Epidemics on networks: the risky and the at-risk

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Vulnerability

Epidemics on Networks

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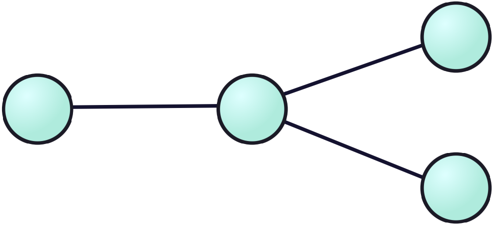
Consider the SIR model on a network:



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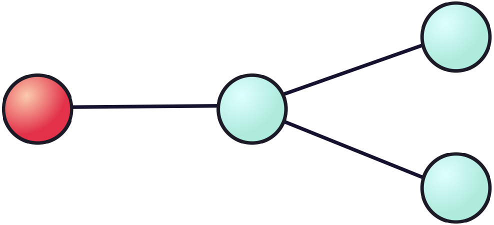

Start with one initial infected individual.

Epidemics on Networks

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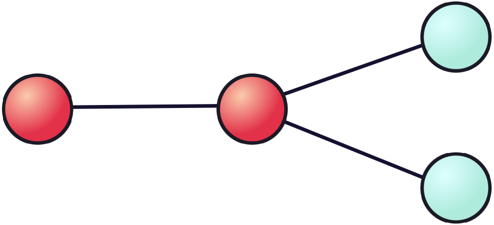

The infection may be passed along the edges of the network with a probability βdt of infection in a small tilmestep dt.

Epidemics on Networks

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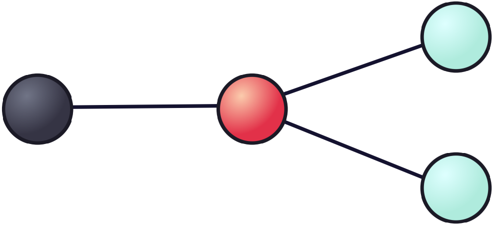

Infected nodes can recover; suppose the time to recovery is randomly distributed with pdf $\gamma(t)$.

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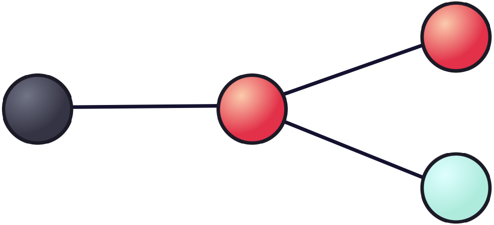

Another infection takes place...

Epidemics on Networks

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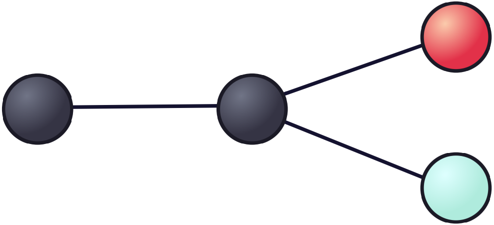

...and another recovery, now the disease cannot progress further...

Epidemics on Networks

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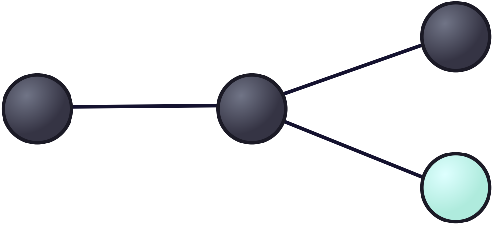

...and must die out. This is the final state.

Transmissibility

What is the probability I catch the disease from my neighbour?

Define the *transmissibility*

$$T = \int_0^\infty \gamma(t)\big(1 - e^{-\beta t}\big)\, dt\,.$$

This is probability that the infection is passed from a node to its neighbour before it recovers.

If T is small, the disease is sure to die out quickly. If T is large, a major outbreak is possible.

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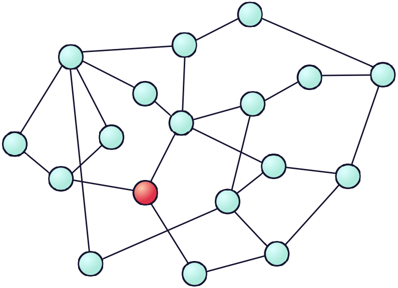
Q: Which nodes are most likely to get infected?

Example

Transmission probability: **90%**



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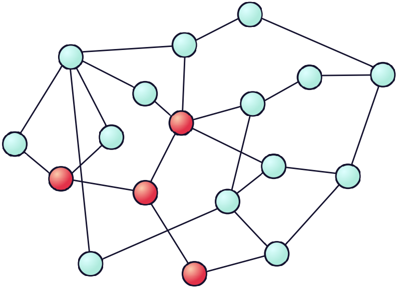

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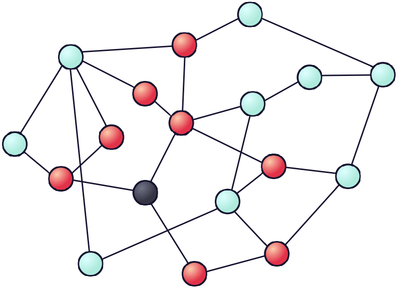

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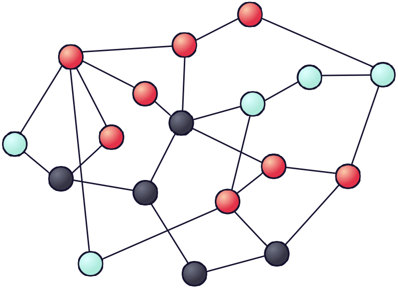

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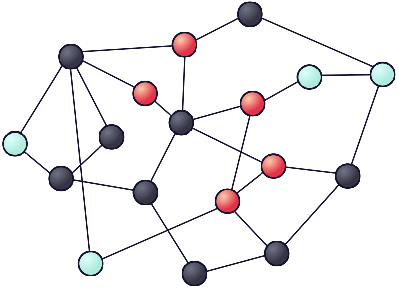

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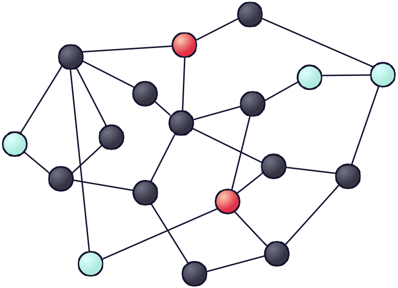

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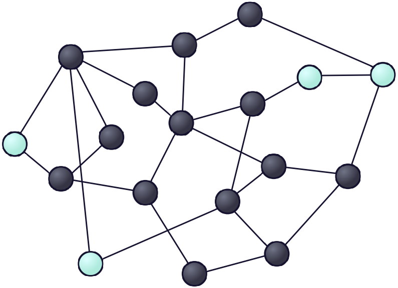

A Guessing Game

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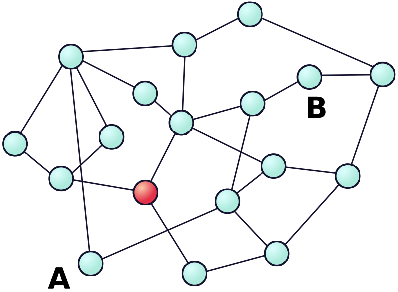

Which node is more vulnerable to the infection, A or B?

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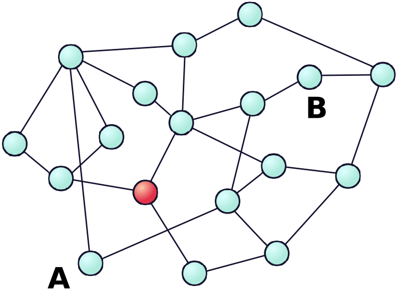

B is more vulnerable — it is closer (in the network) to the source.

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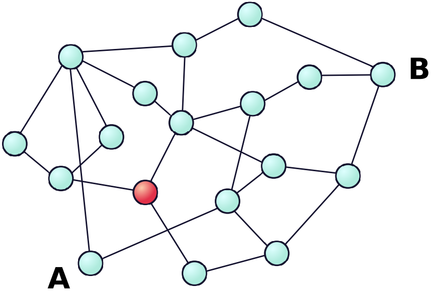

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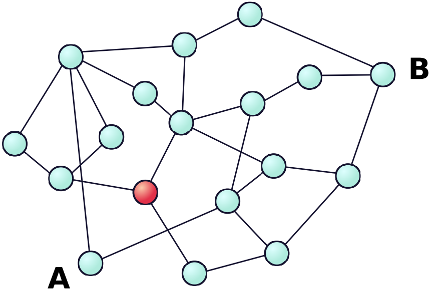
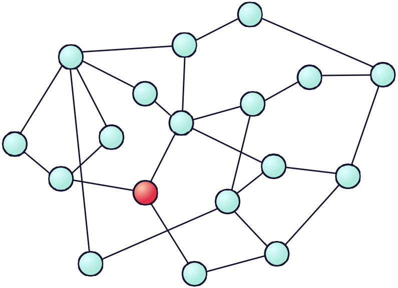


B is more vulnerable — it has more neighbours,
who are likely to get sick themselves.

A Guessing Game

Transmission probability: **30%**



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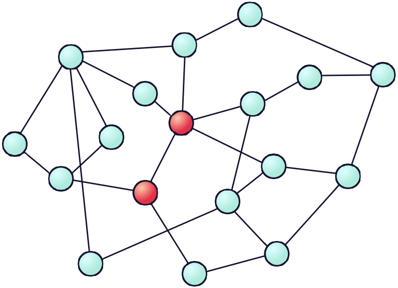

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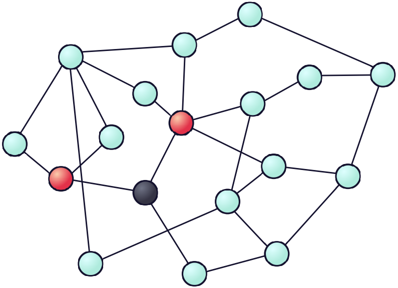

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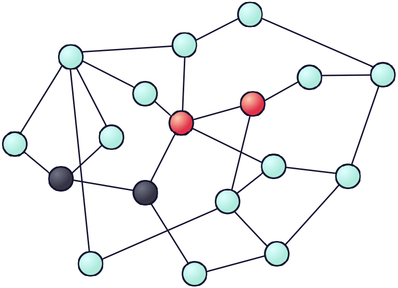

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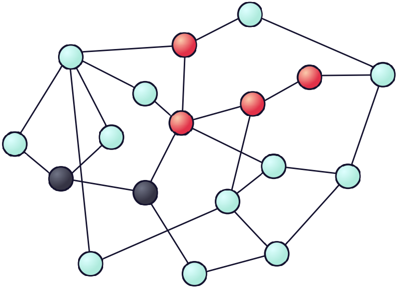

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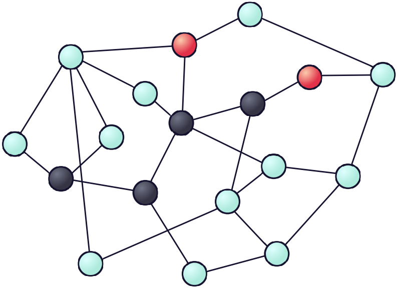

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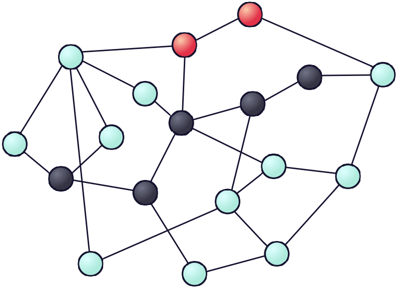

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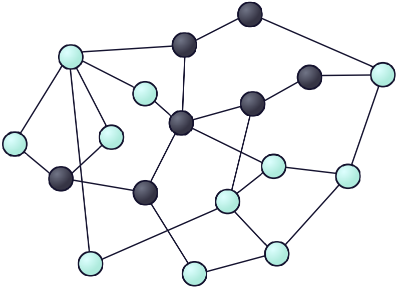

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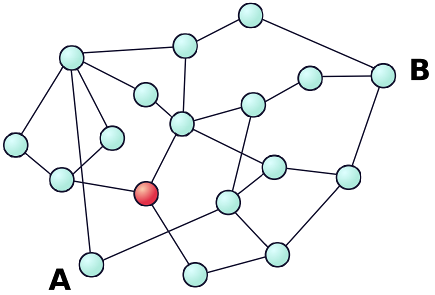

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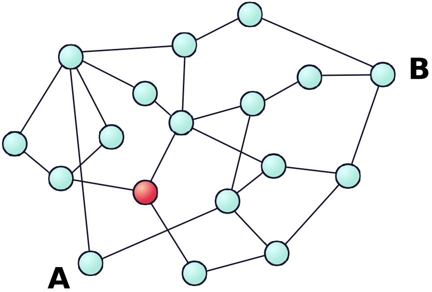

A is more vulnerable — it has more paths between it and the source for the infection to travel down.

Cavity Method

Cavity Method

Write v_i for the probability node i is infected eventually, then

$$v_i = 1 - \prod_{j \in \partial i} (1 - T v_j^{(i)}) \, ,$$

where, $v_j^{(i)}$ is the probability that node j is infected by the disease in the network *with node i removed*.

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$$v_j^{(i)} = 1 - \prod_{l \in \partial j \setminus i} (1 - T v_l^{(j)}) \,.$$

These are the cavity equations.

Cavity Method

Procedure for vulnerability analysis:

1) Compute the transmissibility $T = \int_0^\infty \gamma(t)\big(1 - e^{-\beta t}\big)\, dt$

2) Solve the cavity equations $v_j^{(i)} = 1 - \prod_{l \in \partial j \setminus i}(1 - T v_l^{(j)})$

3) Deduce node vulnerability via $v_i = 1 - \prod_{j \in \partial i}(1 - T v_j^{(i)})$

The cavity equations are a system of $2|E|$ non-linear simultaneous equations. Numerical solution is usually the only option.

Non-Backtracking (Hashimoto) Graph

It will be useful to draw a graph of relationships between cavity variables.

If $G = (V, E)$ is the original graph, define a new directed graph H with

Nodes: ordered pairs (i, j) for $j \in V$, $i \in \partial j$

Edges: $(i, j) \to (k, l)$ if $k = j$ and $l \neq i$

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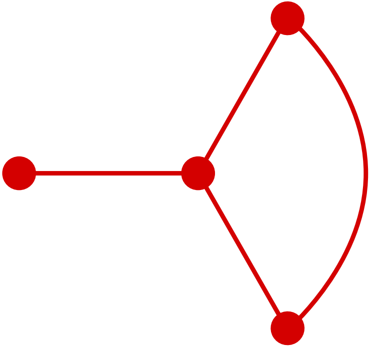

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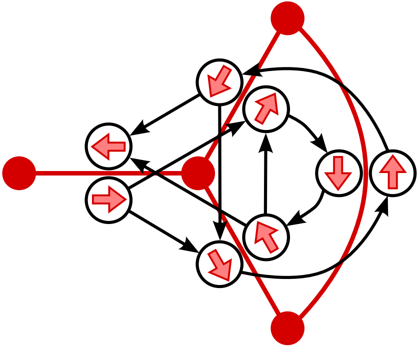

Cavity Equations — Numerical Solution

Define the map $D : \mathbb{R}^{2|E|} \to \mathbb{R}^{2|E|}$

$$D_e(\boldsymbol{v}) = 1 - \prod_{e' \in \partial e} (1 - T v_{e'}) \, .$$

Then solving the cavity equations means finding a fixed point $\boldsymbol{v} = D(\boldsymbol{v})$.

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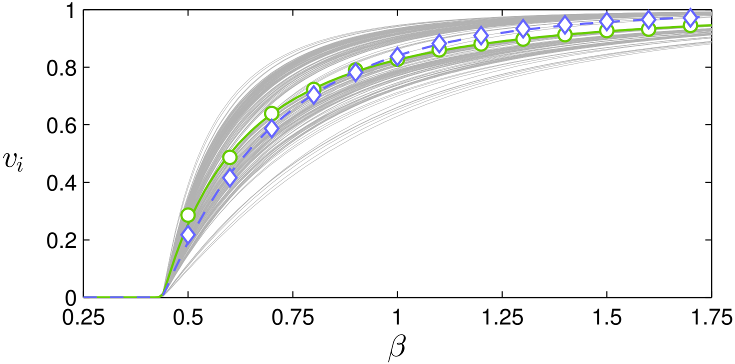
Simple iteration works. $D^n_{(i,j)}(\mathbf{1})$ describes the probability of j eventually being infected in a network with i removed and at nodes of distance n or greater initially infected. As $n \to \infty$ we obtain a solution to the cavity equations.

Vulnerability Ranking



Node vulnerability in a configuration model network with degrees three and five (in 50/50 mix).

Epidemic Threshold

For what value of T is a major outbreak possible?

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So

$$\left. \frac{\partial D_e}{\partial v_{e'}} \right|_{\boldsymbol{v}=\mathbf{0}} = T B_{e,e'} \, ,$$

where B is the adjacency matrix of the Hashimoto graph. Thus a major outbreak is possible only if $T > T_c = 1/\lambda_{\max}(B)$.

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Around $T \approx T_c$ we have $\boldsymbol{v} \approx \mathbf{0}$ so

$$\partial v_e \approx \sum_{e' \in \partial e} T_c \partial v_{e'} \,,$$

that is, $\boldsymbol{\partial v}$ is the eigenvector of B corresponding to the dominant eigenvalue $\lambda_{\max}(B) = 1/T_c$.

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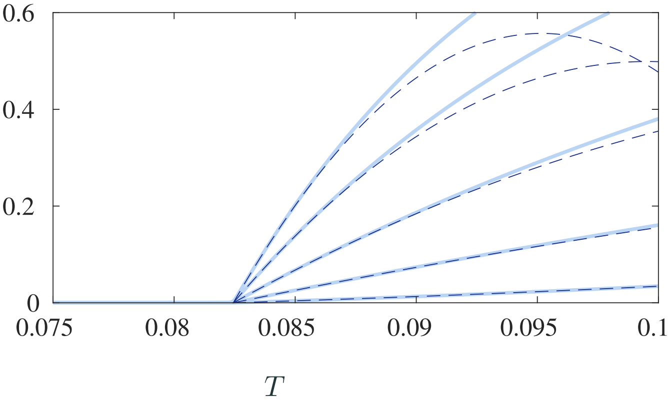
Thus, near T_c, the vulnerability is $v_i \approx (T - T_c) T_c \sum_{j \in \partial i} v_j^{(i)}$.

Vulnerability Ranking — Extremes

Going further, the curvature near T_c can be found by weakly non-linear analysis:

v_i



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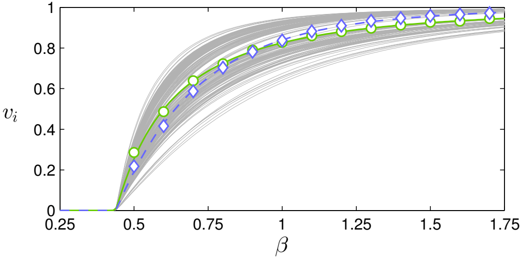
Generally, the first non-zero derivative $\partial^n v_e$ at $T = 1$ is at $n = |\partial e|$.

So node vulnerability ranking for strongly infections diseases depends entirely on degree.

Vulnerability Ranking



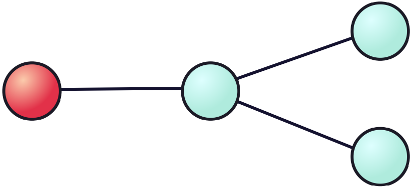
Summarising:

- The epidemic threshold is determined by $T_c = 1/\lambda_{\max}(B)$.
- The rank order near $T = T_c$ depends on the corresponding eigenvector of B.
- The rank order near $T = 1$ depends only on degree.

Risk

Joint Exposure

Suppose we want to compute the probability that a major outbreak happens if a given node is “patient zero”.



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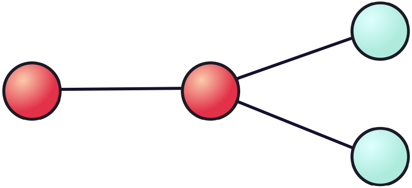

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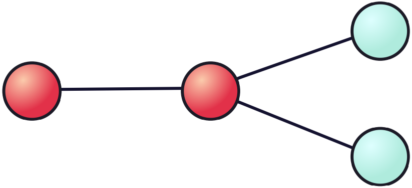

Complication: The fates of the two susceptible nodes here are not independent — they are both exposed to the random lifetime distribution of their infectious neighbour.

Cavity Method

First we need to know the probability that i infects some subset J of it's neighbours (and no-one else):

$$\begin{aligned}\mathbb{P}(i \to J) &= \int_0^\infty \gamma(t) \prod_{j\in J}(1 - e^{\beta t}) \prod_{j\in\partial i\setminus J} e^{-\beta t}\, dt \\ &= \int_0^\infty \gamma(t)(1 - e^{\beta t})^{|J|} e^{-\beta t(|\partial i| - |J|)}\, dt\,.\end{aligned}$$

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Then we can compute the risk posed by i as:

$$r_i = 1 - \sum_{J \subset \partial i} \mathbb{P}(i \to J)(1 - r_J^{(i)})\,,$$

where $r_J^{(i)}$ is the probability of a major outbreak in a network with i removed and all of J initially infected.

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Clearly,

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In tree-like networks this bound is very good, so we assume equality and can write

$$\begin{aligned} r_i &= 1 - \sum_{J \subset \partial i} \mathbb{P}(i \to J)(1 - r_J^{(i)}) \\ &= \ldots = 1 - \sum_{J \subset \partial i} (-1)^{|J|} T_{|J|} \prod_{j \in J} r_j^{(i)} \, , \end{aligned}$$

where $T_n = \int_0^\infty \gamma(t)(1 - e^{-\beta t})^n \, dt$.

Cavity Method

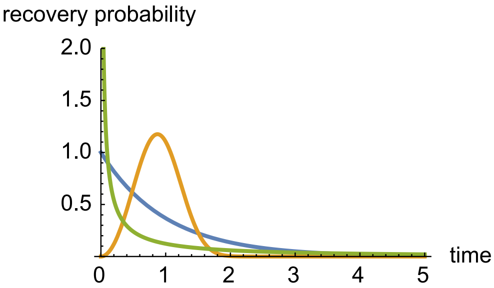
Repeating the calculation for j with i removed we obtain the cavity equations

$$r_j^{(i)} = 1 - \sum_{L \subset \partial j \setminus i} (-1)^{|L|} T_{|L|} \prod_{l \in L} r_l^{(j)} \, .$$

Unlike the node vulnerability, risk depends on the full details of the disease lifetime distribution $\gamma(t)$

Another Guessing Game

Which disease lifetime distribution is most deadly?



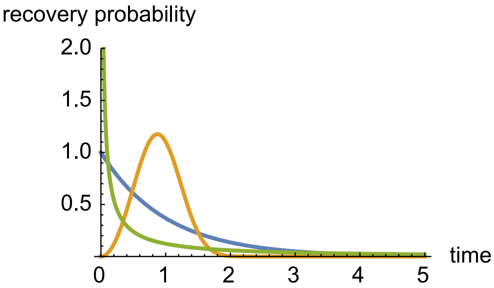
A) Memoryless (blue)

B) Heavy tail (green)

C) Peaked (yellow)

Another Guessing Game

Which disease lifetime distribution is most deadly?



A) Memoryless (blue)

B) Heavy tail (green)

C) **Peaked (yellow)**

Risk Bounds

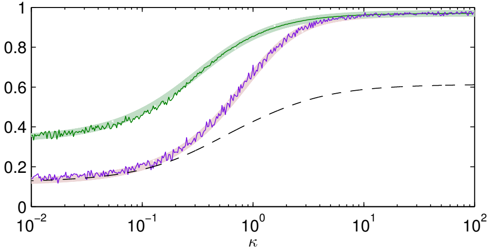
Recalling $T_n = \int_0^\infty \gamma(t)(1 - e^{-\beta t})^n \, dt$, we have

$$T^n \leq T_n \leq T$$

thus

$$1 - \prod_{e' \in \partial e} (1 - T r_{e'}) \geq r_e \geq T \left(1 - \prod_{e' \in \partial e} (1 - r_{e'}) \right) .$$

Risk Bounds



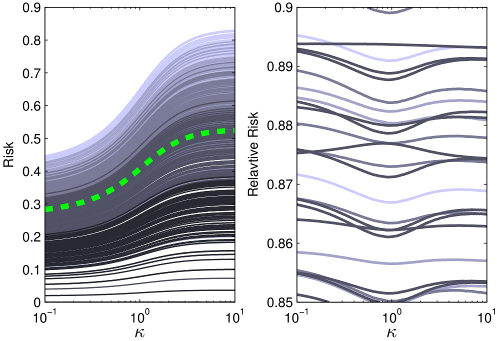
Risk (purple) and vulnerability (green) in a 4-regular graph with Weibull distributed lifetimes

$$\gamma(t) = \kappa e^{-t^{\kappa}} t^{(\kappa-1)}$$

Interpolating between heavy tailed ($\kappa \ll 1$), memoryless ($\kappa = 1$) and delta-function ($\kappa \gg 1$).

Risk Ranking

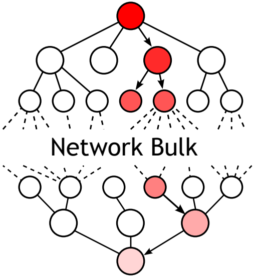
Risk Ranking



Left: Node risk as a function of κ, lines shaded according to degree. The dashed green line is the average risk $\bar{r} = \sum_i r_i$.
Right: Close up of relative risk $r_i/\bar{r}$ for several nodes.

Summary

- Epidemics on networks are confusing
- The cavity method can used to compute node risk and vulnerability to good approximation



Upstream:
Risk of causing
an oubreak

Downstream:
Vulnerability to
ongoing outbreaks

- Lots more to do...