

# Contagion

Complex Networks | @networksvox  
CSYS/MATH 303, Spring, 2016

Prof. Peter Dodds | @peterdodds

Dept. of Mathematics & Statistics | Vermont Complex Systems Center  
Vermont Advanced Computing Core | University of Vermont



Basic Contagion Models

Global spreading condition

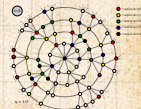
Social Contagion Models

Network version  
All-to-all networks

Theory

Spreading possibility  
Spreading probability  
Physical explanation  
Final size

References



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Models

Global spreading  
condition

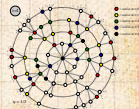
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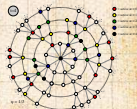
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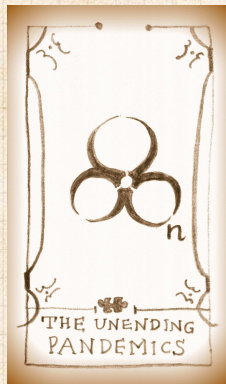
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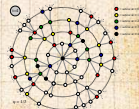
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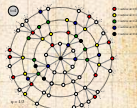
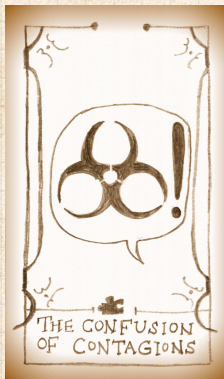
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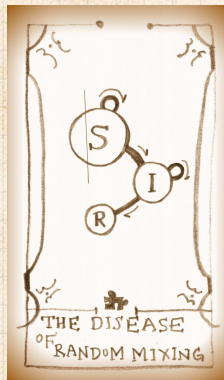
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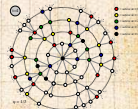
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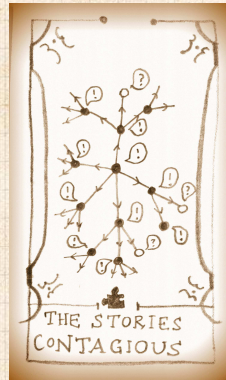
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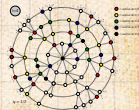
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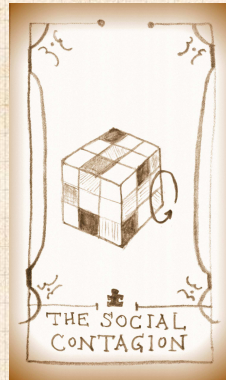
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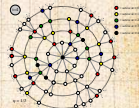
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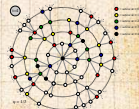
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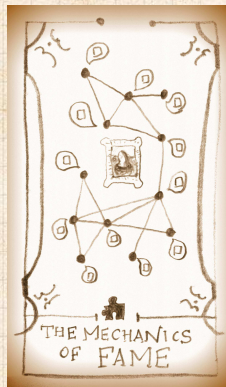
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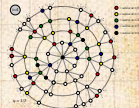
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1. For a given spreading mechanism on a given network, what's the **probability** that there will be global spreading?
2. If spreading does take off, how far will it go?
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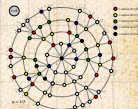
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**Next up:** We'll look at some fundamental kinds of spreading on generalized random networks.

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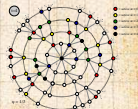
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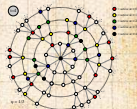
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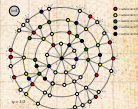
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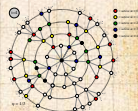
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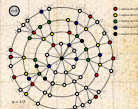
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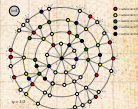
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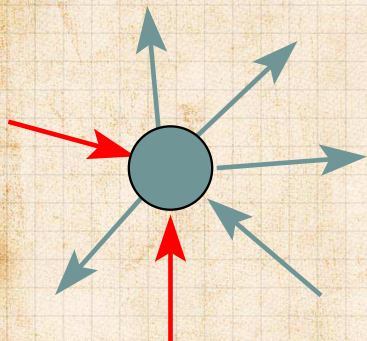
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# Spreading mechanisms



■ uninfected  
■ infected



**General spreading mechanism:**

State of node  $i$  depends on history of  $i$  and  $i$ 's neighbors' states.



Order of entry may be stochastic and history-dependent.



May have multiple, interacting entities spreading at once.

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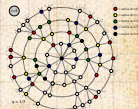
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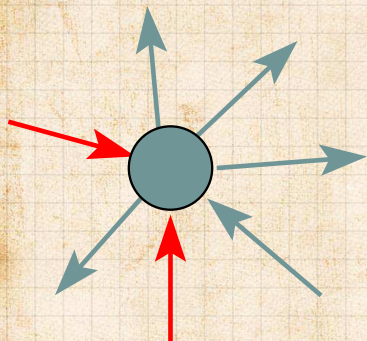
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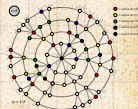
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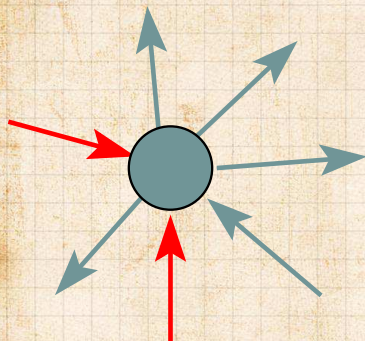
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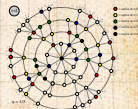
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# Spreading on Random Networks

For random networks, we know local structure is pure branching.

Successful spreading is contingent on single edges infecting nodes.

Focus on binary case with edges and nodes either infected or not.

First big question: for a given network and contagion process, can global spreading from a single seed occur?

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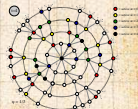
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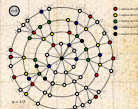
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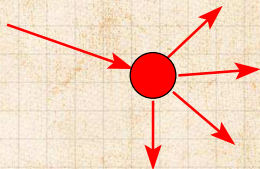


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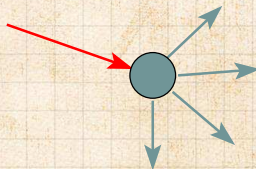
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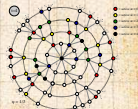
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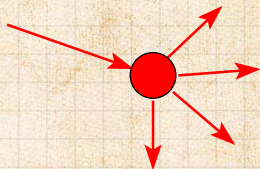


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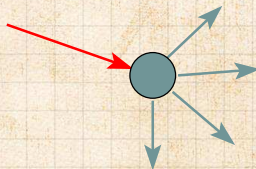
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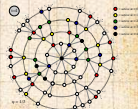
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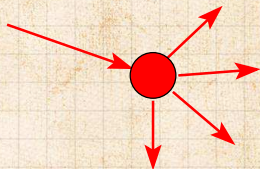


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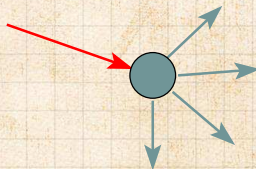
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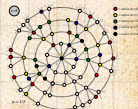
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# Global spreading condition



We need to find: [5]

**R** = the average # of infected edges that one random infected edge brings about.



Call **R** the **gain ratio**.



Define  $B_{k1}$  as the probability that a node of degree  $k$  is infected by a single infected edge.



$$\begin{aligned}
 \mathbf{R} = & \sum_{k=0}^{\infty} \frac{kP_k}{\langle k \rangle} \cdot \frac{(k-1)}{\text{\# outgoing infected edges}} \cdot \frac{B_{k1}}{\text{Prob. of infection}} \\
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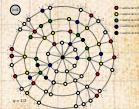
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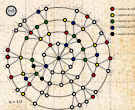
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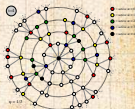
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Basic Contagion Models

Global spreading condition

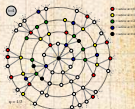
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# Global spreading condition



We need to find: [5]

**R** = the average # of infected edges that one random infected edge brings about.



Call **R** the **gain ratio**.



Define  $B_{k1}$  as the probability that a node of degree  $k$  is infected by a single infected edge.



$$R = \sum_{k=0}^{\infty} \frac{kP_k}{\langle k \rangle} \cdot \underbrace{(k-1)}_{\substack{\# \text{ outgoing} \\ \text{infected} \\ \text{edges}}} \cdot \underbrace{B_{k1}}_{\substack{\text{Prob. of} \\ \text{infection}}}$$

prob. of connecting to a degree  $k$  node

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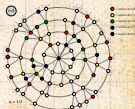
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Basic Contagion Models

Global spreading condition

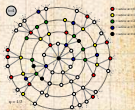
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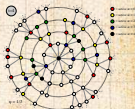
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Basic Contagion Models

Global spreading condition

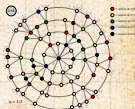
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# Global spreading condition

 Our global spreading condition is then:

$$\mathbf{R} = \sum_{k=0}^{\infty} \frac{kP_k}{\langle k \rangle} \bullet (k-1) \bullet B_{k1} > 1.$$

 **Case 1.** If  $B_{k1} = 1$  then

$$\mathbf{R} = \sum_{k=0}^{\infty} \frac{kP_k}{\langle k \rangle} \bullet (k-1) = \frac{\langle k(k-1) \rangle}{\langle k \rangle} > 1.$$

 **Case 2.** This is just our giant component condition again.

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Global spreading condition

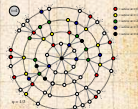
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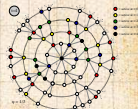
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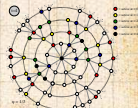
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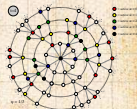
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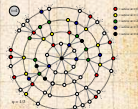
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# Global spreading condition

Case 2: If  $B_{k+1} = \beta < 1$  then

$$R = \sum_{k=0}^{\infty} \frac{k P_k}{\langle k \rangle} \cdot (k-1) \cdot \beta > 1$$

- A fraction  $(1-\beta)$  of edges do not transmit infection.
- Analogous phase transition to giant component case but critical value of  $\langle k \rangle$  is increased.
- Aka bond percolation  $\square$
- Resulting degree distribution  $\tilde{P}_k$ :

$$\tilde{P}_k = \beta^k \sum_{i=k}^{\infty} \binom{i}{k} (1-\beta)^{i-k} P_i$$

Insert question from assignment 9  $\square$

- We can show  $F_{\tilde{P}}(x) = F_P(\beta x + 1 - \beta)$ .

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Global spreading condition

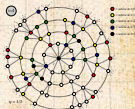
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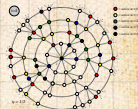
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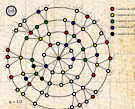
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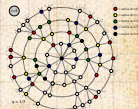
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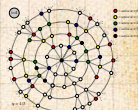
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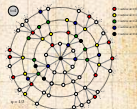
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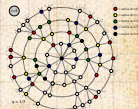
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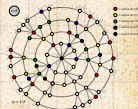
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# Global spreading condition

COCoNuTS



**Cases 3, 4, 5, ...:** Now allow  $B_{k,l}$  to depend on  $l$



**Asymmetry:** Transmission along an edge depends on nodes degree at other end.



**Possibility:**  $B_{k,l}$  increases with  $k$ ... unlikely.



**Possibility:**  $B_{k,l}$  is not monotonic in  $k$ ... unlikely.



**Possibility:**  $B_{k,l}$  decreases with  $k$ ... hmmm



$B_{k,l} \sim \frac{1}{k}$  is a plausible representation of a simple kind of social contagion.



**The story:**

More well connected people are harder to influence.

Basic Contagion Models

Global spreading condition

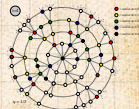
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# Global spreading condition

COcoNuTS

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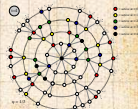
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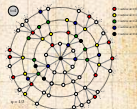
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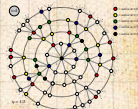
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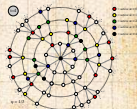
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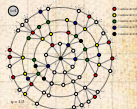
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# Global spreading condition

-  **Cases 3, 4, 5, ...:** Now allow  $B_{k1}$  to depend on  $k$
-  **Asymmetry:** Transmission along an edge depends on node's degree at other end.
-  **Possibility:**  $B_{k1}$  increases with  $k...$  **unlikely.**
-  **Possibility:**  $B_{k1}$  is not monotonic in  $k...$  **unlikely.**
-  **Possibility:**  $B_{k1}$  decreases with  $k...$  hmmm
-   $B_{k1} \searrow$  is a plausible representation of a simple kind of social contagion.
-  **The story:**  
More well connected people are harder to influence.

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Global spreading condition

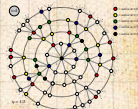
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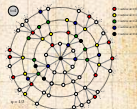
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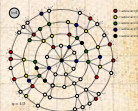
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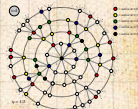
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Since  $R$  is always less than 1, no spreading can occur for this mechanism.



Decay of  $B_{k1}$  is too fast.



Result is independent of degree distribution.

Basic Contagion Models

Global spreading condition

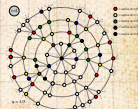
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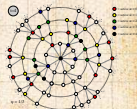
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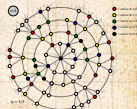
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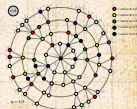
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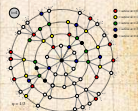
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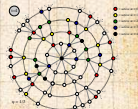
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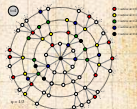
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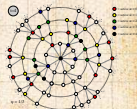
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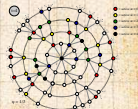
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**Example:**  $B_{k1} = H\left(\frac{1}{k} - \phi\right)$

where  $0 < \phi \leq 1$  is a **threshold** and  $H$  is the Heaviside function .



Infection only occurs for nodes with low degree.



Call these nodes **vulnerable**:  
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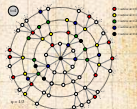
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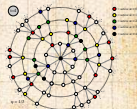
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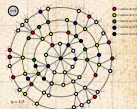
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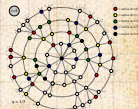
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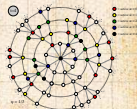
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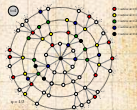
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# Global spreading condition

- The uniform threshold model global spreading condition:

$$\mathbf{R} = \sum_{k=1}^{\lfloor \frac{1}{\phi} \rfloor} (k-1) \cdot \frac{kP_k}{\langle k \rangle} > 1.$$

- As  $\phi \rightarrow 0$ , all nodes become resilient and  $r \rightarrow 0$ .
- As  $\phi \rightarrow 1$ , all nodes become vulnerable and the contagion condition matches up with the giant component condition.
- Key:** If we fix  $\phi$  and then vary  $\langle k \rangle$ , we may see two phase transitions.
- Added to our standard giant component transition, we will see a cut off in spreading as nodes become more connected.

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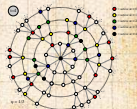
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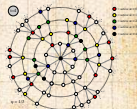
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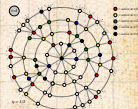
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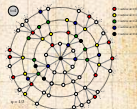
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# Global spreading condition

-  The uniform threshold model global spreading condition:

$$\mathbf{R} = \sum_{k=1}^{\lfloor \frac{1}{\phi} \rfloor} (k-1) \cdot \frac{kP_k}{\langle k \rangle} > 1.$$

-  As  $\phi \rightarrow 1$ , all nodes become resilient and  $r \rightarrow 0$ .
-  As  $\phi \rightarrow 0$ , all nodes become vulnerable and the contagion condition matches up with the giant component condition.
-  **Key:** If we fix  $\phi$  and then vary  $\langle k \rangle$ , we may see **two** phase transitions.
-  Added to our standard giant component transition, we will see a cut off in spreading as nodes become more connected.

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Global spreading condition

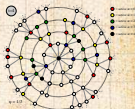
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# Virtual contagion: Corrupted Blood, a 2005 virtual plague in World of Warcraft:

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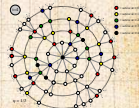
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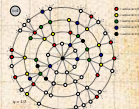
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## Some important models (recap from CSYS 300)

### Tipping models—Schelling (1971)<sup>[11, 12, 13]</sup>

- Simulation on checker boards.
- Idea of thresholds.

### Threshold models—Granovetter (1978)<sup>[14]</sup>

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- Social learning: the class of contagion cascades

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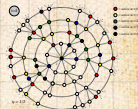
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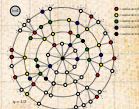
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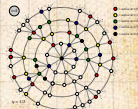
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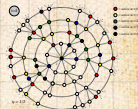
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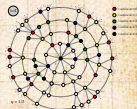
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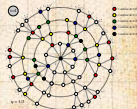
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# Threshold model on a network

COCoNuTS

Original work:



"A simple model of global cascades on random networks" 

Duncan J. Watts,  
Proc. Natl. Acad. Sci., **99**, 5766–5771,  
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Basic Contagion Models

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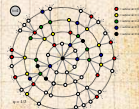
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 Individuals now have a limited view of the world





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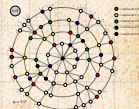
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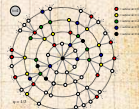
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COcoNuTS

Interactions between individuals now represented by a network

Network is **sparse**

Individual  $i$  has  $k_i$  contacts

Influence on each link is **reciprocal** and of **unit weight**

Each individual  $i$  has a fixed threshold  $\alpha_i$

Individuals repeatedly poll contacts on network

Synchronous, discrete time updating

Individual  $i$  becomes active when number of active contacts  $\alpha_i \geq \alpha_i k_i$

Activation is permanent (SI)

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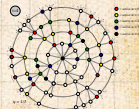
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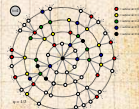
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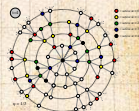
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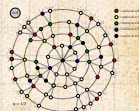
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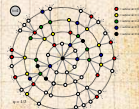
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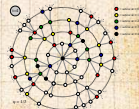
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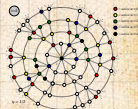
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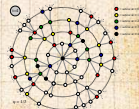
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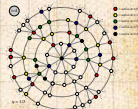
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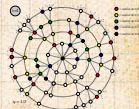
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 All nodes have threshold  $\phi = 0.2$ .





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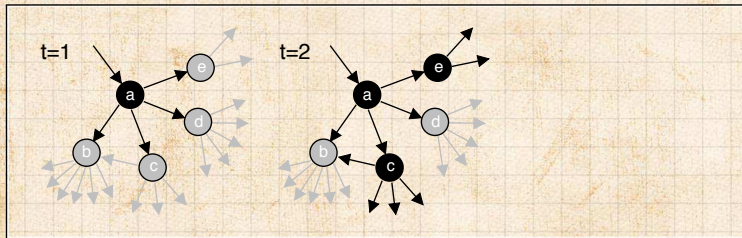
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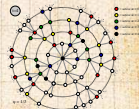
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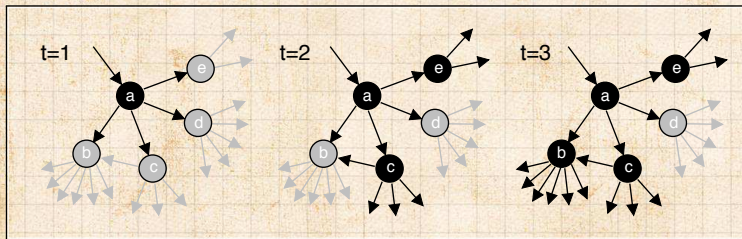
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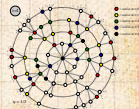
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# The most gullible

## Vulnerables:

- Recall definition: individuals who can be activated by just one contact being active are **vulnerables**.
- The vulnerability condition for node  $i$ :  $1/k_i \geq \phi_i$ .
- Means # contacts  $k_i \leq \lfloor 1/\phi_i \rfloor$ .
- Key:** For global spreading events (cascades) on random networks, must have a **global component of vulnerables**.
- For a uniform threshold  $\phi$ , our global spreading condition tells us when such a component exists:

$$R = \sum_{k=1}^{\lfloor \frac{1}{\phi} \rfloor} \frac{k P_k}{\langle k \rangle} \cdot (k-1) > 1.$$

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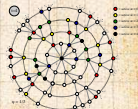
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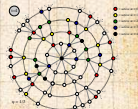
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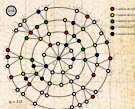
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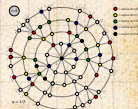
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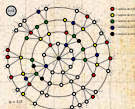
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☒ **Key:** For global spreading events (cascades) on random networks, must have a *global component of vulnerables* <sup>[15]</sup>

☒ For a uniform threshold  $\phi$ , our global spreading condition tells us when such a component exists:

$$\mathbf{R} = \sum_{k=1}^{\lfloor \frac{1}{\phi} \rfloor} \frac{k P_k}{\langle k \rangle} \bullet (k - 1) > 1.$$

Basic Contagion Models

Global spreading condition

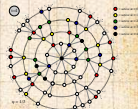
Social Contagion Models

Network version  
All-to-all networks

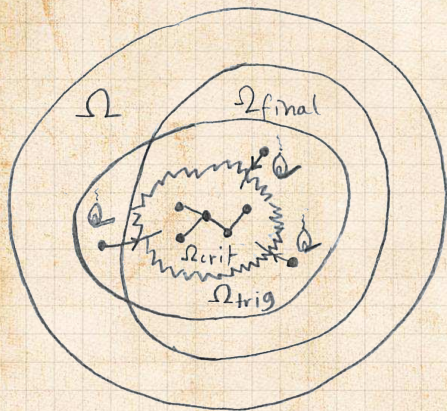
Theory


Spreading possibility  
Spreading probability  
Physical explanation  
Final size


References





# Example random network structure:



  $\Omega_{crit}$  = critical mass = global vulnerable component

  $\Omega_{trig}$  = triggering component

  $\Omega_{final}$  = potential extent of spread

  $\Omega$  = entire network

Basic Contagion Models

Global spreading condition

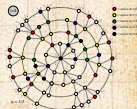
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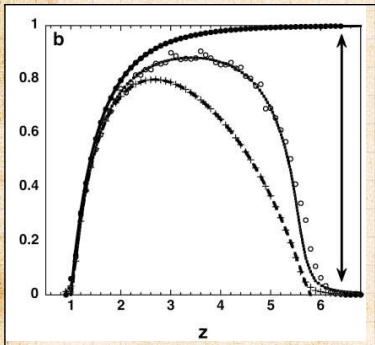
References



$$\Omega_{crit} \subset \Omega_{trig}; \Omega_{crit} \subset \Omega_{final}; \text{ and } \Omega_{trig}, \Omega_{final} \subset \Omega.$$



# Global spreading events on random networks <sup>[15]</sup>



$$z = \langle k \rangle$$



**Top curve:** final fraction infected if successful.



**Middle curve:** chance of starting a global spreading event (cascade).



**Bottom curve:** fractional size of vulnerable subcomponent. <sup>[15]</sup>

Global spreading events occur only if size of vulnerable subcomponent  $> 0$ .

System is robust-yet-fragile just below upper boundary <sup>[3, 4, 14]</sup>

'Ignorance' facilitates spreading.

Basic Contagion Models

Global spreading condition

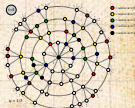
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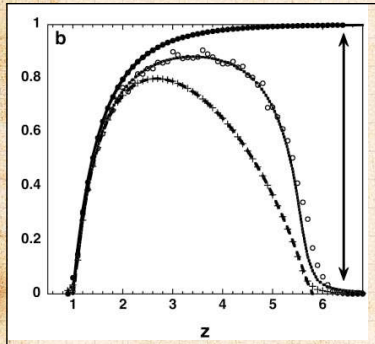
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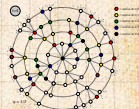
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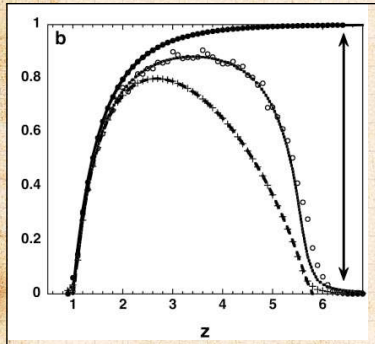
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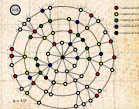
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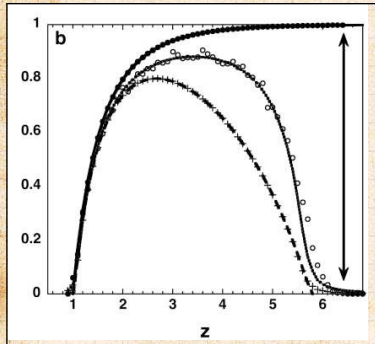
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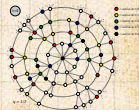
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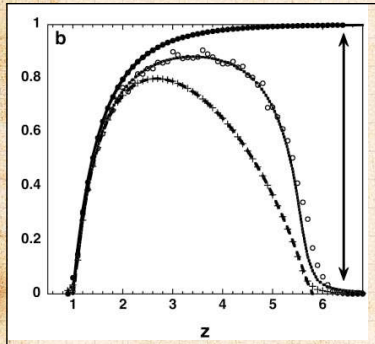
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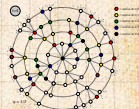
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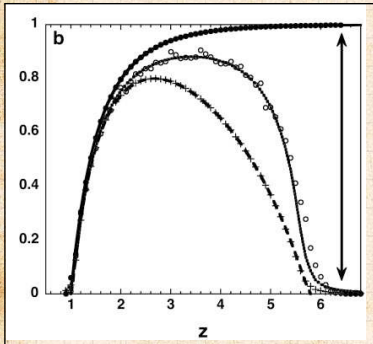
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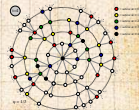
Social Contagion Models

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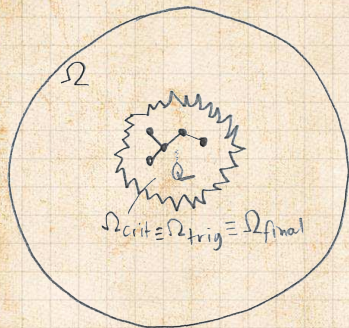
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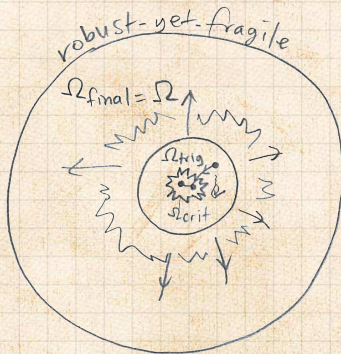





# Cascades on random networks



 Above lower phase transition



 Just below upper phase transition

Basic Contagion Models

Global spreading condition

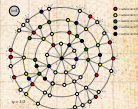
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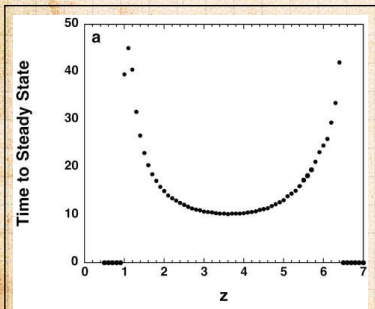
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# Cascades on random networks



Time taken for cascade to spread through network. <sup>[15]</sup>



Two phase transitions.

(n.b.,  $z = \langle k \rangle$ )



Largest vulnerable component = critical mass.



Now have endogenous mechanism for spreading from an individual to the critical mass and then beyond.

Basic Contagion Models

Global spreading condition

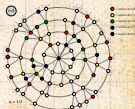
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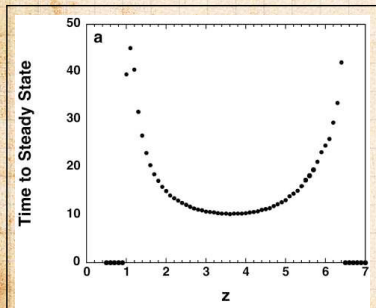
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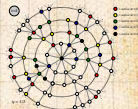
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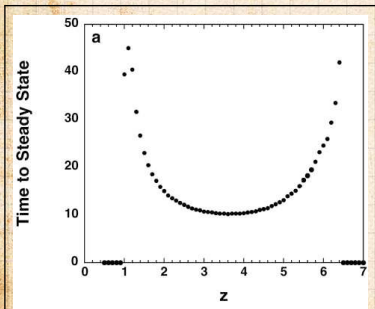
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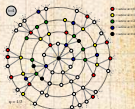
Social Contagion Models

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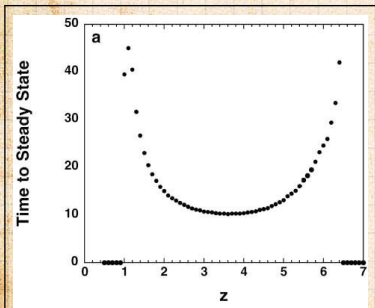
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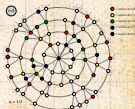
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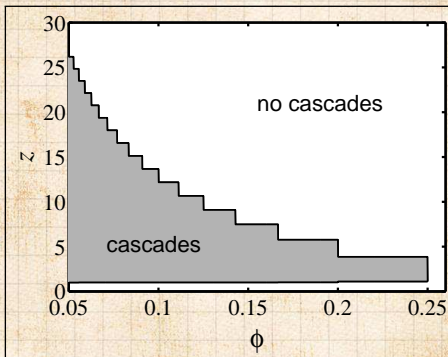
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# Cascade window for random networks



(n.b.,  $z = \langle k \rangle$ )

 Outline of cascade window for random networks.

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Global spreading condition

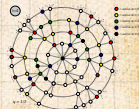
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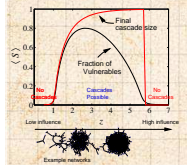
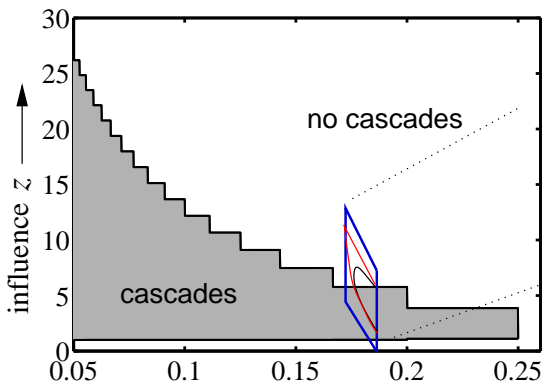
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# Cascade window for random networks



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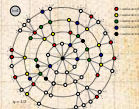
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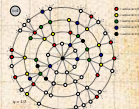
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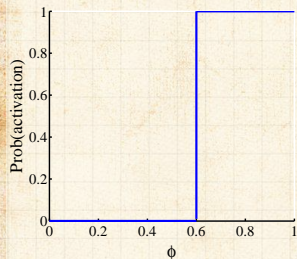
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## Granovetter's Threshold model—recap



Assumes deterministic response functions



$\phi_*$  = threshold of an individual.



$f(\phi_*)$  = distribution of thresholds in a population.



$F(\phi_*)$  = cumulative distribution =  $\int_{\phi'_*=0}^{\phi_*} f(\phi'_*)d\phi'_*$



$\phi_t$  = fraction of people 'rioting' at time step  $t$ .

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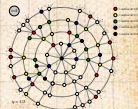
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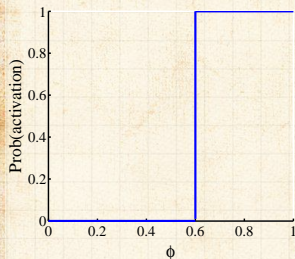
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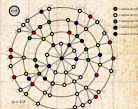
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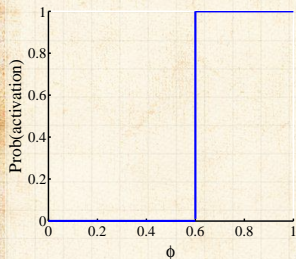
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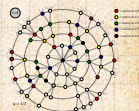
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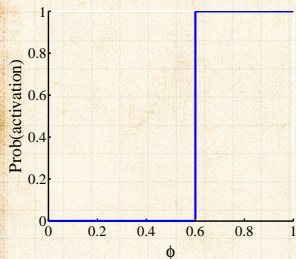
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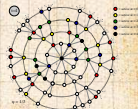
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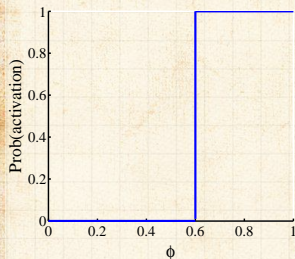
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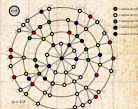
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At time  $t + 1$ , fraction rioting = fraction with

$$\phi_* \leq \phi_t.$$



$$\phi_{t+1} = \int_0^{\phi_t} f(\phi_*) d\phi_* = F(\phi_*) \Big|_0^{\phi_t} = F(\phi_t)$$



⇒ Iterative maps of the unit interval  $[0, 1]$ .

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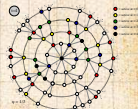
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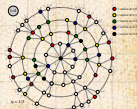
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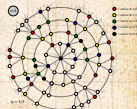
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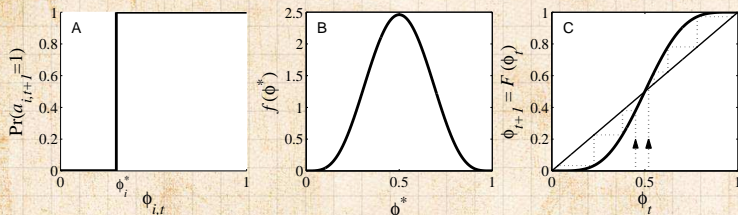


$\Rightarrow$  Iterative maps of the unit interval  $[0, 1]$ .



# Social Sciences—Threshold models

Action based on perceived behavior of others.



- Two states: S and I
- Recover now possible (SIS)
- $\phi$  = fraction of contacts 'on' (e.g., rioting)
- Discrete time, synchronous update (strong assumption!)
- This is a **critical mass model**

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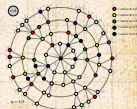
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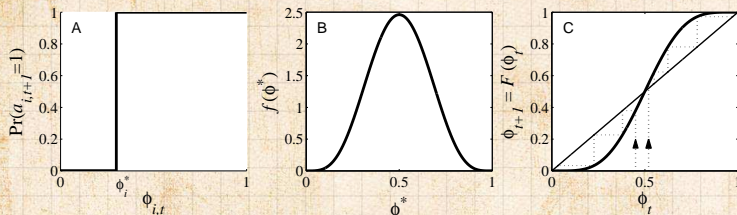
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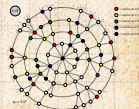
Spreading possibility

Spreading probability

Physical explanation

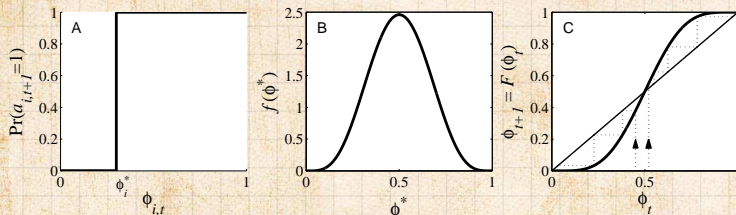
Final size

References





Action based on perceived behavior of others.



- Two states: S and I
- Recover now possible (SIS)
- $\phi$  = fraction of contacts 'on' (e.g., rioting)
- Discrete time, synchronous update (strong assumption!)
- This is a **Critical mass model**

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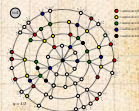
Spreading possibility

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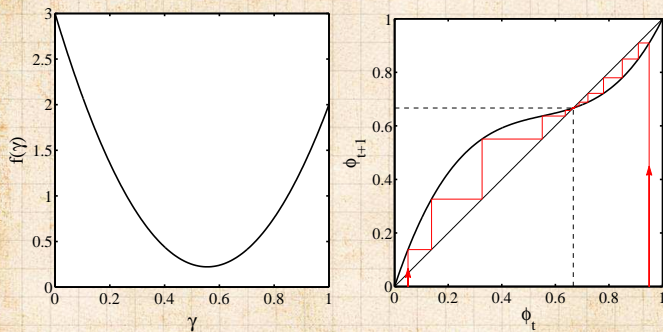
Physical explanation

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# Social Sciences—Threshold models



 Example of single stable state model

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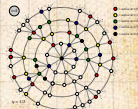
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## Implications for collective action theory:

1. Collective uniformity  $\Rightarrow$  individual uniformity
2. Small individual changes  $\Rightarrow$  large global changes

## Next:

- Connect mean-field model to network model.
- Single seed for network model:  $1/N \rightarrow 0$ .
- Comparison between network and mean-field model sensible for vanishing seed size for the latter.

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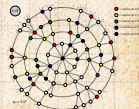
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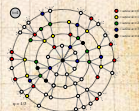
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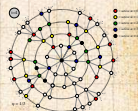
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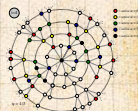
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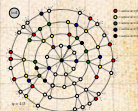
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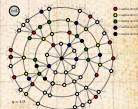
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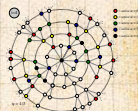
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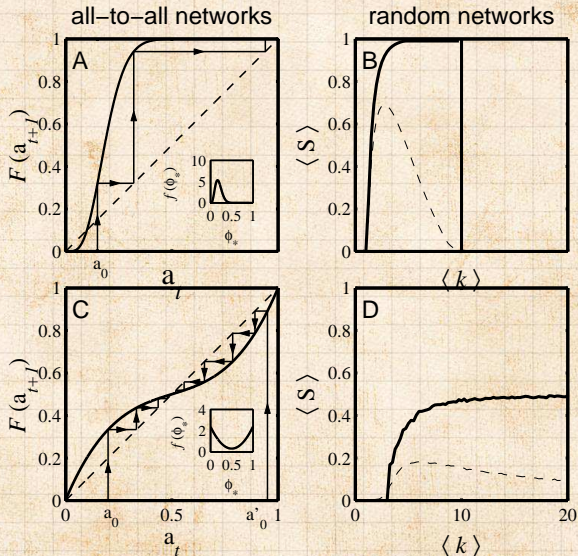
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# All-to-all versus random networks



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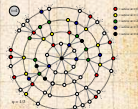
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# Spreadworthiness: Cat videos

## Bowling with Ragdolls:

COcoNuTS

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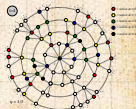
Final size

References

<https://www.youtube.com/v/XX-g2nmqL9Q?rel=0>

 Organic extreme outlier?

 Success did not spread to other videos.



# Threshold contagion on random networks

COcoNuTS

Three key pieces to describe analytically:

1. The fractional size of the largest subcomponent of vulnerable nodes,  $S_{\text{vuln}}$ .
2. The chance of starting a global spreading event,  $P_{\text{trig}} = S_{\text{trig}}$ .
3. The expected final size of any successful spread,  $S$ .

• In the distribution,  $S$  is almost always 0 or 1

Basic Contagion Models

Global spreading condition

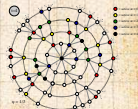
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2. The chance of starting a global spreading event,  $P_{\text{trig}} = S_{\text{trig}}$ .

3. The expected final size of any successful spread,  $S$ .

•  $S$  is the distribution on  $S$ , which is most always unimodal

Basic Contagion Models

Global spreading condition

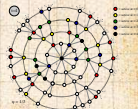
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3. The expected final size of any successful spread,  $S$ .

• In the distribution on the right, almost always spread

Basic Contagion Models

Global spreading condition

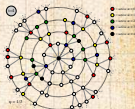
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n.b., the distribution of  $S$  is almost always bimodal.

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Global spreading condition

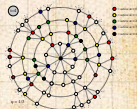
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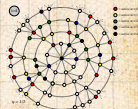
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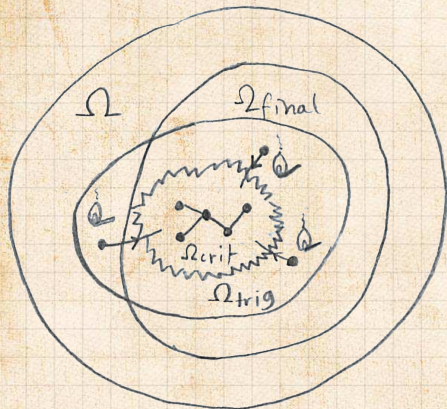
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# Example random network structure:



  $\Omega_{crit} = \Omega_{vuln} =$   
critical mass =  
global  
vulnerable  
component

  $\Omega_{trig} =$   
triggering  
component

  $\Omega_{final} =$   
potential  
extent of  
spread

  $\Omega =$  entire  
network

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Global spreading  
condition

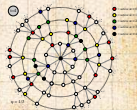
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$$\Omega_{crit} \subset \Omega_{trig}; \Omega_{crit} \subset \Omega_{final}; \text{ and } \Omega_{trig}, \Omega_{final} \subset \Omega.$$

# Outline

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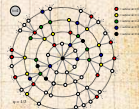
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# Threshold contagion on random networks

 **First goal:** Find the largest component of vulnerable nodes.

 Recall that for finding the giant component's size, we had to solve:

$$F_V(x) = xF_P(F_V(x)) \text{ and } F_P(x) = xF_R(F_V(x))$$

 We'll find a similar result for the subset of nodes that are vulnerable.

 This is a node-based percolation problem.

 For a general monotonic threshold distribution  $f(\phi)$ , a degree  $k$  node is vulnerable with probability

$$B_{k,1} = \int_0^{1/k} f(\phi) d\phi.$$

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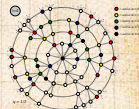
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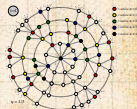
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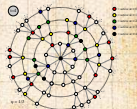
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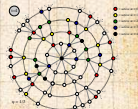
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 We'll find a similar result for the subset of nodes that are vulnerable.

 This is a node-based percolation problem.

 For a general monotonic threshold distribution  $f(\phi)$ , a degree  $k$  node is vulnerable with probability

$$B_{k1} = \int_0^{1/k} f(\phi) d\phi.$$

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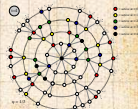
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# Threshold contagion on random networks



We now have a generating function for the probability that a randomly chosen node is vulnerable and has degree  $k$ :

$$F_P^{(\text{vuln})}(x) = \sum_{k=0}^{\infty} P_k B_{k1} x^k.$$



The generating function for friends-of-friends distribution is similar to before:

$$F_R^{(\text{vuln})}(x) = \sum_{k=0}^{\infty} \frac{k P_k}{\langle k \rangle} B_{k1} x^{k-1} = \frac{\frac{d}{dx} F_P^{(\text{vuln})}(x)}{\frac{d}{dx} F_P(x)} = \frac{\frac{d}{dx} F_R^{(\text{vuln})}(x)}{F_R(x)}$$



Note that we still have the underlying degree distribution involved in the denominator.

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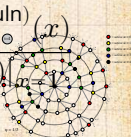
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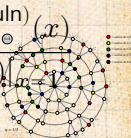
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# Threshold contagion on random networks

Functional relations for component size g.f.'s are almost the same ...

$$F_{\pm}^{(\text{vuln})}(x) = \underbrace{1 - F_P^{(\text{vuln})}(1)}_{\substack{\text{central node} \\ \text{is not} \\ \text{vulnerable}}} + x F_P^{(\text{vuln})}(F_P^{(\text{vuln})}(x))$$

$$F_0^{(\text{vuln})}(x) = \underbrace{1 - F_R^{(\text{vuln})}(1)}_{\substack{\text{first node} \\ \text{is not} \\ \text{vulnerable}}} + x F_R^{(\text{vuln})}(F_P^{(\text{vuln})}(x))$$

Can now solve as before to find

$$c_{\text{vuln}} = 1 - F_{\pm}^{(\text{vuln})}(1)$$

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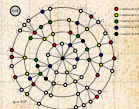
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# Threshold contagion on random networks



Functional relations for component size g.f.'s are almost the same ...

$$F_{\pi}^{(\text{vuln})}(x) = \underbrace{1 - F_P^{(\text{vuln})}(1)}_{\text{central node is not vulnerable}} + x F_P^{(\text{vuln})}(F_{\rho}^{(\text{vuln})}(x))$$

central node  
is not  
vulnerable

$$F_{\rho}^{(\text{vuln})}(x) = \underbrace{1 - F_R^{(\text{vuln})}(1)}_{\text{first node is not vulnerable}} + x F_R^{(\text{vuln})}(F_{\rho}^{(\text{vuln})}(x))$$

first node  
is not  
vulnerable



Can now solve as before to find

$$c_{\text{vuln}} = 1 - F_{\pi}^{(\text{vuln})}(1)$$

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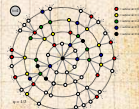
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Can now solve as before to find

$$c_{\text{vuln}} = 1 - F_{\pi}^{(\text{vuln})}(1)$$

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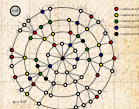
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# Threshold contagion on random networks



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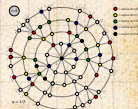
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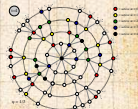
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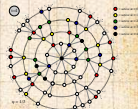
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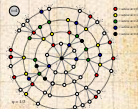
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 **Second goal:** Find probability of triggering largest vulnerable component.

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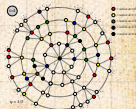
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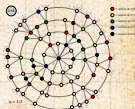
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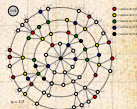
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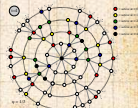
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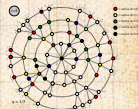
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# Physical derivation of possibility and probability of global spreading:

🧩 Possibility: binary indicator of phase. Global spreading events are either possible or can never happen.

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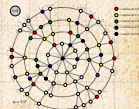
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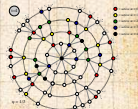
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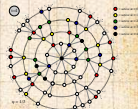
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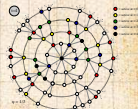
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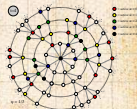
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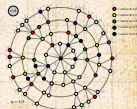
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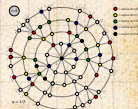
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Probability an infected edge leads to a global spreading event:

  $Q_{\text{trig}}$  must satisfy a one-step recursion relation.

 Follow an infected edge and use three pieces:

1. Probability of reaching a given  $k$  node  $P_k$
  2. The node reaches a global spreading event with probability  $B_{k1}$
  3. At least one of the node's outgoing edges leads to a global spreading event with probability  $1 - (1 - Q_{\text{trig}})^{k-1}$
- So  $Q_{\text{trig}} = \sum_k \frac{kP_k}{\langle k \rangle} \cdot B_{k1} \cdot [1 - (1 - Q_{\text{trig}})^{k-1}]$ .

 Put everything together and solve for  $Q_{\text{trig}}$ :

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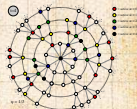
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$$Q_k = \frac{k P_k}{\langle k \rangle}$$

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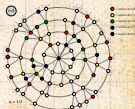
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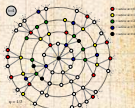
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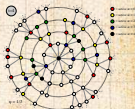
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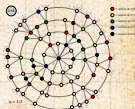
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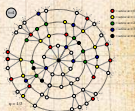
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Global spreading is possible if the fractional size  $S_{\text{vuln}}$  of the largest component of vulnerables is “giant”.

Interpret  $S_{\text{vuln}}$  as the probability a randomly chosen node is vulnerable and that infecting it leads to a global spreading event:

$$S_{\text{vuln}} = \sum_k P_k \cdot B_{k1} \cdot [1 - (1 - Q_{\text{trig}})^k] > 0.$$

Amounts to having  $Q_{\text{trig}} > 0$ .

Probability of global spreading differs only in that we don't care if the initial seed is vulnerable or not:

$$P_{\text{trig}} = S_{\text{trig}} = \sum_k P_k \cdot [1 - (1 - Q_{\text{trig}})^k]$$

As for  $S_{\text{vuln}}$ ,  $P_{\text{trig}}$  is non-zero when  $Q_{\text{trig}} > 0$ .

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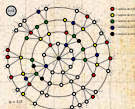
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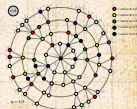
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Amounts to having  $Q_{\text{trig}} > 0$ .

Probability of global spreading differs only in that we don't care if the initial seed is vulnerable or not:

$$P_{\text{trig}} = S_{\text{trig}} = \sum_k P_k \cdot [1 - (1 - Q_{\text{trig}})^k]$$

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Basic Contagion Models

Global spreading condition

Social Contagion Models

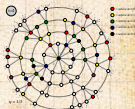
Network version  
All-to-all networks

Theory

Spreading possibility  
Spreading probability

Physical explanation  
Final size

References





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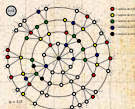
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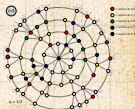
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## Connection to generating function results:

 We found that  $F_\rho^{(\text{vuln})}(1)$ —the probability that a random edge leads to a finite vulnerable component—satisfies

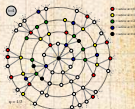
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$$Q_{\text{trig}} = \sum_{k=0}^{\infty} \frac{k P_k}{\langle k \rangle} \cdot B_{k1} \cdot \left[ 1 - (1 - Q_{\text{trig}})^{k-1} \right]$$






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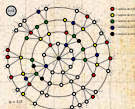
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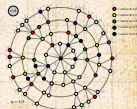
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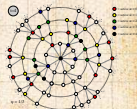
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# Fractional size of the largest vulnerable component:



The generating function approach gave

$S_{\text{vuln}} = 1 - F_{\pi}^{(\text{vuln})}(1)$  where

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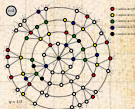
$F_P^{(\text{vuln})}(x) = \sum_{k=0}^{\infty} P_k B_{k1} x^k$ , we have:

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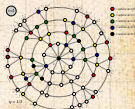
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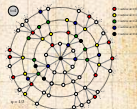
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# Triggering probability for single-seed global spreading events:

🧱 Slight adjustment to the vulnerable component calculation.

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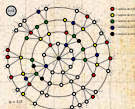
$$F_{\pi}^{(\text{trig})}(1) = 1 \cdot F_P \left( F_P^{(\text{vuln})}(1) \right).$$

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$$1 - S_{\text{trig}} = 1 + \sum_{k=0}^{\infty} P_k (1 - Q_{\text{trig}})^k.$$

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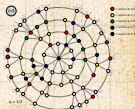
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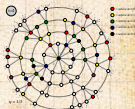
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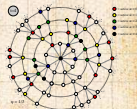
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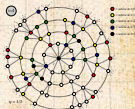
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$$\mathbf{R} = \sum_{k=0}^{\infty} \frac{kP_k}{\langle k \rangle} \cdot (k-1) \cdot B_{k1} > 1.$$

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- It really would be just so totally awesome.
- Must come from our basic edge triggering probability equation:

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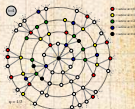
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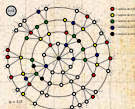
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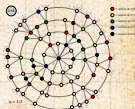
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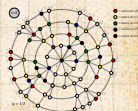
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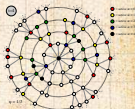
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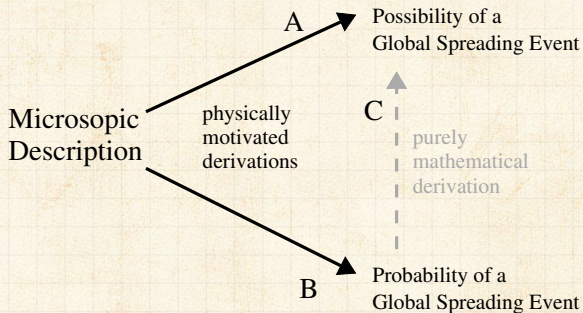
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# What we're doing:



Basic Contagion Models

Global spreading condition

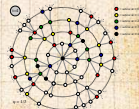
Social Contagion Models


Network version  
All-to-all networks

Theory

Spreading possibility  
Spreading probability  
Physical explanation  
Final size

References



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$$\Rightarrow Q_{\text{trig}} = \sum_k \frac{kP_k}{\langle k \rangle} \cdot B_{k1} \cdot (k-1)Q_{\text{trig}}$$

$$\Rightarrow 1 = \sum_k \frac{kP_k}{\langle k \rangle} \cdot (k-1) \cdot B_{k1}$$

 Only defines the phase transition points (i.e.,  $R = 1$ ).

 Inequality?

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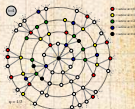
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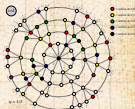
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 Only defines the phase transition points (i.e.,  $R = 1$ ).

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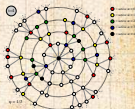
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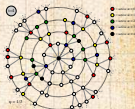
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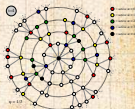
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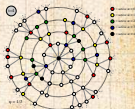
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Again take  $Q_{\text{trig}} \rightarrow 0^+$ , but keep next higher order term:

$$Q_{\text{trig}} = \sum_k \frac{k P_k}{\langle k \rangle} \cdot B_{k1} \cdot \left[ 1 - \left( 1 - (k-1)Q_{\text{trig}} + \binom{k-1}{2} Q_{\text{trig}}^2 \right) \right]$$

$$\Rightarrow Q_{\text{trig}} = \sum_k \frac{k P_k}{\langle k \rangle} \cdot B_{k1} \cdot \left[ (k-1)Q_{\text{trig}} - \binom{k-1}{2} Q_{\text{trig}}^2 \right]$$

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We have  $Q_{\text{trig}} > 0$  if  $\sum_k \frac{k P_k}{\langle k \rangle} \cdot (k-1) \cdot B_{k1} > 1$ .

Repeat: Above is a mathematical connection between two physically derived equations.

From this connection, we don't know anything about a gain ratio  $\mathbf{R}$  or how to arrange the pieces.



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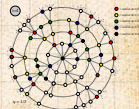
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# Threshold contagion on random networks

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 **Third goal:** Find expected fractional size of spread.

 Not obvious even for uniform threshold problem.

 Difficulty is in figuring out if and when nodes that need  $\geq 2$  hits switch on.

 Problem solved for infinite seed case by Gleeson and Cahalane:

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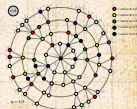
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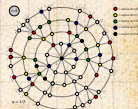
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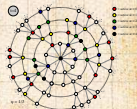
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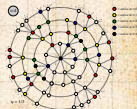
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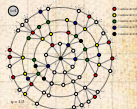
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# Expected size of spread

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- ☰ Randomly turn on a fraction  $\phi_0$  of nodes at time  $t = 0$
- ☰ Capitalize on local branching network structure of random networks (again)
- ☰ Now think about what must happen for a specific node  $i$  to become active at time  $t$ :
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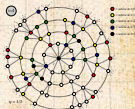
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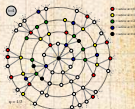
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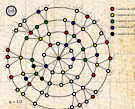
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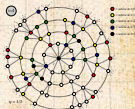
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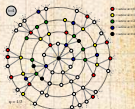
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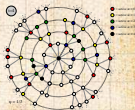
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  - $t = n$ : enough nodes within  $n$  hops of  $i$  switched on at  $t = 0$  and their effects have propagated to reach  $i$ .

Basic Contagion Models

Global spreading condition

Social Contagion Models

Network version

All-to-all networks

Theory

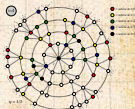
Spreading possibility

Spreading probability

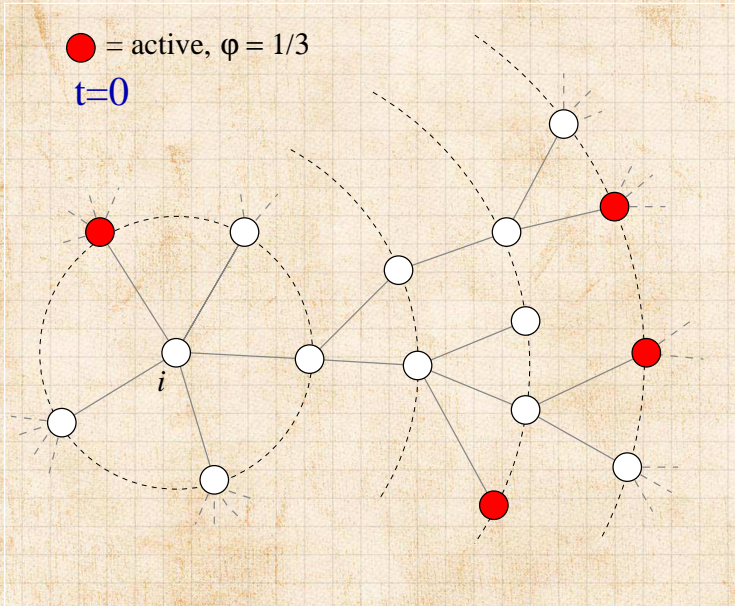
Physical explanation

Final size

References



# Expected size of spread



Basic Contagion Models

Global spreading condition

Social Contagion Models

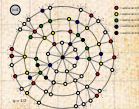
Network version  
All-to-all networks

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Spreading possibility  
Spreading probability  
Physical explanation

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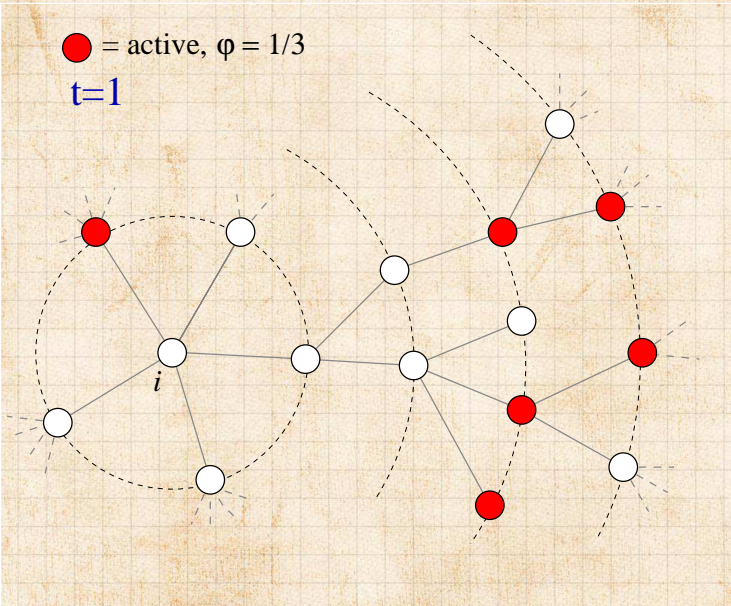




# Expected size of spread

● = active,  $\phi = 1/3$

$t=1$



Basic Contagion Models

Global spreading condition

Social Contagion Models

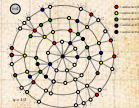
Network version  
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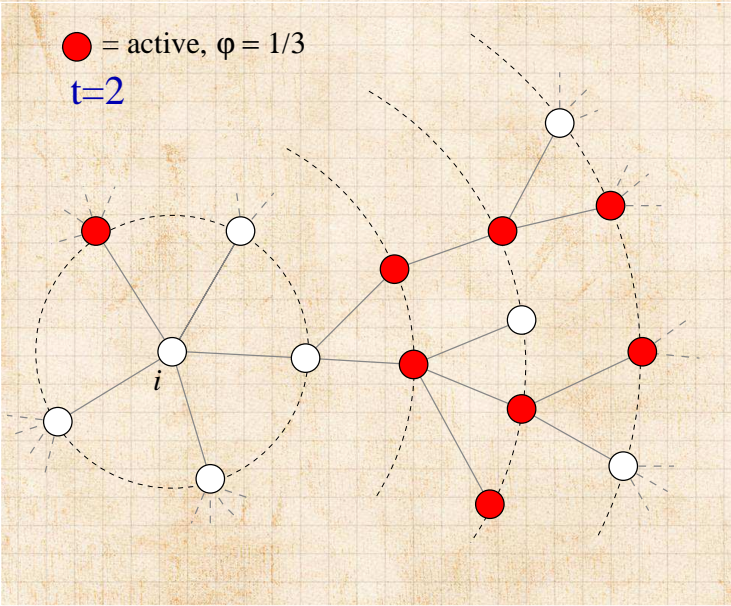
References



# Expected size of spread

● = active,  $\phi = 1/3$

$t=2$



Basic Contagion Models

Global spreading condition

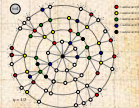
Social Contagion Models

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Spreading possibility  
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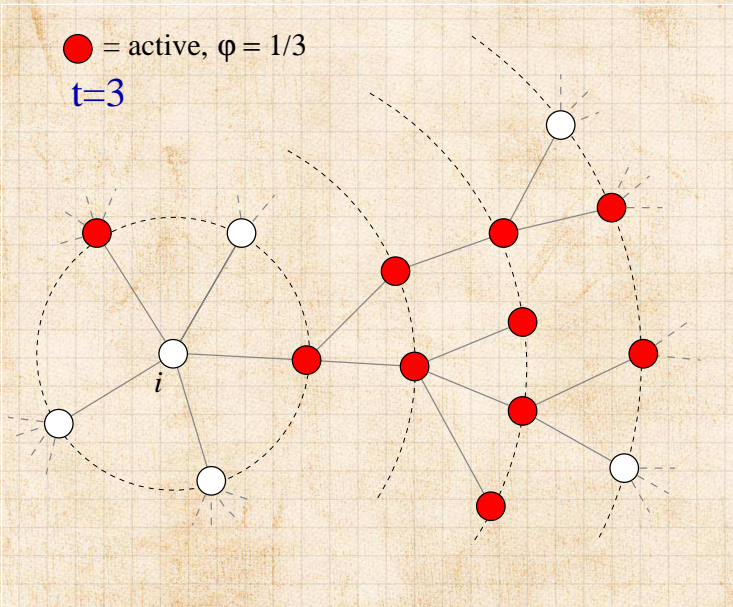
References



# Expected size of spread

● = active,  $\phi = 1/3$

$t=3$



Basic Contagion Models

Global spreading condition

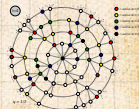
Social Contagion Models

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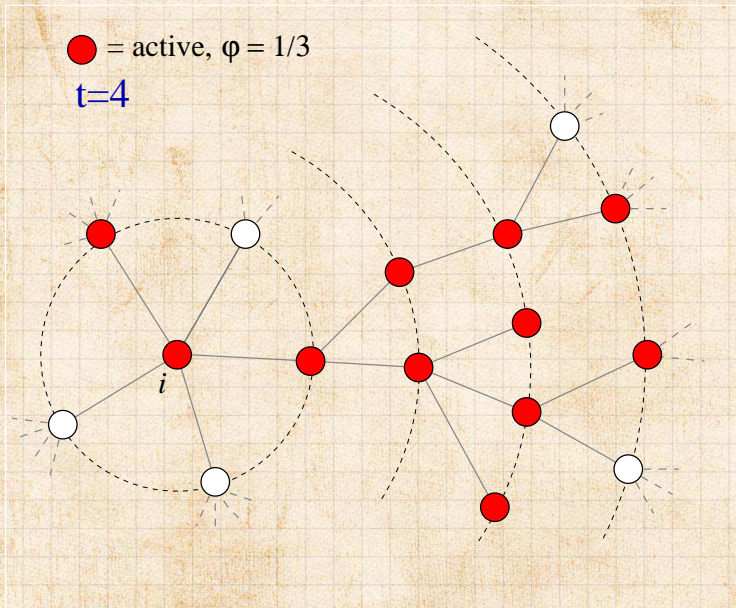
Spreading possibility  
Spreading probability  
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# Expected size of spread



Basic Contagion Models

Global spreading condition

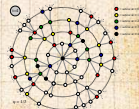
Social Contagion Models

Network version  
All-to-all networks

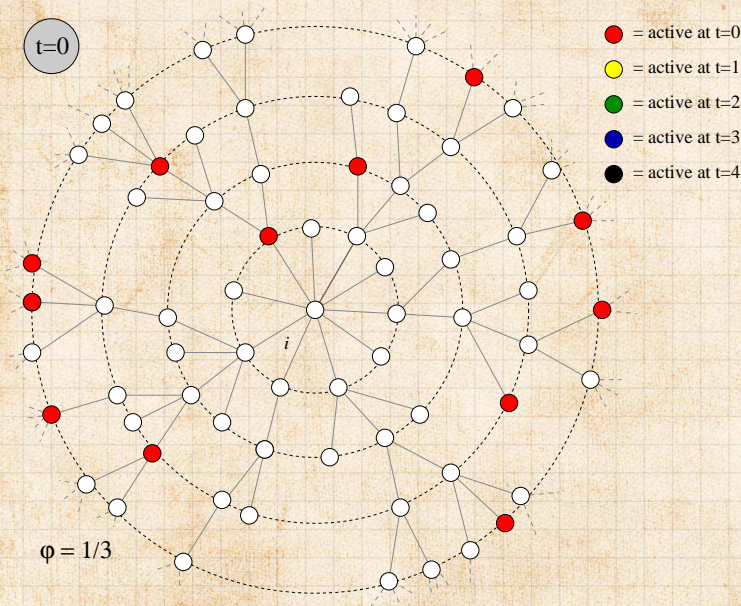
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# Expected size of spread



Basic Contagion Models

Global spreading condition

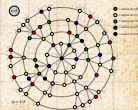
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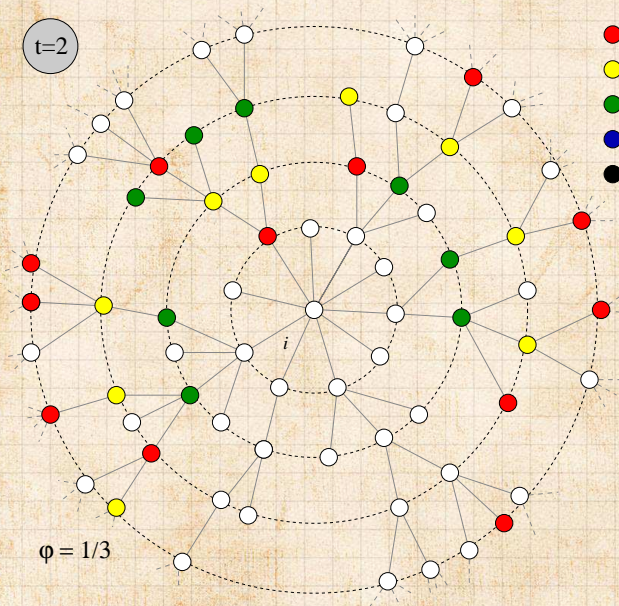
References







# Expected size of spread



- = active at  $t=0$
- = active at  $t=1$
- = active at  $t=2$
- = active at  $t=3$
- = active at  $t=4$

Basic Contagion Models

Global spreading condition

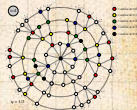
Social Contagion Models

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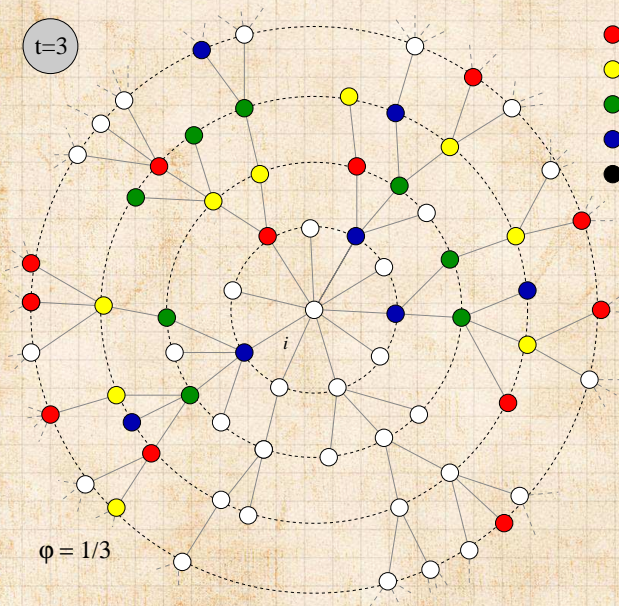
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# Expected size of spread



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- = active at  $t=1$
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Basic Contagion Models

Global spreading condition

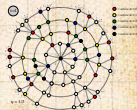
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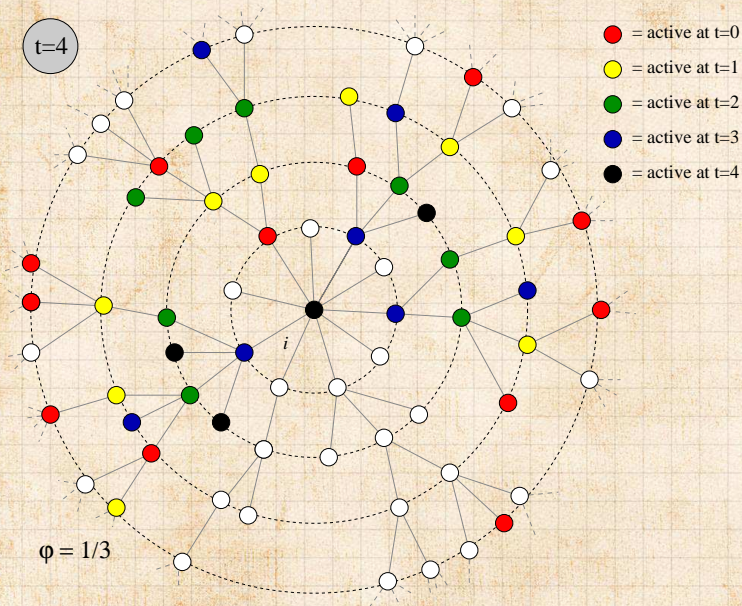
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# Expected size of spread



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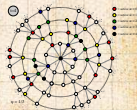
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# Expected size of spread

## Notes:

- Calculations presume nodes do not become inactive (strong restriction, liftable)
- Not just for threshold model—works for a wide range of contagion processes.
- We can analytically determine the entire time evolution, not just the final size.
- We can in fact determine  $\Pr(\text{node of degree } k \text{ switches on at time } t)$ .
- Even more, we can compute:  $\Pr(\text{specific node } i \text{ switches on at time } t)$ .
- Asynchronous updating can be handled too.

Basic Contagion Models

Global spreading condition

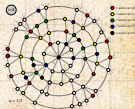
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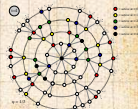
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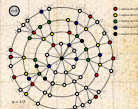
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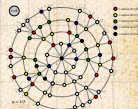
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Basic Contagion Models

Global spreading condition

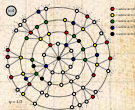
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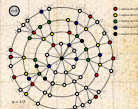
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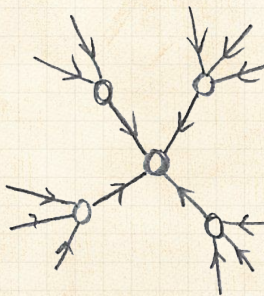
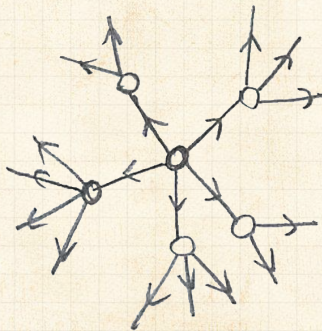


# Expected size of spread

## Pleasantness:

📦 Taking off from a single seed story is about **expansion** away from a node.

📦 Extent of spreading story is about **contraction** at a node.



Basic Contagion Models

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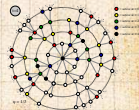
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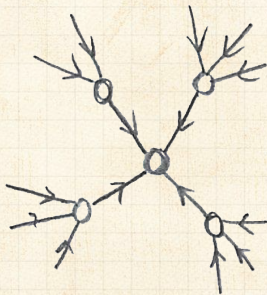
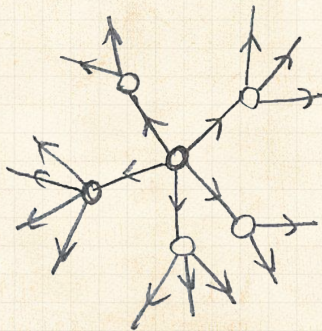
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- ☰ Extent of spreading story is about **contraction** at a node.



Basic Contagion Models

Global spreading condition

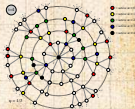
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# Expected size of spread



## Notation:

$\phi_{k,t} = \Pr(\text{a degree } k \text{ node is active at time } t).$



$B_{k,j} = \Pr(\text{a degree } k \text{ node becomes active if } j \text{ neighbors are active}).$



Our starting point:  $\phi_{k,0} = \phi_0.$



$(1 - \phi_0)^j = \Pr(j \text{ of a degree } k \text{ node's neighbors were seeded at time } t = 0).$



Probability a degree  $k$  node was a seed at  $t = 0$  is  $\phi_0$  (as above).



Probability a degree  $k$  node was not a seed at  $t = 0$  is  $1 - \phi_0$ .



Combining everything, we have:

$$\phi_{k,t} = \phi_0 + (1 - \phi_0) \sum_{j=0}^k \binom{k}{j} \phi_0^j (1 - \phi_0)^{k-j} B_{k,j}$$

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Social Contagion Models

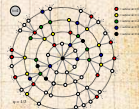
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# Expected size of spread



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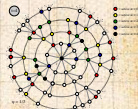
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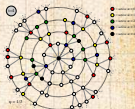
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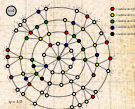
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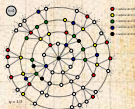
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Combining everything, we have:

$$\phi_{k,t} = \phi_0 + \sum_{j=0}^{k-1} \binom{k}{j} \phi_0^j (1 - \phi_0)^{k-j} B_{kj}$$

Basic Contagion Models

Global spreading condition

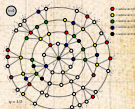
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Probability a degree  $k$  node was not a seed at  $t = 0$  is  $(1 - \phi_0).$



Combining everything, we have:

$$\phi_{k,1} = \phi_0 + (1 - \phi_0) \sum_{j=0}^k \binom{k}{j} \phi_0^j (1 - \phi_0)^{k-j} B_{kj}.$$

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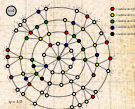
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# Expected size of spread

For general  $t$ , we need to know the probability an edge coming into a degree  $k$  node at time  $t$  is active.

**Assumption:** call this probability  $\theta_t$ .

We already know  $\theta_0 = \phi_0$ .

Story analogous to  $t = 1$  case. For specific node  $i$ :

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So we need to compute  $\theta_t, \dots$

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Theory

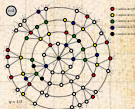
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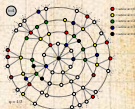
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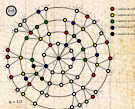
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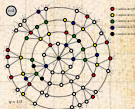
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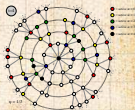
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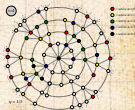
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So we need to compute  $\theta_t$ ... massive excitement...

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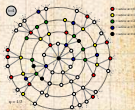
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# Expected size of spread


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  $\frac{k P_k}{\langle k \rangle} = Q_k = \mathbf{Pr}$  (edge connects to a degree  $k$  node).

  $\sum_{j=0}^{k-1}$  piece gives  $\mathbf{Pr}$  (degree node  $k$  activates if  $j$  of its  $k - 1$  incoming neighbors are active).

  $\phi_0$  and  $(1 - \phi_0)$  terms account for state of node at time  $t = 0$ .

 See this all generalizes to give  $\theta_{t+1}$  in terms of  $\theta_t \dots$

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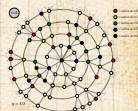
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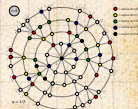
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# Expected size of spread

Two pieces: edges first, and then nodes

$$1. \theta_{t+1} = \underbrace{\phi_0}_{\text{exogenous}}$$

$$+(1 - \phi_0) \underbrace{\sum_{k=1}^{\infty} \frac{k P_k}{\langle k \rangle} \sum_{j=0}^{k-1} \binom{k-1}{j} \theta_t^j (1 - \theta_t)^{k-1-j} B_{kj}}_{\text{social effects}}$$

with  $\theta_0 = \phi_0$ .

$$2. \phi_{t+1} =$$

$$\underbrace{\phi_0}_{\text{exogenous}} + (1 - \phi_0) \underbrace{\sum_{k=0}^{\infty} P_k \sum_{j=0}^k \binom{k}{j} \theta_t^j (1 - \theta_t)^{k-j} B_{kj}}_{\text{social effects}}$$

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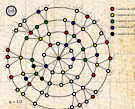
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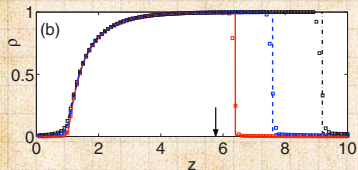
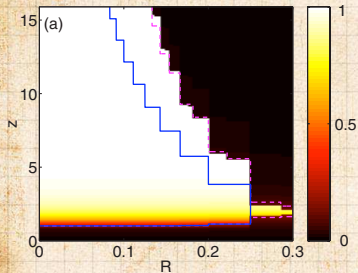
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# Comparison between theory and simulations



From Gleeson and Cahalane [7]



Pure random networks with simple threshold responses



$R =$  uniform threshold (our  $\phi_*$ );  $z =$  average degree;  $\rho = \phi$ ;  $q = \theta$ ;  $N = 10^5$ .



$\phi_0 = 10^{-3}$ ,  $0.5 \times 10^{-2}$ , and  $10^{-2}$ .



Cascade window is for  $\phi_0 = 10^{-2}$  case.



Sensible expansion of cascade window as  $\phi_0$  increases.

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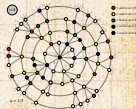
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First, if self-starters are present, some activation is assured:

$$G(0; \phi_0) = \sum_{k=1}^{\infty} \frac{k P_k}{\langle k \rangle} \bullet B_{k0} > 0$$

meaning  $B_{k0} > 0$  for at least one value of  $k \geq 1$ .

If  $\theta = 0$  is a fixed point of  $G$  (i.e.,  $G(0; \phi_0) = 0$ ) then spreading occurs for a small seed if

$$G'(0; \phi_0) = \sum_{k=0}^{\infty} \frac{k P_k}{\langle k \rangle} \bullet (k-1) \bullet B_{k1} > 1.$$

Insert question from assignment 10 

Basic Contagion Models

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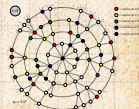
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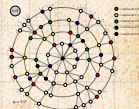
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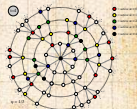
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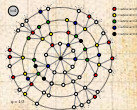
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## In words:

🧩 If  $G(0; \phi_0) > 0$ , spreading must occur because some nodes turn on for free.

🧩 If  $G$  has an **unstable fixed point** at  $\theta = 0$ , then cascades are also always possible.

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🧩 Cascade condition is more complicated for  $\phi_0 > 0$ .

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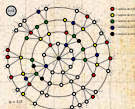
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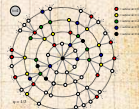
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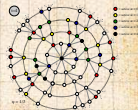
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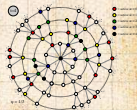
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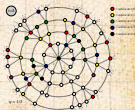
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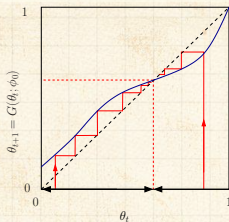
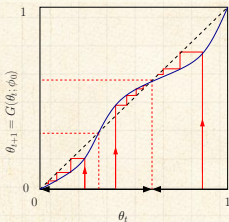
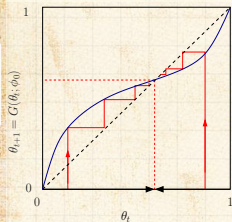
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# General fixed point story:



Given  $\theta_0 (= \phi_0)$ ,  $\theta_\infty$  will be the nearest stable fixed point, either above or below.

n.b., adjacent fixed points must have opposite stability types.

**Important:** Actual form of  $G$  depends on  $\phi_0$ .

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Basic Contagion Models

Global spreading condition

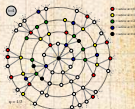
Social Contagion Models

Network version  
All-to-all networks

Theory

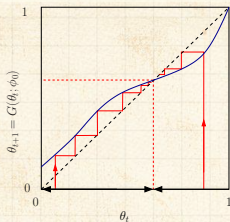
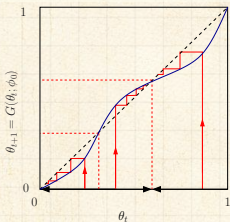
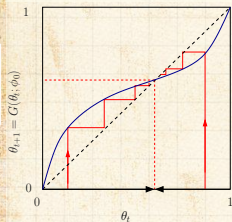
Spreading possibility  
Spreading probability  
Physical explanation  
Final size

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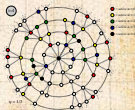
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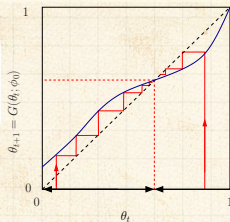
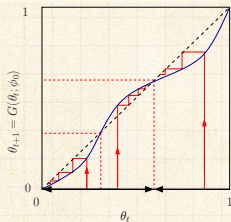
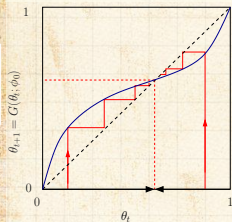
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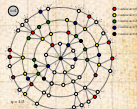
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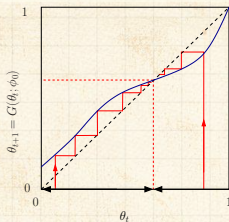
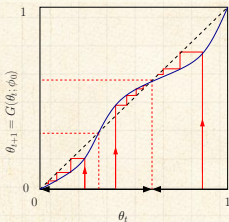
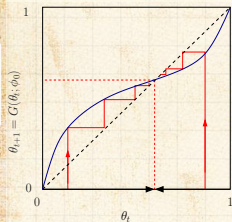
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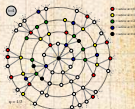
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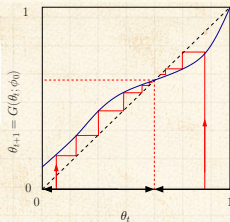
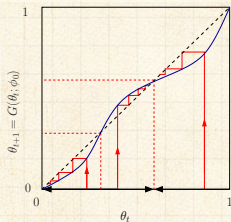
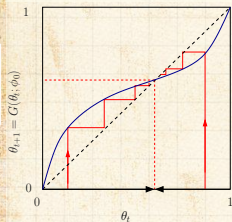
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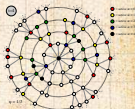
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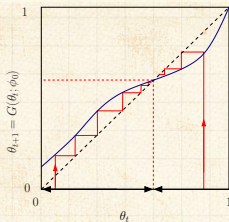
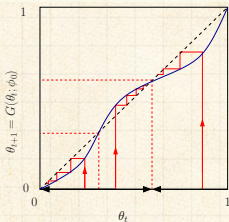
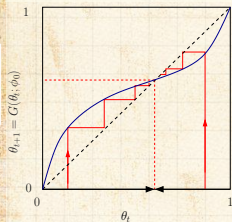
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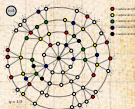
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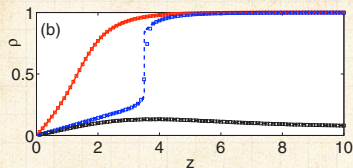
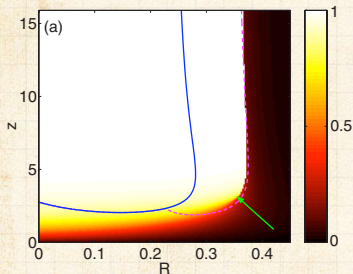
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Final size

References



## Interesting behavior:



Now allow thresholds to be distributed according to a Gaussian with mean  $R$ .



$R = 0.2, 0.362,$  and  $0.38; \sigma = 0.2.$



$\phi_0 = 0$  but some nodes have thresholds  $\leq 0$  so effectively  $\phi_0 > 0$ .



Now see a (nasty) discontinuous phase transition for low  $\langle k \rangle$ .

Basic Contagion Models

Global spreading condition

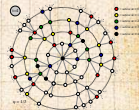
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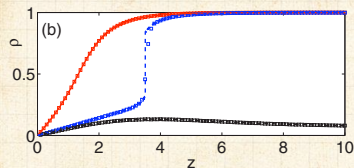
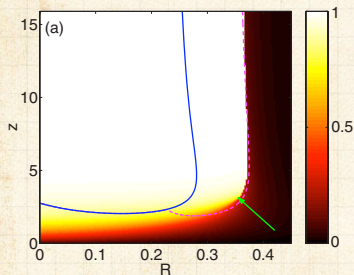
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From Gleeson and Cahalane [7]



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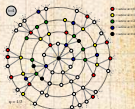
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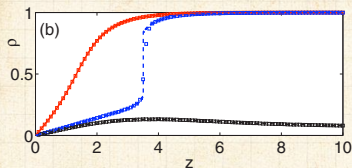
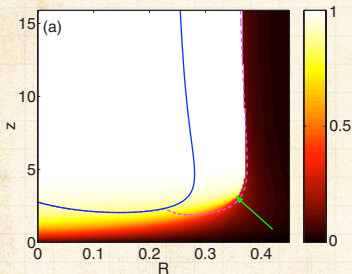
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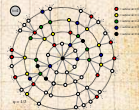
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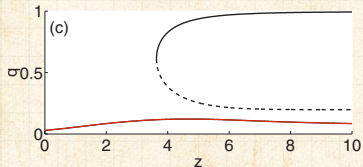
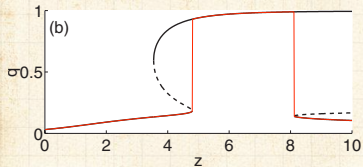
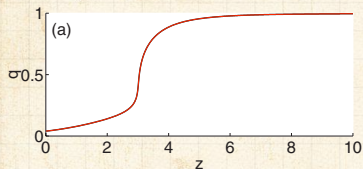
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## Interesting behavior:



Plots of stability points for  $\theta_{t+1} = G(\theta_t; \phi_0)$ .



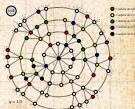
n.b.: 0 is not a fixed point here:  $\theta_0 = 0$  always takes off.



Top to bottom:  $R = 0.35, 0.371, \text{ and } 0.375$ .



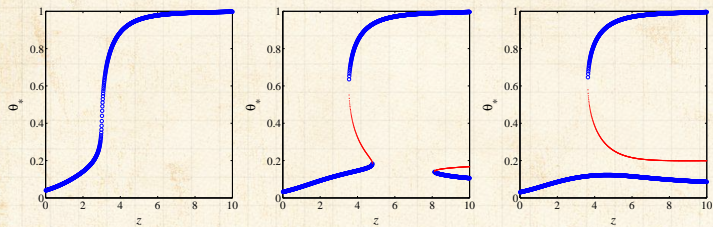
Saddle node bifurcations appear and merge (b and c).



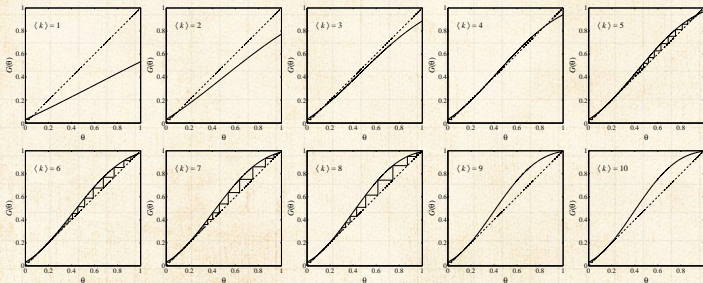
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# What's happening:



Fixed points slip above and below the  $\theta_{t+1} = \theta_t$  line:



Basic Contagion Models

Global spreading condition

Social Contagion Models

Network version

All-to-all networks

Theory

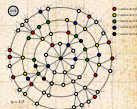
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## Synchronous update

- Done: Evolution of  $\phi_t$  and  $\theta_t$  given exactly by the maps we have derived.

## Asynchronous updates

- Update nodes with probability  $\alpha$
- As  $\alpha \rightarrow 0$ , updates become effectively independent
- Now can talk about  $\langle \phi \rangle$  and  $\langle \theta \rangle$

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Global spreading condition

Social Contagion Models

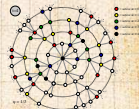
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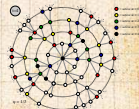
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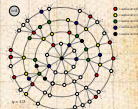
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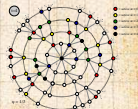
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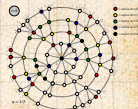
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# Nutshell:

 Solid dive into understanding contagion on generalized random networks.


 Threshold model leads to idea of vulnerables and a critical mass. [15-21]

 Generating function approaches provided first breakthroughs and gave possibility and probability of spreading. [10, 16]

 Later: A probabilistic, physical method solved the whole story for a fractional seed—final size, dynamics, ... [7, 6]

 Much can be generalized for more realistic kinds of networks: degree-correlated, modular, bipartite, ...

 The single seed contagion condition and triggering probability can be fully developed using a physical story. [5, 9]

 Many connections to other kinds of models: Voter models, Ising models, ...

COCoNuTS

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Global spreading condition

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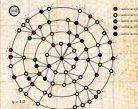
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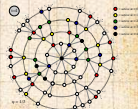
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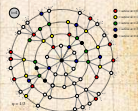
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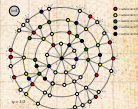
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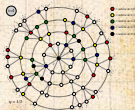
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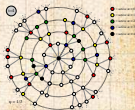
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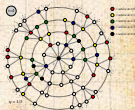
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- Generating function approaches provided first breakthroughs and gave possibility and probability of spreading. [10, 16]
- Later: A probabilistic, physical method solved the whole story for a fractional seed—final size, dynamics, ... [7, 6]
- Much can be generalized for more realistic kinds of networks: degree-correlated, modular, bipartite, ...
- The single seed contagion condition and triggering probability can be fully developed using a physical story. [5, 9]
- Many connections to other kinds of models: Voter models, Ising models, ...





# Nutshell:

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# Neural reboot (NR):

Pangolin happiness:

COcoNuTS

Basic Contagion  
Models

Global spreading  
condition

Social Contagion  
Models

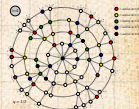
Network version  
All-to-all networks

Theory

Spreading possibility  
Spreading probability  
Physical explanation



Final size

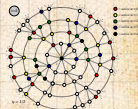
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<https://www.youtube.com/v/LMiYjkG4onM?rel=0>

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Basic Contagion Models

Global spreading condition

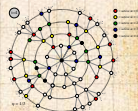
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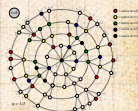
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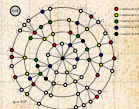
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