Epidemics in Networks
Part I — Introduction

Joel C. Miller & Tom Hladish

18–20 July 2018

Who are we?

- Joel C. Miller:
  - Former math and biology faculty at Penn State and later Monash University (Melbourne).
  - Now senior research scientist at Institute for Disease Modeling
  - Co-author of "Mathematics of Epidemics on Networks": http://bit.ly/EpidemicSonnetWorks
  - Developer of python package EoN: http://epidemicsonnetworks.readthedocs.io/en/latest/
  - 8th year teaching this course.
- Thomas J. Hladish
  - Biology and Emerging Pathogens Institute faculty at the University of Florida
  - Developer of C++ EpiFire, AbcSmc packages: https://github.com/tjhladish/
  - 10th year teaching this course

Layout of course

The course will consist of a mixture of theory and computer labs.

- Theory
  - Properties of diseases and networks
  - Analytic predictions of disease behavior
- Computer Lab
  - Python and EpiFire-based stochastic simulation of epidemics on networks.
- Notes are available at http://sismid.hladish.com

Disease spread

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- Immune response / natural history.

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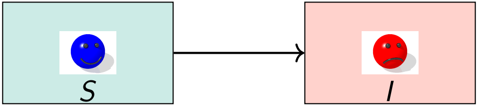

HIV, Tuberculosis (without treatment), Hepatitis (sometimes),

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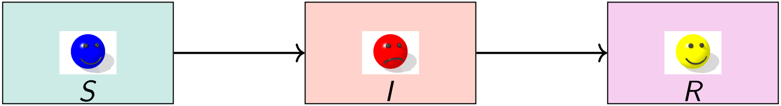

Measles, Mumps, Rubella, Pertussis, . . .

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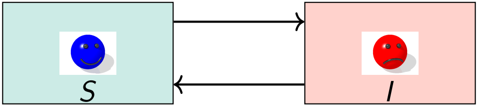

Many parasites (e.g., lice), Many bacteria, Many STDs, ...

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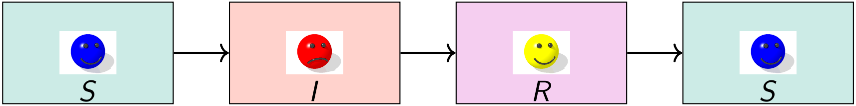

Dengue (sort of), Pertussis, Influenza (because of genetic drift of virus).

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Lots of things to think about

For SIR, we are typically interested in

- $\mathcal{P}$, the probability of an epidemic.
- $\mathcal{A}$, the "attack rate": the fraction infected (better named the attack ratio)
- $\mathcal{R}_0$, the average number of infections caused by those infected early in the epidemic.
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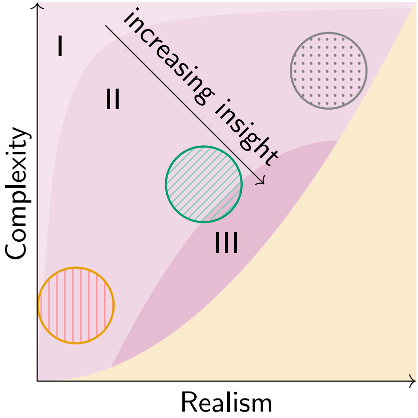
For SIS, we are typically interested in

- $\mathcal{P}$
- $I(\infty)$, the equilibrium level of infection
- $\mathcal{R}_0$
- $I(t)$

Modeling options



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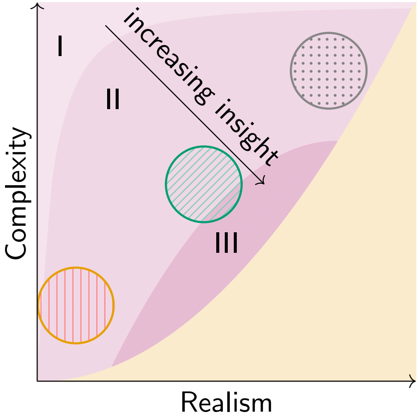

- ◍: Compartmental models

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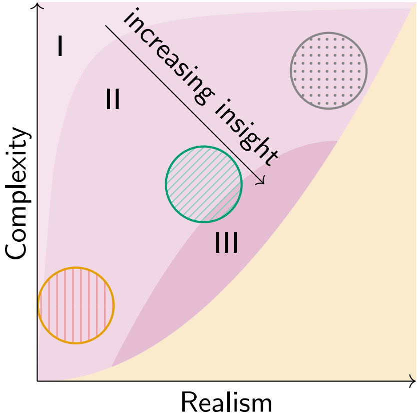

- ▥: Compartmental models
- ░: Agent-based models

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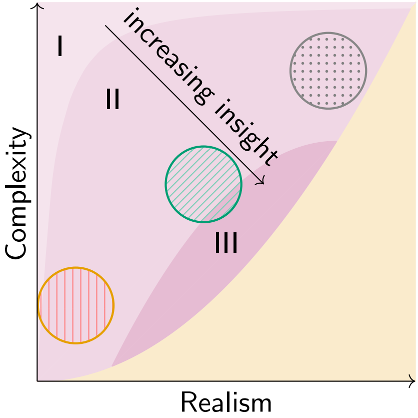

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- ▨: Network models
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We will analyze compartmental models in detail later to provide context for network models.

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- Directed
- . . .

Other important types of networks

The nodes don't have to be individuals. They can be communities.

- Airline network
- Connected communities
- Livestock movement
- . . .

Network definition

- A network is a collection of nodes which are joined into pairs by edges.
- Two nodes that are joined together are called neighbors. The number of neighbors a given node has is its degree, k.
- There is no real difference between the definitions of "network" and "graph".
- I will tend to use the terminology "partner" for neighbor and "partnership" for "edge" [the term "contact" is also commonly used but can be ambiguous].

Network Properties

There are a number of things we can measure:

- Degree distribution: $P(k)$, the proportion of nodes with degree k.

High degree nodes tend to be infected early and in turn infect more nodes. So the early growth is more affected by the presence of high-degree nodes than by the average degree.

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- Degree distribution: $P(k)$, the proportion of nodes with degree k.
- Clustering: frequency of short cycles [not common in sexual networks].

Clustering tends to slow the spread of a disease, but often does not significantly affect whether a disease occurs or how large it gets. Its role is reduced as typical degrees increase.

Network Properties

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- Degree distribution: $P(k)$, the proportion of nodes with degree k.
- Clustering: frequency of short cycles [not common in sexual networks].
- Partnership duration: Network may be dynamics, with partnerships changing in time. Individuals may enter/leave the population.

Changing partnerships reduces the effect of local "susceptible depletion"

More Network Properties

There are a number of things we can measure:

- Edge weights: some edges may have higher transmission probabilities than others.

Edge weights and many other effects are generally less significant (but what if weights inversely correlated with degree?)

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- Assortativity: Individuals may actively select similar partners. In particular, partners with similar degree.

Assortative mixing by degree tends to make it easier for a disease to get established because the core of high-degree nodes provides a good place to spread. However, it often reduces the total size of the epidemic because the low degree nodes tend to connect only to low degree nodes.

More Network Properties

There are a number of things we can measure:

- Edge weights: some edges may have higher transmission probabilities than others.
- Assortativity: Individuals may actively select similar partners. In particular, partners with similar degree.
- Modularity: some parts of the network may be more densely connected than others.

The existence of subcommunities may influence how a disease spreads (and when it is detected).

A preliminary glance at SIR disease in networks

- To give context to our first computer simulations, we take a preliminary look at SIR disease in a simple network.

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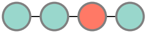
- To give context to our first computer simulations, we take a preliminary look at SIR disease in a simple network.
- We take a very simple network: 4 nodes in a line.
- We take a very simple SIR disease: in a time step nodes transmit to neighbors with probability p and then recover with immunity.

Modeling Disease Spread in a network



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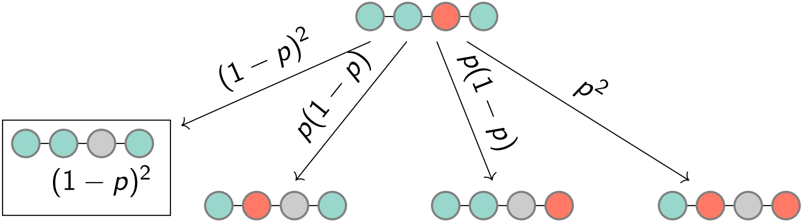

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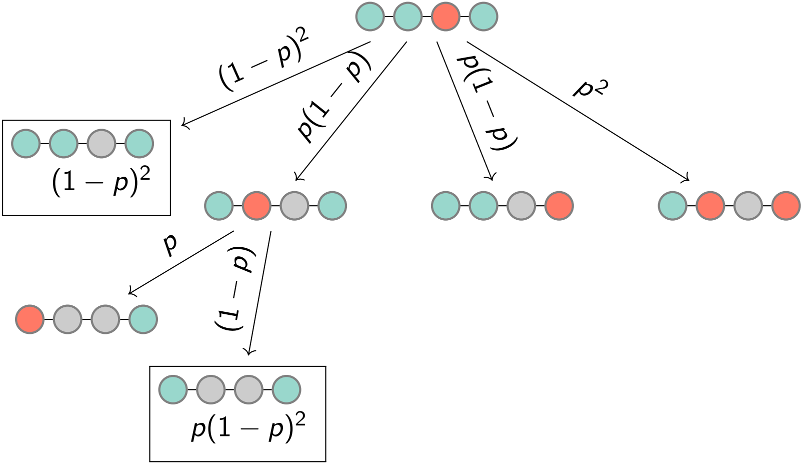

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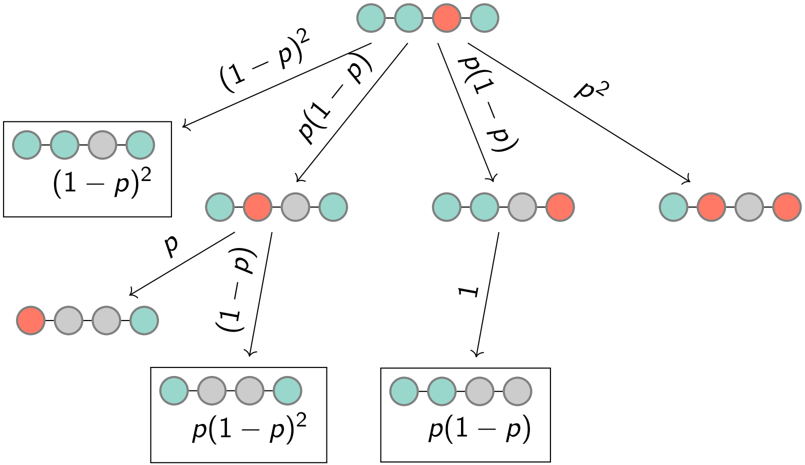

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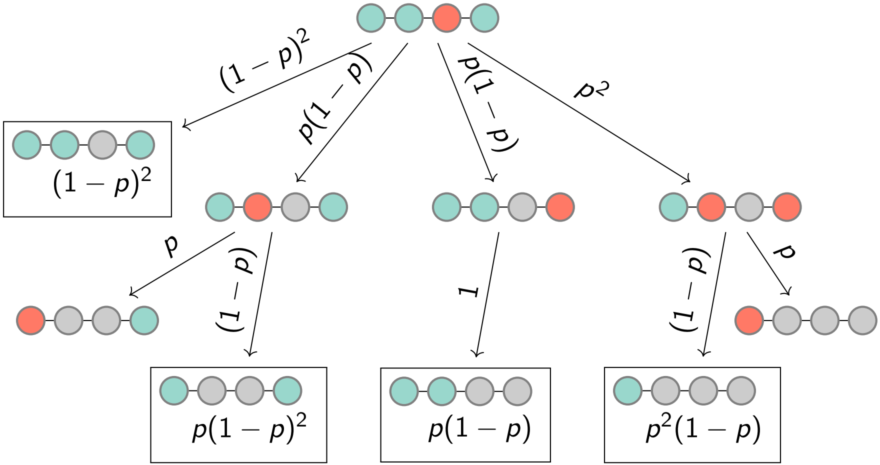

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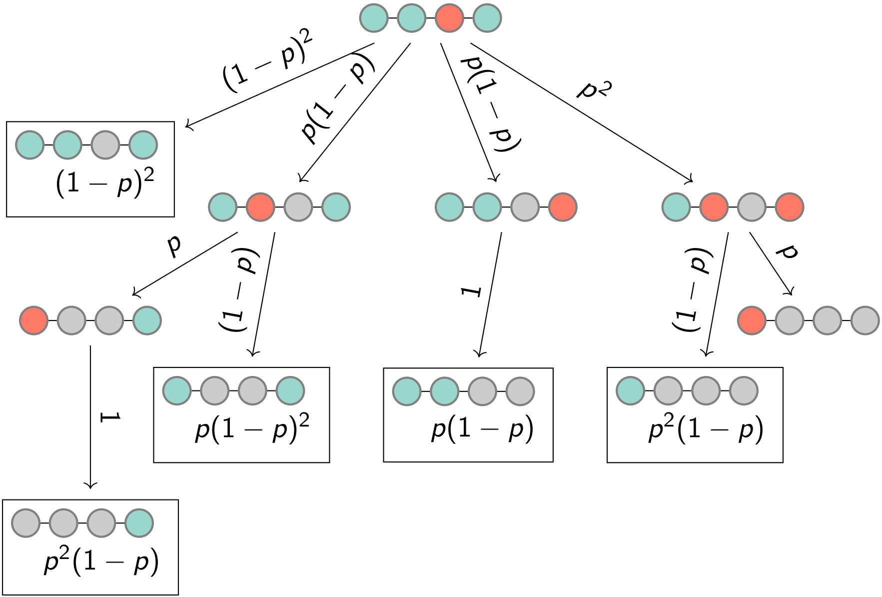

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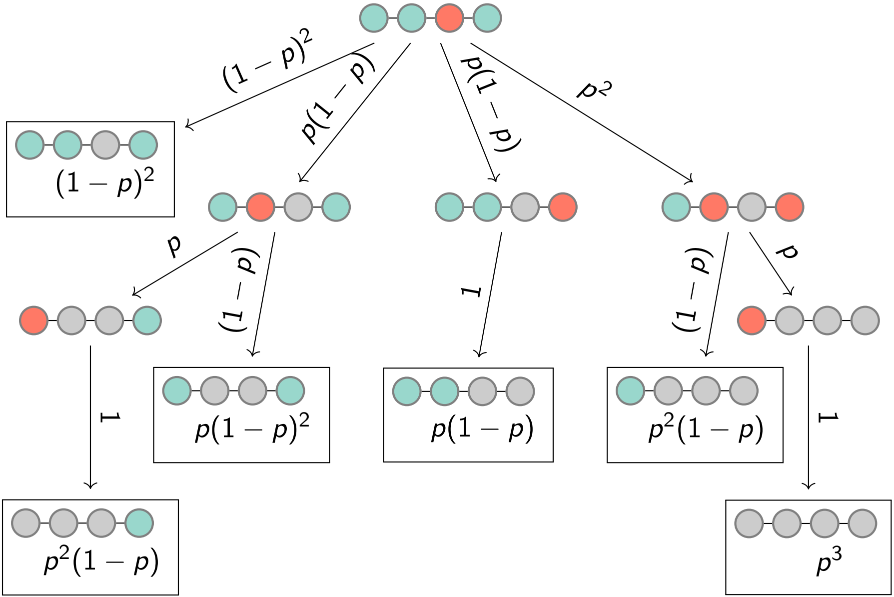
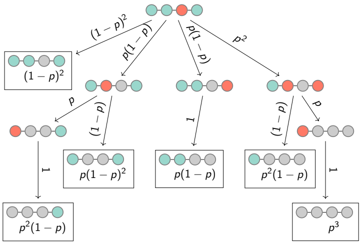


Alternative perspective



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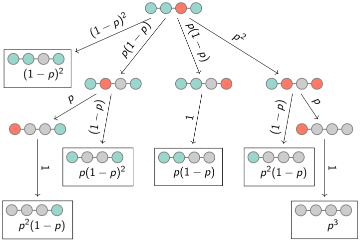
- 

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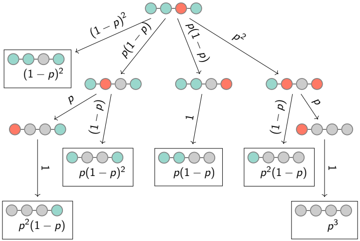
- 

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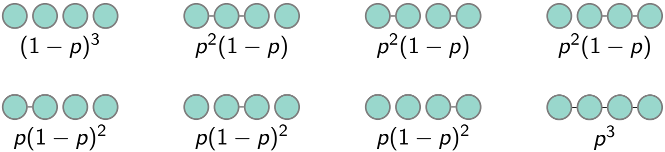
- 

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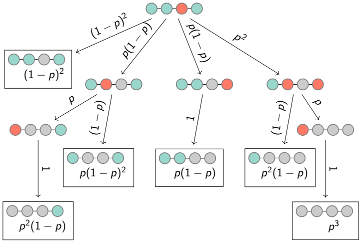
- 

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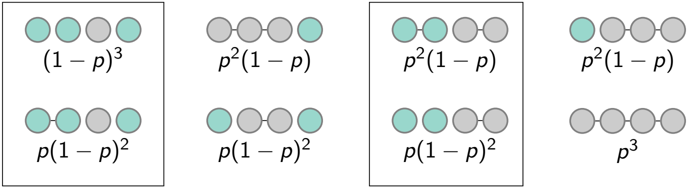
- 

Random networks

We rarely have exact data about a population's contact structure. Instead we have measurements of a few important features.

- We want to generate a random network that captures these properties.
- If these properties are the relevant properties, then disease spread in the simulated network will accurately reproduce dynamics in the real population.
- Ideally we can analytically predict the dynamics in the model network.
- An interesting challenge [outside our scope] is finding ways to generate random networks with specified properties which are analytically tractible.

Common random network models

- Small World networks
- Barabási-Albert
- Configuration Model
- Exponential Random Graph Model [ERGM]

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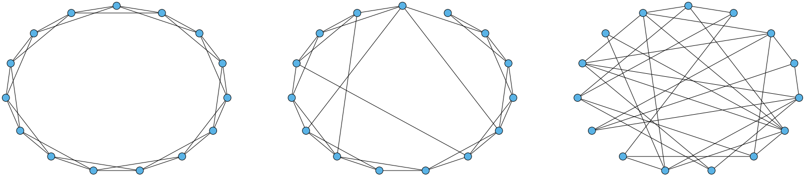
Small-world networks



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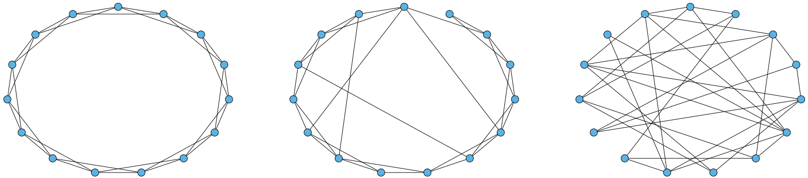

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- Rewire a fraction p of the edges.
- The resulting network has short typical path lengths and high "clustering".

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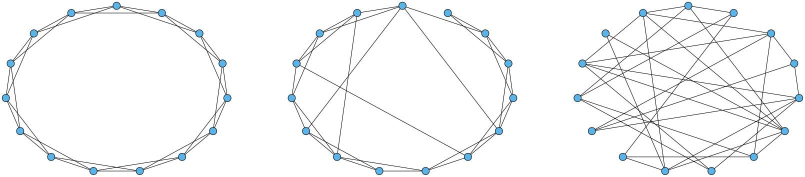

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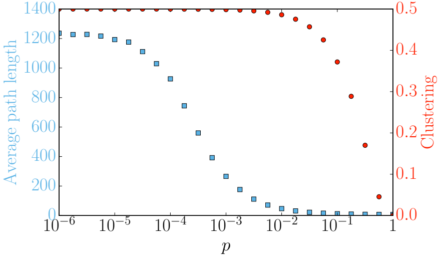

Epidemics in Small-world networks: theory vs simulation

(theory to come later)
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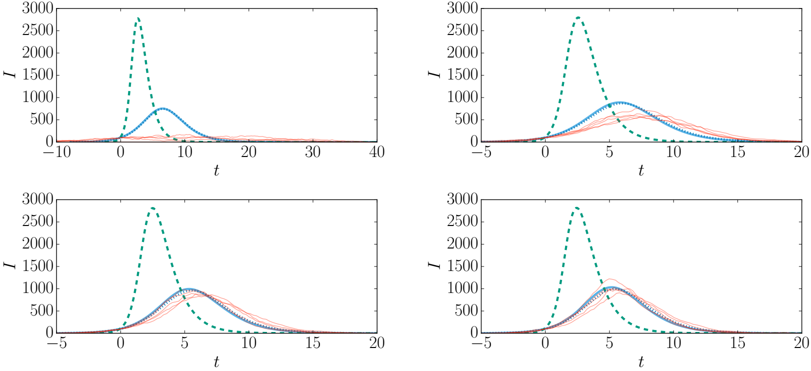

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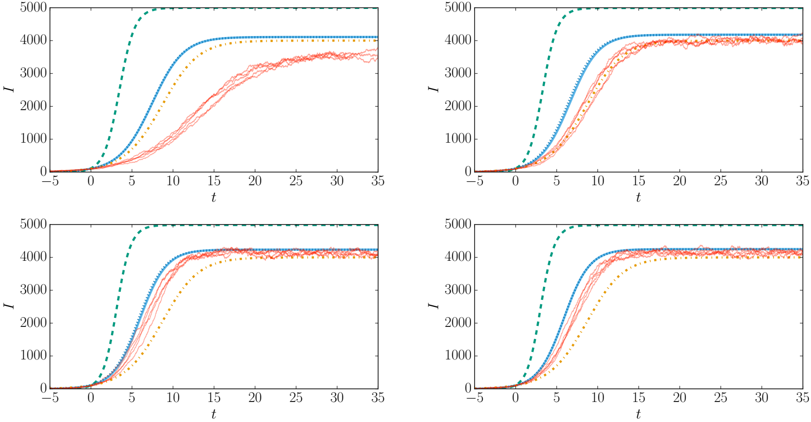
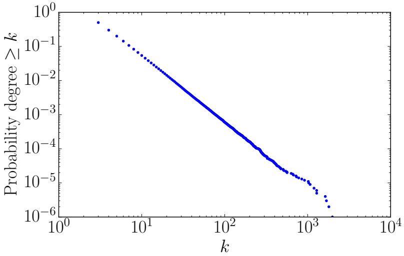


Barabási–Albert networks

- Start with $m + 1$ nodes all connected to each other.
- Add a node, connect it to m previously existing nodes
- Repeat, each time selecting the previously existing nodes with probability proportional to their degree.



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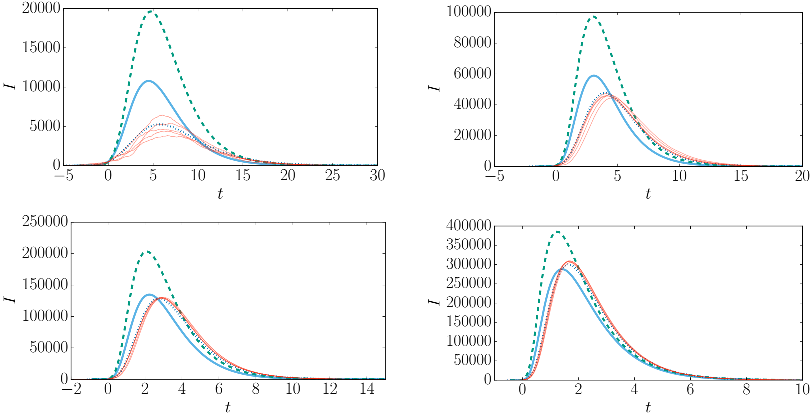

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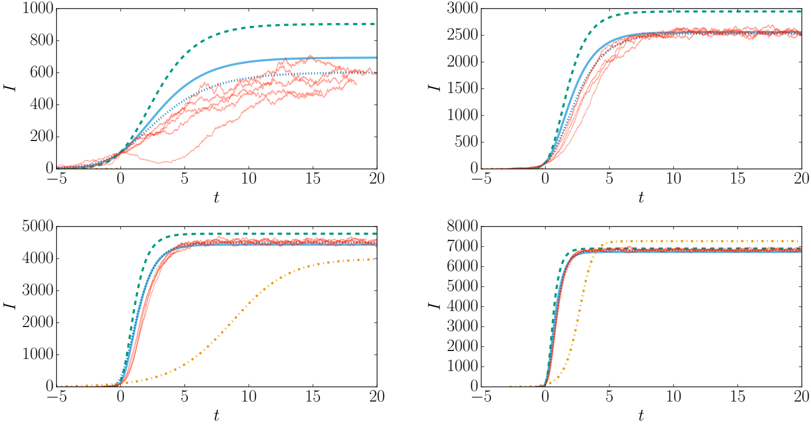

Configuration Model

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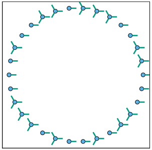

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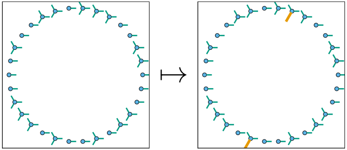

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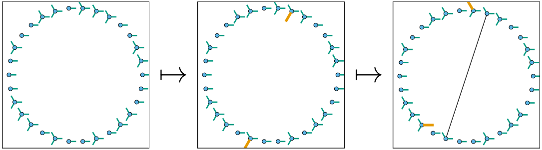

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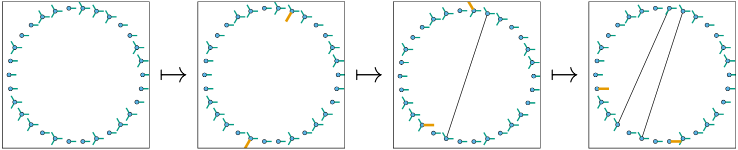

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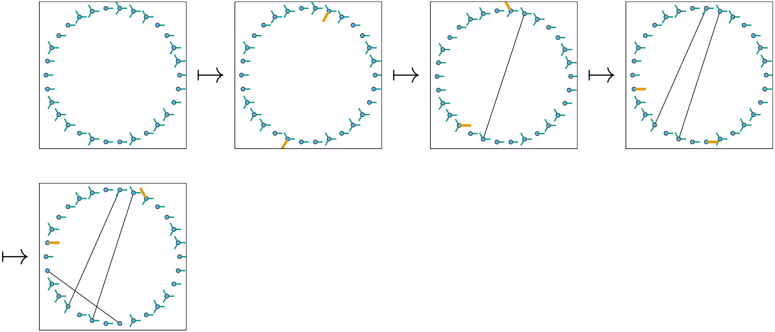

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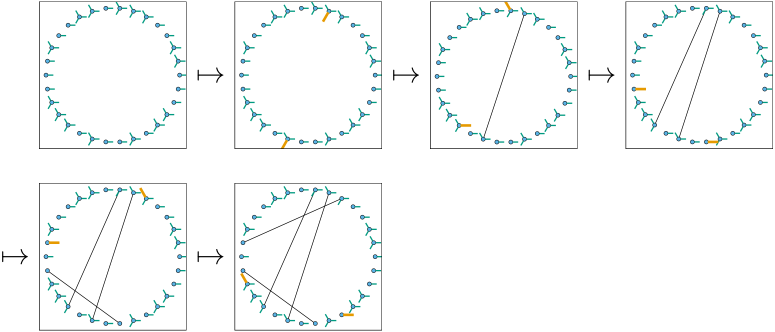

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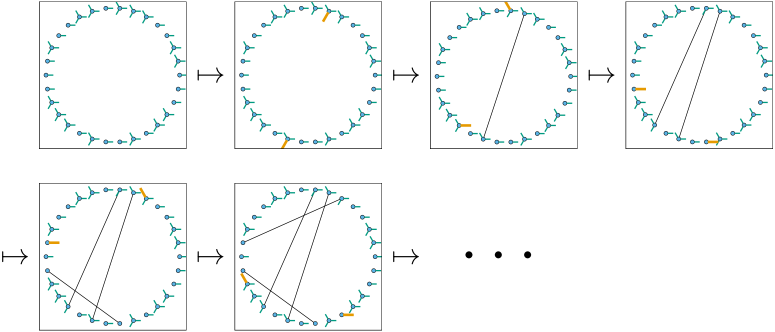

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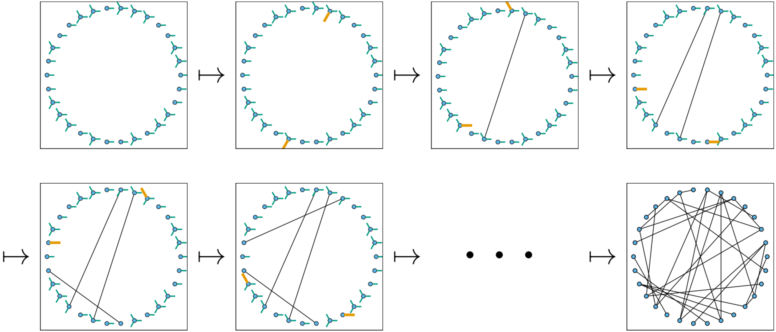

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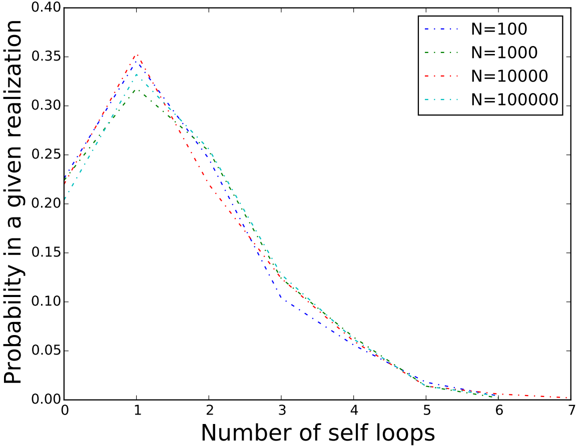
What can go wrong?
Create the graph at the last step:
$L = [7, 6, 5, 6, 2, 2, 4, 7, 1, 3, 6, 5, 4, 5]$

Density of "short" cycles is small for large N



Configuration model networks, all degrees equal 4.

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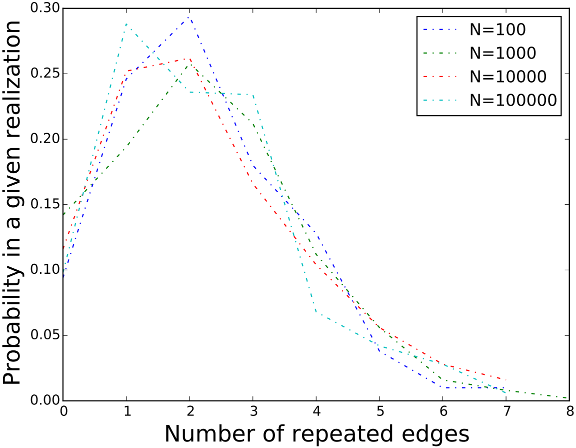

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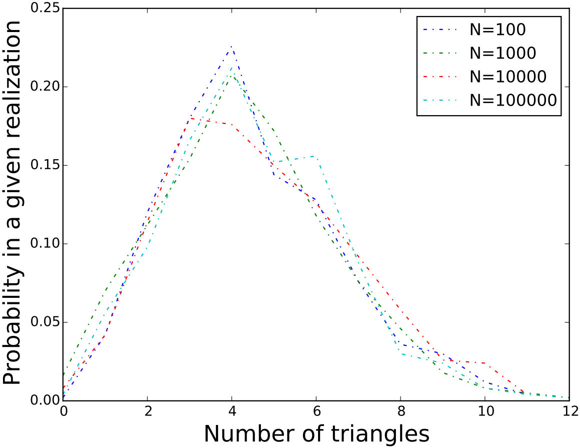
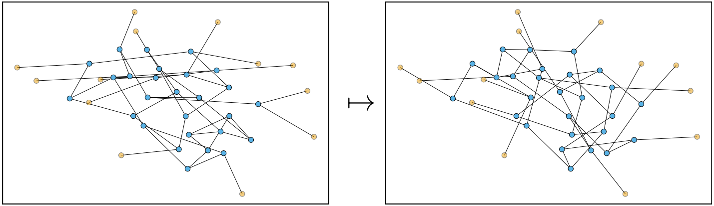


Configuration model networks, all degrees equal 4.

“Annealed” Configuration Model



- The annealed network version assumes that at every moment the network looks like a Configuration model network.
- However, at every moment, an individual changes all of its partners.
- In practice this is appropriate if partnerships are so short or disease transmission so rare that an individual is unlikely to ever transmit to the same individual twice or transmit back to its infector.
- People who use the term “annealed network” call the static version a “quenched network”.

Exponential Random Graph Model (ERGM)

- Given some vector of parameters θ and statistical measurements s on a graph G, choose G with probability proportional to
$$\exp[\theta \cdot s]$$
- Generally a network is chosen through MCMC.
- Computational power significantly constrains the network size

Do your friends have more friends than you do (on average)?

Given a configuration model network G with a heterogeneous degree distribution:

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Given a configuration model network G with a heterogeneous degree distribution:

If we choose a random individual in a configuration model network, is its expected degree

1. higher
2. lower
3. the same
4. depends on the degree distribution

than the expected degree of a random partner?

Size Bias

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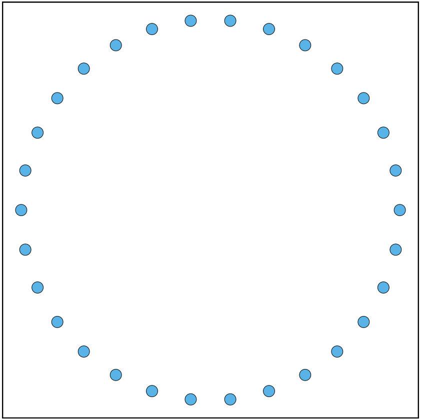

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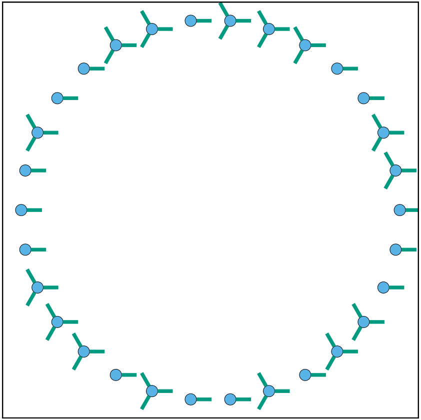

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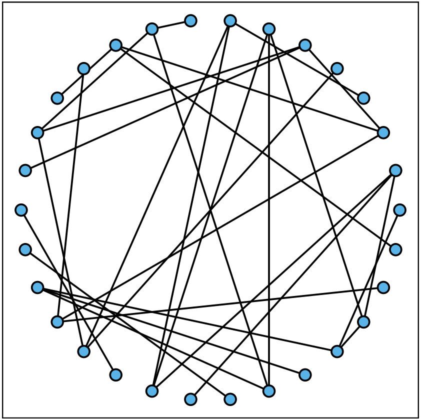

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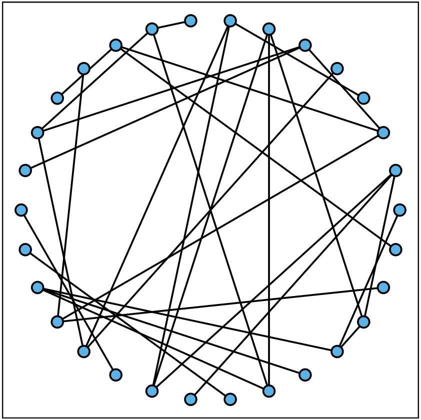

The probability a partner has degree k is $P_n(k) = kP(k)/\langle K \rangle$.

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- A random individual has degree k with probability $P(k)$
- What about a random partner? What is $P_n(k)$, the probability a partner has degree k?

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- A partner's partner also has degree k with probability $P_n(k)$.

Size Bias

I cannot stress enough that if $P(k)$ is the probability a random individual has k partners, then

$$P_n(k) = kP(k) / \langle K \rangle$$

is the probability a random partner has k partners.

Social networks

- facebook
- linkedin
- twitter
- . . .

These may be more appropriate for spread of ideas or opinions.

Contact networks

- The network of physical interactions.
- Often highly clustered.
- Appropriate for respiratory diseases.
- Sometimes measured by giving people devices that measure physical proximity.

Sexual networks

- Appropriate for sexually transmitted diseases.
- Often low clustering.
- Often highly heterogeneous.
- Transient partnerships may play a large role.

Location–Location networks

- Cities connected by travel of people between them [spread of H1N1, Ebola].
- Farms connected by movement of animals [foot and mouth].
- Habitats connected by bird migrations [West Nile].

Empirical networks

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- Romantic networks [10]

Sample location–location networks

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- Seasonal population movements [16]: study of seasonal population movements for malaria control (phone data, census, satellite imagery).

Agent-based models

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- South Africa: Simulation by George Seage’s group at HSPH for HIV transmission ($\approx$ 6 million?)

Review

- Disease dynamics depend on immune response and population structure
- Simple SIR disease can be modeled through percolation.
- We will focus on "Configuration model" populations and hope that they are close enough to real populations.
- There is a size-biasing effect by which higher degree nodes are more likely to be infected early on and then transmit to more nodes.

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