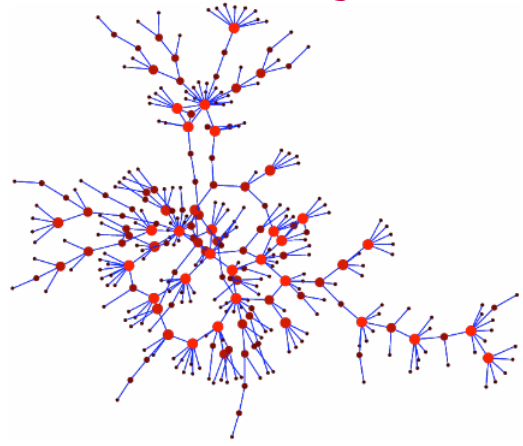
01RMHNG–03RMHPF–01RMING
Network Dynamics
Week 8
Epidemics and Pairwise Interacting Network Systems



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The birth of epidemic models

1927: Two Sottish biochemists Kermack and McKendrick propose a general mathematical model for the diffusion of epidemics. Most of the models used today are derived from Kermack and McKendrick's one.

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1927: Two Sottish biochemists Kermack and McKendrick propose a general mathematical model for the diffusion of epidemics. Most of the models used today are derived from Kermack and McKendrick's one.

- Population divided into groups:
  - S susceptible people that are currently healthy and that can be infected
  - I infected people that can transmit the infection
  - R removed people that had the infection but that can no longer infect (because immune, or isolated or dead)
- Mechanism that describes how contagion takes place (pairwise interaction) and how a person becomes removed.

The most used epidemics models are known for their acronyms:

SI, *SIS*, *SIR*

SI epidemics

- (undirected) graph $\mathcal{G} = (\mathcal{V}, \mathcal{E}, W)$
- parameter $\beta > 0$
- nodes $i \in \mathcal{V}$ have state $X_i(t) \in \{S, I\}$

SI epidemics

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- links $(i, j) \leftrightarrow$ independent rate-βW_{ij} Poisson clocks

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- if link (i,j)-th clock ticks at time t then

$$X_i(t^-) = S \quad X_j(t^-) = I \qquad \Longrightarrow \qquad \underbrace{X_i(t) = I}_{\text{contagion}} \quad X_{-i}(t) = X_{-i}(t^-)$$

otherwise $X(t) = X(t^-)$

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- if node i-th clock ticks at time t then

$$X_i(t^-) = I \qquad \Longrightarrow \qquad \underbrace{X_i(t) = S}_{\text{recovery}} \quad X_{-i}(t) = X_{-i}(t^-)$$

otherwise $X(t) = X(t^-)$

SIR epidemics

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- if node i-th clock ticks at time t then

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otherwise $X(t) = X(t^-)$

- if node i-th clock ticks at time t then

$$X_i(t^-) = I \qquad \Longrightarrow \qquad \underbrace{X_i(t) = R}_{\text{recovery}} \quad X_{-i}(t) = X_{-i}(t^-)$$

$$X_i(t^-) = R \qquad \Longrightarrow \qquad \underbrace{X_i(t) = S}_{\text{loss of immunity}} \quad X_{-i}(t) = X_{-i}(t^-)$$

otherwise $X(t) = X(t^-)$

Voter model

Pairwise interacting models are used in other contexts

- graph $\mathcal{G} = (\mathcal{V}, \mathcal{E}, W)$, parameter $\beta > 0$
- nodes $i \in \mathcal{V}$ have state $X_i(t) \in \mathcal{A}$ (*opinions*)

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The stochastic update law:

- links $(i, j) \leftrightarrow$ independent rate-βW_{ij} Poisson clocks
- if link (i, j)-th clock ticks at time t then

$$\underbrace{X_i(t) = X_j(t^-)}_{\text{copy}} \quad X_{-i}(t) = X_{-i}(t^-)$$

Evolutionary dynamics

- (undirected) graph $\mathcal{G} = (\mathcal{V}, \mathcal{E}, W)$, parameter $\beta > 0$
- nodes $i \in \mathcal{V}$ have state $X_i(t) \in \{0, 1\}$ (*competing species*)
- $f_0, f_1 \in [0, 1]$ (*fitness*)

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- $f_0, f_1 \in [0, 1]$ (*fitness*)

The stochastic update law:

- links $(i, j) \leftrightarrow$ independent rate-βW_{ij} Poisson clocks
- if link (i, j)-th clock ticks at time t then

with probability $f_{X_j(t^-)}$ $\quad \underbrace{X_i(t) = X_j(t^-)}_{\text{invasion}} \quad X_{-i}(t) = X_{-i}(t^-)$

with probability $1 - f_{X_j(t^-)}$ $\quad X(t) = X(t^-)$

Pairwise interacting network systems

- (undirected) graph $\mathcal{G} = (\mathcal{V}, \mathcal{E}, W)$, parameter $\beta > 0$
- nodes $i \in \mathcal{V}$ have state $X_i(t) \in \mathcal{A}$
- *mutation kernel*: stochastic matrix $\psi \in \mathbb{R}^{\mathcal{A} \times \mathcal{A}}$
- *interaction kernel*: stoc. mat. $\varphi(c) \in \mathbb{R}^{\mathcal{A} \times \mathcal{A}}$, $c \in \mathcal{A}$

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- nodes equipped with rate 1 clocks, edges with rate-βW_{ij} clocks
- if link (i,j)-th clock ticks at time t then

$$X_i(t^-) = a \quad X_j(t^-) = c \qquad \Longrightarrow \qquad \underbrace{X_i(t) = b}_{\text{interaction}} \text{ with prob. } \varphi_{a,b}(c)$$

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- if node i-th clock ticks at time t then

$$X_i(t^-) = a \qquad \Longrightarrow \qquad \underbrace{X_i(t) = b}_{\text{mutation}} \text{ with prob. } \psi_{a,b}$$

Pairwise interacting network systems: examples

- SI Epidemics, $\mathcal{A} = \{S, I\}$

$$\psi = \begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix} \qquad \varphi(S) = \begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix} \qquad \varphi(I) = \begin{bmatrix} 0 & 1 \\ 0 & 1 \end{bmatrix}$$

- SIS Epidemics, $\mathcal{A} = \{S, I\}$

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- SIR Epidemics, $\mathcal{A} = \{S, I, R\}$

$$\psi = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 0 & 1 \\ 0 & 0 & 1 \end{bmatrix} \qquad \varphi(S) = \varphi(R) = Id \qquad \varphi(I) = \begin{bmatrix} 0 & 1 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix}$$

Pairwise interacting network systems: examples

- Voter model

$$\psi = Id \qquad \varphi(c) = \mathbb{1}(\delta^{(c)})^T$$

- Evolutionary dynamics

$$\psi = Id \qquad \varphi(c) = (1 - f_c)I + f_c \mathbb{1}(\delta^{(c)})^T$$

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$X(t)$ cont.-time Markov chain over *configuration space* $\mathcal{X} = \mathcal{A}^{\mathcal{V}}$ with transition rates

$$\Lambda_{xy} = \begin{cases} 0 & \text{if} \quad x_i \neq y_i \text{ for more than one } i \\ \psi_{x_i y_i} + \beta \sum_j W_{ij} \varphi_{x_i y_i}(x_j) & \text{if} \quad x_i \neq y_i \text{ and } x_{-i} = y_{-i} \end{cases}$$

$\mathcal{G}_\Lambda$ graph describing the non-zero transition probability rates in $\mathcal{X}$.

Extensions: *heterogenous nodes* with different mutation and interaction kernels.

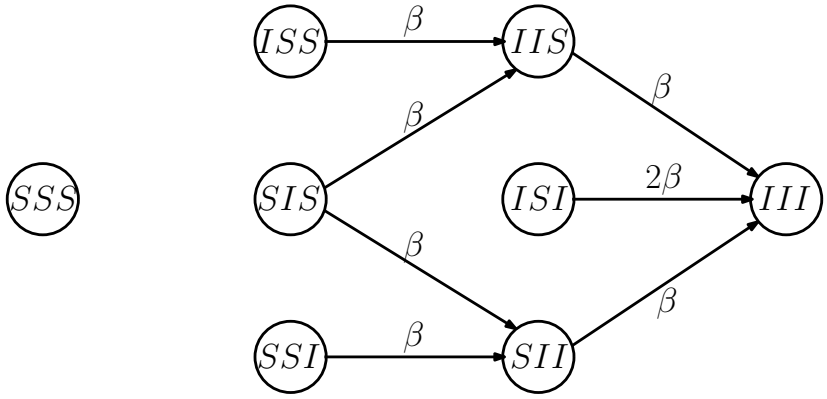
Warning: two graphs not to be confused!

- The graph $\mathcal{G}$ describing the interaction among nodes
- The graph $\mathcal{G}_\Lambda$ in the configuration space

Example:

$\mathcal{G}$

The corresponding $\mathcal{G}_\Lambda$ for the SI epidemics model



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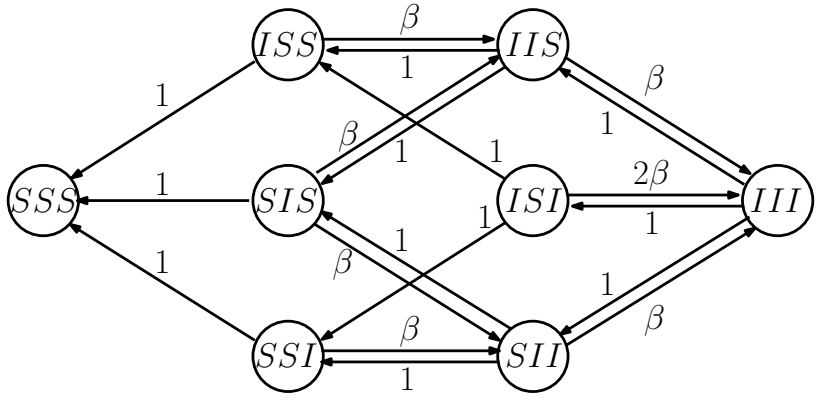

Absorbing configurations

$\mathcal{G} = (\mathcal{V}, \mathcal{E}, W)$ connected, $\beta > 0$

In all the examples considered, $X(t)$ is not ergodic (e.g. $\mathcal{G}_\Lambda$ is not connected). There exist absorbing configurations:

- SI Epidemics: $\{\text{absorbing config.}\} = \{S\mathbb{1}, I\mathbb{1}\}$
- SIS Epidemics: $\{\text{absorbing config.}\} = \{S\mathbb{1}\}$
- SIR Epidemics: $\{\text{absorbing config.}\} = \{S, R\}^{\mathcal{V}}$
- Voter model, Ev. Dyn.: $\{\text{absorbing config.}\} = \{c\mathbb{1} : c \in \mathcal{A}\}$

Fact: from every initial configuration, there exists a walk in the configuration graph leading to an absorbing configuration (exercise)

Consequence: with probability 1 in finite time, the process $X(t)$ will be absorbed in one of the absorbing configurations

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Questions:

- expected absorbing time for SI and SIS
- absorbing probabilities for SIR, voter and evolutionary dynamics

For general graphs the computation or estimation of most of these quantities is a challenging problem.

Binary Pairwise Interacting Systems

- $\mathcal{A} = \{0, 1\}$, $\beta > 0$, $\varphi_{ab}(a) = 0 \ \forall a \neq b \in \{0, 1\}$, $\mathcal{G} = (\mathcal{V}, \mathcal{E}, W)$
- $N(t) = \sum_i X_i(t) =$ number of 1's

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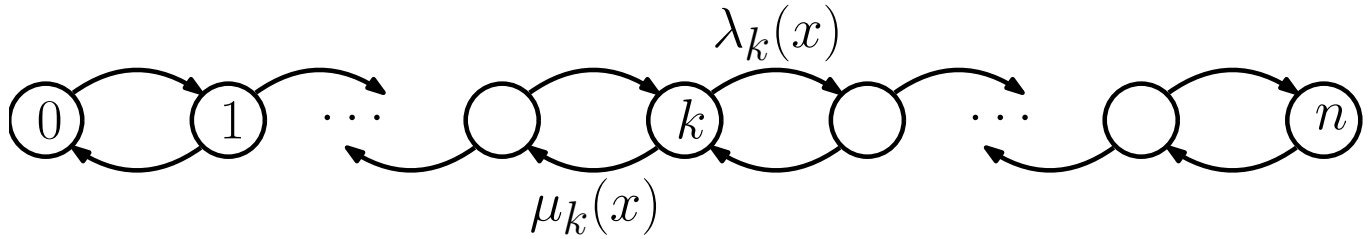
- $N(t) = \sum_i X_i(t) =$ number of 1'snot a Markov chain in general:



$$\lambda_k(x) = (n-k)\psi_{0,1} + \zeta_+(x)\beta\varphi_{01}(1) \qquad \mu_k(x) = k\psi_{1,0} + \zeta_-(x)\beta\varphi_{10}(0)$$

depend on both k and active in- and out-boundaries:

$$\zeta_+(x) = \sum_{i,j} W_{ij}(1 - x_i)x_j, \qquad \zeta_-(x) = \sum_{i,j} W_{ij}x_i(1 - x_j)$$

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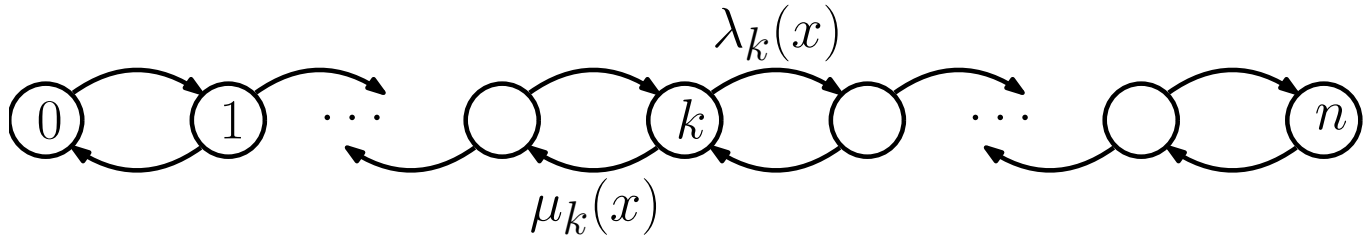

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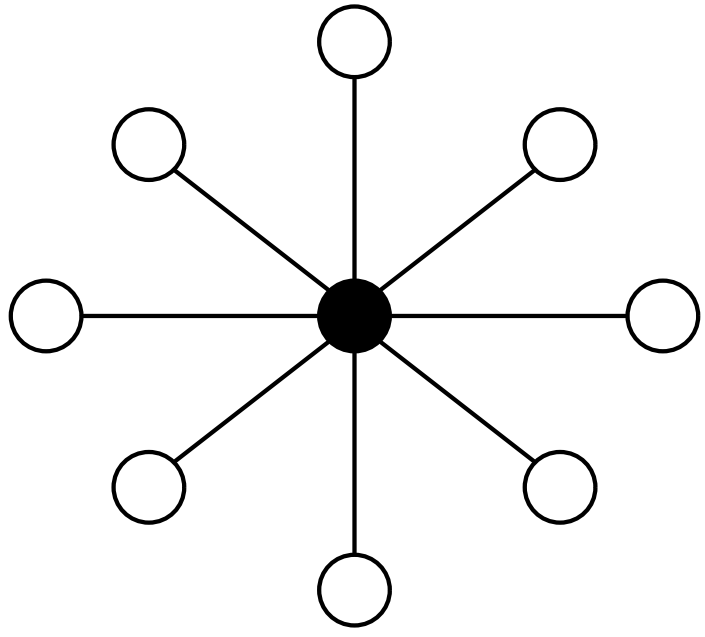
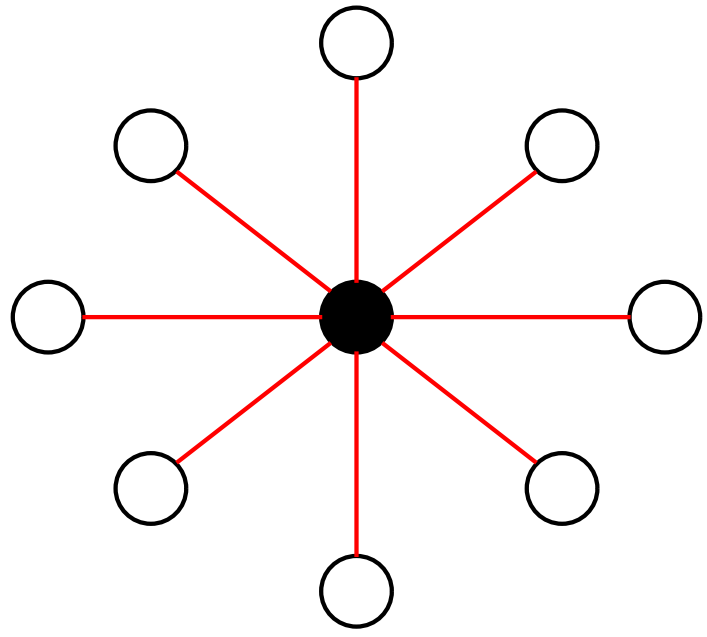
- $N(t)$ birth-and-death chain in those special cases where $\zeta_+(x)$, $\zeta_-(x)$ are function of $k = \sum_i x_i$
- E.g., $\mathcal{G} = K_n$ complete $\Longrightarrow \zeta_+(x) = \zeta_+(x) = k(n-k)$

Absorbing time for SI on the star graph



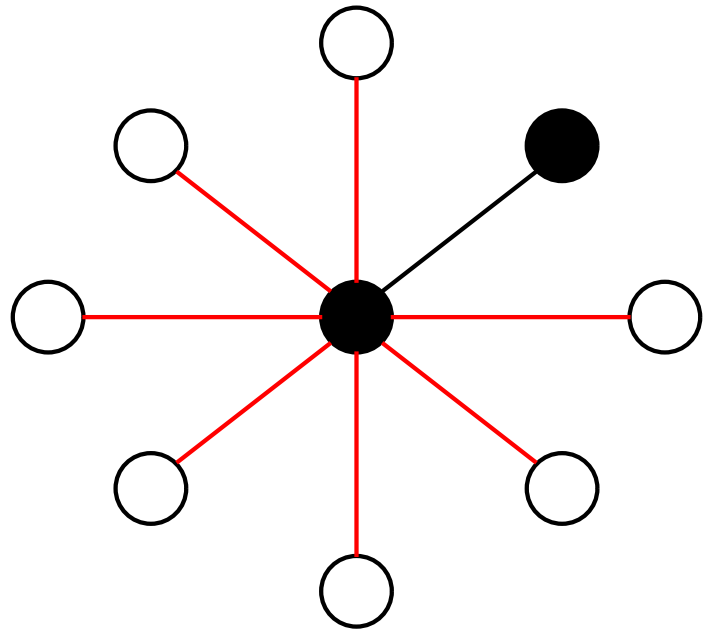
- Star graph with only center node initially infected: $N(0) = 1$

Absorbing time for SI on the star graph



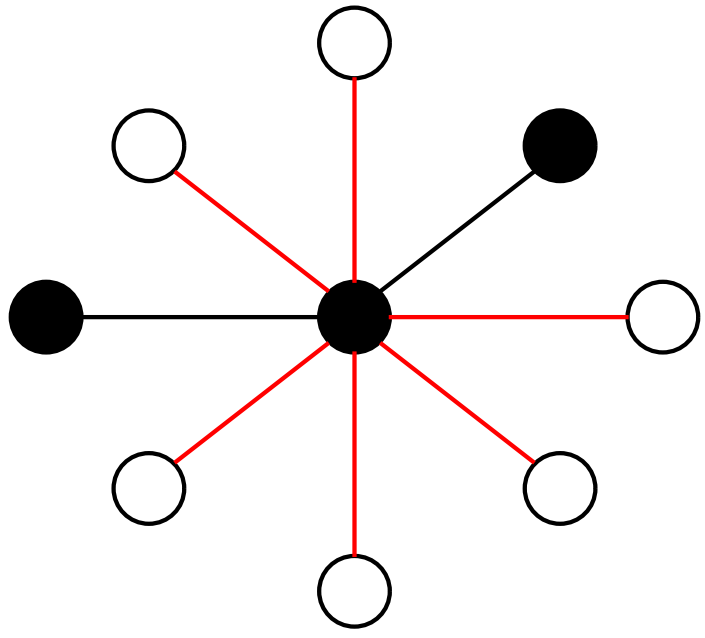
- $N(t) = 1$
- active boundary: $\zeta_+(X(t)) = n - 1$
- Expected time to next infection $1/(n-1)\beta$

Absorbing time for SI on the star graph



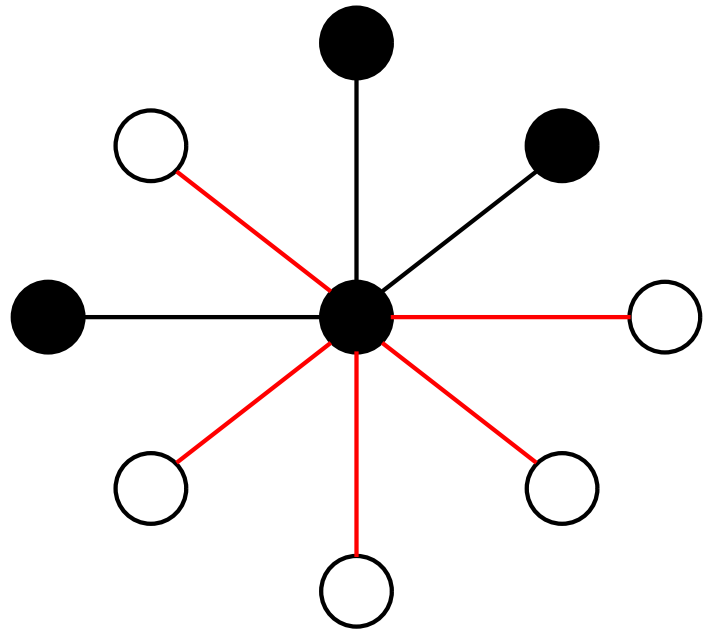
- $N(t) = 2$
- active boundary: $\zeta_+(X(t)) = n - 2$
- Expected time to next infection $1/(n-2)\beta$

Absorbing time for SI on the star graph



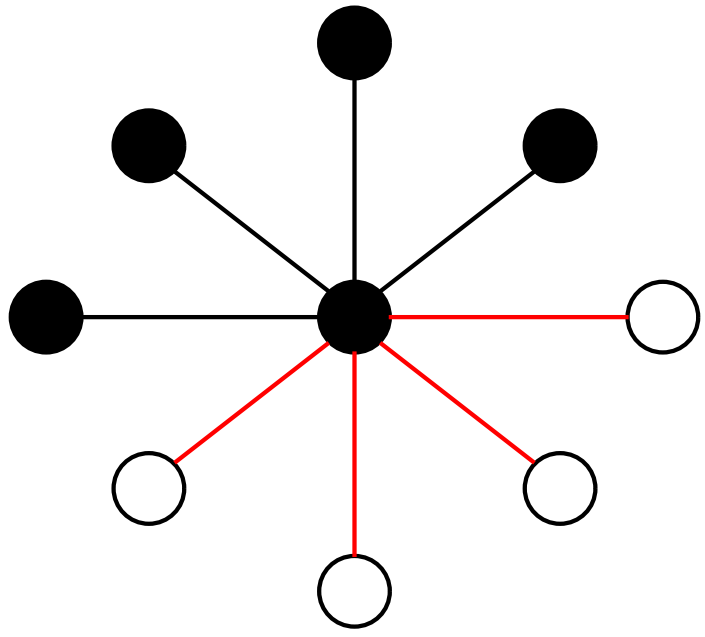
- $N(t) = 3$
- active boundary: $\zeta_+(X(t)) = n - 3$
- Expected time to next infection $1/(n-3)\beta$

Absorbing time for SI on the star graph



- $N(t) = k$
- active boundary: $\zeta_+(X(t)) = n - k$
- Expected time to next infection $1/(n-k)\beta$

Absorbing time for SI on the star graph



- $N(t) = k$
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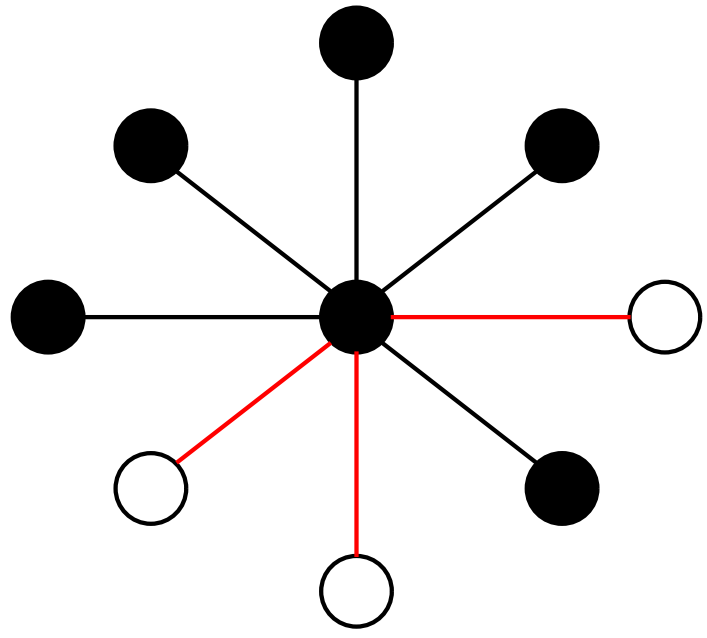
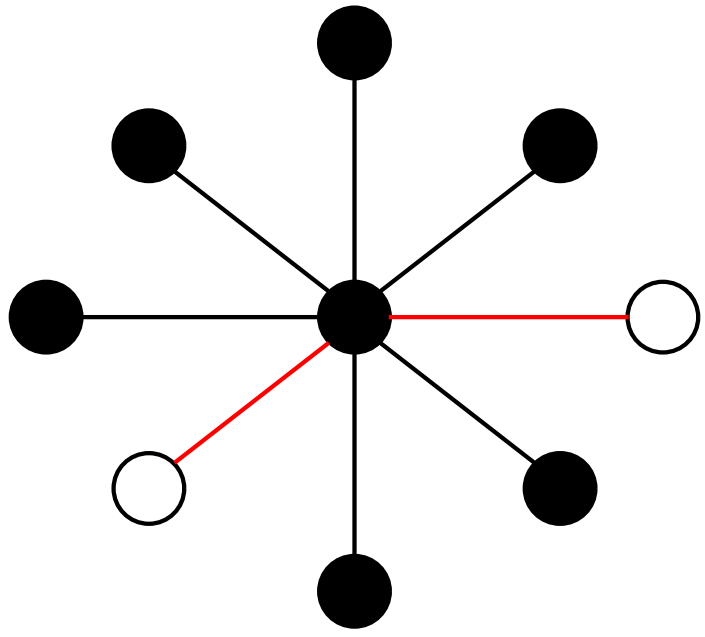
- Expected time to next infection $1/(n-k)\beta$

Absorbing time for SI on the star graph



- $N(t) = k$
- active boundary: $\zeta_+(X(t)) = n - k$
- Expected time to next infection $1/(n-k)\beta$

Absorbing time for SI on the star graph



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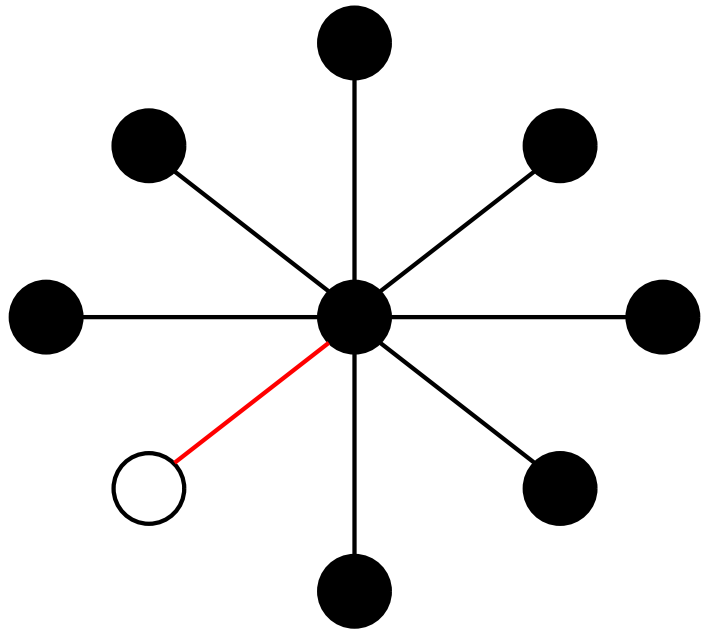
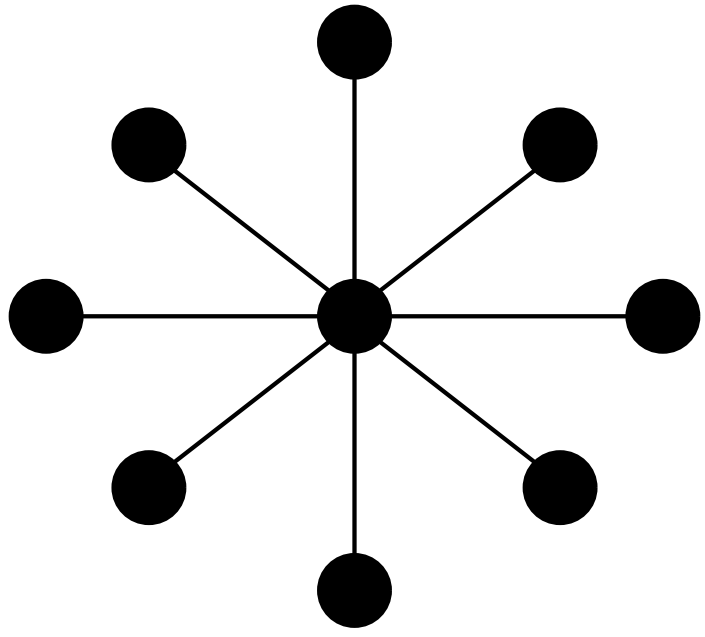


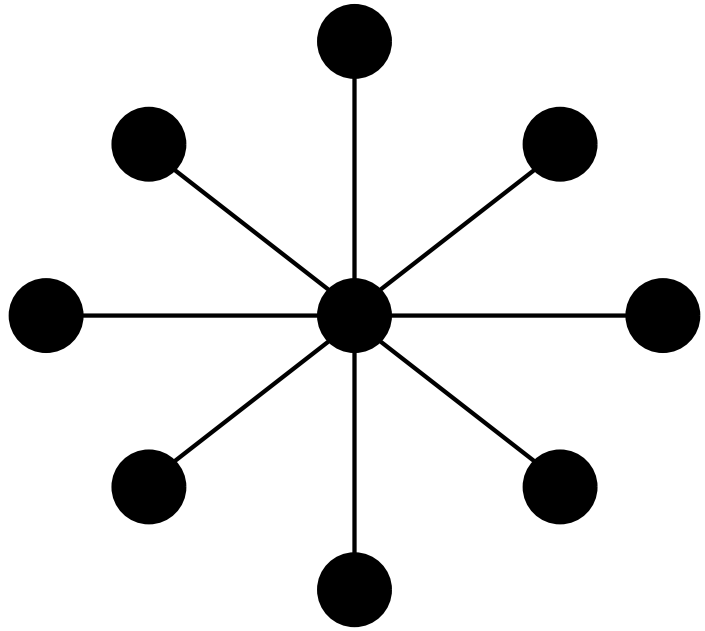
- $N(t) = n - 1$
- active boundary: $\zeta_+(X(t)) = 1$
- Expected time to next infection $1/\beta$

Absorbing time for SI on the star graph



- $N(t) = n$
- active boundary: $\zeta_+(X(t)) = 0$
- reached full infection

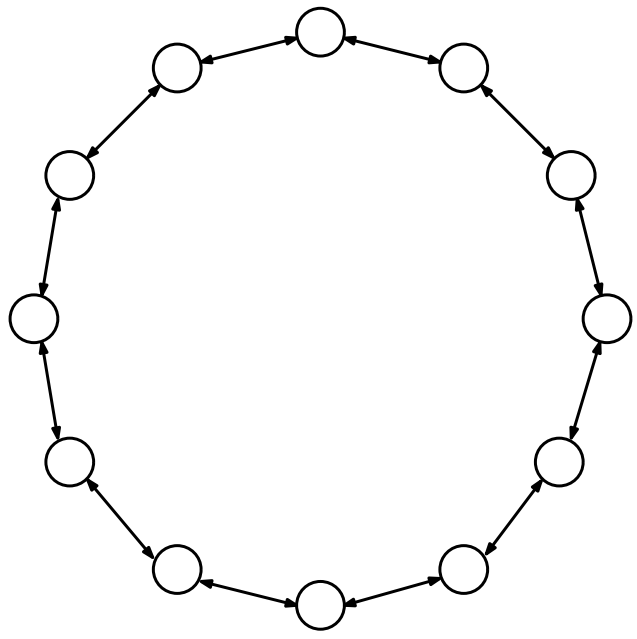
Absorbing time for SI on the star graph



- Expected time to full infection

$$\begin{aligned}
\mathbb{E}[T|X(0) = (1\ldots0)] &= \frac{1}{\beta(n-1)} + \frac{1}{\beta(n-2)} + \ldots + \frac{1}{\beta} \\
&= \frac{1}{\beta}\sum_{k=1}^{n-1}\frac{1}{n-k} = \frac{1}{\beta}\sum_{k=1}^{n-1}\frac{1}{k} \\
&= \frac{H_{n-1}}{\beta} \sim \frac{\log n}{\beta}
\end{aligned}$$

Absorbing time for SI on the ring graph



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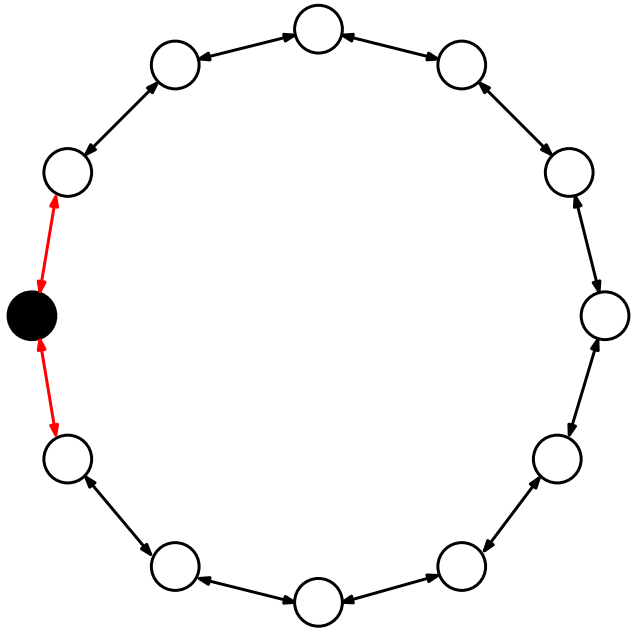
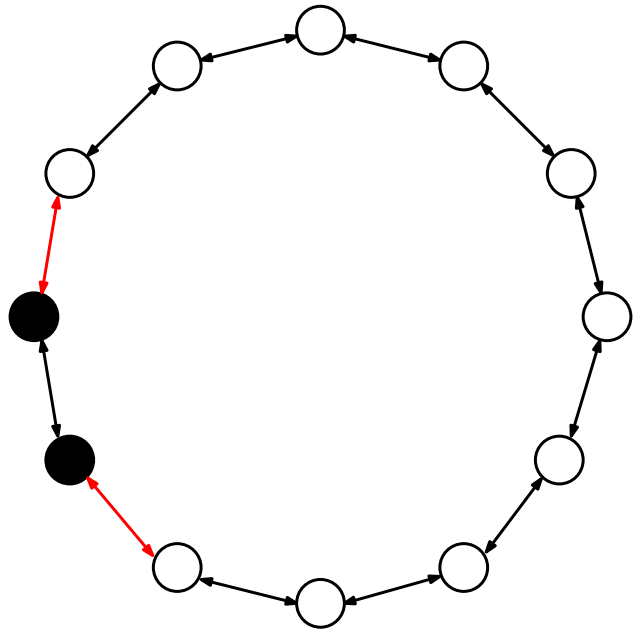


Absorbing time for SI on the ring graph



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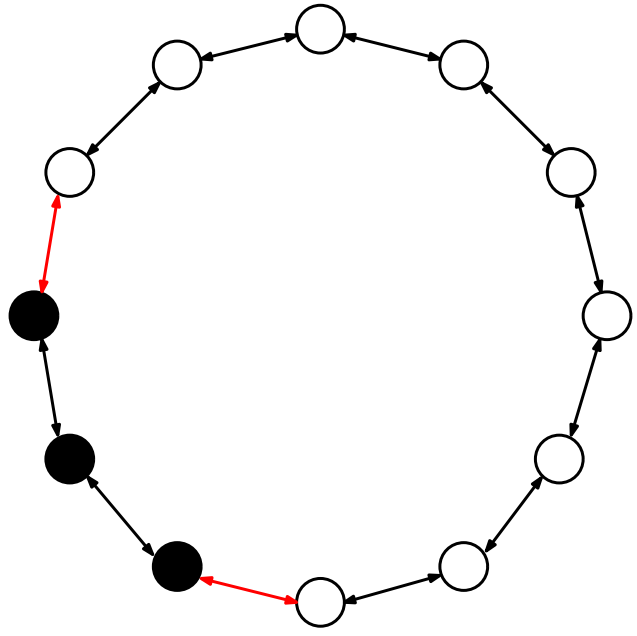

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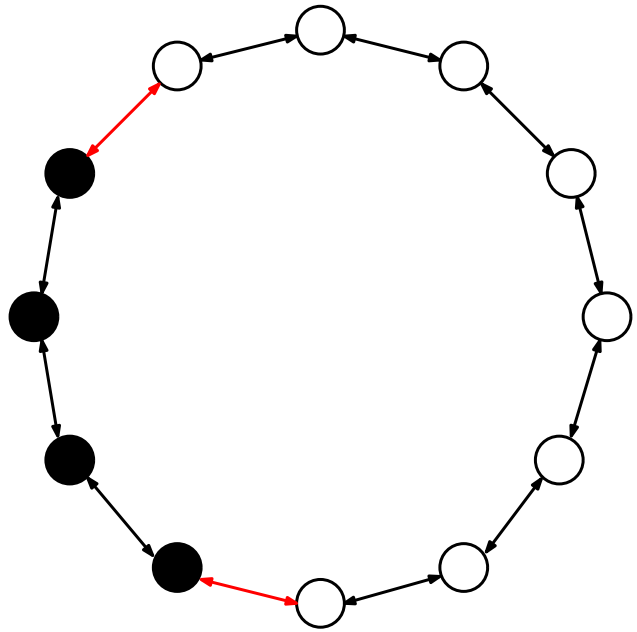

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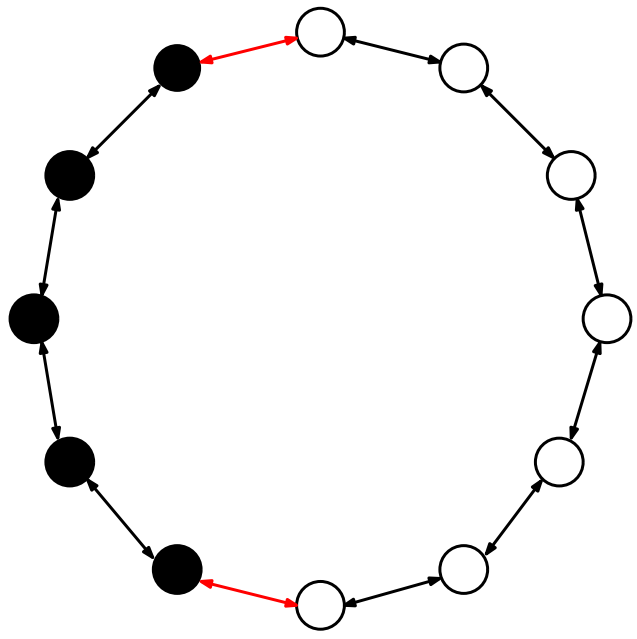

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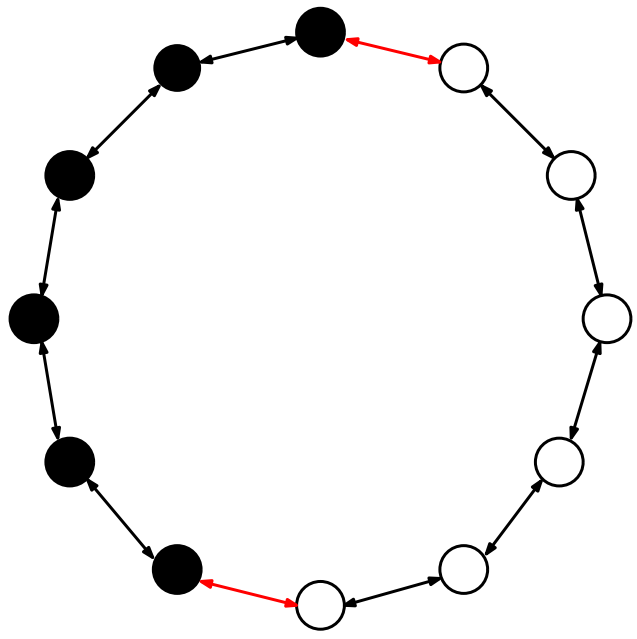

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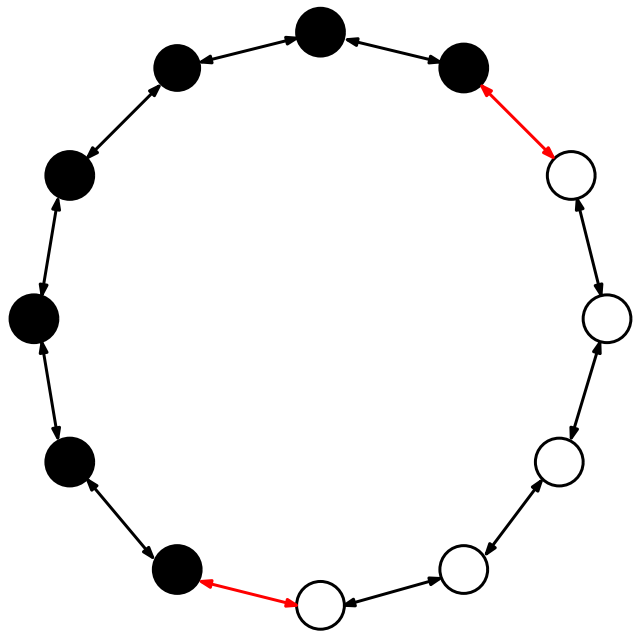

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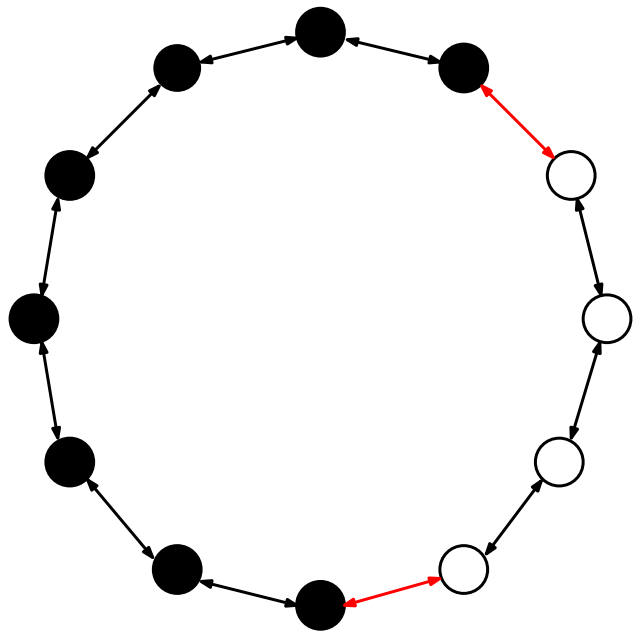

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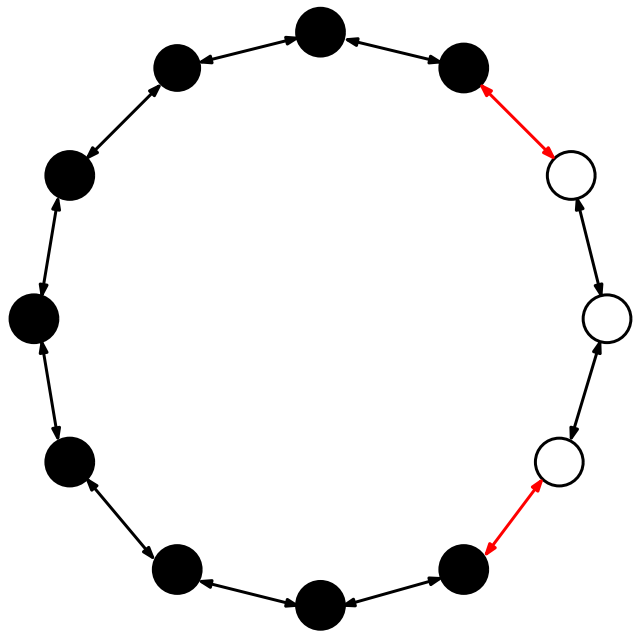

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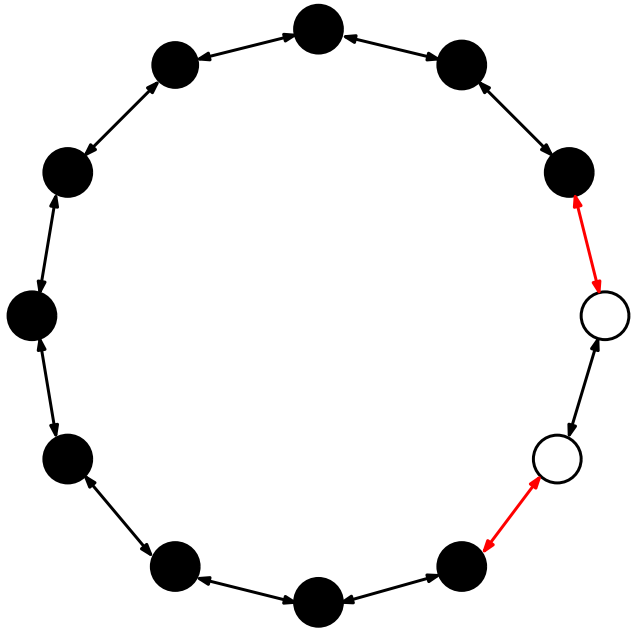

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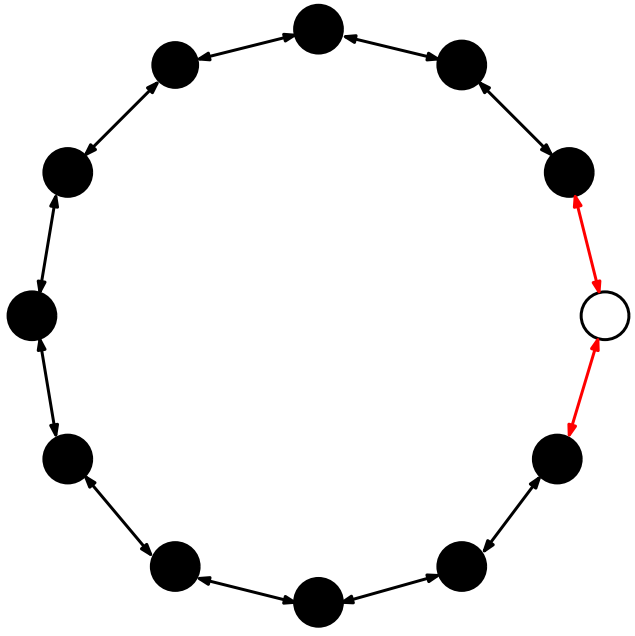

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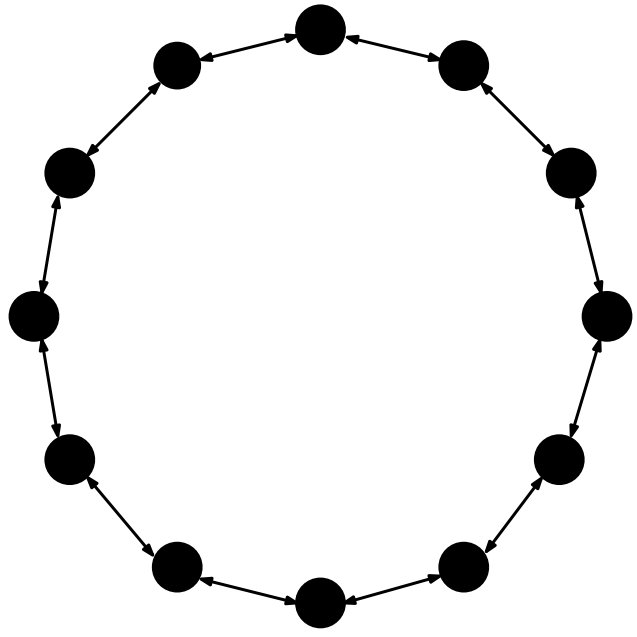

- Expected time to full infection

$$\mathbb{E}[T|X(0) = \delta^{(i)}] = \frac{1}{2\beta} + \frac{1}{2\beta} + \cdots \frac{1}{2\beta} = \frac{n-1}{2\beta}$$

Absorbing time for SI on the complete graph

Expected absorbing time: $X(t) = I\mathbb{1} \Leftrightarrow N(t) = n$

- $N(t) = k \Rightarrow$ active boundary: $\zeta_+(X(t)) = k(n-k)$
- Expected time to next infection $1/\beta$

$$\tau_n = 0 \qquad \tau_k = \frac{1}{k(n-k)\beta} + \tau_{k+1}, \quad 0 \leq k < n$$

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$$\tau_1 = \sum_{k=1}^{n-1} \frac{1}{k(n-k)\beta} = \frac{2}{\beta n} \sum_{k=1}^{n-1} \frac{1}{k} \sim \frac{2}{\beta} \frac{\log n}{n}$$

Extinction time for SIS epidemics on the complete graph

- $N(t)$ continuous-time birth-and-death chain:

  $$\mu_k(x) = k, \quad 1 \le k \le n, \qquad \lambda_k(x) = \beta k(n-k), \quad 1 \le k < n$$

- unique globally reachable absorbing state 0

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$$\mu_k(x) = k, \quad 1 \le k \le n, \qquad \lambda_k(x) = \beta k(n-k), \quad 1 \le k < n$$

- unique globally reachable absorbing state 0
- expected extinction times $\tau_k = \mathbb{E}[T_0 | N(0) = k]$ satisfy

$$\tau_0 = 0 \qquad \tau_k = \frac{1 + k\tau_{k-1} + \beta k(n-k)\tau_{k+1}}{k + \beta k(n-k)} \qquad \tau_n = \frac{1}{n} + \tau_{n-1}$$

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- Proposition: SIS epidemics on K_n, $\beta = \alpha/n$. Then,

(i) $\alpha < 1 \Longrightarrow \tau_k \le \tau_n \sim \dfrac{\log n}{1-\alpha}$

(ii) $\alpha > 1 \Longrightarrow \tau_k \ge \tau_1 \sim \dfrac{e^{ng(\alpha)}}{\alpha n}$

$$g(\alpha) = \max_{\frac{1}{\alpha} \le \gamma \le 1} (1-\gamma)\log(\alpha\gamma) > 0$$

SIS on general graph

▶ Theorem: Consider the SIS epidemics on a connected undirected graph $\mathcal{G} = (\mathcal{V}, \mathcal{E}, W)$. Then,

$$\beta\lambda_W < 1 \qquad \Longrightarrow \qquad \mathbb{E}_x[T_0] \leq \frac{1 + \log n}{1 - \beta\lambda_W} \qquad \forall x \in \mathcal{X}$$

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▶ The existence of a slow extinction regime depends on other connectivity properties of a graph. It can be investigated for some special graph families (e.g., Erdos-Renyi random graphs)

Fixation probability for evolutionary dynamics

- Theorem: Evolutionary dynamics on connected $\mathcal{G} = (\mathcal{V}, \mathcal{E}, W)$, binary states $\{0, 1\}$, fitness ratio $\rho = f_1/f_0$. If $\mathcal{G}$ undirected, then

$$\mathbb{P}_x\left(\lim_{t\to+\infty} X(t) = \mathbb{1}\right) = \begin{cases} k/n & \text{if} \quad \rho = 1 \\ \dfrac{1-\rho^{-k}}{1-\rho^{-n}} & \text{if} \quad \rho \neq 1 \end{cases}$$

where $k = \sum_i x_i$.

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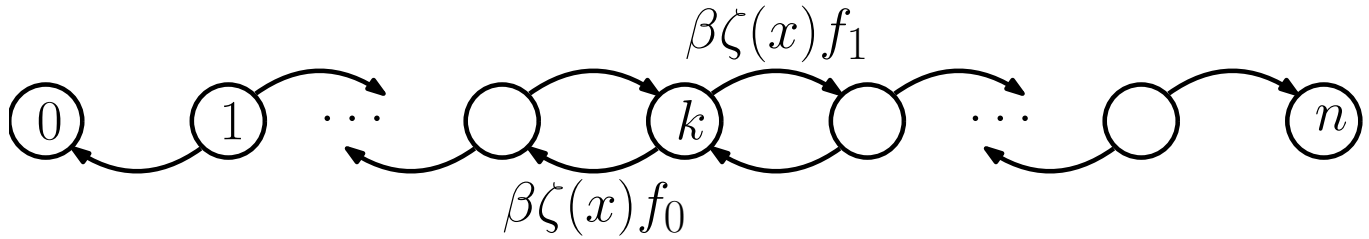
- Proof: $N(t)$ is not a continuous-time Markov chain ...



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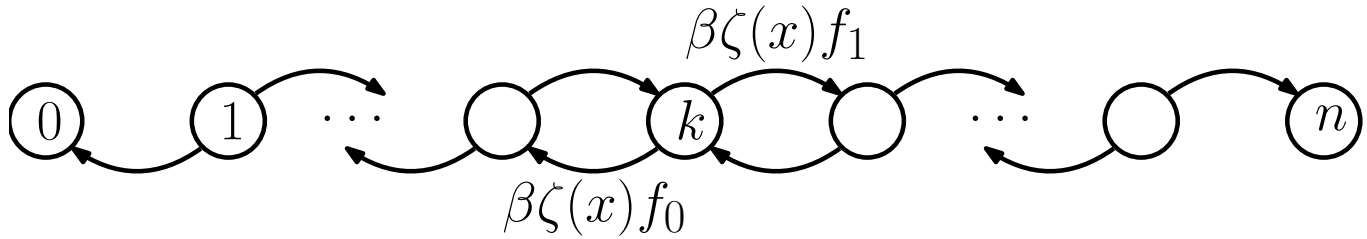
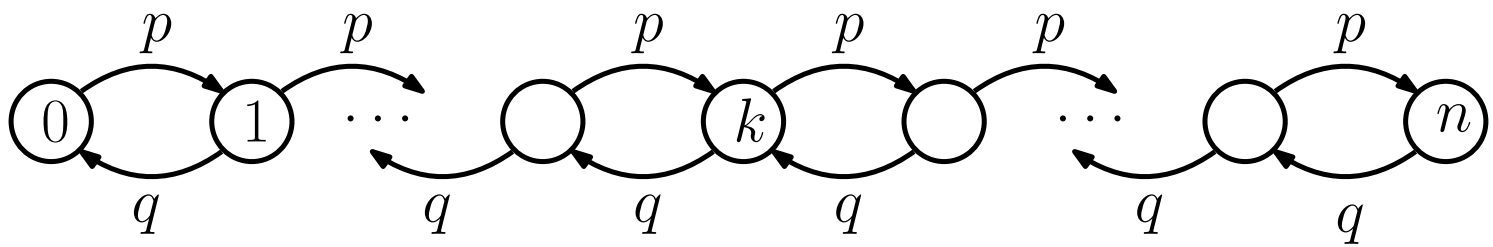


... but has the same absorbing probabilities as its jump chain



where $p = f_1/(f_0 + f_1)$ and $q = f_0/(f_0 + f_1)$.

Fixation probability for evolutionary dynamics (cont'd)

- Theorem: Evolutionary dynamics on connected $\mathcal{G} = (\mathcal{V}, \mathcal{E}, W)$, binary states $\{0, 1\}$, fitness ratio $\rho = f_1/f_0$. If $\mathcal{G}$ undirected, then

$$\mathbb{P}\left(\lim_{t\to+\infty} X(t) = \mathbb{1}|X(0)\right) = \begin{cases} k/n & \text{if} \quad \rho = 1 \\ \dfrac{1-\rho^{-k}}{1-\rho^{-n}} & \text{if} \quad \rho \neq 1 \end{cases}$$

where $k = \sum_i X_i(0)$.

- Biological interpretation: if you start with a native population of 0's and introduce a single genetic mutant 1 with evolutionary advantage $f_1 > f_0$, then the probability the mutant specie 1 replaces the native specie 0 is

$$\mathbb{P}\left(\lim_{t\to+\infty} X(t) = \mathbb{1}|X(0)\right) = \frac{1-\rho^{-1}}{1-\rho^{-n}}$$

independently from the position of the initial mutant.

Absorbing probabilities for the voter model

- Theorem: Voter model on connected $\mathcal{G} = (\mathcal{V}, \mathcal{E}, W)$. Then,

$$\mathbb{P}_x \left(\lim_{t \to +\infty} X(t) = a\mathbb{1} \right) = \sum_{i : x_i = a} \overline{\pi}_i$$

where $\overline{\pi}$ is the Laplace-invariant distribution of $\mathcal{G}$.

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- Proof: $p_i^a(t) = \mathbb{P}_x(X_i(t) = a)$ satisfies $p_i^a(0) = \delta_{x_i}^{(a)}$ and

$$\frac{\mathrm{d}}{\mathrm{d}t} p_i^a(t) = \beta \sum_{j \in \mathcal{V}} W_{ij} \left(p_j^a(t) - p_i^a(t) \right)$$

so that $\dfrac{\mathrm{d}}{\mathrm{d}t} \sum_i \overline{\pi}_i p_i^a(t) = 0$. Then

$$\sum_{i : x_i = a} \overline{\pi}_i = \sum_i \overline{\pi}_i p_i^a(0) = \sum_i \overline{\pi}_i p_i^a(t) \overset{t \to +\infty}{\longrightarrow} \mathbb{P}_x \left(\lim_{t \to +\infty} X(t) = a\mathbb{1} \right)$$

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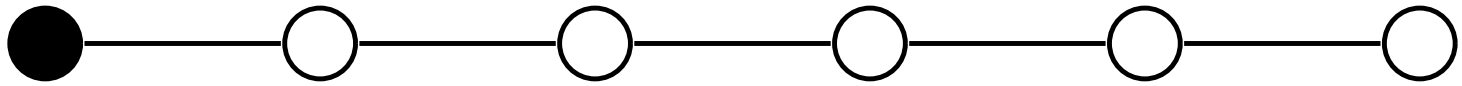
- Corollary: Voter model on connected balanced $\mathcal{G} = (\mathcal{V}, \mathcal{E}, W)$. Then,

$$\mathbb{P}_x \left(\lim_{t \to +\infty} X(t) = a\mathbb{1} \right) = \frac{1}{n} \left| \{ i \in \mathcal{V} : x_i = a \} \right|$$

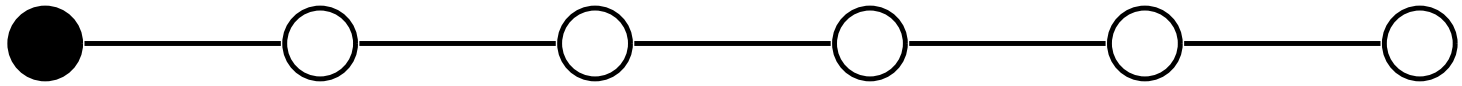
- Proof: in balanced connected graph $\overline{\pi}$ is uniform
- $\mathcal{G}$ undirected $\Rightarrow$ π uniform (c.f. previous result in case $|\mathcal{A}| = 2$)

Final number of recovered for SIR epidemics on line graph



- Let $N =$ total nr of nodes in final state R
- If $X(0) = x \in \{I, S\}^{\mathcal{V}}$, then $N =$ total nr of nodes that get infected at some time

Final number of recovered for SIR epidemics on line graph



- Let $N =$ total nr of nodes in final state R
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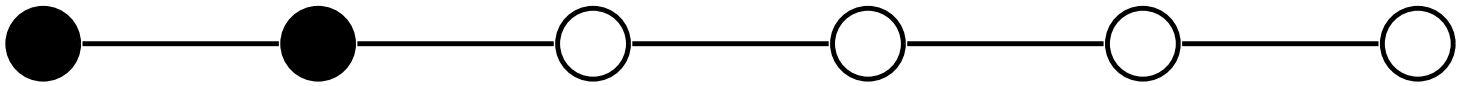
- Consider $x = (I, S, S, \ldots, S)$. Then,

$$\mathbb{P}_x(N \geq 1) = 1$$

$$\mathbb{P}_x(N = 1) = \frac{1}{1+\beta}$$

Final number of recovered for SIR epidemics on line graph



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- Consider $x = (I, S, S, \ldots, S)$. Then,

$$\mathbb{P}_x(N \geq 2) = \frac{\beta}{1+\beta} \qquad \mathbb{P}_x(N = 2 | N \geq 2) = \frac{1}{1+\beta}$$

$$\mathbb{P}_x(N = 2) = \mathbb{P}_x(N \geq 2)\mathbb{P}_x(N = 2 | N \geq 2) = \frac{\beta}{(1+\beta)^2}$$

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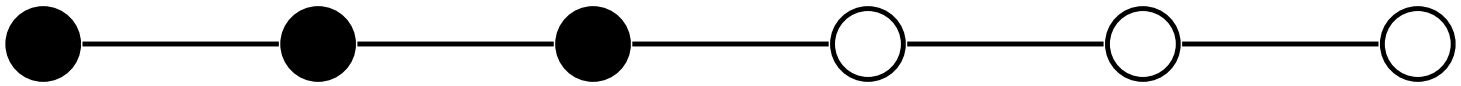

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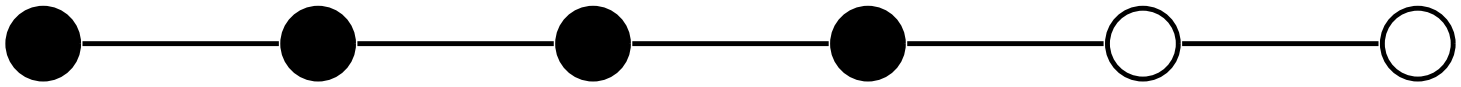
- Consider $x = (I, S, S, \ldots, S)$. Then,

$$\mathbb{P}_x(N \geq 3) = \left(\frac{\beta}{1+\beta}\right)^2 \qquad \mathbb{P}_x(N = 3 | N \geq 3) = \frac{1}{1+\beta}$$

$$\mathbb{P}_x(N = 3) = \mathbb{P}_x(N \geq 3)\mathbb{P}_x(N = 3 | N \geq 3) = \frac{\beta^2}{(1+\beta)^3}$$

Final number of recovered for SIR epidemics on line graph



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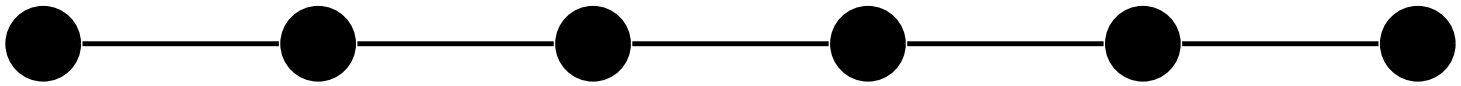
$$\mathbb{P}_x(N \geq k) = \left(\frac{\beta}{1+\beta}\right)^{k-1} \qquad \mathbb{P}_x(N = k | N \geq k) = \frac{1}{1+\beta}$$

$$\mathbb{P}_x(N = k) = \mathbb{P}_x(N \geq k)\mathbb{P}_x(N = k | N \geq k) = \frac{\beta^{k-1}}{(1+\beta)^k}$$

Final number of recovered for SIR epidemics on line graph



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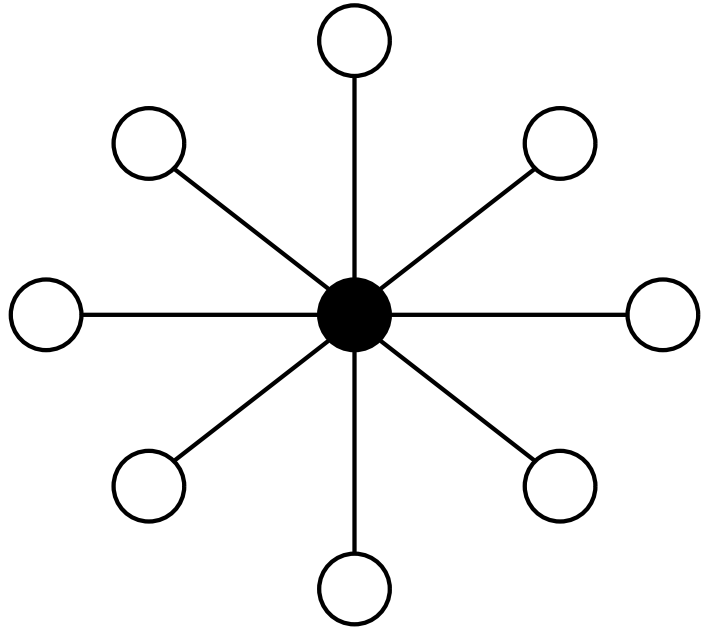
- If $X(0) = x \in \{I, S\}^{\mathcal{V}}$, then $N =$ total nr of nodes that get infected at some time
- Consider $x = (I, S, S, \ldots, S)$. Then,

$$\mathbb{P}_x(N \geq n) = \left(\frac{\beta}{1+\beta}\right)^{n-1} \qquad \mathbb{P}_x(N = k | N \geq n) = 1$$

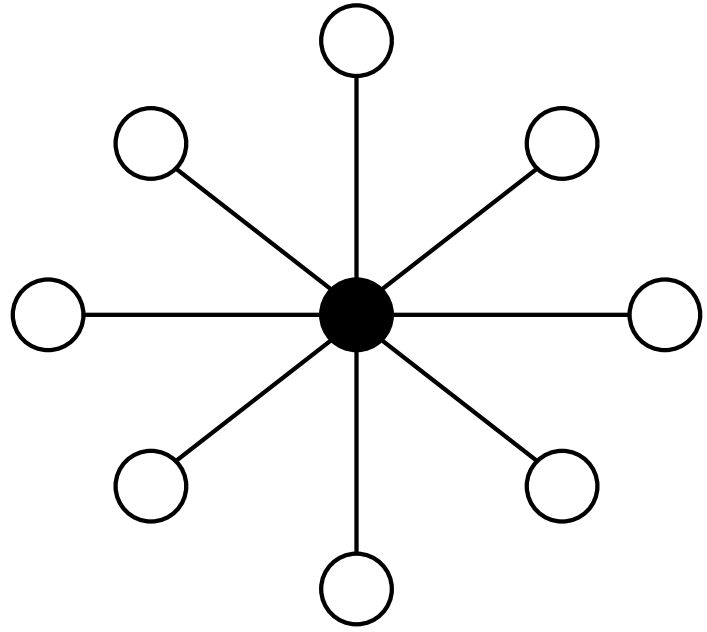
$$\mathbb{P}_x(N = k) = \mathbb{P}_x(N \geq k)\mathbb{P}_x(N = k | N \geq k) = \left(\frac{\beta}{1+\beta}\right)^{n-1}$$

Final number of recovered for SIR epidemics on star graph



- Let $N =$ total nr of nodes in final state R
- Consider $x = (I, S, S, \ldots, S)$. Then,

Final number of recovered for SIR epidemics on star graph

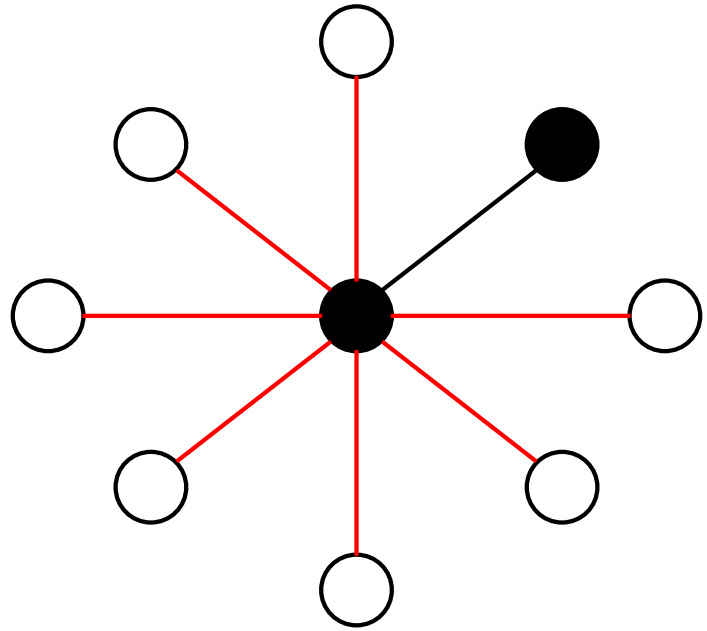


- Let $N =$ total nr of nodes in final state R
- Consider $x = (I, S, S, \ldots, S)$. Then,

$$\mathbb{P}_x(N \geq 1) = 1$$

$$\mathbb{P}_x(N = 1) = \frac{1}{1 + (n-1)\beta}$$

Final number of recovered for SIR epidemics on star graph

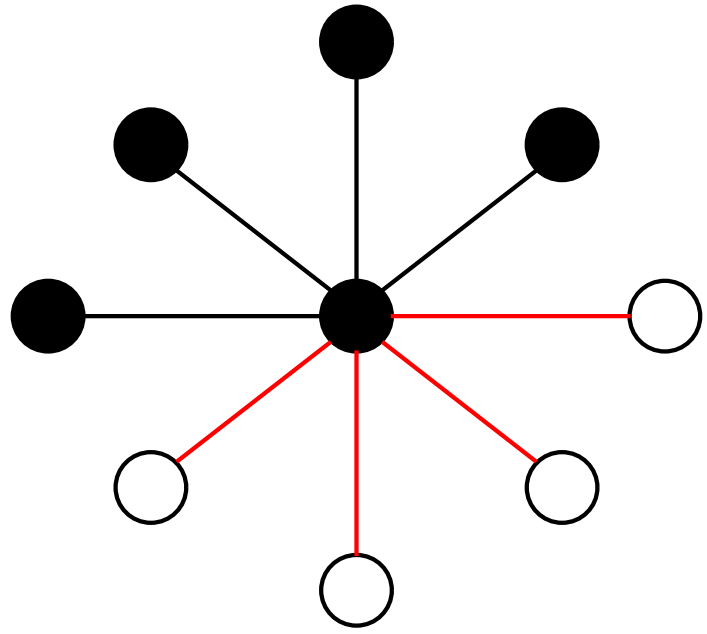


- Let $N =$ total nr of nodes in final state R
- Consider $x = (I, S, S, \ldots, S)$. Then,

$$\mathbb{P}_x(N \geq 2) = \frac{(n-1)\beta}{1+(n-1)\beta} \qquad \mathbb{P}_x(N = 2|N \geq 2) = \frac{1}{1+(n-2)\beta}$$

$$\mathbb{P}_x(N = 2) = \mathbb{P}_x(N \geq 2)\mathbb{P}_x(N = 2|N \geq 2) = \frac{(n-1)\beta}{1+(n-1)\beta}\frac{1}{1+(n-2)\beta}$$

Final number of recovered for SIR epidemics on star graph



- Let $N =$ total nr of nodes in final state R
- Consider $x = (I, S, S, \ldots, S)$. Then,

$$\mathbb{P}_x(N \geq k+1) = \frac{(n-k)\beta}{1+(n-k)\beta}\mathbb{P}_x(N \geq k)$$

$$\mathbb{P}_x(N = k+1 | N \geq k+1) = \frac{1}{1+(n-k-1)\beta}$$