# Epidemics in Networks
# Small network examples

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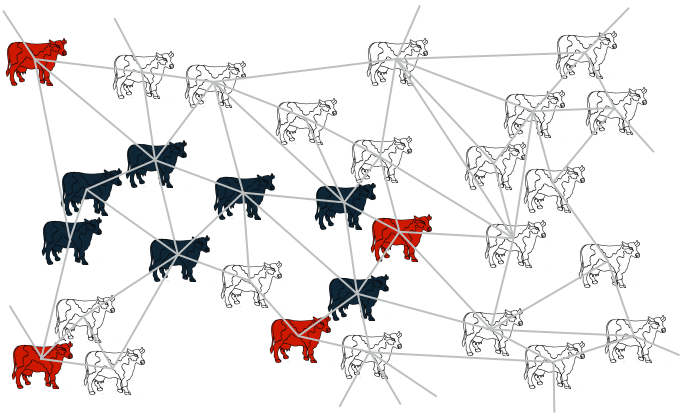
## SIR disease

Take Reed–Frost/chain–binomial model:

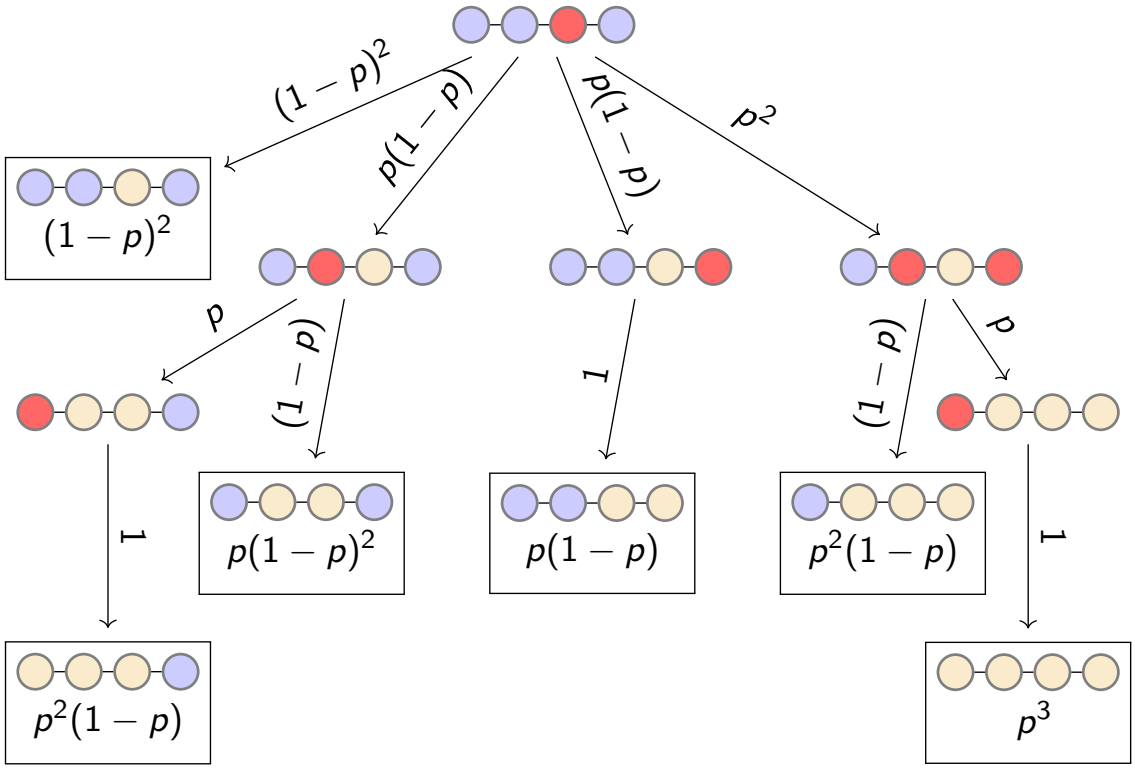
- Assume $u$ susceptible, with $n$ infected partners at time $t$.
- Each transmits independently with probability $p$.
- Then at $t+1$, $u$ is infected with probability $1-(1-p)^n$.
- After one timestep infected, nodes recover.



## Example



## Example



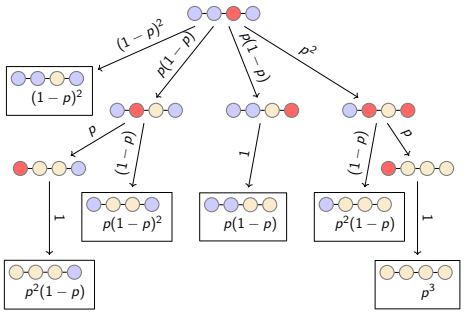


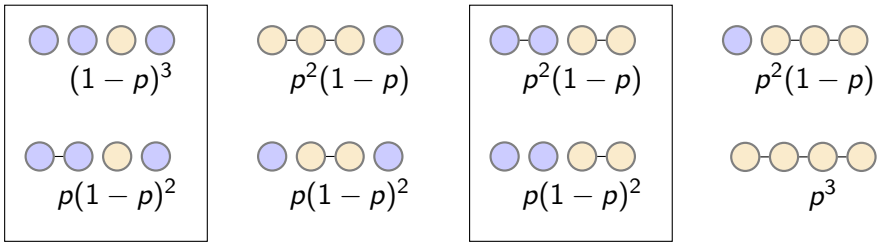

## Percolation analogy

Let's think about simulating this process.

- I use Tom as a random number generator.
- I put him under pressure to quickly say "yes" or "no" each time I ask whether an edge transmits.
- He has the network in advance, and he cheats!!
  - He erases each edge in his copy with probability $1 - p$.
  - When asked about an edge, if it's in his copy, he says "yes" otherwise "no".
- On the basis of one simulation, could I get any evidence he's cheating?

## Alternative perspective

- 


  At each step, if there is an edge to cross, it is crossed with probability $p$. No edge is ever crossed twice.
- It is equivalent to decide in advance whether the edges will be crossed if encountered.
- 




## Percolation Equivalence

The following processes produce Indistinguishable output:

- Normal Epidemic Simulation:
  - Take a network.
  - Choose an initial infected individual.
  - Trace the disease spread, transmitting with probability $p$ at each step.
- Percolation-based simulation:
  - Take a network.
  - Generate a new network, with each edge existing with probability $p$, the probability the edge will transmit if given the chance. (Percolation!)
  - Choose an initial infected individual.
  - Trace the disease spread, transmitting if the edge is in the new network.

## Major consequence of percolation

The eventually infected nodes are exactly the nodes that are in the same component as the index case.
So the size distribution is equal to the distribution of sizes of components in percolated networks.



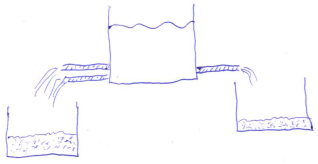
## Continuous time

- We begin epidemics with a single infected node.
- It recovers at rate $\gamma$ (which we can assume is 1)
- It transmits independently to each partner with rate $\beta$.

## Swimming pool analogy

I'll refer to the "swimming pool analogy" several times.

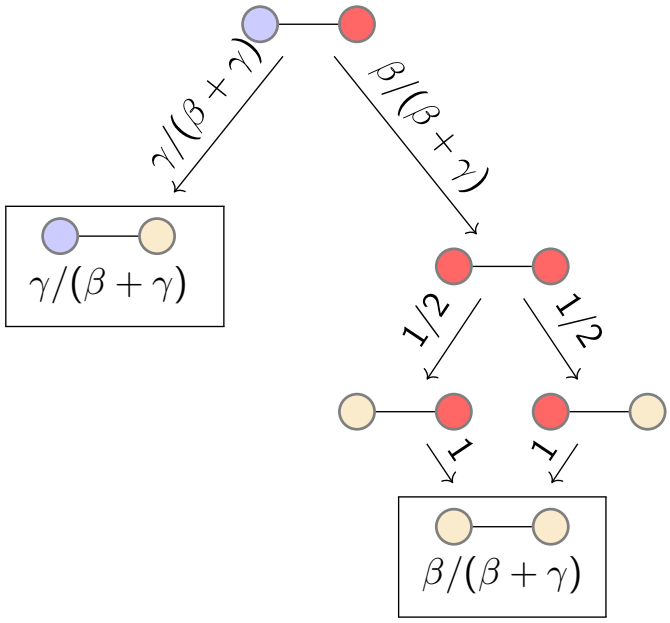
- Imagine that there is a source of water, from which two swimming pools are filled.



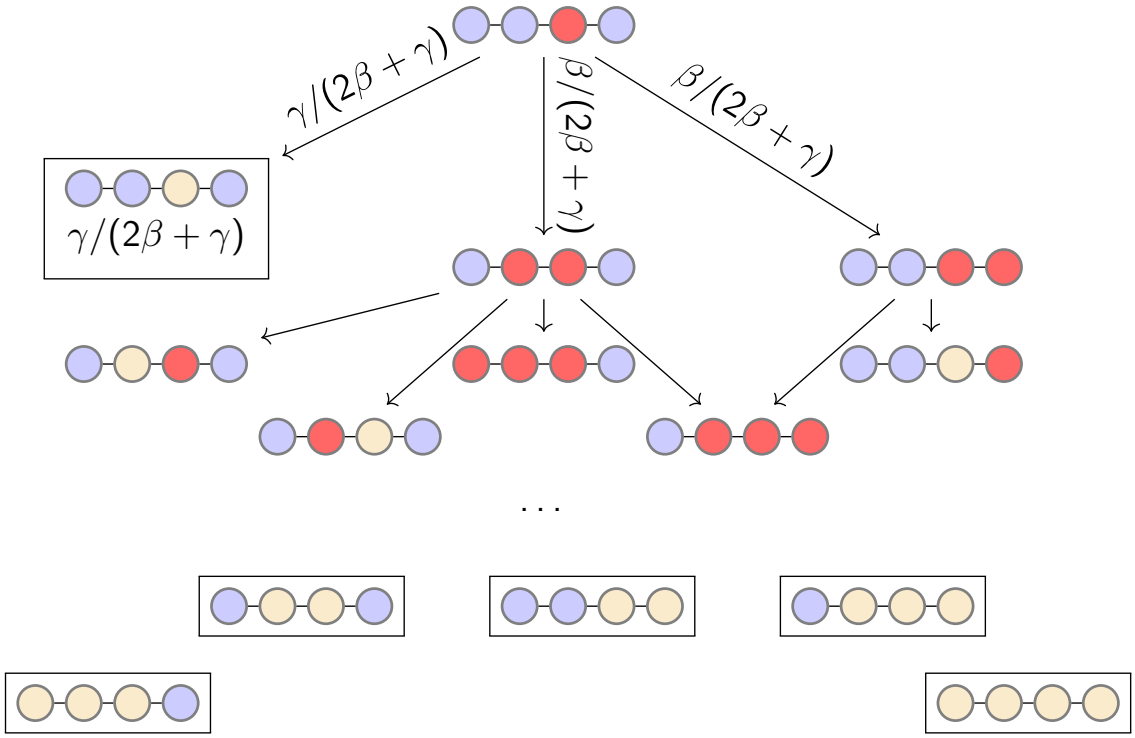
- If both pools start empty, and at all times one receives $c$ times as much flow as the other, then it will always have $c$ times as much water in it.
- If the source is additionally finite, then when all the water has left the source, the first will have $c/(1+c)$ of the initial water and the second will have $1/(1+c)$ of the initial water.



## Transmission Probability




The probability an edge will transmit infection is $\beta/(\beta+\gamma)$. However, transmission across two edges from the same node are not independent. They both depend on the duration of infection of the same node.






## Directed Percolation Equivalence

The following processes produce Indistinguishable output:

- Normal Epidemic Simulation:
  - Take a network.
  - Choose an initial infected individual.
  - Allow edges to transmit until the random time the individual recovers.
- Percolation-based simulation:
  - Take a network.
  - Generate a new directed network:
    - For each individual $u$, assign a duration $d$ of infection.
    - For each edge from $u$, determine delay $\tau$ until transmitting.
    - If $\tau < d$, place directed edge into network with associated time.
  - Choose an initial infected individual.
  - Trace the disease spread, transmitting after given time if an edge is in the new network.

## More comments on directed percolation

- Directed percolation can be used more generally when there are other sources of heterogeneity in infectiousness and/or susceptibility.
- The eventually infected nodes are exactly those nodes in the out-component of the index case.
- The probability a random node is infected follows from the size of its in-component.



SIR

SIS

Moving towards larger networks

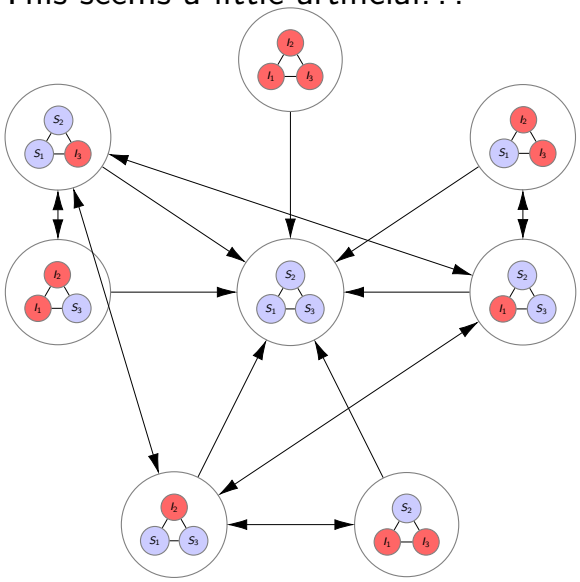
## SIS in discrete time

- There is some freedome in how we choose to model this. We're forcing a continuous process into a discrete framework.
- Nodes are infected for one time step, then become susceptible.
- A susceptible node with $n$ infected neighbors is infected with probability $1 - (1 - p)^n$.
- If Tom were to cheat in this case, I would be able to tell, because the same edge would transmit over and over.
- There is no mapping between SIS and percolation.
- Can an infected node remain infected in the next time step if a neighbor transmits to it?



## Example

This seems a little artificial...

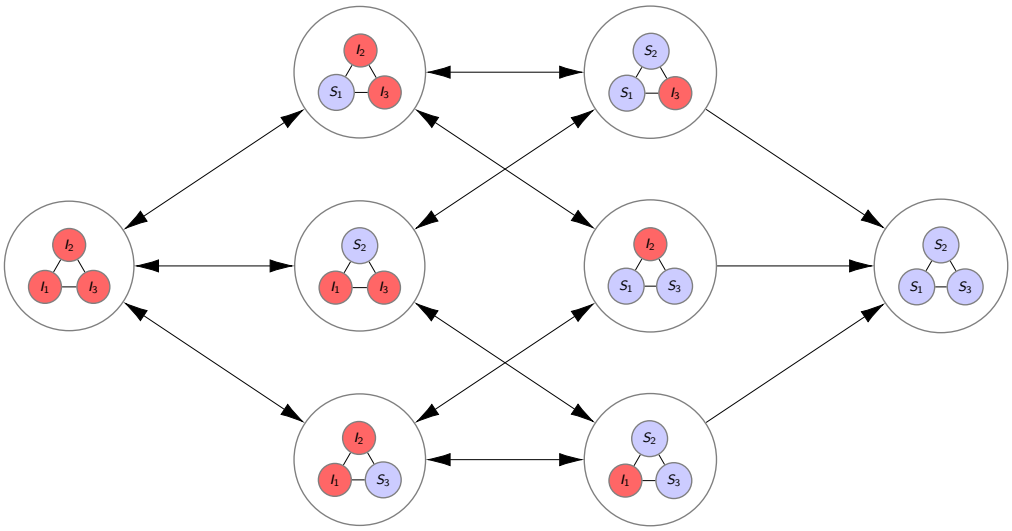


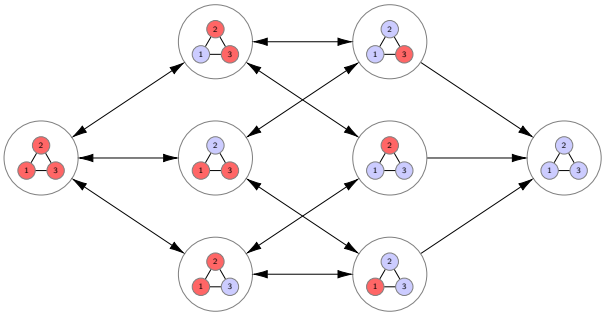
## SIS in continuous time

- Infected nodes recover (to susceptible) at rate $\gamma$.
- Edges between susceptible and infected nodes transmit at rate $\beta$.
- No relation to directed percolation.



## Example





$$
\begin{aligned}
\dot{X}_{SSS} &= \gamma(X_{SSI} + X_{SIS} + X_{ISS}),\\
\dot{X}_{SSI} &= \gamma(X_{SII} + X_{ISI}) - (2\beta + \gamma)X_{SSI},\\
\dot{X}_{SIS} &= \gamma(X_{SII} + X_{IIS}) - (2\beta + \gamma)X_{SIS},\\
\dot{X}_{ISS} &= \gamma(X_{ISI} + X_{IIS}) - (2\beta + \gamma)X_{ISS},\\
\dot{X}_{SII} &= \gamma X_{III} + \beta(X_{SSI} + X_{SIS}) - 2(\beta + \gamma)X_{SII},\\
\dot{X}_{ISI} &= \gamma X_{III} + \beta(X_{SSI} + X_{ISS}) - 2(\beta + \gamma)X_{ISI},\\
\dot{X}_{IIS} &= \gamma X_{III} + \beta(X_{SIS} + X_{ISS}) - 2(\beta + \gamma)X_{IIS},\\
\dot{X}_{III} &= -3\gamma X_{III} + 2\beta(X_{SII} + X_{ISI} + X_{IIS}).
\end{aligned}
$$



- Way too many equations for these small networks.
- We can take advantage of some symmetries.
- Set

$$
\begin{aligned}
x_0 &= X_{SSS}\\
x_1 &= X_{ISS} + X_{SIS} + X_{SSI}\\
x_2 &= X_{SII} + X_{ISI} + X_{IIS}\\
x_3 &= X_{III}
\end{aligned}
$$

- Because of symmetries:

$$
\begin{aligned}
\dot{x}_0 &= \gamma x_1,\\
\dot{x}_1 &= 2\gamma x_2 - \gamma x_1 - 2\beta x_1,\\
\dot{x}_2 &= 2\beta x_1 - 2\gamma x_2 - 2\beta x_2 + 3\gamma x_3,\\
\dot{x}_3 &= 2\beta x_2 - 3\gamma x_3.
\end{aligned}
$$

## Larger networks

- It will be hopeless to find equations for all possible states: $2^N$ for SIS and $3^N$ for SIR.
- Instead we can try to calculate "population-scale" quantities such as proportion infected.
- Perhaps surprisingly, SIR is easier to work with. Although there are more states, there are fewer transitions possible.
- Working with SIS will require more dubious assumptions.