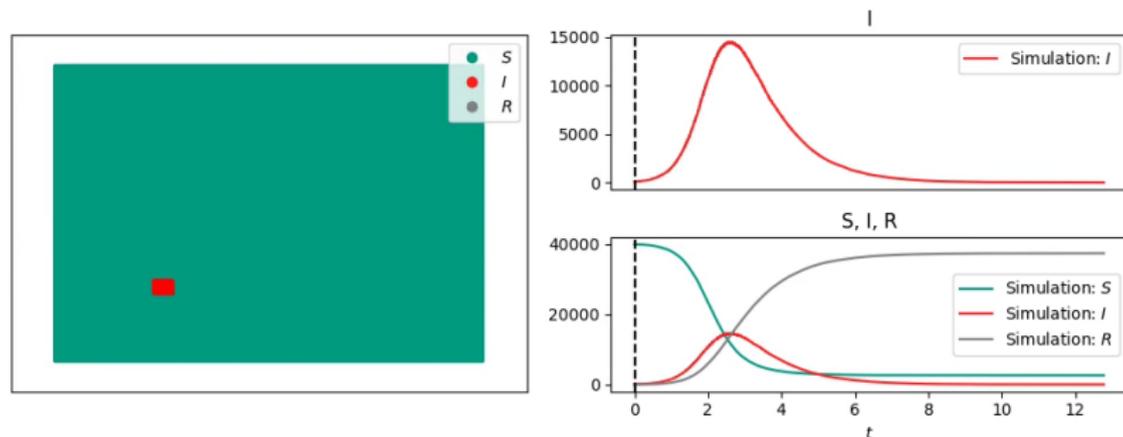
Few shortcuts, clustering coefficient ≈ 0.45

Disease spread in 2D Watts–Strogatz-style small-world networks



Nothing but shortcuts, clustering coefficient ≈ 0

Disease spread in 2D Watts–Strogatz-style small-world networks



Nothing but shortcuts, clustering coefficient ≈ 0

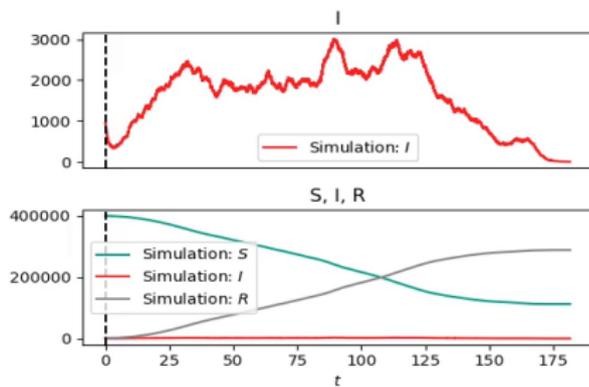
Why is the second case different from and similar to the first and the third?

Shameless plug

The simulations and visualizations were generated with the open source Python package Epidemics on Networks (EoN) v0.99.2:
<http://epidemicsonnetworks.readthedocs.io/en/latest/EoN.html>

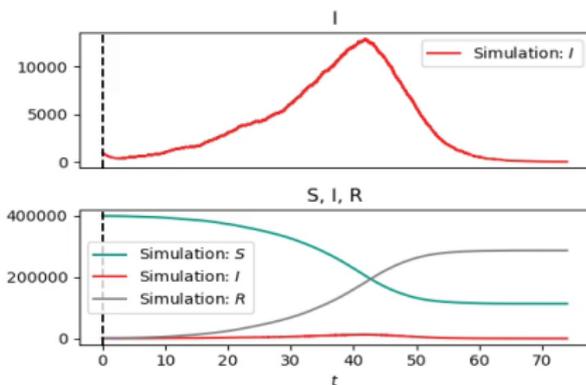
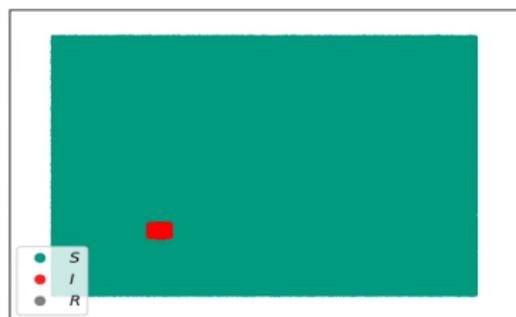
```
...: beta=0.55
...: gamma = 1.0
...: initial_infecteds = [(u,v) for (u,v) in G if 45<u<55 and 45<v<55]
...: sim = EoN.fast_SIR(G, beta, gamma, initial_infecteds = initial_infecteds,
...:                   return_full_data=True)
...: pos = {node:node for node in G}
...: sim.set_pos(pos)
...: ani=sim.animate(ts_plots=['I', 'SIR'], node_size = 4)
...: ani.save(filename, fps=5, extra_args=['-vcodec', 'libx264'])
```

Disease spread with varying distance kernels in RSNs



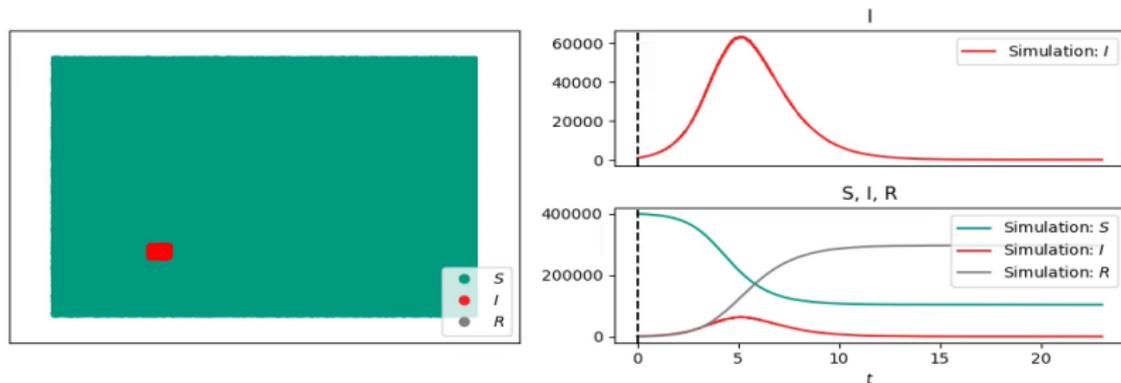
f only allows local connections: clustering coefficient ≈ 0.05

Disease spread with varying distance kernels in RSNs



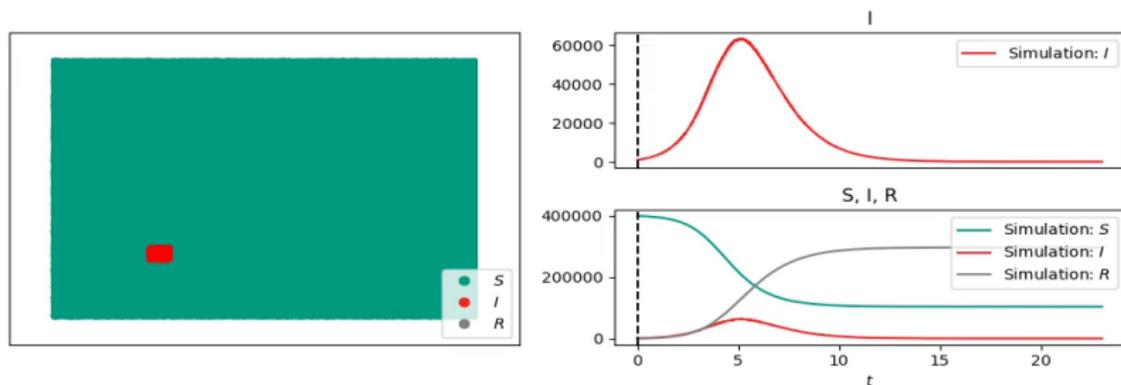
f mostly local, but small amount of global connections: clustering coefficient ≈ 0.05

Disease spread with varying distance kernels in RSNs



f allows all connections with equal probability, clustering coefficient ≈ 0

Disease spread with varying distance kernels in RSNs

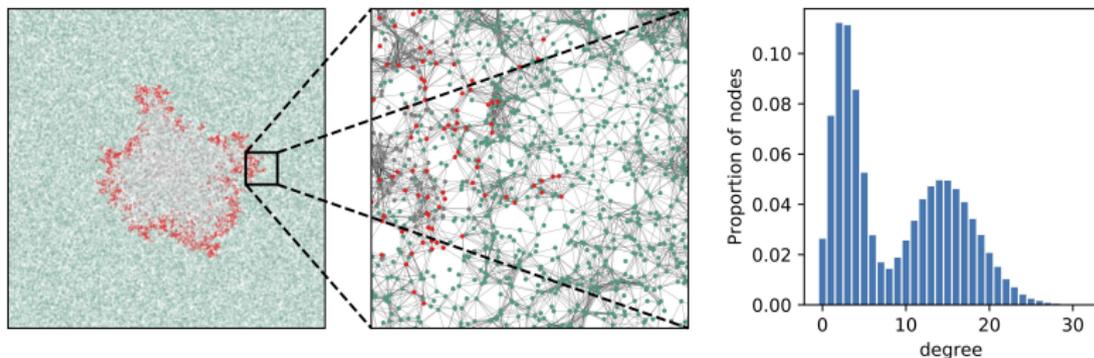


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Disease spread at varying density in RSNs

$\rho = 100000$:



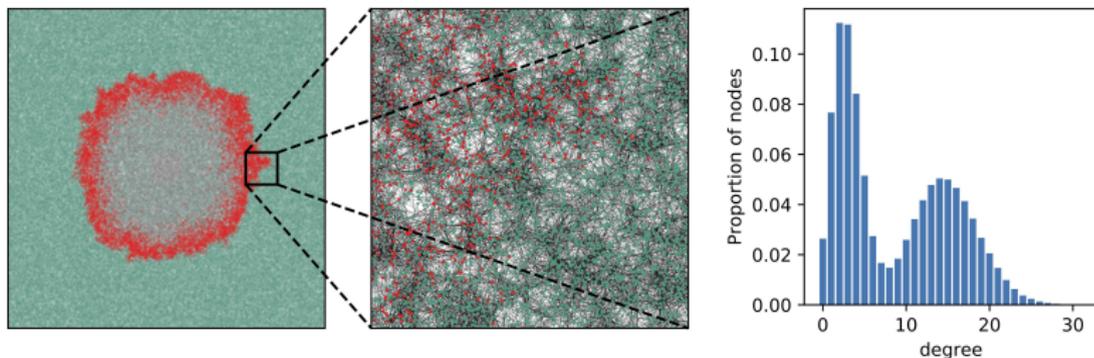
Snapshots of infection spread at specific time with infection initiated near center.

$$f(d) = \begin{cases} \frac{1}{0.01^2 \pi} & d < 0.01 \\ 0 & d \geq 0.01 \end{cases}$$

$$P(\kappa = 3) = P(\kappa = 15) = 0.5$$

Disease spread at varying density in RSNs

$\rho = 500000$:



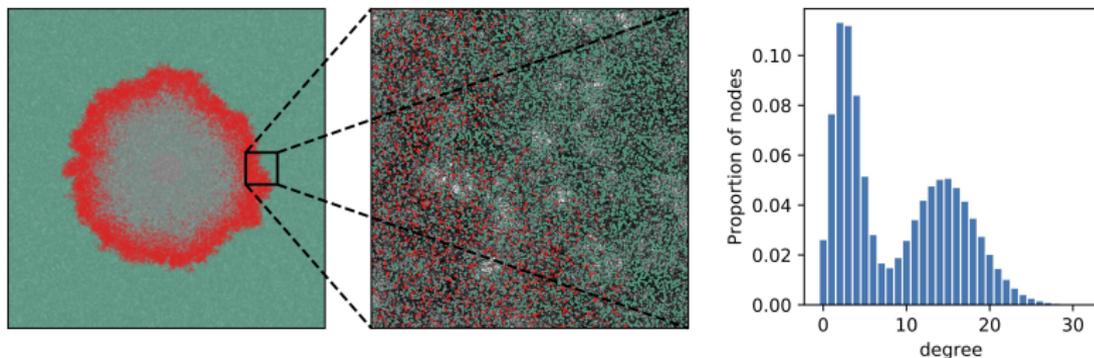
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Disease spread at varying density in RSNs

$\rho = 1000000$:



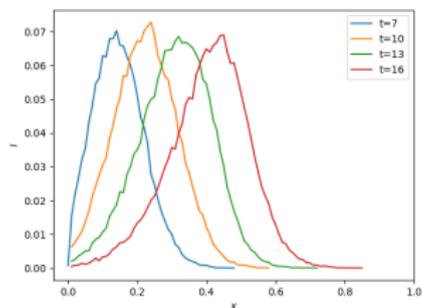
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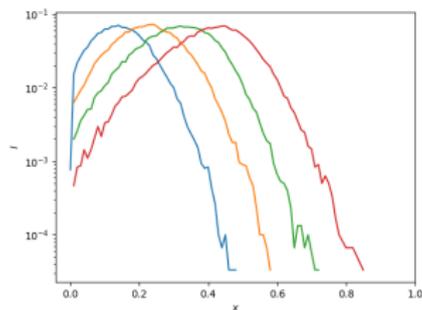
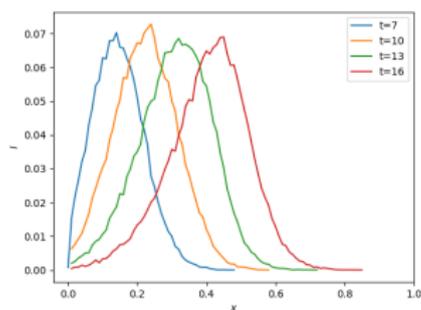
Disease Spread in 1-Dimension

Consider SIR Disease spread in a 1-dimensional RSN.



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The front has an exponentially decaying leading edge.

Signposting

- ▶ Derivation of analytic equations.
- ▶ Comparison with simulation.
- ▶ Predictions about traveling waves.
- ▶ Limitations & what constitutes a “small-world”.

The large-population limit

Our simulations suggest that (at least for localized distance kernels), a coherent traveling wave emerges in large populations.
Can we study this limit analytically?

Deriving the SIR governing equations

If $1 - \Theta(\mathbf{x}, t)$ is the expected number of edges to transmit to a node with $\kappa = 1$ at \mathbf{x} by time t (only the first transmission has any impact), then

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- ▶ and $e^{-\kappa(1 - \Theta(\mathbf{x}, t))}$ is the probability a node with given κ has not received a transmission.
- ▶ So

$$S(\mathbf{x}, t) = S(\mathbf{x}, 0)\Psi(\Theta(\mathbf{x}, t)) = S(\mathbf{x}, 0) \int_0^\infty e^{-\kappa(1 - \Theta(\mathbf{x}, t))} P(\kappa) d\kappa$$

is the probability an arbitrary node is susceptible at \mathbf{x} and t .

Governing Equations

With some effort (not shown here) we can find an equation for Θ .

$$\frac{\partial}{\partial t} \Theta(\mathbf{x}, t) = -\beta \Theta(\mathbf{x}, t) + \gamma(1 - \Theta(\mathbf{x}, t)) \\ + \beta \frac{\int_V S(\hat{\mathbf{x}}, 0) \Psi'(\Theta(\hat{\mathbf{x}}, t)) f(|\hat{\mathbf{x}} - \mathbf{x}|) d\hat{\mathbf{x}}}{\langle \kappa \rangle}$$

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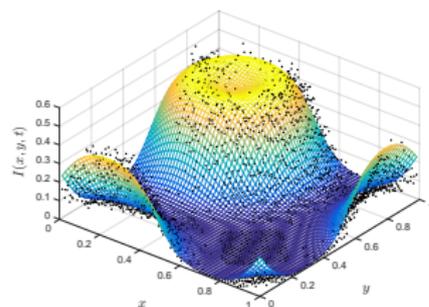
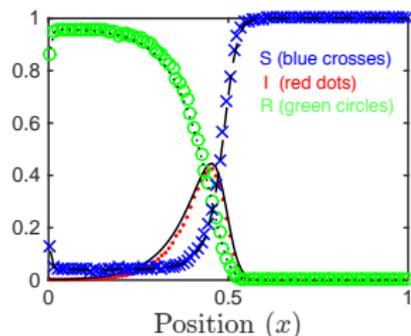
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with

$$\Psi(\Theta(\mathbf{x}, t)) = \int_0^\infty e^{-\kappa(1-\Theta(\mathbf{x}, t))} P(\kappa) d\kappa$$

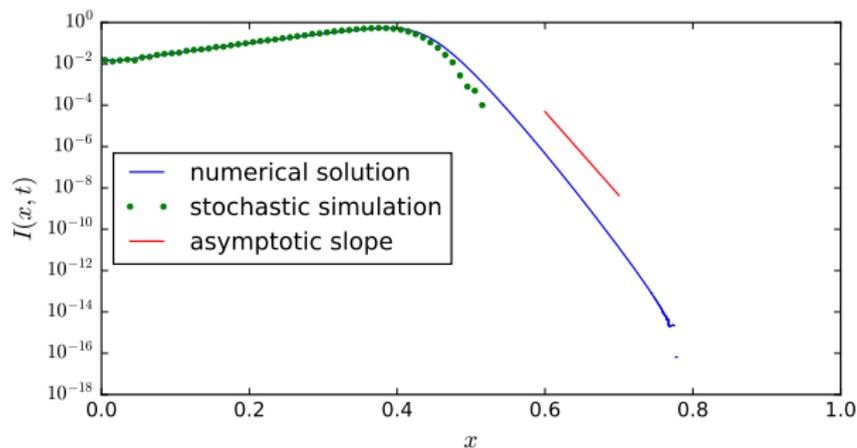
Equations versus simulations



Does well at predicting both 1D and 2D simulations [with narrow kernel f].

Studying the traveling wave

If we assume that the front has an exponentially decaying leading edge: $I \propto e^{-\alpha(x-ct)}$, we can linearize and study it.



- ▶ The wavenumber α satisfies

$$\alpha \mathcal{L}[xf(|x|)](\alpha) + \mathcal{L}[f](\alpha) = \frac{1}{\mathcal{R}_0}$$

where $\mathcal{R}_0 = \beta \langle K^2 \rangle / \langle K \rangle (\beta + \gamma)$ is the reproductive number.

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$$c = -\beta \frac{\langle \kappa^2 \rangle}{\langle \kappa \rangle} \mathcal{L}[xf(|x|)](\alpha) = -(\beta + \gamma) \mathcal{R}_0 \mathcal{L}[xf(|x|)](\alpha)$$

Where $\mathcal{L}[f](\alpha)$ is the two-sided Laplace Transform

$$\mathcal{L}[g](\alpha) = \int_{-\infty}^{\infty} g(x) e^{-\alpha x} dx$$

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Where $\mathcal{L}[f](\alpha)$ is the two-sided Laplace Transform

$$\mathcal{L}[g](\alpha) = \int_{-\infty}^{\infty} g(x) e^{-\alpha x} dx$$

- ▶ For what functions $f(|x|)$ does $\mathcal{L}[f](\alpha)$ diverge?

- ▶ The wavenumber α satisfies

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where $\mathcal{R}_0 = \beta \langle K^2 \rangle / \langle K \rangle (\beta + \gamma)$ is the reproductive number.

- ▶ The wavespeed c satisfies

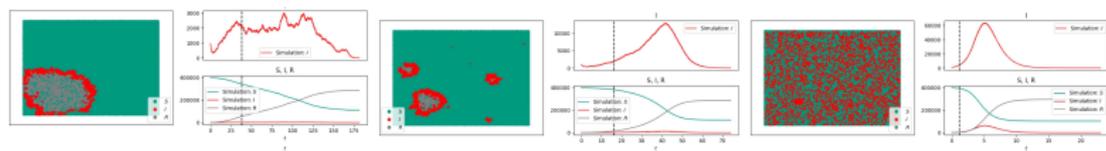
$$c = -\beta \frac{\langle \kappa^2 \rangle}{\langle \kappa \rangle} \mathcal{L}[xf(|x|)](\alpha) = -(\beta + \gamma) \mathcal{R}_0 \mathcal{L}[xf(|x|)](\alpha)$$

Where $\mathcal{L}[f](\alpha)$ is the two-sided Laplace Transform

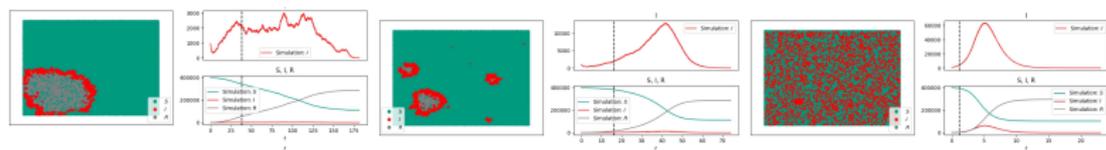
$$\mathcal{L}[g](\alpha) = \int_{-\infty}^{\infty} g(x) e^{-\alpha x} dx$$

- ▶ For what functions $f(|x|)$ does $\mathcal{L}[f](\alpha)$ diverge?
If f decays slower than exponentially, there is no finite wavespeed.

Limitations on deterministic model

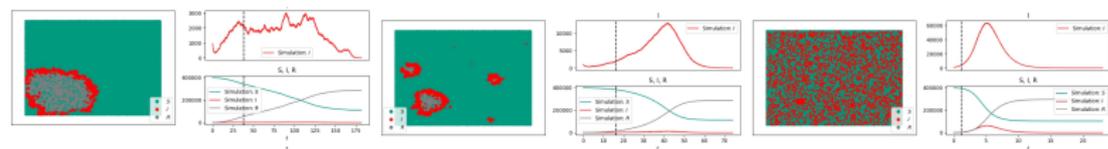


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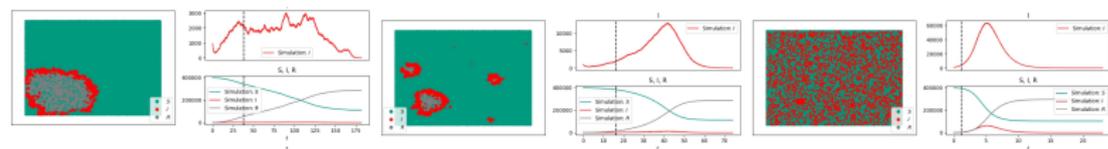
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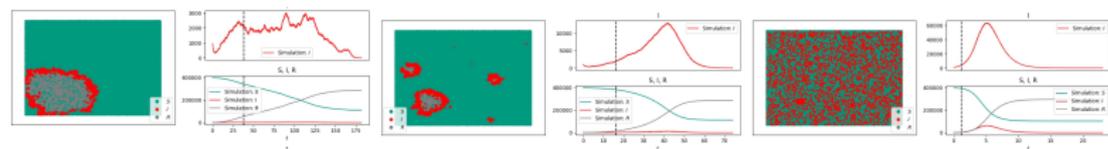
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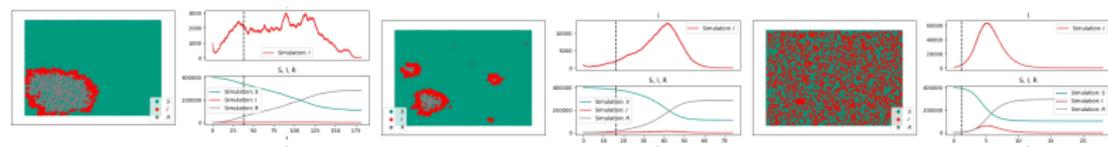
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- ▶ Because the disease grows exponentially locally, a rare transmission has a significant effect.
- ▶ If f decays too slowly, then stochastic jumps will occur, and we cannot predict their locations in a deterministic model.
- ▶ Nevertheless, in some cases we can estimate how many jumps should have occurred and use this to predict the combined global dynamics.

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- ▶ What constitutes a small-world network depends on the spreading process.

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- ▶ For complex contagions, the small-world effect doesn't seem to occur easily.

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- ▶ We can create a class of Random Spatial Networks which allow us to explore small-world networks as a special case.
- ▶ We can analytically explore SIR transmission on these networks.
- ▶ We can use predictions from these models to give a quantitative prediction of what a small-world network is.

Acknowledgments

Parts of this work were done in collaboration with

- ▶ Hans De Sterck (Monash University & Waterloo)



- ▶ John Lang (Waterloo & UCLA)



- ▶ Jamieson L. Kaiser (Monash University)

