

Contagion

Last updated: 2018/03/23, 12:08:15

Complex Networks | @networksvox
CSYS/MATH 303, Spring, 2018

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

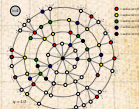
Social Contagion Models

Network version
All-to-all networks

Theory

Spreading possibility
Spreading probability
Physical explanation
Final size

References



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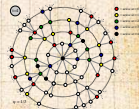
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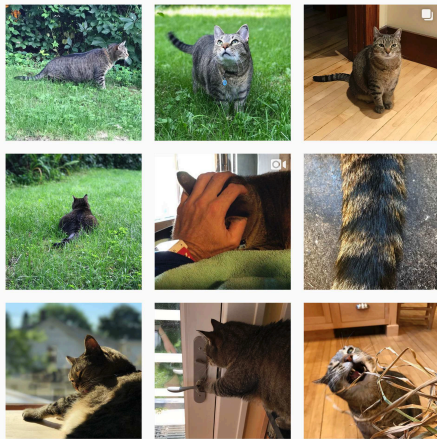
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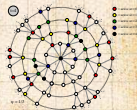
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 On Instagram at [pratchett_the_cat](https://www.instagram.com/pratchett_the_cat) 



Outline

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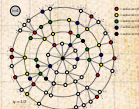
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Contagion models

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Some large questions concerning network contagion:

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?
3. How do the **details** of the network affect the outcome?
4. How do the **details** of the spreading mechanism affect the outcome?
5. What if the seed is one or many nodes?

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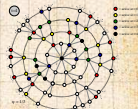
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Next up: We'll look at some fundamental kinds of spreading on generalized random networks.

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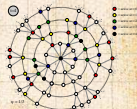
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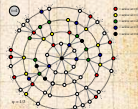
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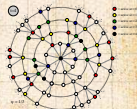
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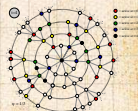
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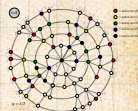
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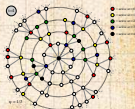
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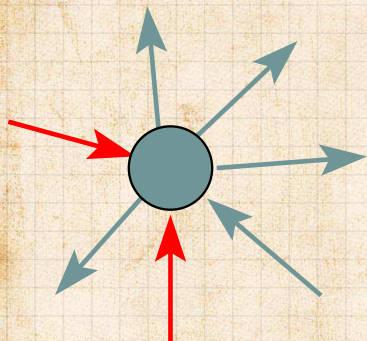
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Spreading mechanisms



■ uninfected
■ infected



General spreading mechanism:

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



Process of entity may be stochastic and history-dependent.



May have multiple, interacting entities spreading at once.

Basic Contagion Models

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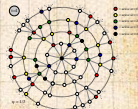
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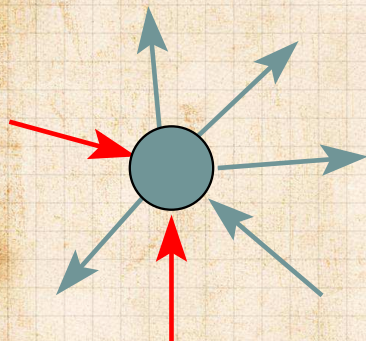
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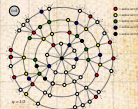
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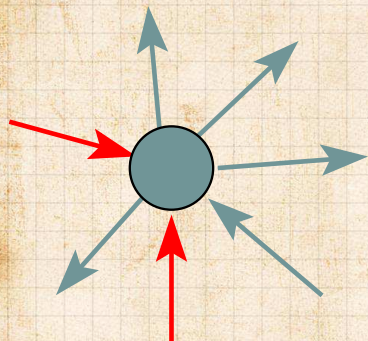
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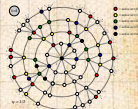
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Spreading on Random Networks

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

Successful spreading is contingent on single edge 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?

Basic Contagion Models

Global spreading condition

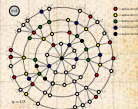
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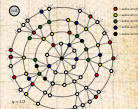
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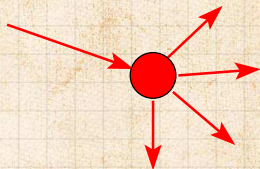


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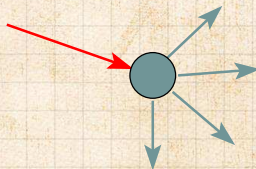
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Success



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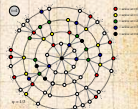
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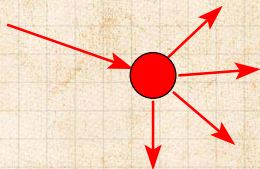


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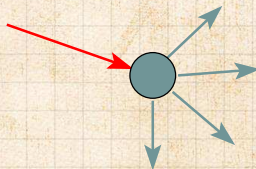
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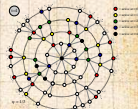
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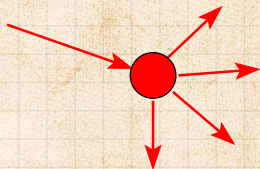


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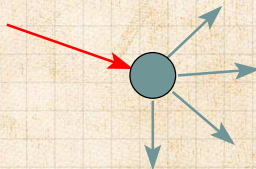
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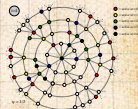
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We need to find: [5]

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.



$$R = \sum_{k=0}^{\infty} \frac{k P_k}{\langle k \rangle}$$

$\frac{k P_k}{\langle k \rangle}$
 prob. of
 connecting to
 a degree k node



$(k-1)$
 # outgoing
 infected
 edges



B_{k1}
 Prob. of
 infection

$$+ \sum_{k=0}^{\infty} \frac{k P_k}{\langle k \rangle}$$

0
 # outgoing
 infected
 edges



$(1 - B_{k1})$
 Prob. of
 no infection

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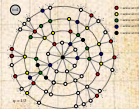
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$\cdot \underbrace{(k-1)}_{\text{\# outgoing infected edges}}$

$\cdot \underbrace{B_{k1}}_{\text{Prob. of infection}}$

$+ \sum_{k=0}^{\infty} \frac{kP_k}{\langle k \rangle} \cdot \underbrace{0}_{\text{\# outgoing infected edges}}$

$\cdot \underbrace{(1 - B_{k1})}_{\text{Prob. of no infection}}$

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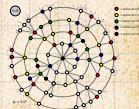
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prob. of connecting to a degree k node

$$1 - \sum_{k=0}^{\infty} \frac{k P_k}{\langle k \rangle} \cdot \underbrace{0}_{\substack{\# \text{ outgoing} \\ \text{infected} \\ \text{edges}}} \cdot \underbrace{(1 - B_{k-1})}_{\substack{\text{Prob. of} \\ \text{no infection}}}$$

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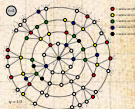
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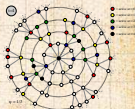
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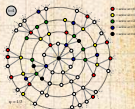
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prob. of connecting to a degree k node
outgoing infected edges
Prob. of infection

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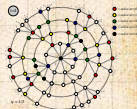
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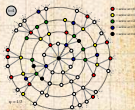
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Basic Contagion Models

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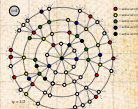
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Global spreading condition

 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

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

Basic Contagion Models

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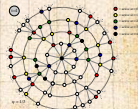
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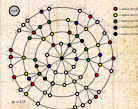
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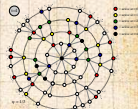
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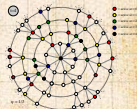
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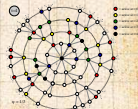
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Global spreading condition

 **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 
-  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 

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

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Global spreading condition

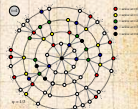
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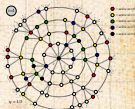
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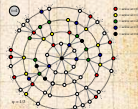
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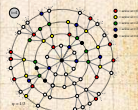
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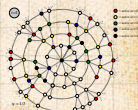
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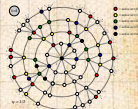
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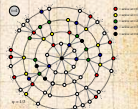
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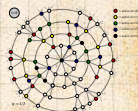
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Global spreading condition

- 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 l ... unlikely.
- Possibility: $B_{k,l}$ is not monotonic in l ... unlikely.
- Possibility: $B_{k,l}$ decreases with l ... hmmm
- $B_{k,l} \searrow$ 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

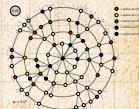
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Global spreading condition

COcoNuTS

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

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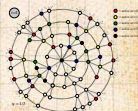
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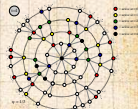
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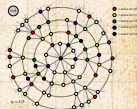
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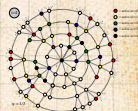
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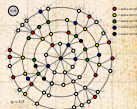
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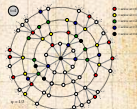
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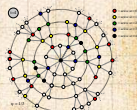
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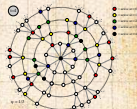
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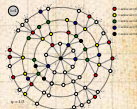
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Global spreading condition

 **Example:** $B_{k1} = 1/k$.



$$\begin{aligned} R &= \sum_{k=1}^{\infty} \frac{k P_k}{\langle k \rangle} \cdot (k-1) \cdot B_{k1} = \sum_{k=1}^{\infty} (k-1) \cdot \frac{k P_k}{\langle k \rangle} \cdot \frac{1}{k} \\ &= \sum_{k=1}^{\infty} \frac{P_k}{\langle k \rangle} \cdot (k-1) = 1 - \frac{1 - P_0}{\langle k \rangle} \end{aligned}$$

 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

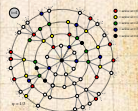
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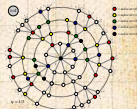
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Basic Contagion Models

Global spreading condition

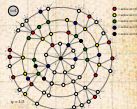
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Global spreading condition



Example: $B_{k1} = 1/k$.



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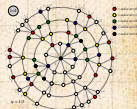
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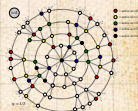
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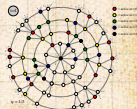
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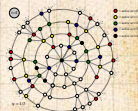
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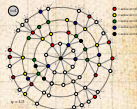
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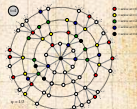
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Global spreading condition



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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$$R = \sum_{k=1}^{\infty} \frac{kP_k}{\langle k \rangle} \bullet (k-1) \bullet B_{k1} = \sum_{k=1}^{\infty} \frac{kP_k}{\langle k \rangle} \bullet (k-1) \bullet H\left(\frac{1}{k} - \phi\right)$$

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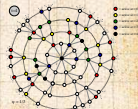
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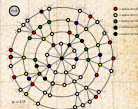
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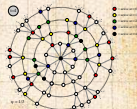
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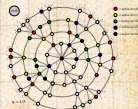
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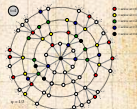
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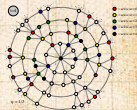
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Global spreading condition

- The uniform threshold model global spreading condition:

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

- 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 ϕ 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.

Basic Contagion Models

Global spreading condition

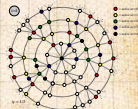
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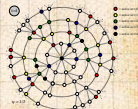
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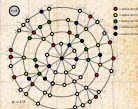
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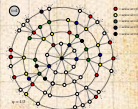
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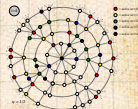
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Virtual contagion: Corrupted Blood, a 2005 virtual plague in World of Warcraft:

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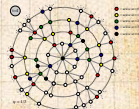
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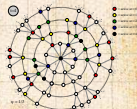
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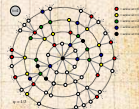
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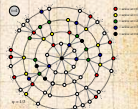
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 Social learning: the case of online social cascades

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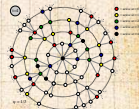
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 Social learning: the class of contagion cascades

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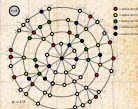
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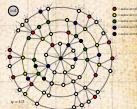
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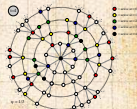
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Threshold model on a network

COCoNuTS

Original work:



"A simple model of global cascades on random networks" 

Duncan J. Watts,
Proc. Natl. Acad. Sci., **99**, 5766–5771,
2002. ^[15]

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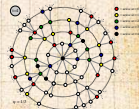
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References

 Mean field Granovetter model → network model

 Individuals now have a limited view of the world



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,
2002. ^[15]

Basic Contagion Models

Global spreading condition


Social Contagion Models

Network version
All-to-all networks

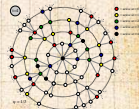
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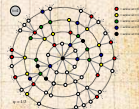
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COcoNuTS

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 α_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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Global spreading condition

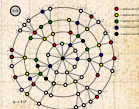
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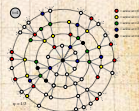
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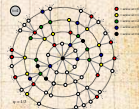
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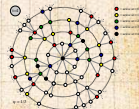
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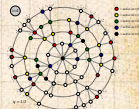
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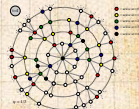
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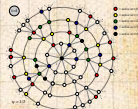
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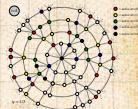
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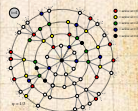
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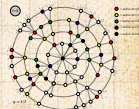
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 All nodes have threshold $\phi = 0.2$.



Threshold model on a network

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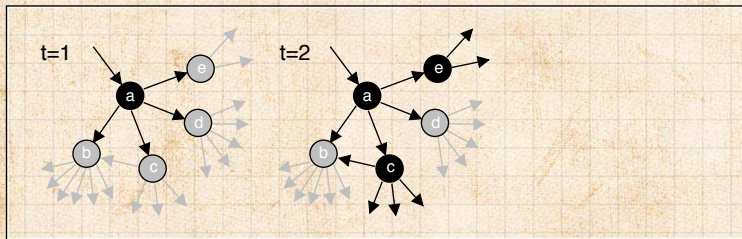
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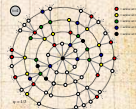
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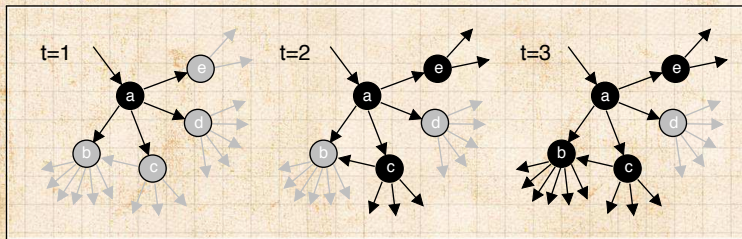
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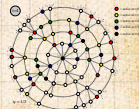
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The most gullible

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 ϕ , our global spreading condition tells us when such a component exists:

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

Basic Contagion Models

Global spreading condition

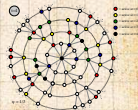
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Basic Contagion Models

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Social Contagion Models

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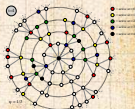
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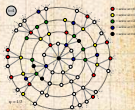
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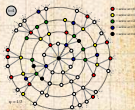
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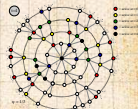
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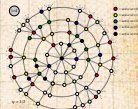
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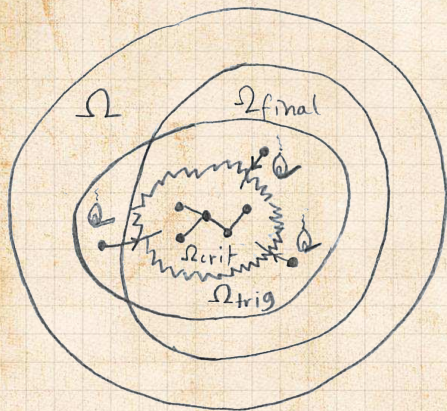
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Example random network structure:



 Ω_{crit} = critical mass = global vulnerable component

 Ω_{trig} = triggering component

 Ω_{final} = potential extent of spread

 Ω = entire network

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Global spreading condition

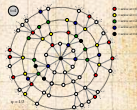
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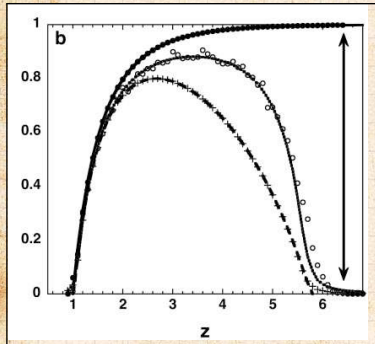
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$$\Omega_{crit} \subset \Omega_{trig}; \Omega_{crit} \subset \Omega_{final}; \text{ and } \Omega_{trig}, \Omega_{final} \subset \Omega.$$

Global spreading events on random networks ^[15]



$$z = \langle k \rangle$$



Top curve: final fraction infected if successful.



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



Bottom curve: fractional size of vulnerable subcomponent. ^[15]

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

System is robust-yet-fragile just below upper boundary ^[3, 4, 14]

'Ignorance' facilitates spreading.

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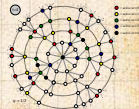
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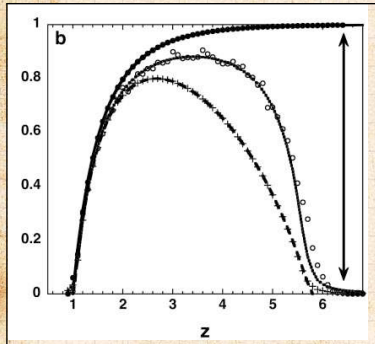
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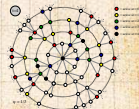
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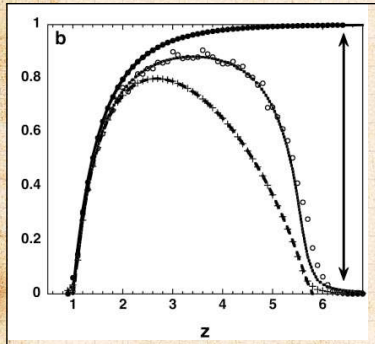
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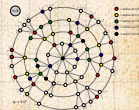
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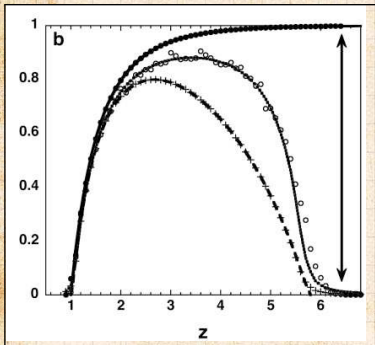
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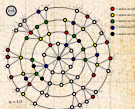
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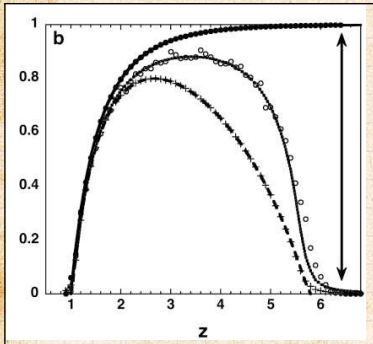
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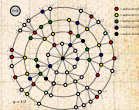
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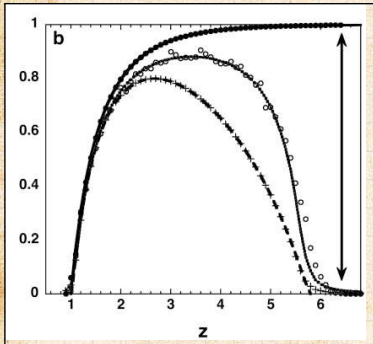
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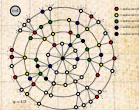
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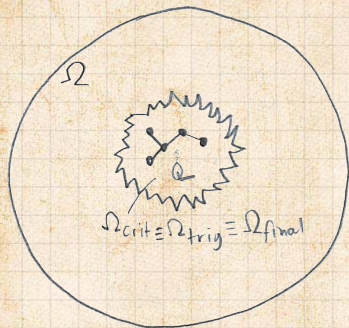
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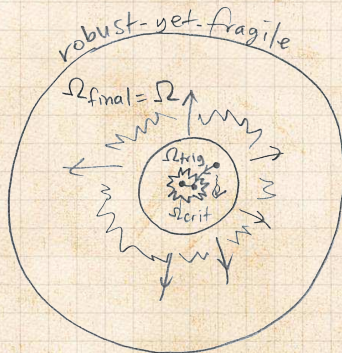
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Cascades on random networks



 Above lower phase transition



 Just below upper phase transition

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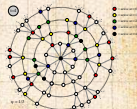
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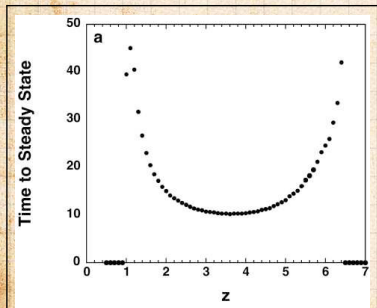
Theory

- Spreading possibility
- Spreading probability
- Physical explanation
- Final size

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Cascades on random networks



Time taken for cascade to spread through network.^[15]



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

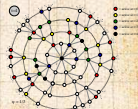
Social Contagion Models

Network version
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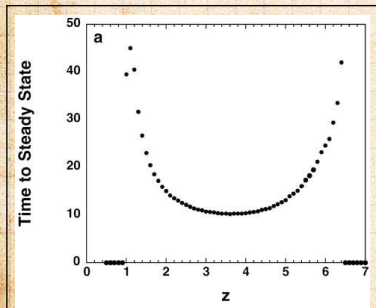
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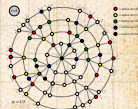
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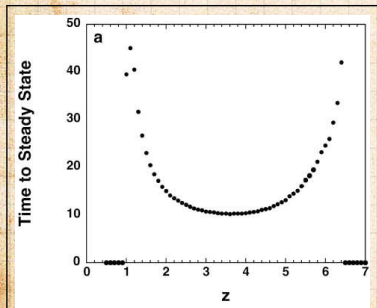
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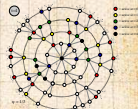
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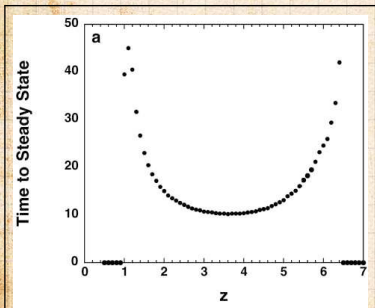
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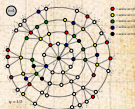
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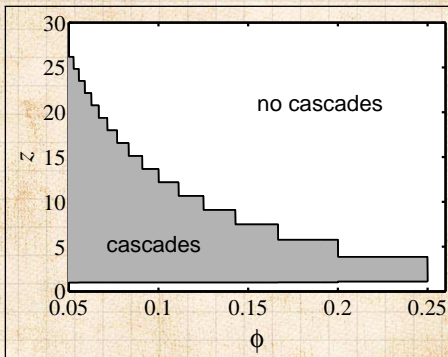
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Cascade window for random networks



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

 Outline of cascade window for random networks.

Basic Contagion Models

Global spreading condition

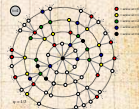
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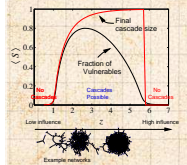
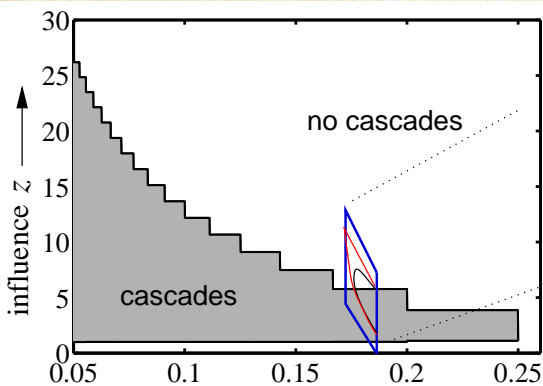
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Global spreading condition

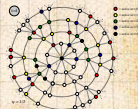
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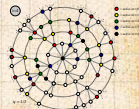
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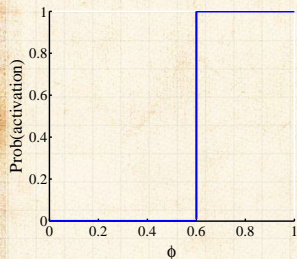
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Granovetter's Threshold model—recap



 Assumes deterministic response functions

 ϕ_* = threshold of an individual.

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

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

 ϕ_t = fraction of people 'rioting' at time step t .

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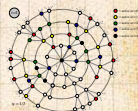
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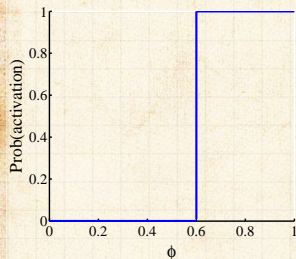
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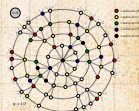
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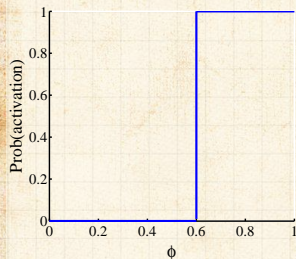
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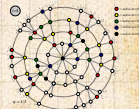
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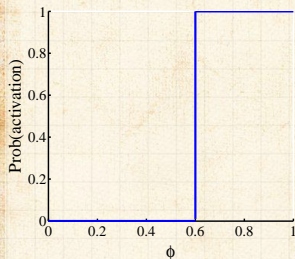
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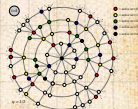
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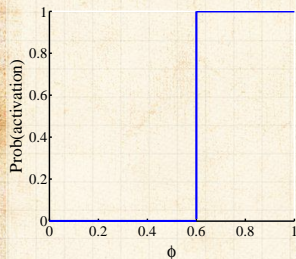
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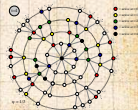
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At time $t + 1$, fraction rioting = fraction with

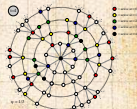
$$\phi_* \leq \phi_t.$$



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



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



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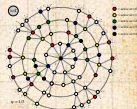
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⇒ iterative maps of the unit interval $[0, 1]$.



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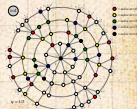
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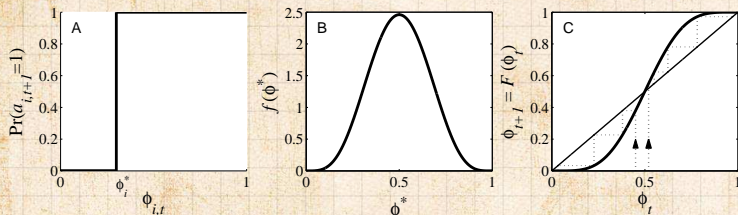


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Social Sciences—Threshold models

Action based on perceived behavior of others.



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

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Theory

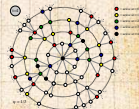
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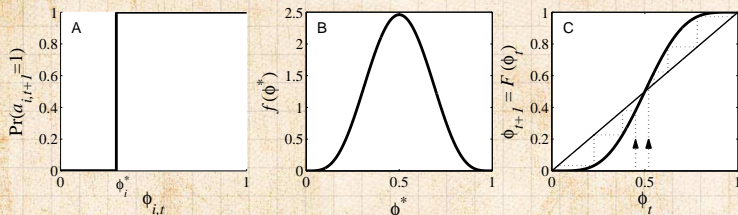
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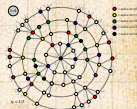
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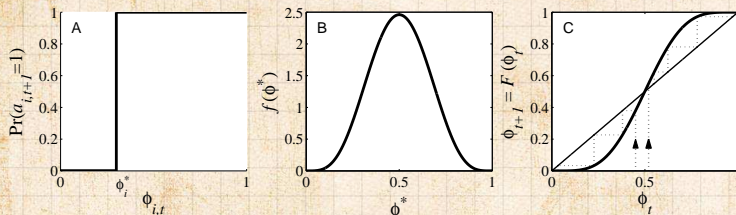
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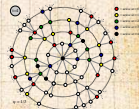
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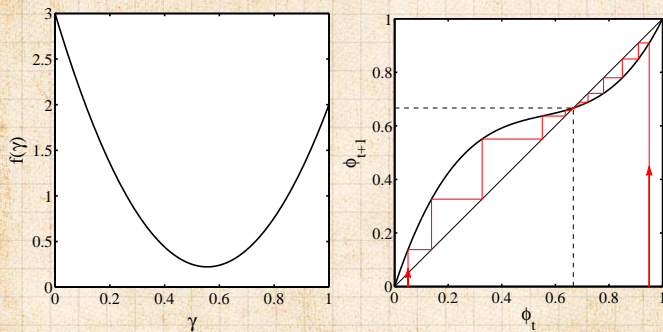
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Social Sciences—Threshold models



Example of single stable state model

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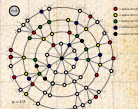
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Implications for collective action theory:

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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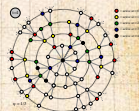
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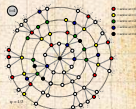
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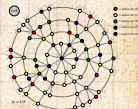
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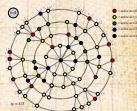
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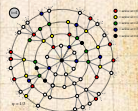
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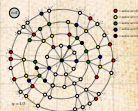
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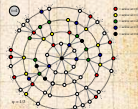
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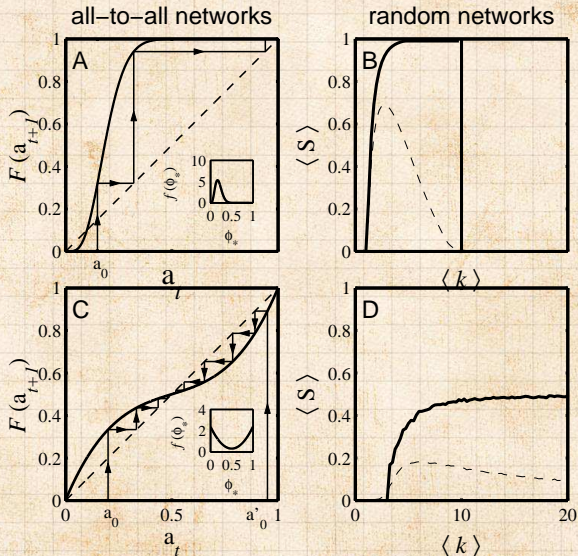
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All-to-all versus random networks



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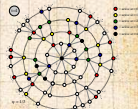
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Spreadworthiness: Cat videos

Bowling with Ragdolls:

COcoNuTS

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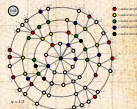
Final size

References

<https://www.youtube.com/watch?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_{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 on S , it is not always unimodal

Basic Contagion Models

Global spreading condition

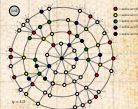
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• In the distribution on S , it is almost always 0 or 1

Basic Contagion Models

Global spreading condition

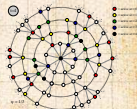
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• In the distribution on any network, almost always spreadable

Basic Contagion Models

Global spreading condition

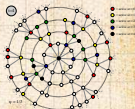
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Threshold contagion on random networks

COcoNuTS

Three key pieces to describe analytically:

1. The fractional size of the largest subcomponent of vulnerable nodes, S_{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 .

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

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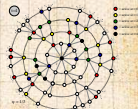
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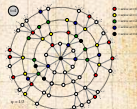
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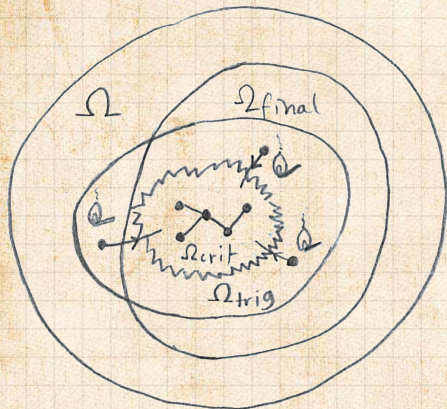
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Example random network structure:



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

 $\Omega_{trig} =$
 triggering
 component

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

 $\Omega =$ entire
 network

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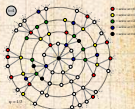
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$$\Omega_{crit} \subset \Omega_{trig}; \Omega_{crit} \subset \Omega_{final}; \text{ and } \Omega_{trig}, \Omega_{final} \subset \Omega.$$

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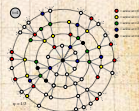
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Threshold contagion on random networks

 **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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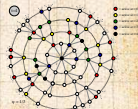
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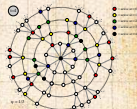
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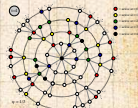
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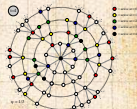
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 This is a node-based percolation problem.

 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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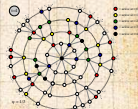
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Threshold contagion on random networks

-  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:

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

-  Detail: We still have the underlying degree distribution involved in the denominator.

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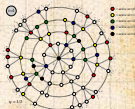
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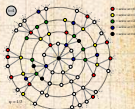
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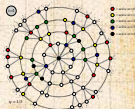
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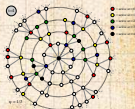
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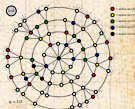
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Threshold contagion on random networks



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

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

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



Can now solve as before to find

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

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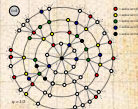
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$$F_{\rho}^{(\text{vuln})}(x) = \underbrace{1 - F_R^{(\text{vuln})}(1)}_{\substack{\text{first node} \\ \text{is not} \\ \text{vulnerable}}} + x F_R^{(\text{vuln})}(F_{\pi}^{(\text{vuln})}(x))$$



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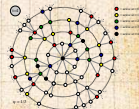
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Can now solve as before to find

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

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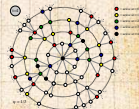
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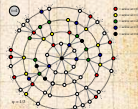
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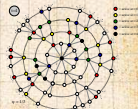
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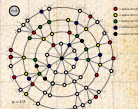
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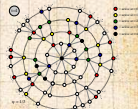
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Threshold contagion on random networks

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

 Assumption is **first node** is randomly chosen.

 Same set up as for vulnerable component except now we don't care if the initial node is vulnerable or not:

$$F_{\tau}^{(\text{trig})}(x) = x F_p^{(\text{vuln})}(F_R^{(\text{vuln})}(x))$$

$$F_p^{(\text{vuln})}(x) = 1 - F_R^{(\text{vuln})}(1) + x F_R^{(\text{vuln})}(F_p^{(\text{vuln})}(x))$$

 Solve as before to find $F_{\text{trig}} = S_{\text{trig}} = 1 - F_{\tau}^{(\text{trig})}(1)$.

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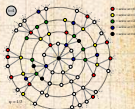
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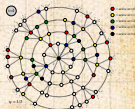
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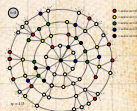
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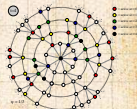
Social Contagion Models

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All-to-all networks

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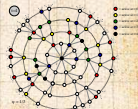
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Physical derivation of possibility and probability of global spreading:

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

🧩 For random networks, global spreading possibility is understood as meaning a giant component of vulnerable nodes exists.

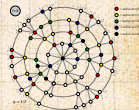
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🧩 Call this P_{trig} .

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🧩 Call this Q_{trig} .

🧩 Later: Generalize to more complex networks involving assortativity of all kinds.



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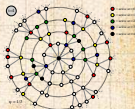
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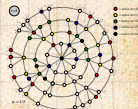
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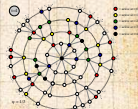
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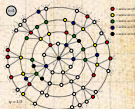
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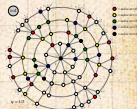
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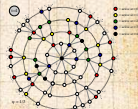
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 Q_{trig} must satisfy a one-step recursion relation.

 Follow an infected edge and use three pieces:

1. The node has k outgoing edges. Use k nodes.
2. The node reaches a global spreading event with probability Q_{trig} .
3. At least one of the node's outgoing edges leads to a global spreading event. (Probability no edges do so = $(1 - Q_{\text{trig}})^k$.)

 Put everything together and solve for Q_{trig} :

$$Q_{\text{trig}} = \sum_k \frac{k P_k}{\langle k \rangle} \cdot B_{k-1} \cdot [1 - (1 - Q_{\text{trig}})^{k-1}] .$$

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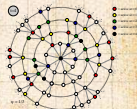
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 Follow an infected edge and use three pieces:

1. Probability of reaching a degree k node is

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

2. The node reached is vulnerable with probability

$$B_{k1}$$

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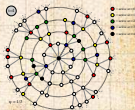
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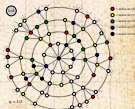
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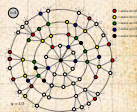
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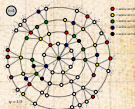
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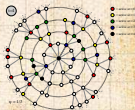
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Good things about our equation for Q_{trig} :


$$Q_{\text{trig}} = \sum_k \frac{kP_k}{\langle k \rangle} \cdot B_{k1} \cdot [1 - (1 - Q_{\text{trig}})^{k-1}] = f(Q_{\text{trig}}; P_k, B_{k1})$$

 $Q_{\text{trig}} = 0$ is always a solution.


 Spreading occurs if a second solution exists for which $0 < Q_{\text{trig}} \leq 1$.

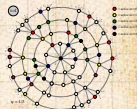
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 The function f increases monotonically with Q_{trig} .

 We can therefore use an iterative cobwebbing approach to find the solution:


$$Q_{\text{trig}}^{(n+1)} = f(Q_{\text{trig}}^{(n)}; P_k, B_{k1}).$$


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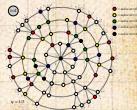
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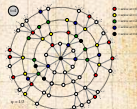
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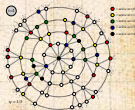
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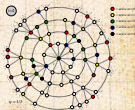


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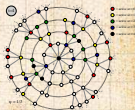
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Global spreading is possible if the fractional size S_{vuln} of the largest component of vulnerables is “giant”.

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

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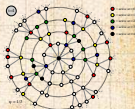
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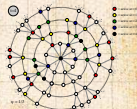
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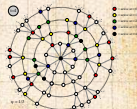
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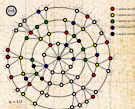
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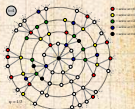
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Connection to generating function results:

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

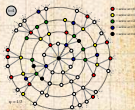
$$F_\rho^{(\text{vuln})}(1) = 1 - F_R^{(\text{vuln})}(1) + 1 \cdot F_R^{(\text{vuln})}(F_\rho^{(\text{vuln})}(1)).$$

- 📦 We set $F_\rho^{(\text{vuln})}(1) = 1 - Q_{\text{trig}}$ and deploy


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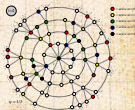
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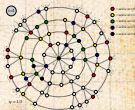
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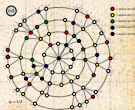
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Fractional size of the largest vulnerable component:



The generating function approach gave

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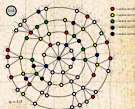
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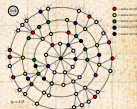
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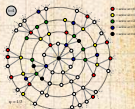
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Triggering probability for single-seed global spreading events:

- 🧱 Slight adjustment to the vulnerable component calculation.

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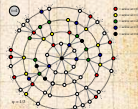
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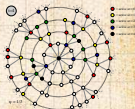
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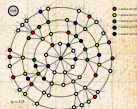
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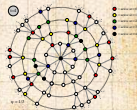
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Connection to simple gain ratio argument:

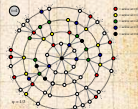
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$$\mathbf{R} = \sum_{k=0}^{\infty} \frac{kP_k}{\langle k \rangle} \bullet (k-1) \bullet B_{k1} > 1.$$

- We would very much like to see that $\mathbf{R} > 1$ matches up with $Q_{\text{trig}} > 0$.
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- Must come from our basic edge triggering probability equation:

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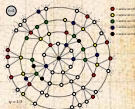
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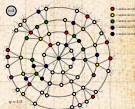
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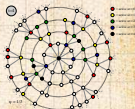
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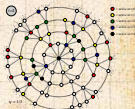
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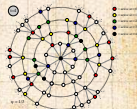
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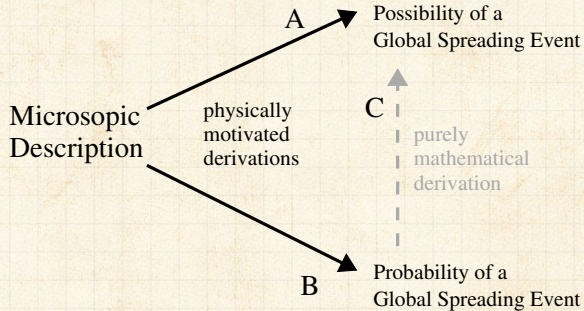
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What we're doing:



Basic Contagion Models

Global spreading condition

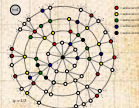
Social Contagion Models


Network version
All-to-all networks

Theory

Spreading possibility
Spreading probability
Physical explanation
Final size

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 Inequality?

Basic Contagion Models

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Social Contagion Models

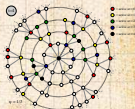
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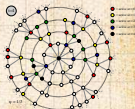
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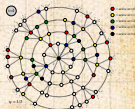
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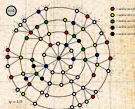
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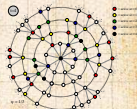
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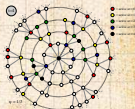
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Again take $Q_{\text{trig}} \rightarrow 0^+$, but keep next higher order term:

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

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

$$\Rightarrow \sum_k \frac{kP_k}{\langle k \rangle} \bullet (k-1) \bullet B_{k1} = 1 + \sum_k \frac{kP_k}{\langle k \rangle} B_{k1} \binom{k-1}{2} Q_{\text{trig}}$$

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

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

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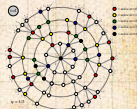
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Threshold contagion on random networks

COcoNuTS

 **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 ≥ 2 hits switch on.

 Problem solved for infinite seed case by Gleeson and Cahalane:

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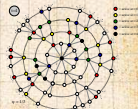
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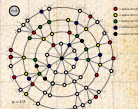
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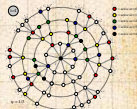
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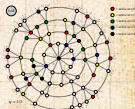
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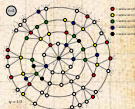
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Meme species:

Periodic Table of Advice Animals

CHEEZ
SOUNGZ Know Your Meme

Advice Dog first arrived on the Internet in 2006 as an avatar image meant as a lighthearted way to give useful, easily read advice. Quickly gaining popularity online, the version of Advice Dog has inspired an endless number of spin-offs.

The format usually includes a stock image in the center with text along the top and bottom.

The text almost always describes a common situation or action in the form of a humorous observation or a pun.

For example, the version known as **Stonor Dog** also brings attention to the etymological relationship (dog root) in the first line and the common phrase "stones up" from the Shakespearean English.

Each iteration eventually identifies a user, large group, or personality through visual selection and modification, "surfing the wave" within its niche and human culture.

Color Blobs

Animals/Dogs
Puppies/Puppies
Animals/Animals
Animals/Animals
Animals/Animals
Animals/Animals
Animals/Animals
Animals/Animals
Animals/Animals
Animals/Animals

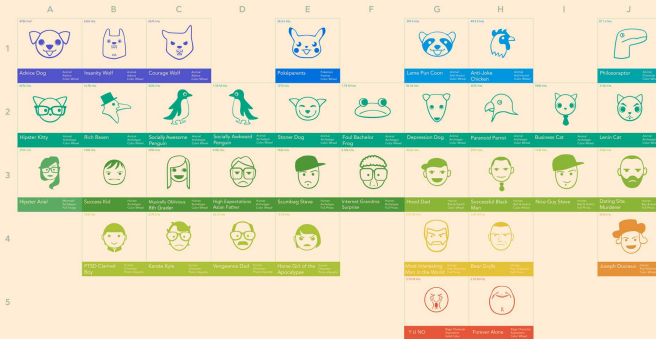
Notes

Advice Dog
Anti-Advice Dog
Stonor Dog
Stonor Dog
Stonor Dog
Stonor Dog
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Stonor Dog
Stonor Dog

Hysterical
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Stonor Dog
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Stonor Dog
Stonor Dog
Stonor Dog



This Periodic Table of Advice Animals is a work of fan art. It is not affiliated with Know Your Meme.

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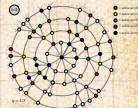
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More here at <http://knowyourmeme.com>

Expected size of spread

Idea:

- ☰ Randomly turn on a fraction ϕ_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 :
 - $t = 0$: i is one of the seeds (prob = ϕ_0)
 - $t = 1$: i was not a seed but enough of i 's friends switched on at time $t = 0$ so that i 's threshold is now exceeded.
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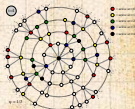
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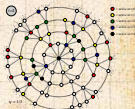
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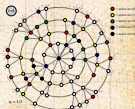
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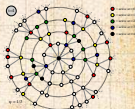
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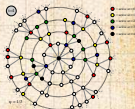
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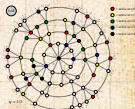
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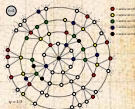
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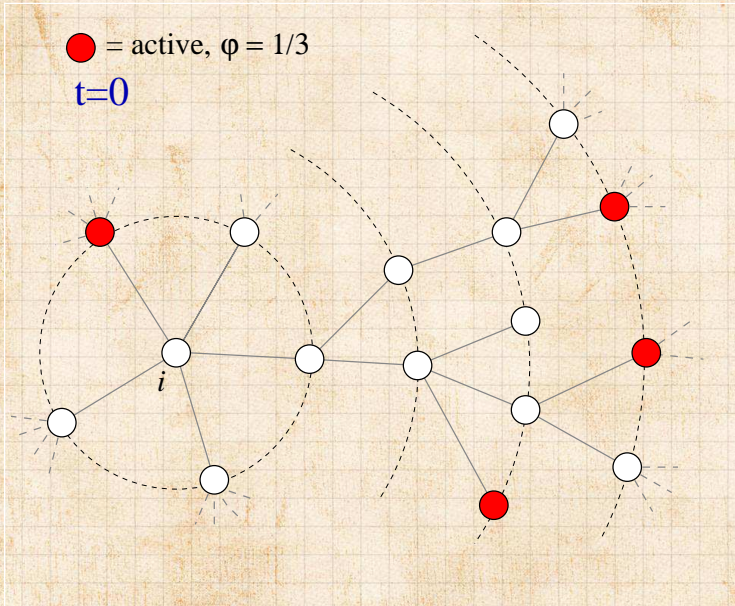
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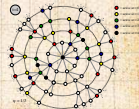
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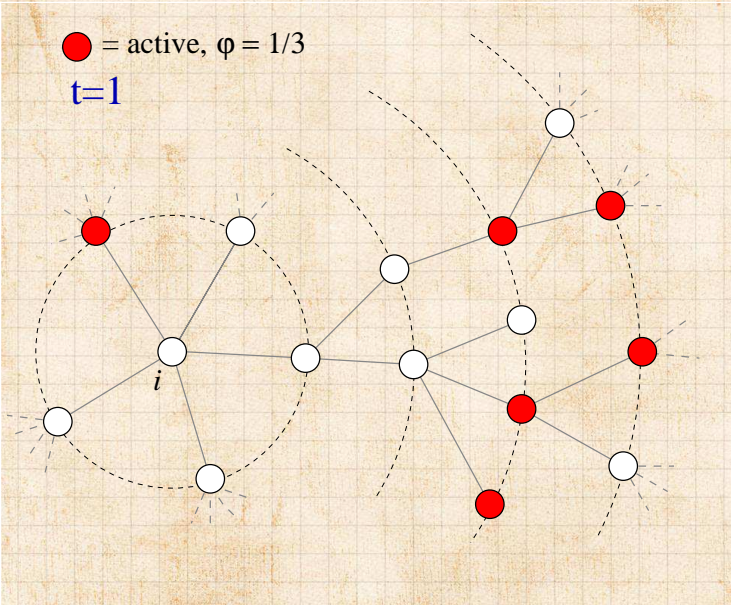
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Expected size of spread

● = active, $\phi = 1/3$

$t=1$



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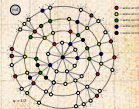
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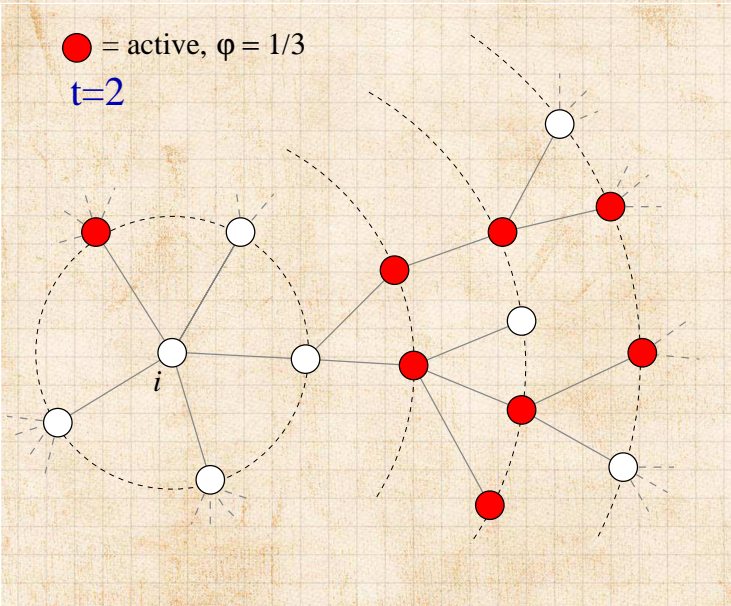
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Expected size of spread

● = active, $\phi = 1/3$

$t=2$



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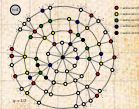
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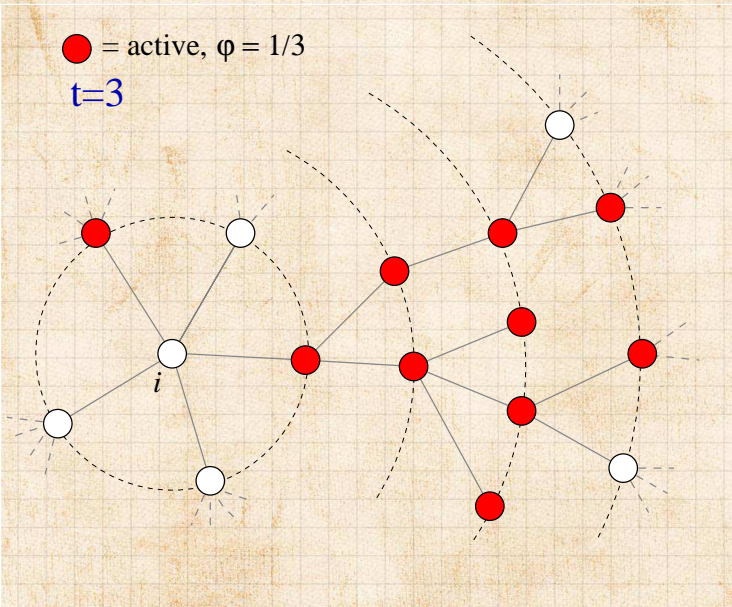
References



Expected size of spread

● = active, $\phi = 1/3$

$t=3$



Basic Contagion Models

Global spreading condition

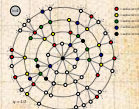
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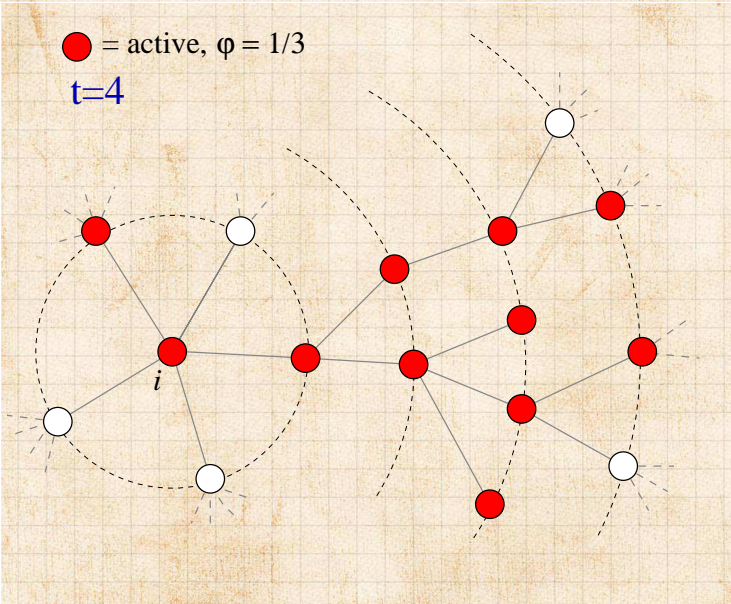
References



Expected size of spread

● = active, $\phi = 1/3$

$t=4$



Basic Contagion Models

Global spreading condition

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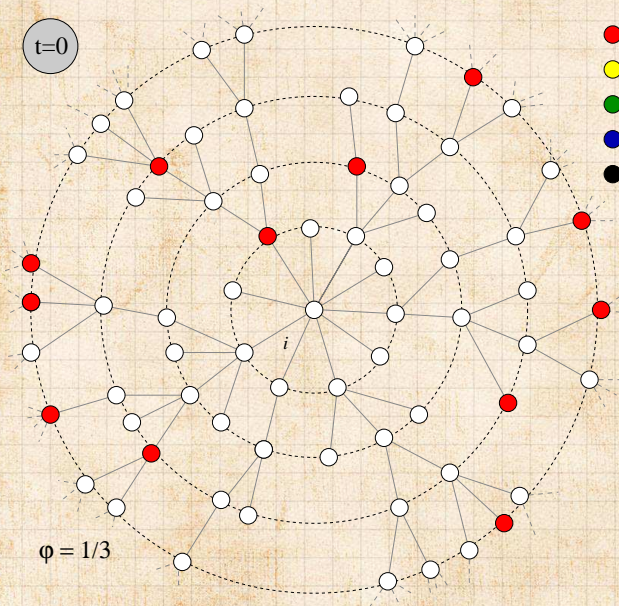
- Spreading possibility
- Spreading probability
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Expected size of spread

t=0



- = 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

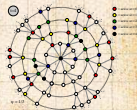
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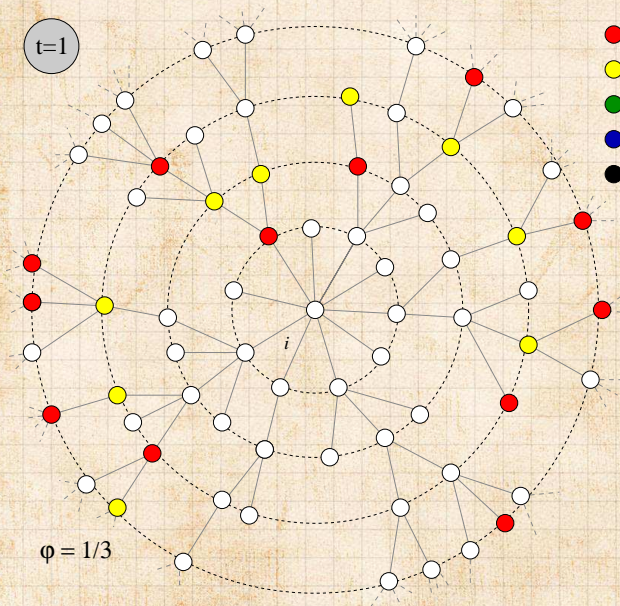
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$$\phi = 1/3$$

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

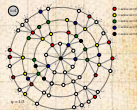
Social Contagion Models

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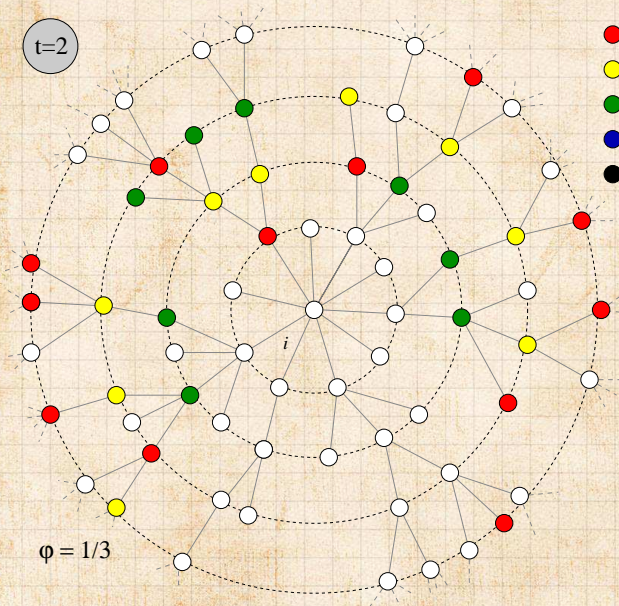
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Expected size of spread



- = 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

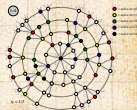
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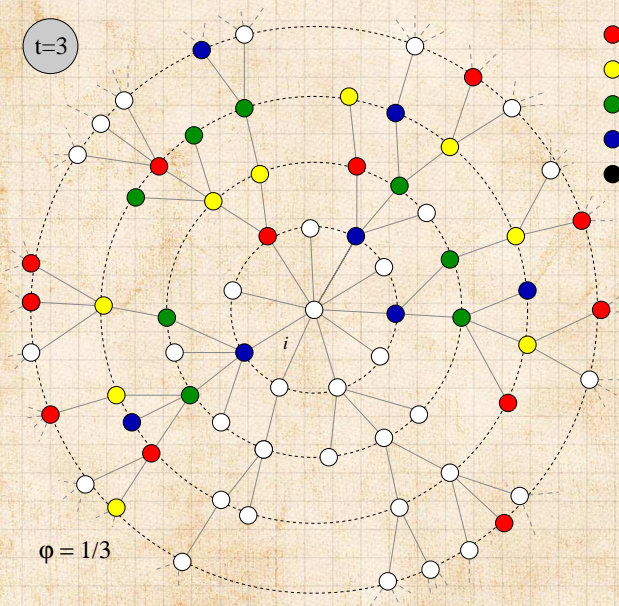
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Expected size of spread



- = active at $t=0$
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- = active at $t=4$

Basic Contagion Models

Global spreading condition

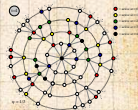
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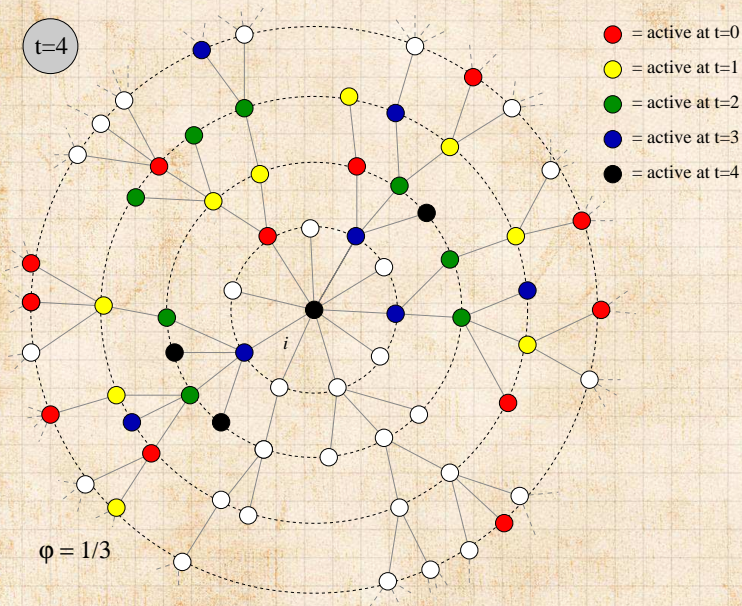
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Expected size of spread



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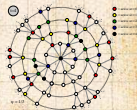
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Expected size of spread

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

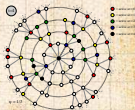
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Global spreading condition

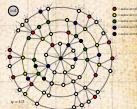
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Basic Contagion Models

Global spreading condition

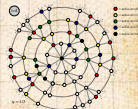
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Global spreading condition

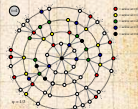
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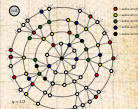
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Basic Contagion Models

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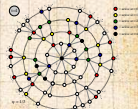
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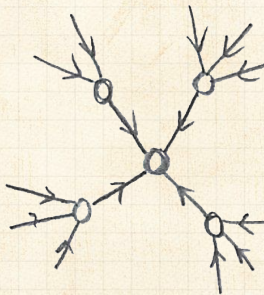
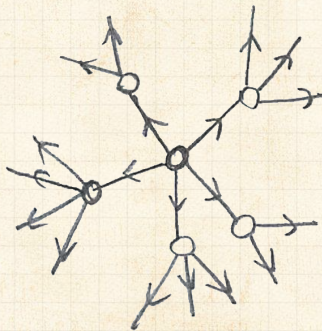


Expected size of spread

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

Global spreading condition

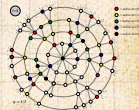
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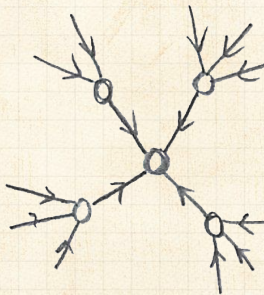
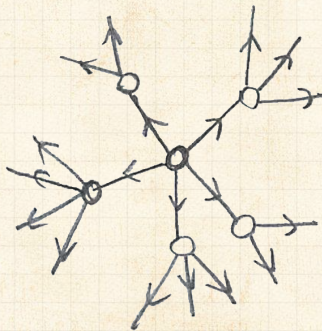
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Expected size of spread

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

Global spreading condition

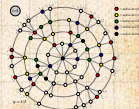
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Expected size of spread



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



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



Probability a degree k node was a seed at $t = 0$ is ϕ_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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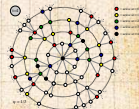
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Expected size of spread



Notation:

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



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



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



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Basic Contagion Models

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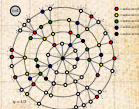
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Our starting point: $\phi_{k,0} = \phi_0.$



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



Probability a degree k node was a seed at $t = 0$ is ϕ_0^k (as above).



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



Combining everything, we have:

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

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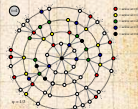
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Expected size of spread



Notation:

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



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



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



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



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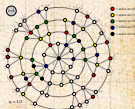
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Expected size of spread



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



Combining everything, we have:

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

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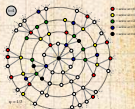
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$\binom{k}{j} \phi_0^j (1 - \phi_0)^{k-j} = \Pr$ (j of a degree k node's neighbors were seeded at time $t = 0$).



Probability a degree k node was a seed at $t = 0$ is ϕ_0 (as above).



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



Combining everything, we have:

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

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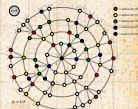
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Expected size of spread



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



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



Probability a degree k node was a seed at $t = 0$ is ϕ_0 (as above).



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



Combining everything, we have:

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

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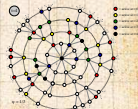
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Expected size of spread

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 θ_t .

We already know $\theta_0 = \phi_0$.

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

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

Average over all nodes with degree k to obtain expression for ϕ_{t+1} :

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

So we need to compute θ_t, \dots

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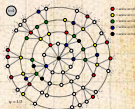
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 Story analogous to $t = 1$ case. For specific node i :

$$\phi_{i,t+1} = 1 + \frac{1}{k_i} \sum_{j=0}^{k_i} \binom{k_i}{j} \theta_t^j (1 - \theta_t)^{k_i - j} B_{k_i, j}$$

 Average over all nodes with degree k to obtain expression for ϕ_{t+1} :

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

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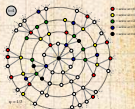
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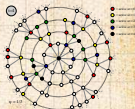
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We already know $\theta_0 = \phi_0$.

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

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

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So we need to compute θ_t, \dots

Basic Contagion Models

Global spreading condition

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Theory

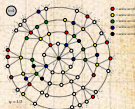
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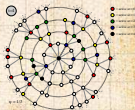
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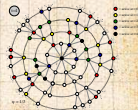
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So we need to compute θ_t ... massive excitement...

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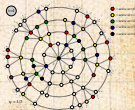
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Expected size of spread


First connect θ_0 to θ_1 :

 $\theta_1 = \phi_0 +$

$$(1 - \phi_0) \sum_{k=1}^{\infty} \frac{k P_k}{\langle k \rangle} \sum_{j=0}^{k-1} \binom{k-1}{j} \theta_0^j (1 - \theta_0)^{k-1-j} B_{kj}$$

 $\frac{k P_k}{\langle k \rangle} = Q_k = \mathbf{Pr}$ (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).

 ϕ_0 and $(1 - \phi_0)$ terms account for state of node at time $t = 0$.

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

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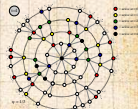
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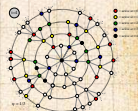
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Expected size of spread

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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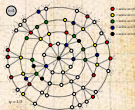
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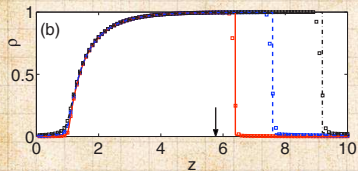
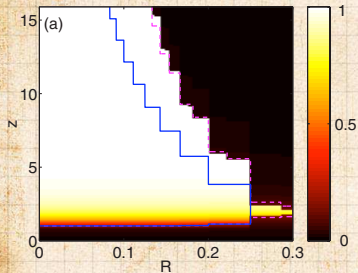
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Comparison between theory and simulations



From Gleeson and Cahalane [7]



Pure random networks with simple threshold responses



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



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



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



Sensible expansion of cascade window as ϕ_0 increases.

Basic Contagion Models

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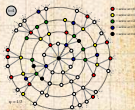
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First, if self-starters are present, some activation is assured:

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

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

Global spreading condition

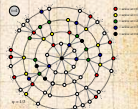
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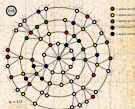
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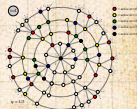
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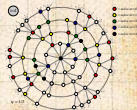
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In words:

🧩 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.

Non-vanishing seed case:

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

🧩 If G has a stable fixed point at $\theta = 0$, and an unstable fixed point for some $0 < \theta_0 < 1$, then for $\phi_0 > \phi_0^*$ spreading takes off.

🧩 Tricky point: G depends on ϕ_0 , so as we change ϕ_0 , we also change G .

Basic Contagion Models

Global spreading condition

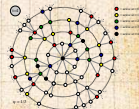
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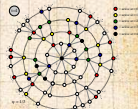
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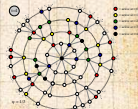
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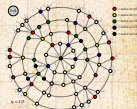
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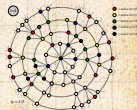
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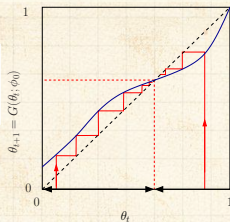
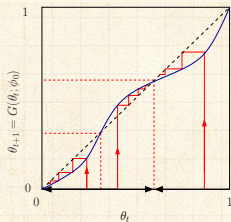
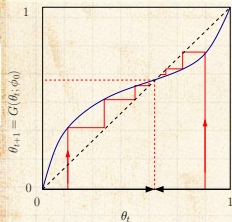
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General fixed point story:



Given $\theta_0 (= \phi_0)$, θ_∞ 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 ϕ_0 .

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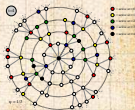
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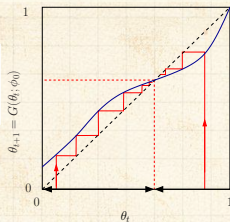
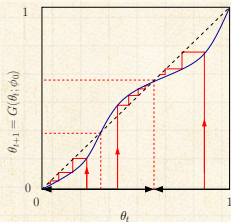
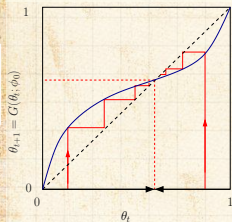
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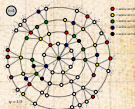
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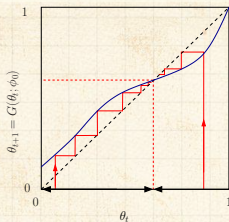
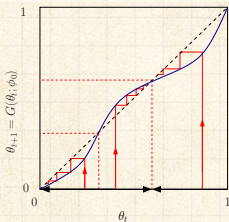
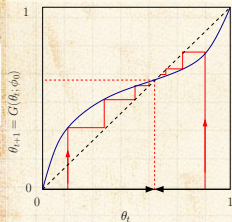
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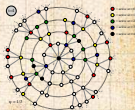
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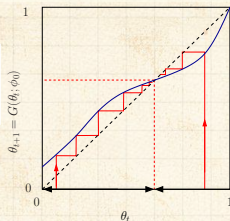
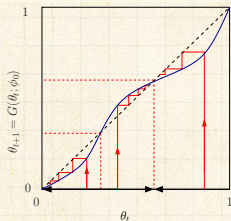
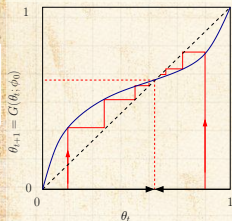
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Basic Contagion Models

Global spreading condition

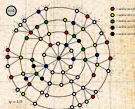
Social Contagion Models

Network version
All-to-all networks

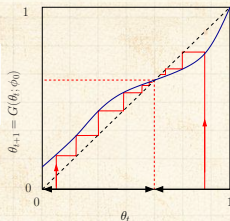
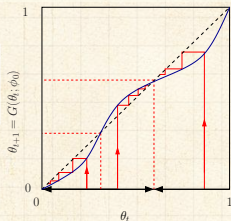
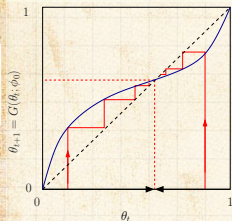
Theory

Spreading possibility
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General fixed point story:



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

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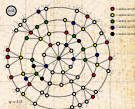
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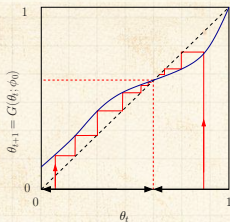
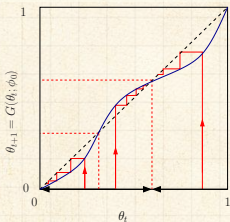
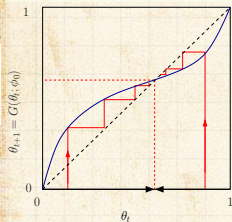
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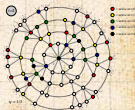
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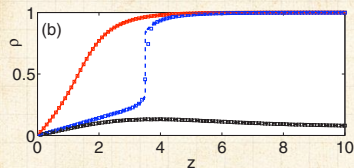
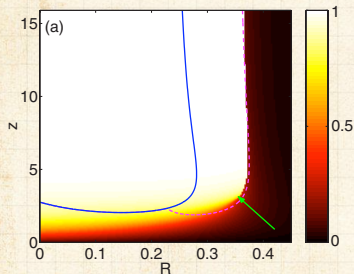
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Physical explanation
Final size

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Interesting behavior:



From Gleeson and Cahalane [7]



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 ≤ 0 so effectively $\phi_0 > 0$.



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

Basic Contagion Models

Global spreading condition

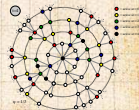
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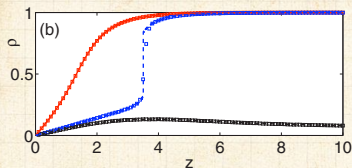
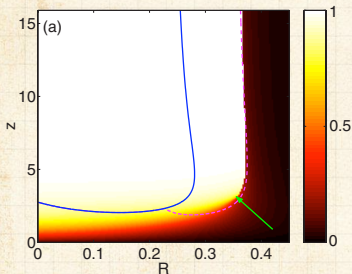
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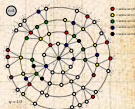
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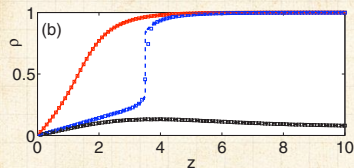
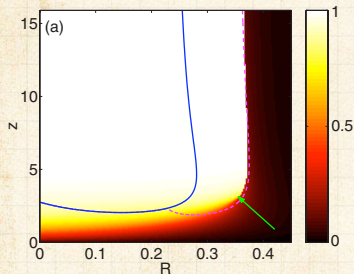
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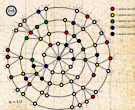
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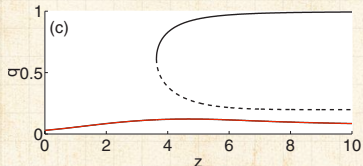
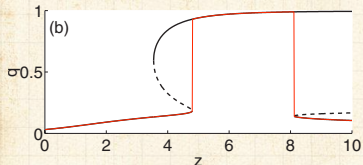
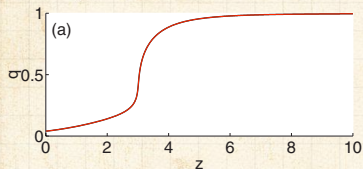
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Interesting behavior:



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



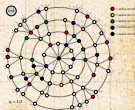
n.b.: 0 is not a fixed point here: $\theta_0 = 0$ always takes off.



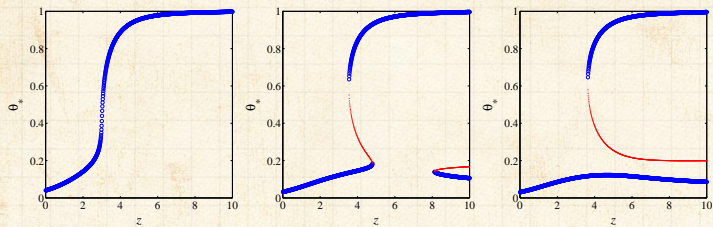
Top to bottom: $R = 0.35, 0.371, \text{ and } 0.375$.



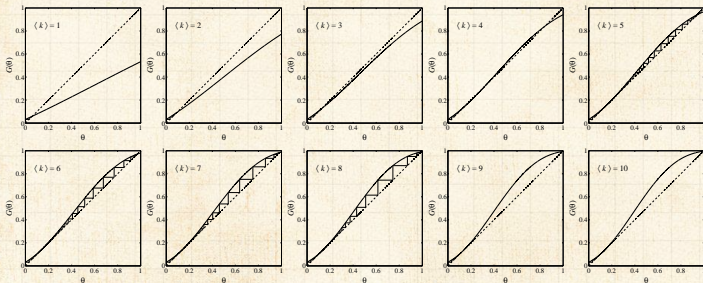
Saddle node bifurcations appear and merge (b and c).



What's happening:



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



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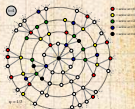
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Synchronous update

- Done: Evolution of ϕ_t and θ_t given exactly by the maps we have derived.

Asynchronous updates

- Update nodes with probability α .
- As $\alpha \rightarrow 0$, updates become effectively independent.
- Now can talk about $\phi(A)$ and $\theta(B)$.

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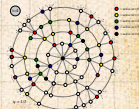
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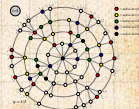
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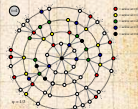
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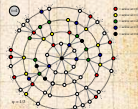
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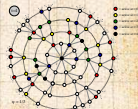
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Nutshell:

 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

Basic Contagion Models

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Social Contagion Models

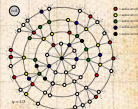
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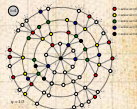
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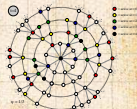
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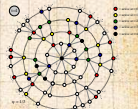
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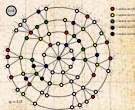
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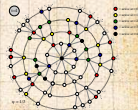
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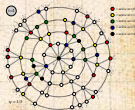
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Neural reboot (NR):

Pangolin happiness:

COcoNuTS

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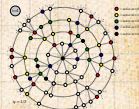
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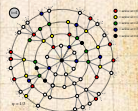
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<https://www.youtube.com/watch?v=LMIYjkG4onM?rel=0> ↗

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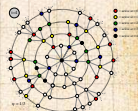
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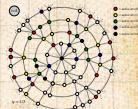
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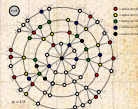
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