

Contagion

Complex Networks

CSYS/MATH 303, Spring, 2011

Prof. Peter Dodds

Department of Mathematics & Statistics
Center for Complex Systems
Vermont Advanced Computing Center
University of Vermont

Contagion

Basic Contagion
Models

Global spreading
condition

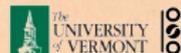
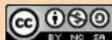
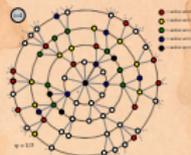
Social Contagion
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All-to-all networks

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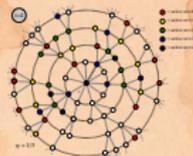
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Contagion models

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

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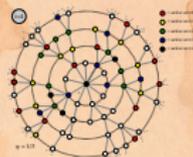
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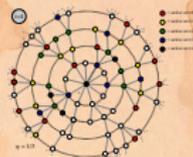
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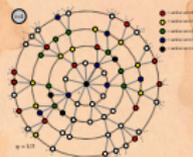
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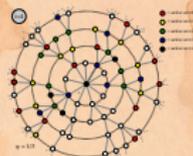
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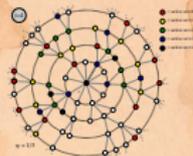
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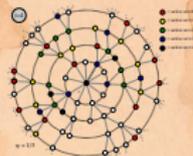
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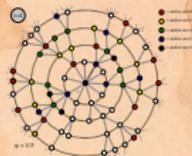
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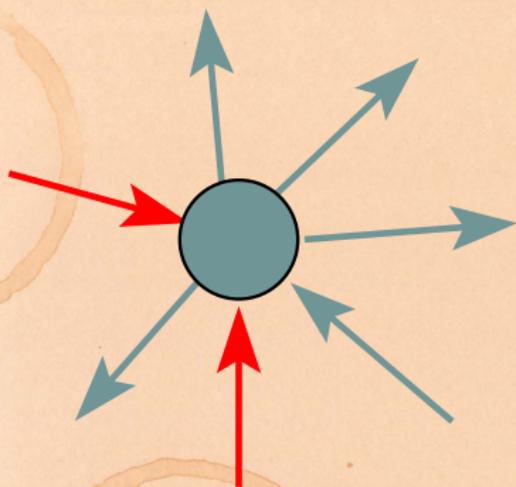
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Spreading mechanisms



■ uninfected
■ infected

- ▶ **General spreading mechanism:**
State of node i depends on history of i and i 's neighbors' states.
- ▶ Doses of entity may be stochastic and history-dependent.
- ▶ May have multiple, interacting entities spreading at once.

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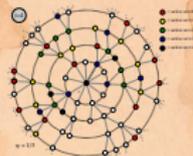
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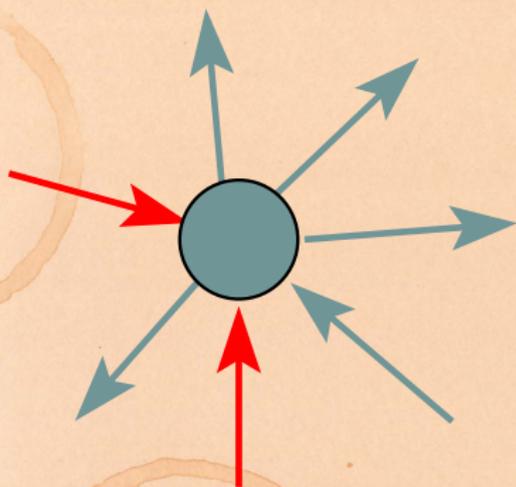
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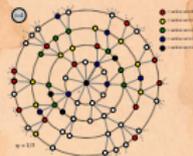
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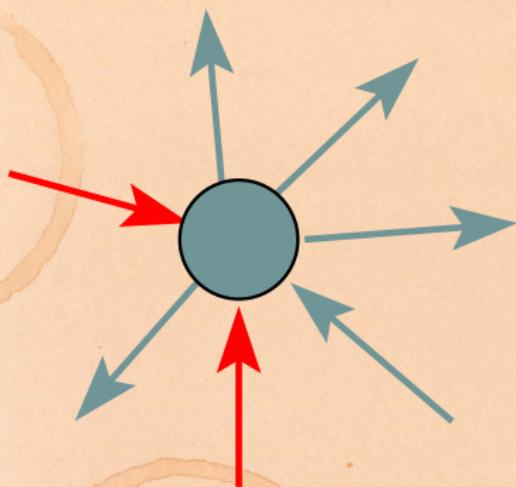
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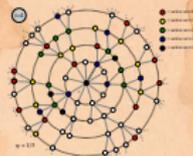
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Spreading on Random Networks

- ▶ For random networks, we know local structure is pure branching.
- ▶ Successful spreading is \therefore contingent on single edges infecting nodes.

- ▶ Focus on binary case with edges and nodes either infected or not.
- ▶ First big question: for a given network and contagion process, can global spreading from a single seed occur?

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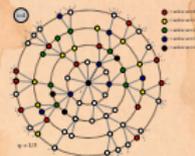
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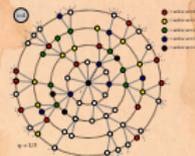
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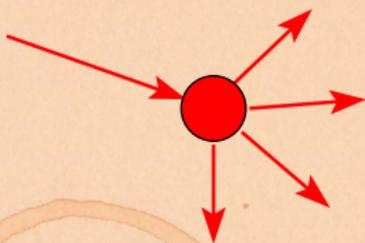
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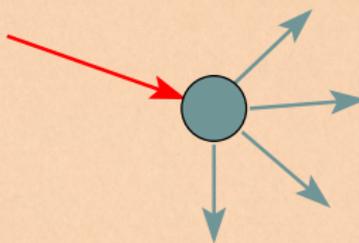
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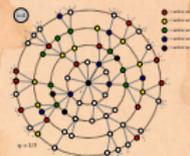
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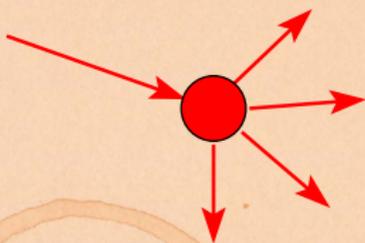
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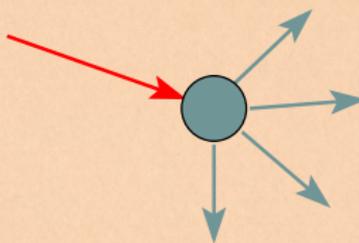
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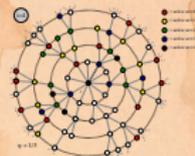
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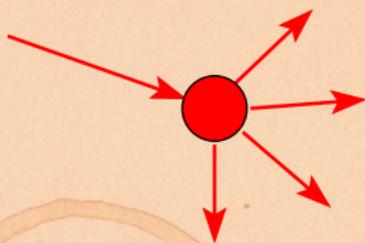
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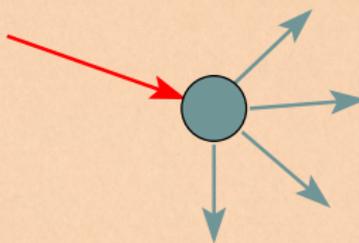
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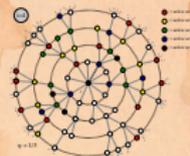
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Global spreading condition

- ▶ We need to find: ^[5]

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

- ▶ Call **R** the **gain ratio**.

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

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

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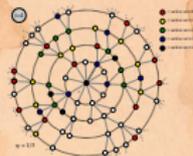
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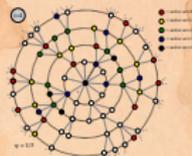
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- ▶

$$R = \sum_{k=0}^{\infty}$$

$$\frac{kP_k}{\langle k \rangle}$$

prob. of connecting to a degree k node

•

$(k-1)$
outgoing infected edges

•

B_{k1}
Prob. of infection

$$+ \sum_{k=0}^{\infty}$$

$$\frac{kP_k}{\langle k \rangle}$$

0

outgoing infected edges

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

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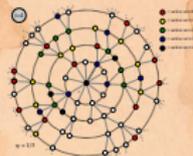
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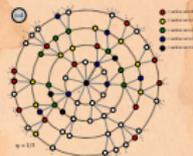
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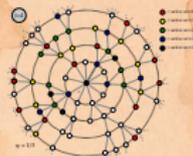
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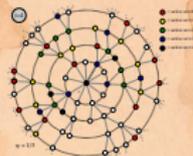
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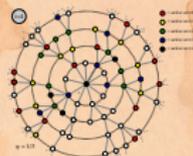
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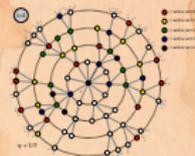
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Global spreading condition

- ▶ Our global spreading condition is then:

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

- ▶ Case 1: If $B_{k1} = 1$ then

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

- ▶ Good: This is just our giant component condition again.

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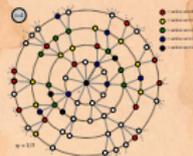
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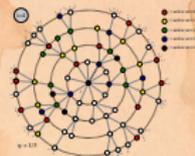
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- ▶ Our global spreading condition is then:

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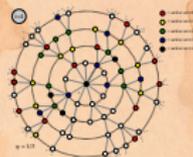
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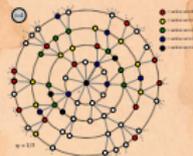
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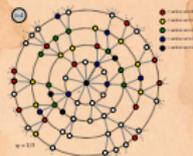
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Insert question from assignment 7 (\boxplus)

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

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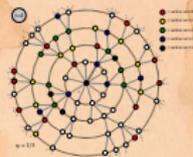
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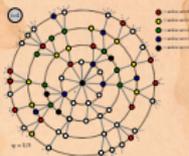
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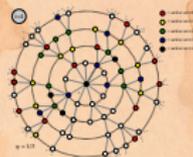
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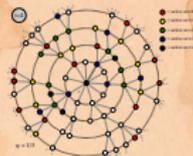
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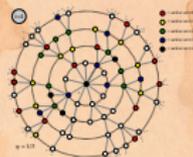
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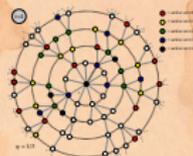
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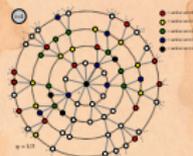
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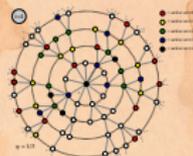
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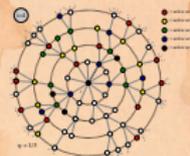
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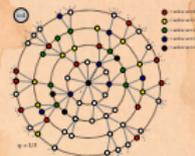
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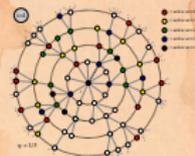
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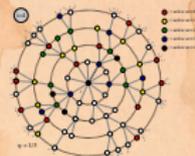
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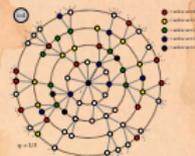
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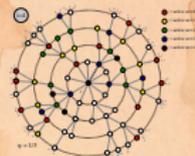
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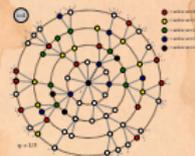
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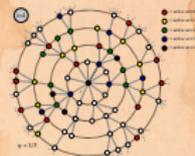
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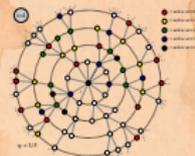
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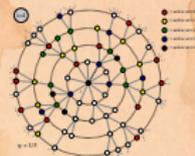
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- ▶ **Example:** $B_{k1} = 1/k$.

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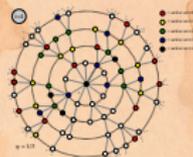
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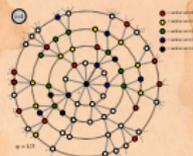
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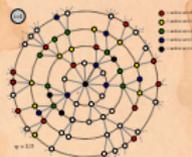
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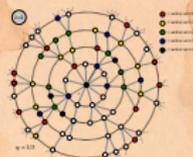
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Contagion

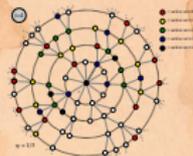
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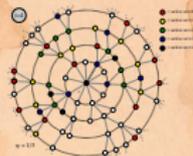
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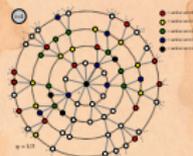
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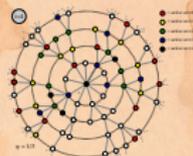
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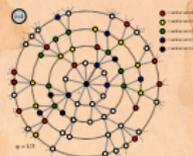
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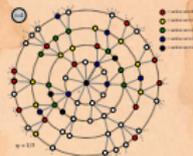
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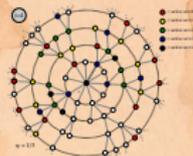
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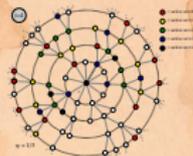
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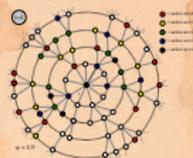
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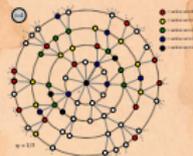
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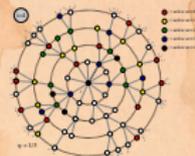
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Global spreading condition

- ▶ 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 $\phi \rightarrow 1$, all nodes become resilient and $r \rightarrow 0$.
- ▶ As $\phi \rightarrow 0$, all nodes become vulnerable and the contagion condition matches up with the giant component condition.
- ▶ Key: If we fix ϕ and then vary $\langle k \rangle$, we may see two phase transitions.
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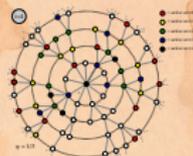
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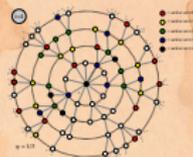
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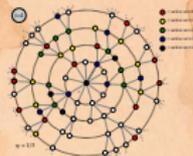
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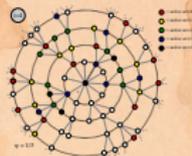
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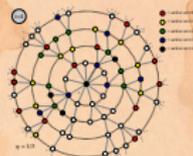
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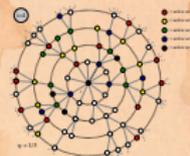
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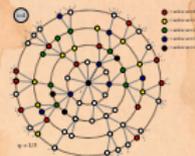
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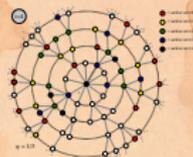
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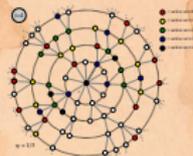
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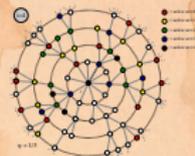
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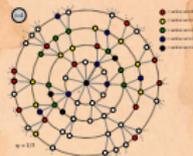
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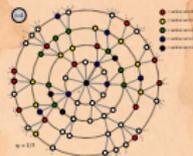
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Threshold model on a network

Original work:

“A simple model of global cascades on random networks”

D. J. Watts. Proc. Natl. Acad. Sci., 2002^[13]

- ▶ Mean field Granovetter model \rightarrow network model
- ▶ Individuals now have a limited view of the world

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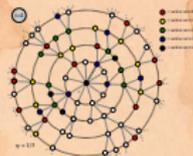
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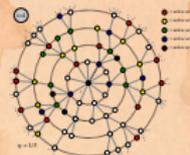
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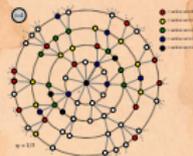
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Threshold model on a network

- ▶ 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 ϕ_i
- ▶ Individuals repeatedly poll contacts on network
- ▶ Synchronous: discrete time updating
- ▶ Individual i becomes active when number of active contacts $a_i \geq \phi_i/k_i$
- ▶ Activation is permanent (SI)

Contagion

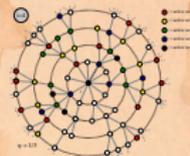
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Contagion

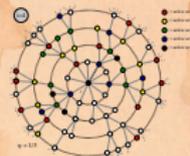
Basic Contagion Models

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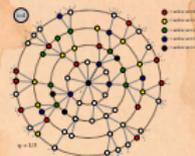
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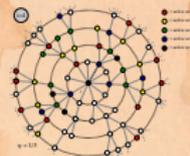
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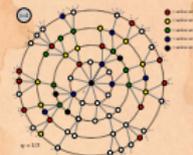
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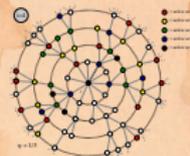
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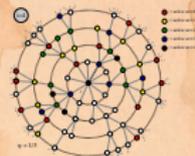
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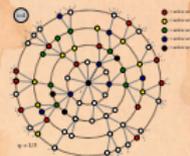
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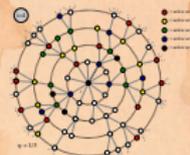
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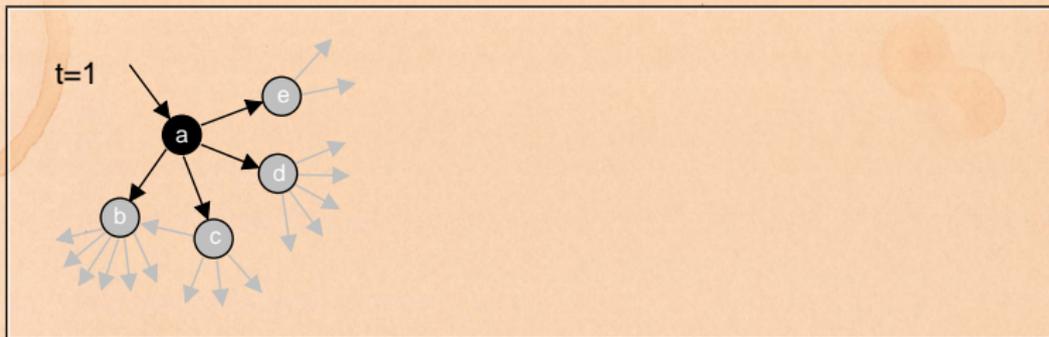
Social Contagion Models

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Threshold model on a network



▶ All nodes have threshold $\phi = 0.2$.

Contagion

Basic Contagion Models

Global spreading condition

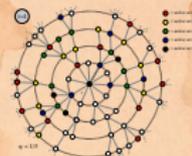
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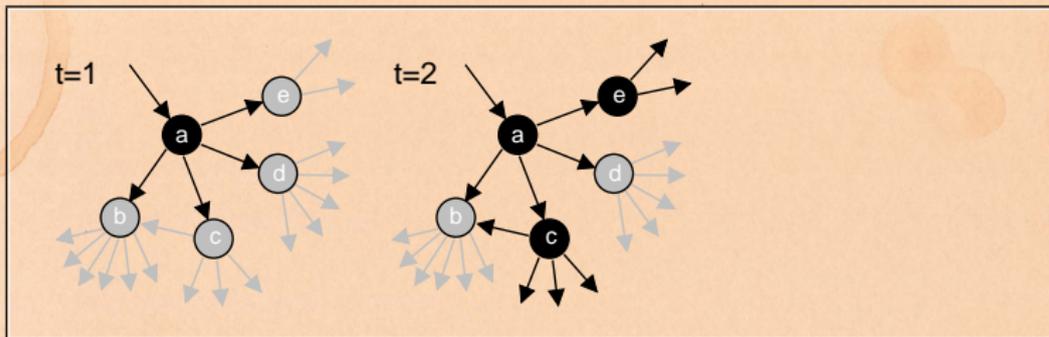
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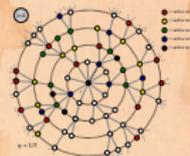
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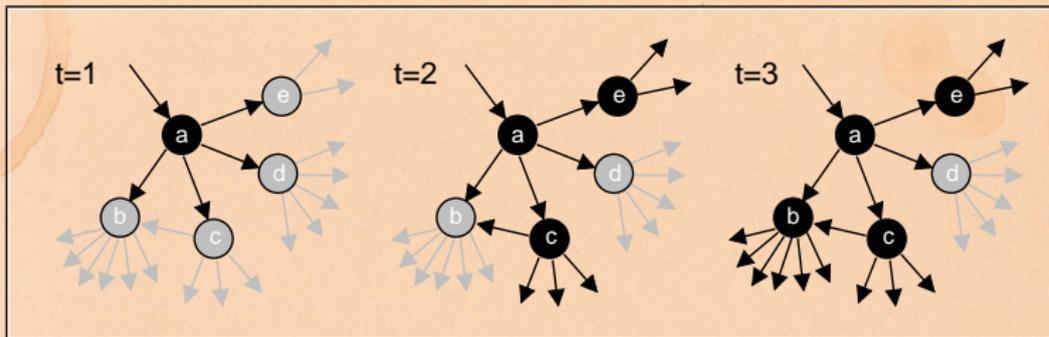
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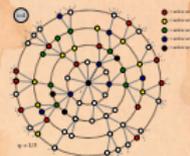
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The most gullible

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* [13]
- ▶ For a uniform threshold ϕ , our global spreading condition tells us when such a component exists:

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

Contagion

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Global spreading condition

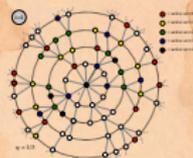
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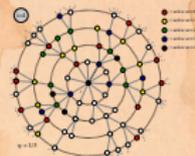
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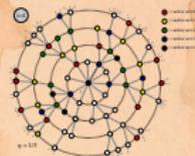
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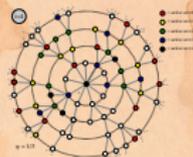
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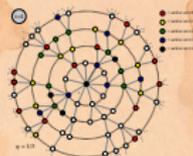
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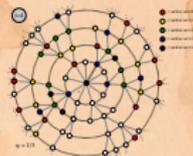
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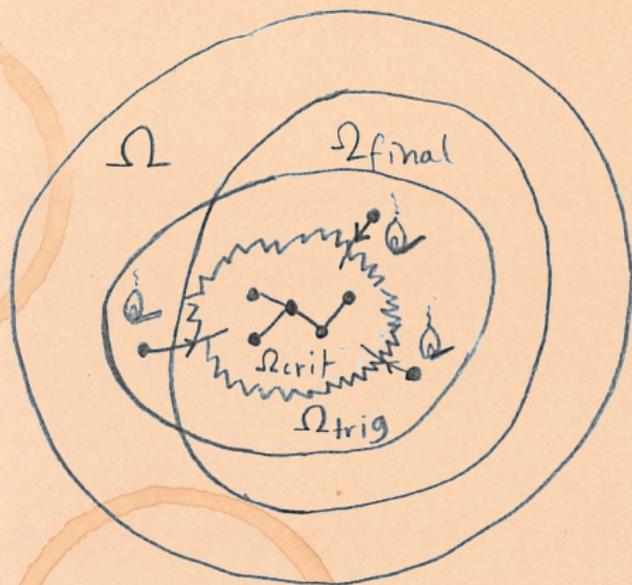
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Example random network structure:



- ▶ Ω_{crit} = critical mass = global vulnerable component
- ▶ Ω_{trig} = triggering component
- ▶ Ω_{final} = potential extent of spread
- ▶ Ω = entire network

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

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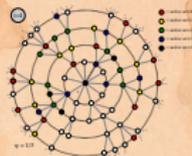
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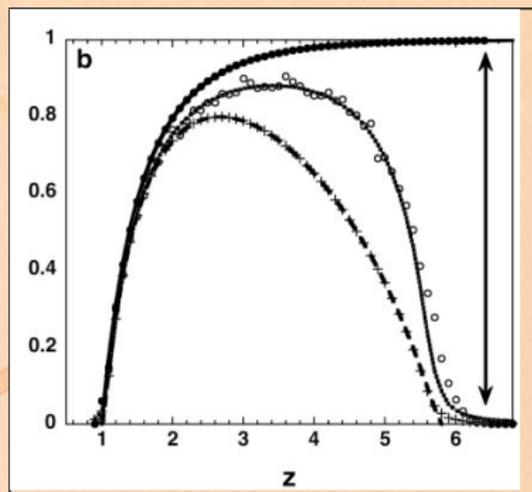
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Global spreading events on random networks



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

- ▶ Global spreading events occur only if size of vulnerable subcomponent > 0 .
- ▶ System is robust-yet-fragile just below upper boundary [3, 4, 12]
- ▶ 'Ignorance' facilitates spreading.

- ▶ **Top curve:** final fraction infected if successful.
- ▶ **Middle curve:** chance of starting a global spreading event (cascade).
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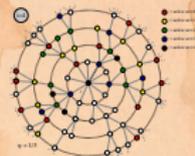
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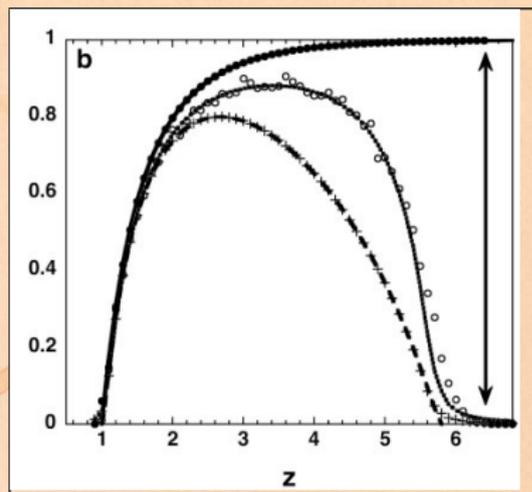
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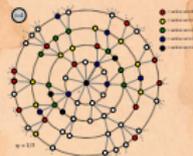
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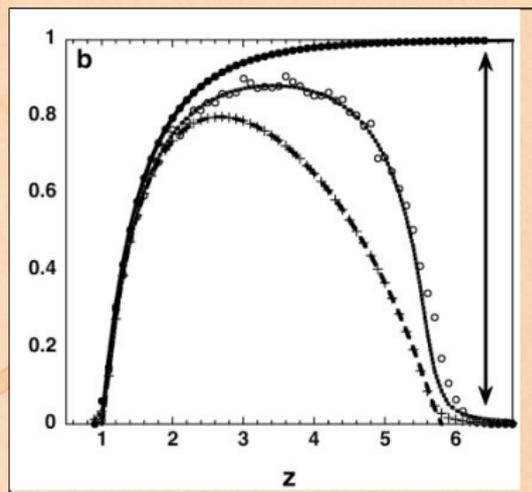
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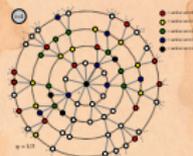
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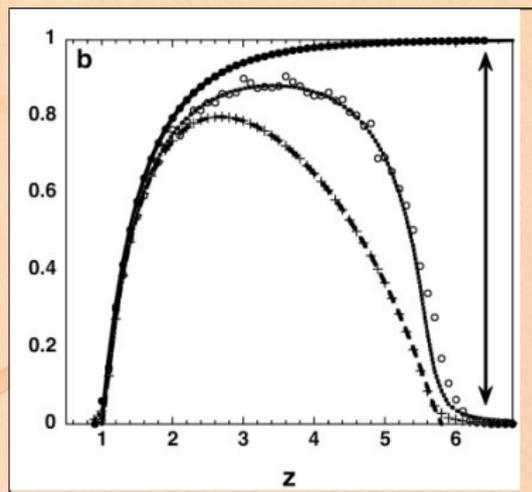
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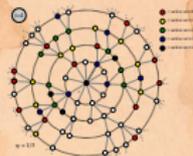
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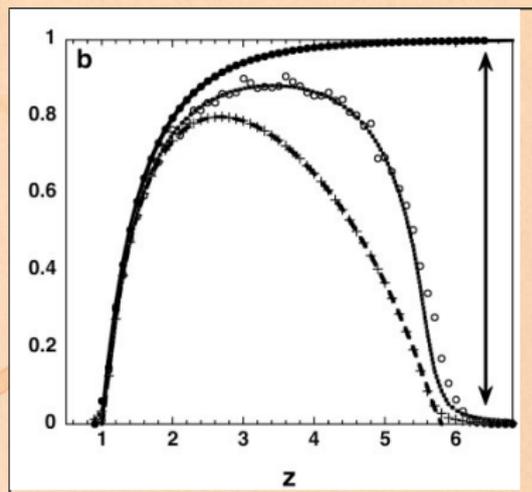
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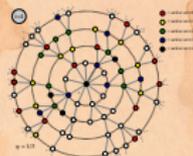
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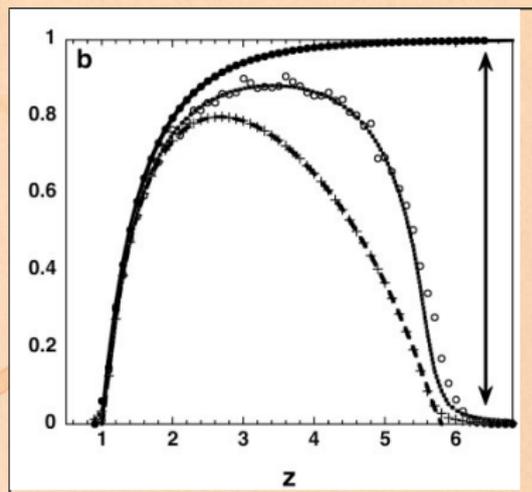
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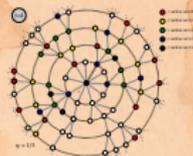
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Cascades on random networks

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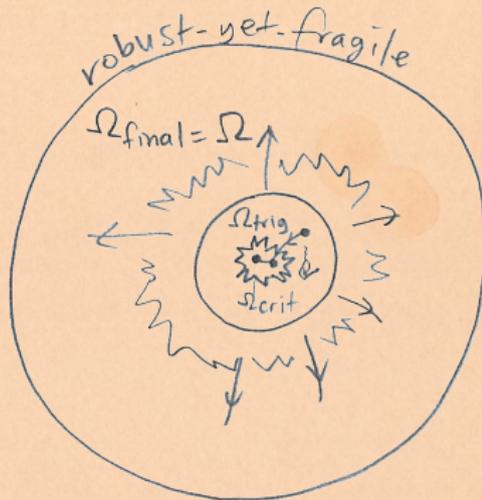
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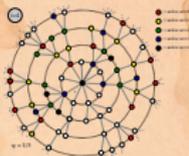
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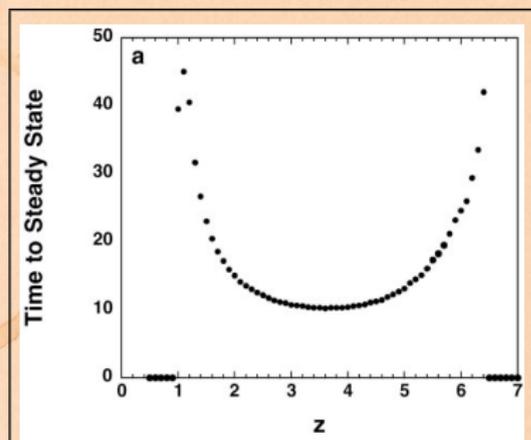
▶ Above lower phase transition



▶ Just below upper phase transition



Cascades on random networks



(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.

- ▶ Time taken for cascade to spread through network. [13]
- ▶ Two phase transitions.

Contagion

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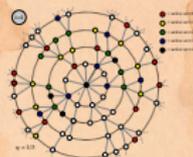
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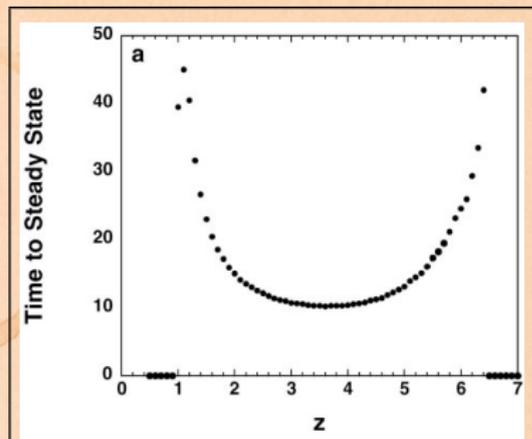
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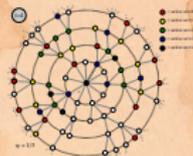
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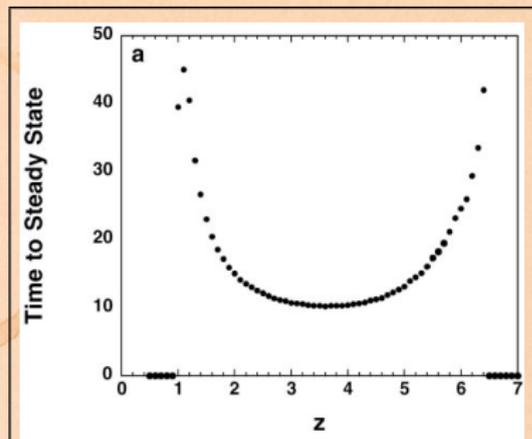
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Basic Contagion Models

Global spreading condition

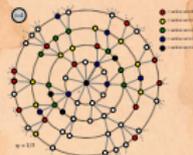
Social Contagion Models

Network version

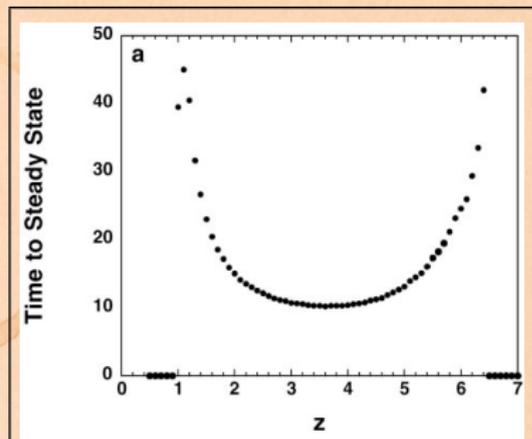
All-to-all networks

Theory

References



Cascades on random networks



(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.

- ▶ Time taken for cascade to spread through network. [13]
- ▶ Two phase transitions.

Contagion

Basic Contagion Models

Global spreading condition

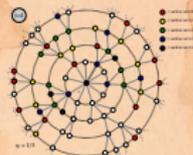
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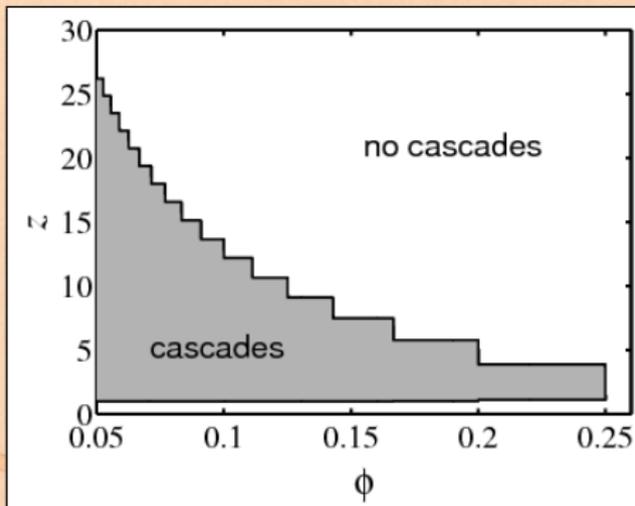
All-to-all networks

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Cascade window for random networks



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

- ▶ Outline of cascade window for random networks.

Contagion

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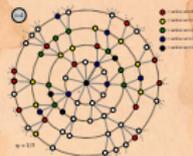
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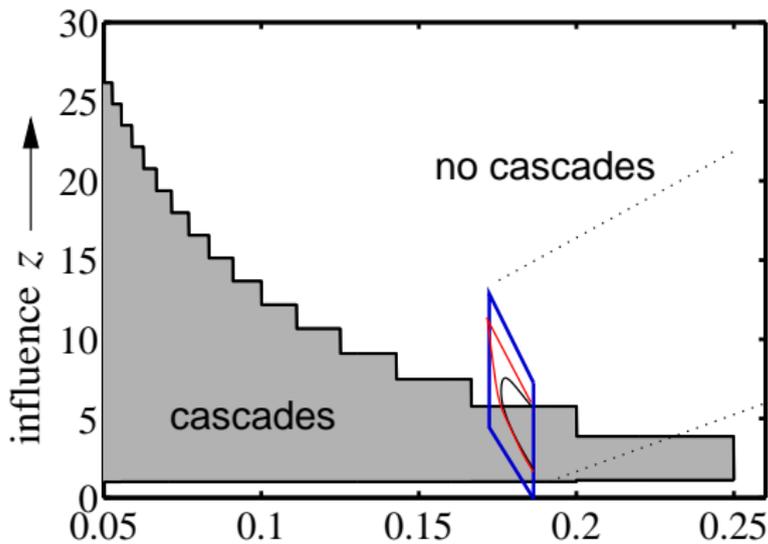
All-to-all networks

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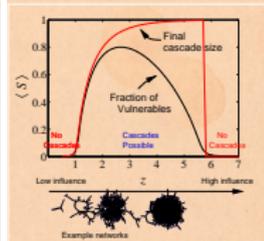
References



Cascade window for random networks



ϕ = uniform individual threshold



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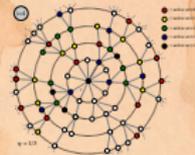
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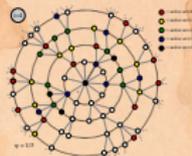
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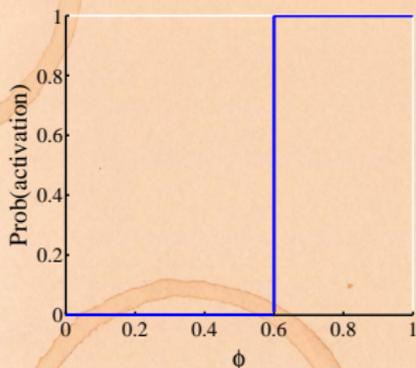
Theory

References



Social Contagion

Granovetter's Threshold model—recap



- ▶ Assumes deterministic response functions

- ▶ ϕ_c = threshold of an individual.

- ▶ $f(\phi_c)$ = distribution of thresholds in a population.

- ▶ $F(\phi_c)$ = cumulative distribution = $\int_{\phi_c}^1 f(\phi_c) d\phi_c$

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

Contagion

Basic Contagion Models

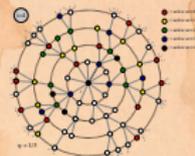
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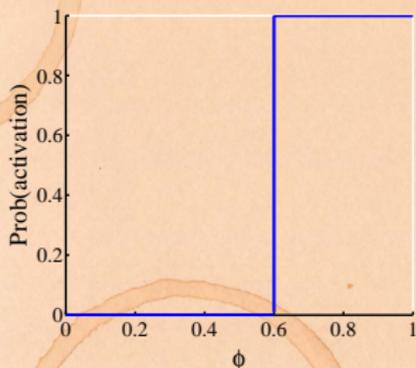
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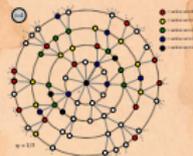
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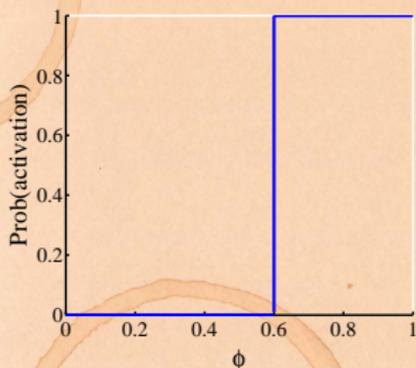
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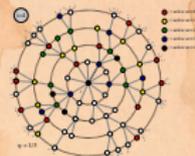
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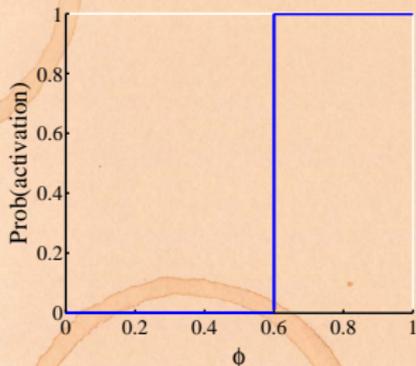
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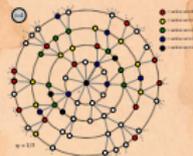
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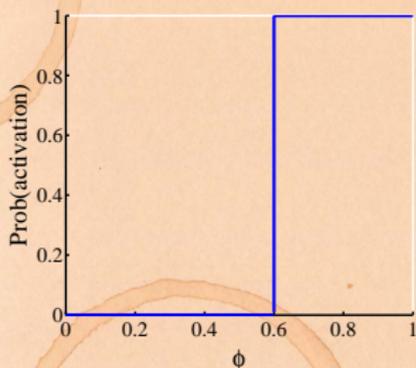
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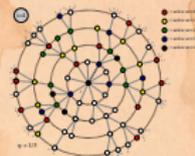
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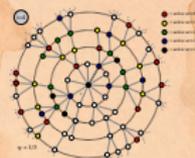
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- ▶ At time $t + 1$, fraction rioting = fraction with $\phi_* \leq \phi_t$.

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

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



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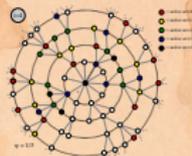
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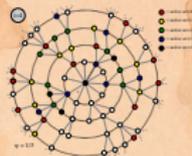
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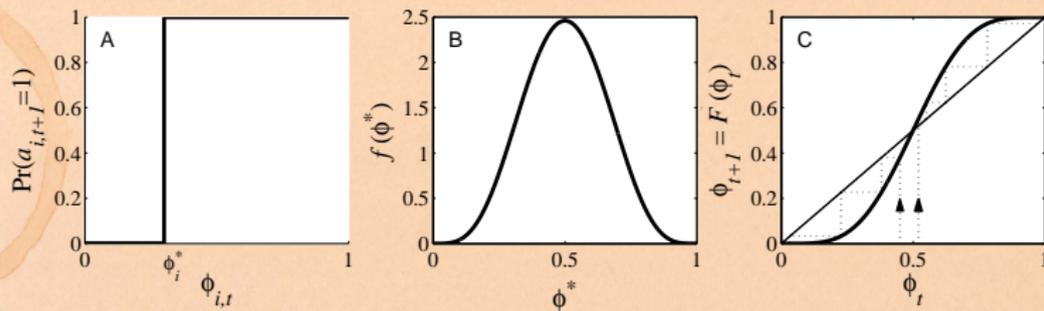
Global spreading condition

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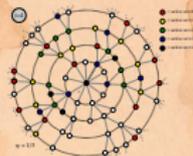
Network version
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References

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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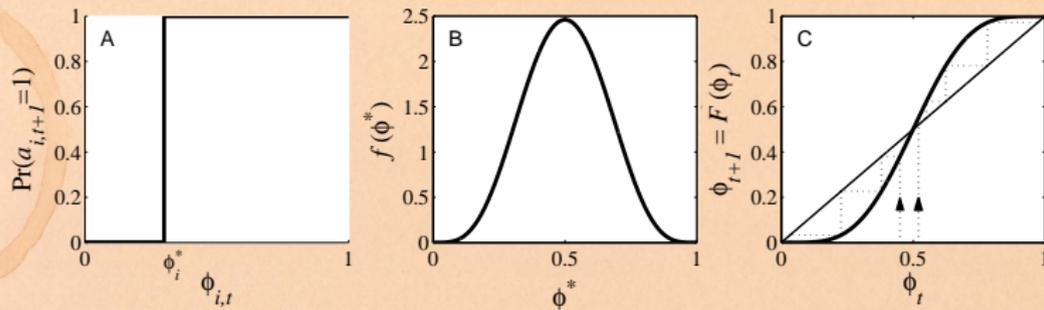
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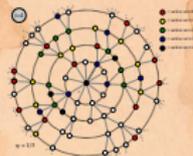
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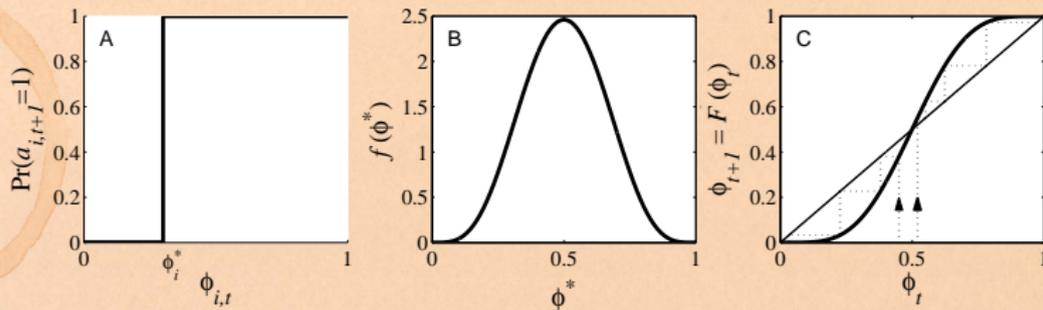
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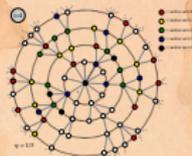
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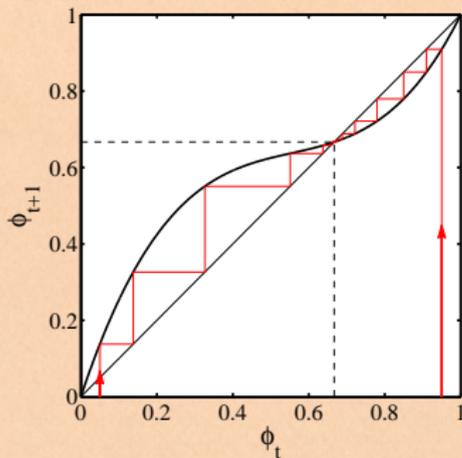
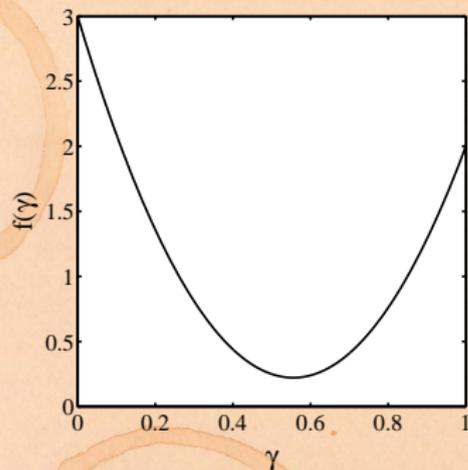
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Social Sciences—Threshold models



- ▶ Example of single stable state model

Contagion

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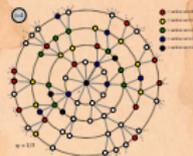
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Social Sciences—Threshold models

Implications for collective action theory:

1. Collective uniformity \nrightarrow 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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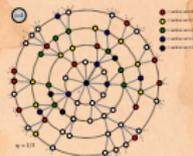
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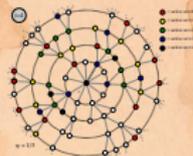
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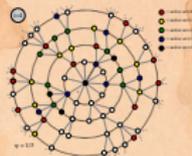
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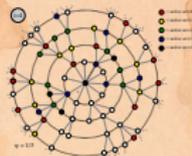
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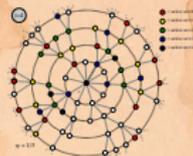
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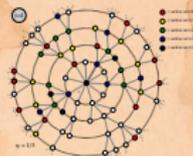
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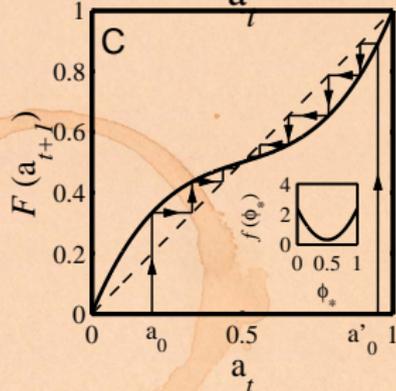
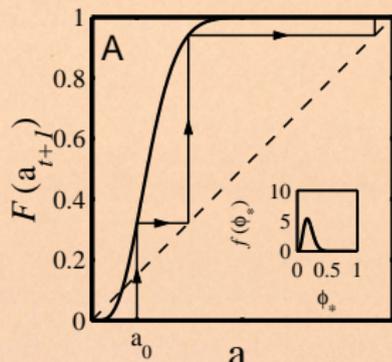
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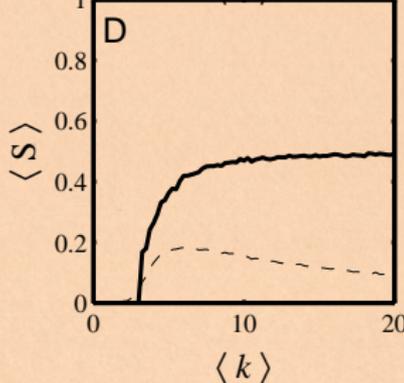
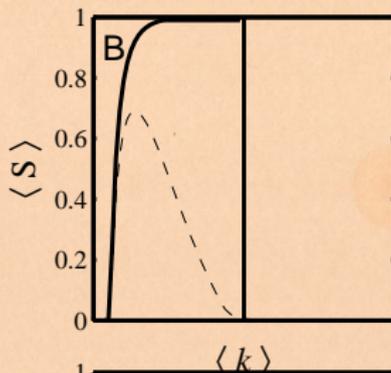


All-to-all versus random networks

all-to-all networks



random networks



Contagion

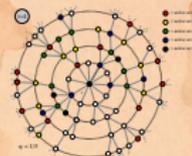
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Threshold contagion on random networks

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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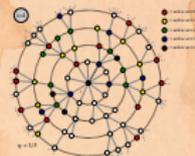
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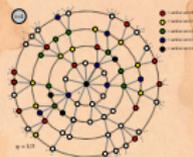
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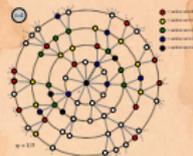
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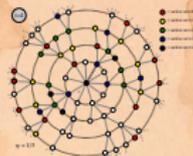
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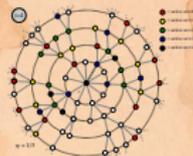
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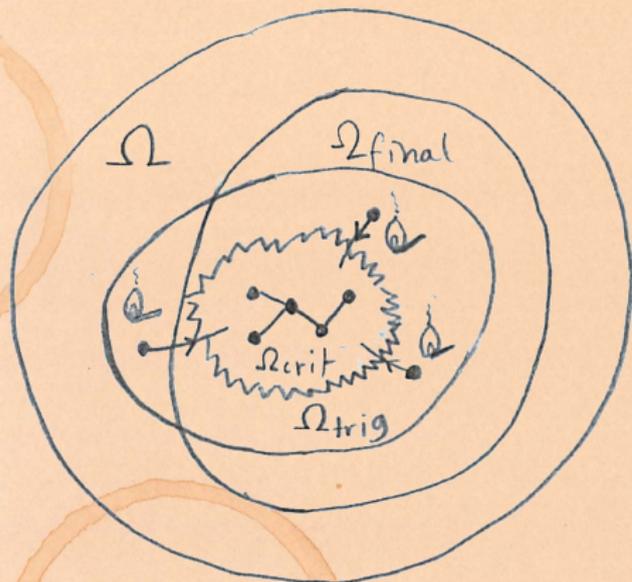
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Example random network structure:



- ▶ $\Omega_{\text{crit}} = \Omega_{\text{vuln}} =$
critical mass =
global
vulnerable
component
- ▶ $\Omega_{\text{trig}} =$
triggering
component
- ▶ $\Omega_{\text{final}} =$
potential extent
of spread
- ▶ $\Omega =$ entire
network

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

Contagion

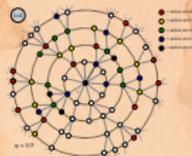
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Threshold contagion on random networks

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

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

$$F_v(x) = xF_P(F_v(x)) \quad \text{and} \quad F_u(x) = xF_R(F_v(x))$$

- ▶ 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

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

Contagion

Basic Contagion Models

Global spreading condition

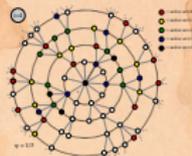
Social Contagion Models

Network version

All-to-all networks

Theory

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Threshold contagion on random networks

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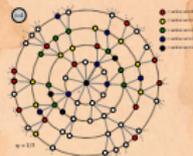
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Contagion

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Global spreading condition

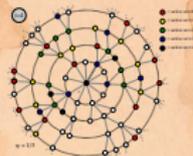
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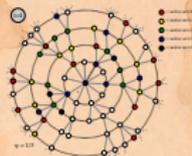
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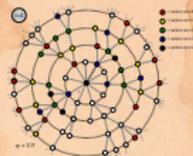
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Threshold contagion on random networks

- ▶ Everything now revolves around the **modified** generating function:

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

- ▶ Generating function for friends-of-friends distribution is related in same way as before:

$$F_A^{(\text{vuln})}(x) = \frac{\frac{d}{dx} F_P^{(\text{vuln})}(x)}{\frac{d}{dx} F_P^{(\text{vuln})}(x)|_{x=1}}$$

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Basic Contagion Models

Global spreading condition

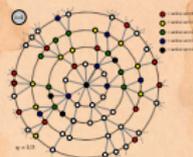
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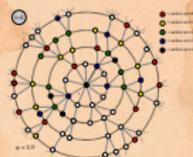
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Threshold contagion on random networks

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

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

central node
is not
vulnerable

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

first node
is not
vulnerable

- ▶ Can now solve as before to find $S_{\text{vuln}} = 1 - F_{\tau}^{(\text{vuln})}(1)$.

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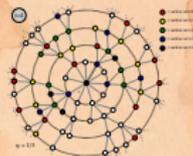
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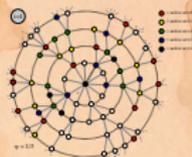
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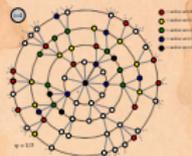
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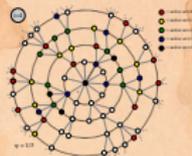
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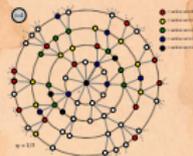
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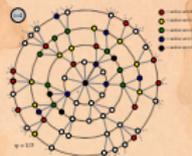
Social Contagion Models

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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:

$$F_x^{(\text{big})}(x) = xF_P \left(F_P^{(\text{vuln})}(x) \right)$$

$$F_P^{(\text{vuln})}(x) = 1 - F_R'(1) + xF_R^{(\text{vuln})} \left(F_P^{(\text{vuln})}(x) \right)$$

- ▶ Solve as before to find $P_{\text{big}} = S_{\text{big}} = 1 - F_x^{(\text{big})}(1)$.

Contagion

Basic Contagion Models

Global spreading condition

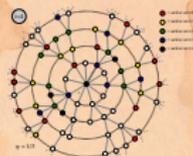
Social Contagion Models

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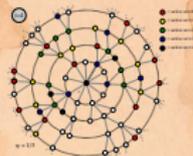
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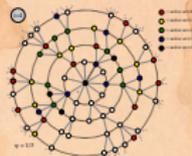
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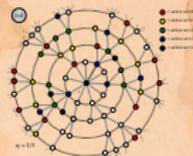
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Threshold contagion on random networks

- ▶ **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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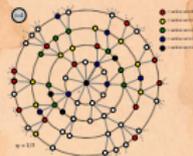
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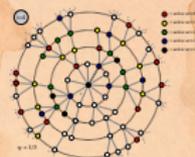
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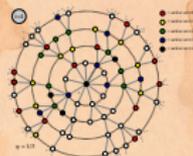
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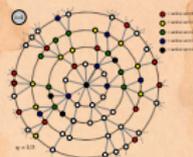
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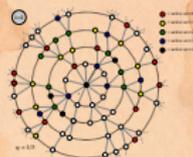
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Expected size of spread

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.
 - $t = 2$: enough of i 's friends and friends-of-friends switched on at time $t = 0$ so that i 's threshold is now exceeded.
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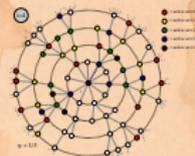
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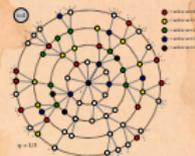
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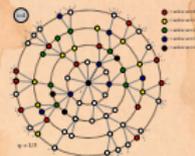
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Global spreading condition

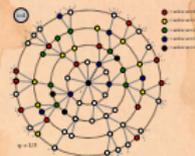
Social Contagion Models

Network version

All-to-all networks

Theory

References



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.
 - $t = 2$: enough of i 's friends and friends-of-friends switched on at time $t = 0$ so that i 's threshold is now exceeded.
 - $t = n$: enough nodes within n hops of i switched on at $t = 0$ and their effects have propagated to reach i .

Contagion

Basic Contagion Models

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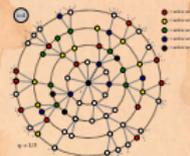
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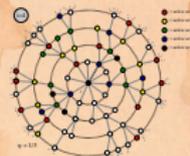
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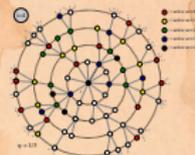
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Expected size of spread

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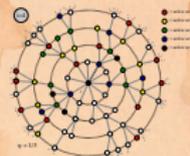
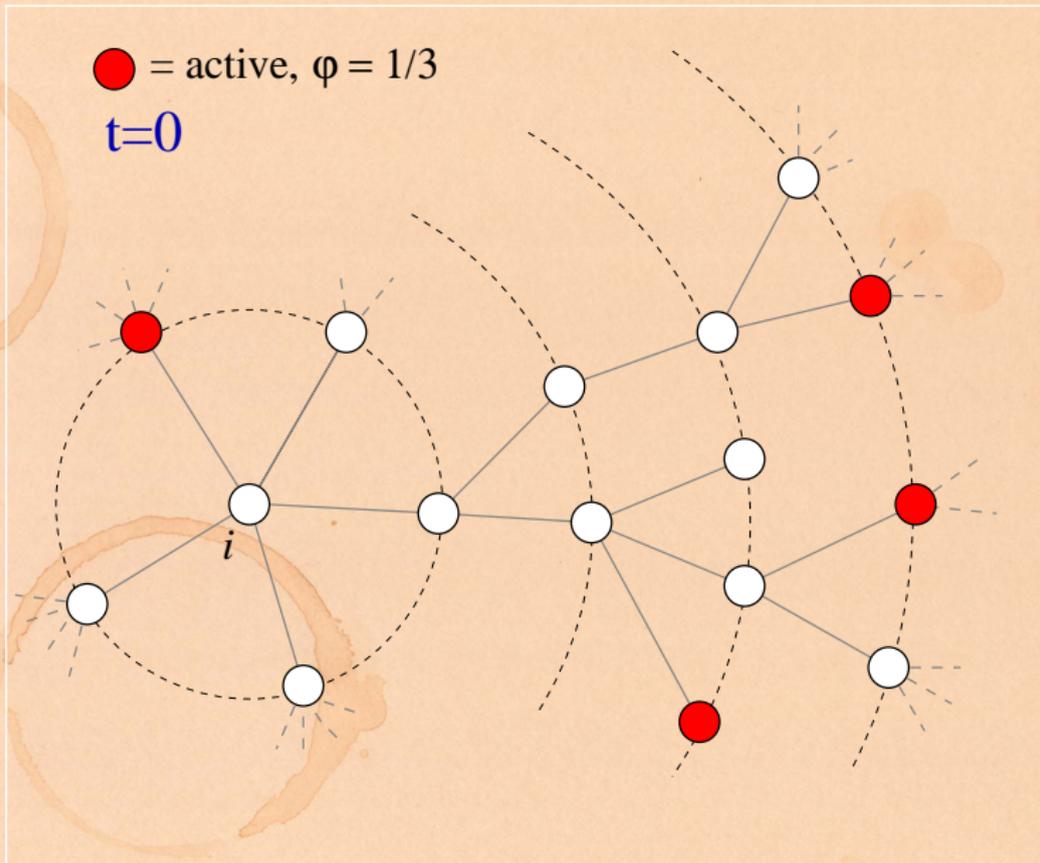
Global spreading condition

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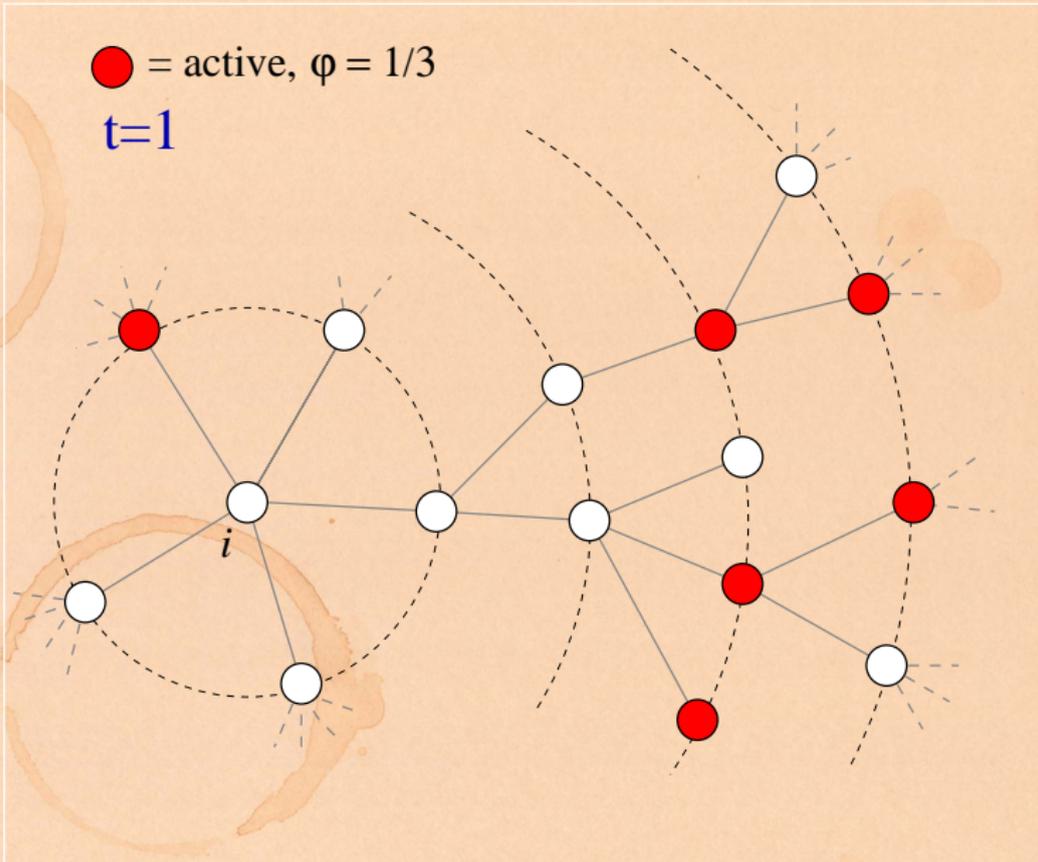
References



Expected size of spread

● = active, $\phi = 1/3$

$t=1$



Contagion

Basic Contagion Models

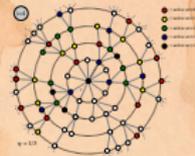
Global spreading condition

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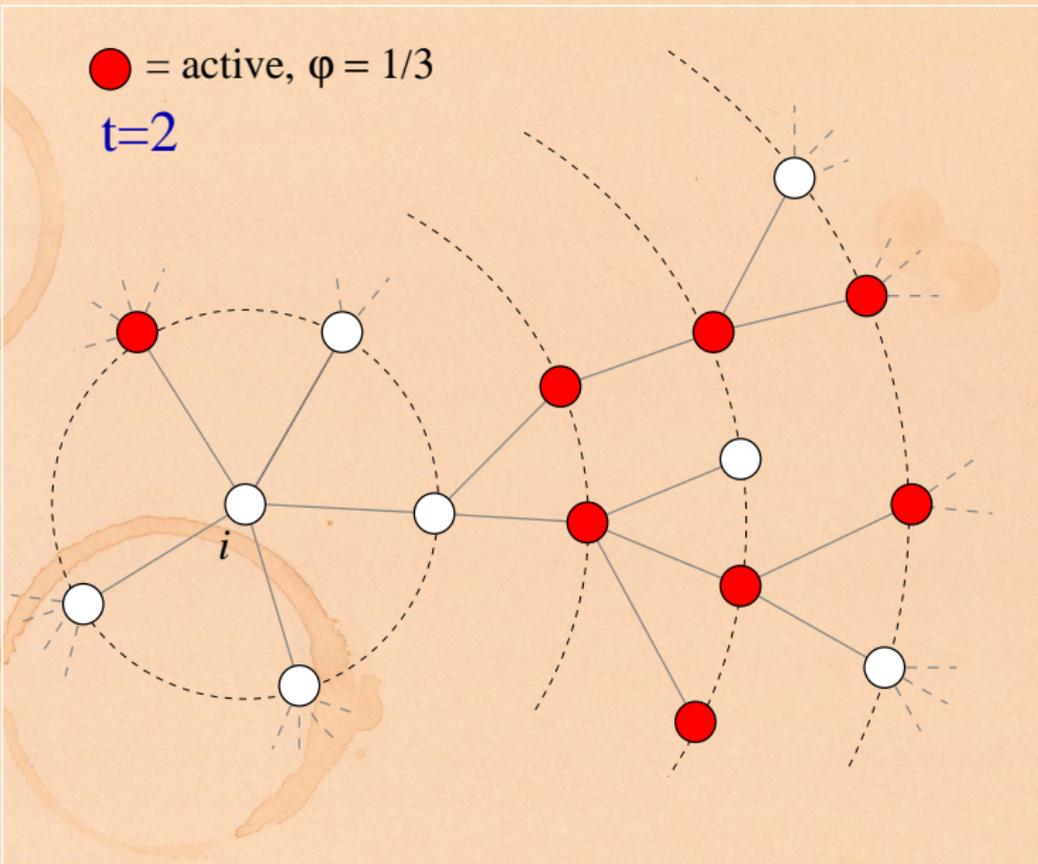
References



Expected size of spread

● = active, $\phi = 1/3$

$t=2$



Contagion

Basic Contagion Models

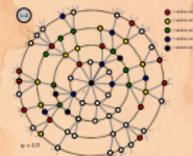
Global spreading condition

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Expected size of spread

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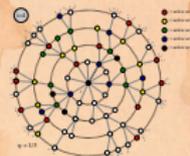
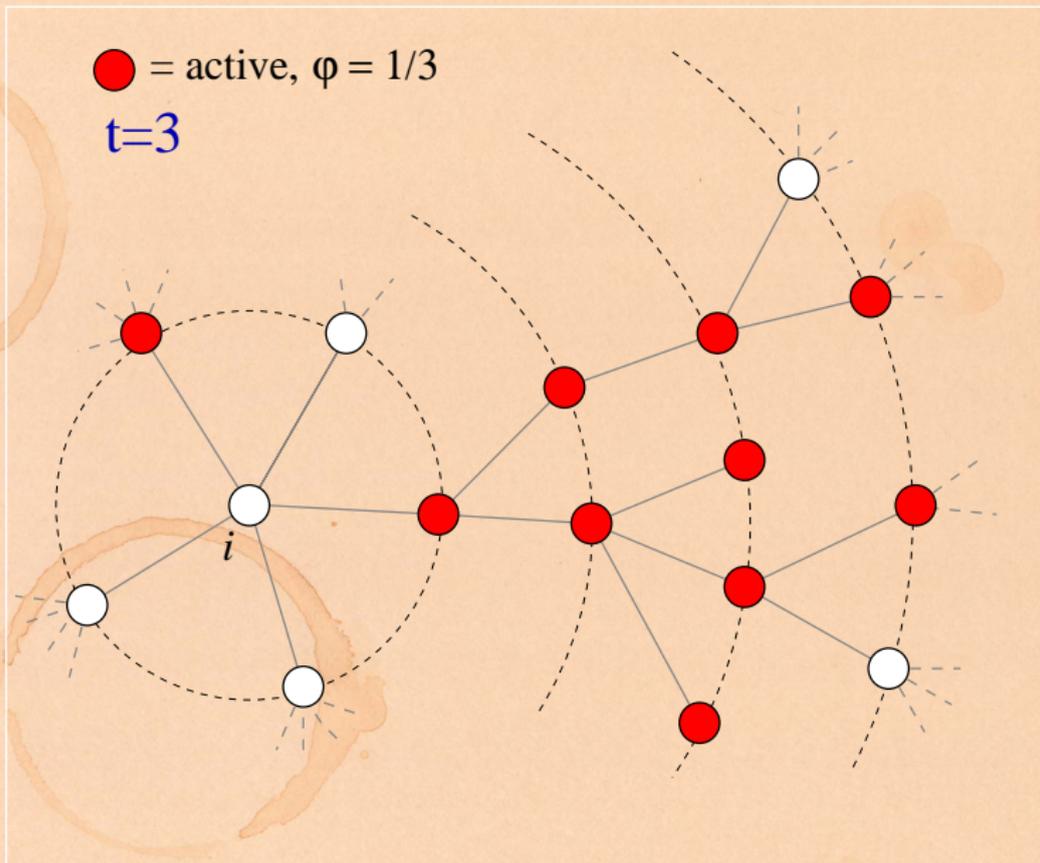
Global spreading condition

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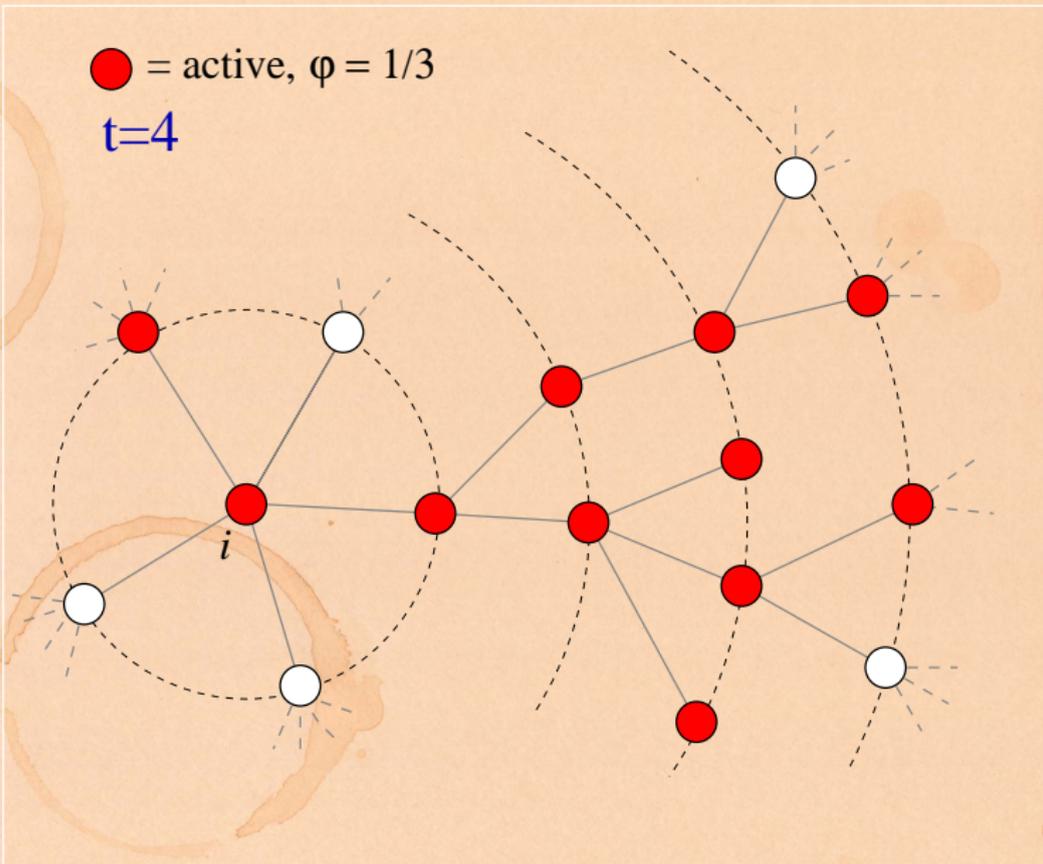
References



Expected size of spread

● = active, $\phi = 1/3$

$t=4$



Contagion

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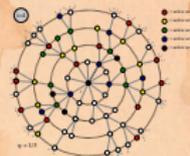
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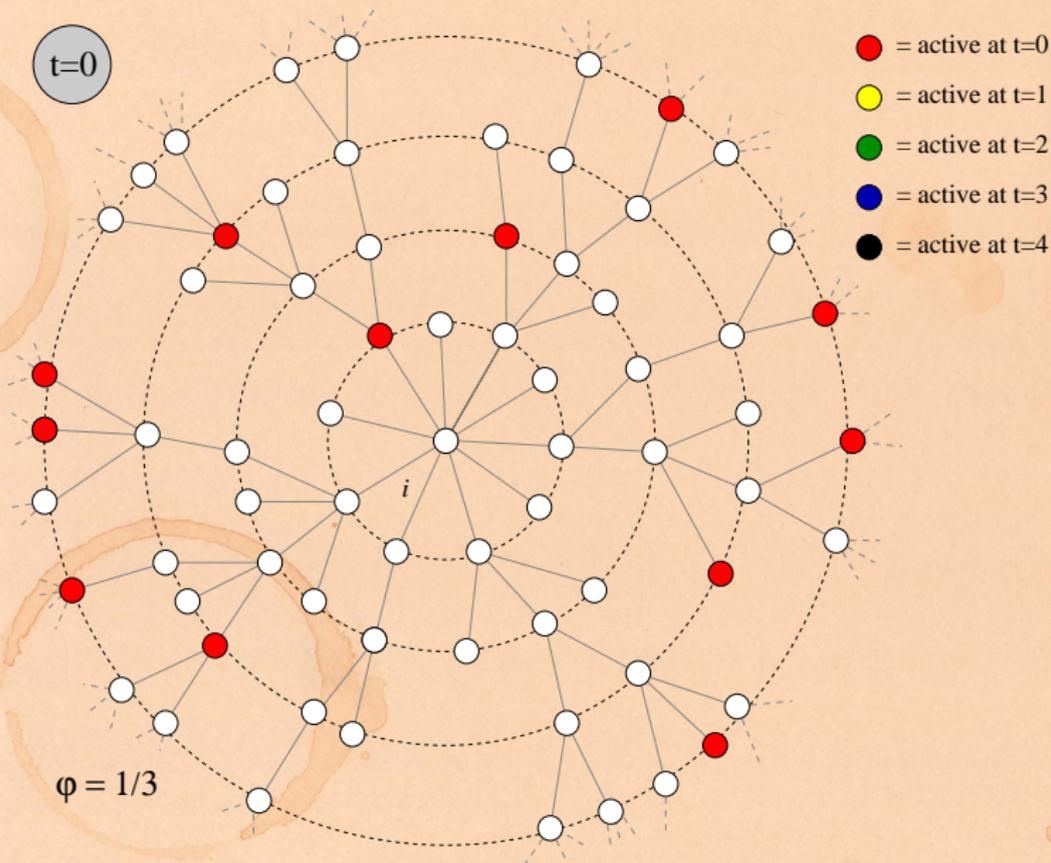
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Expected size of spread



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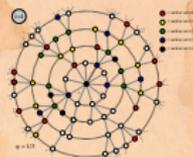
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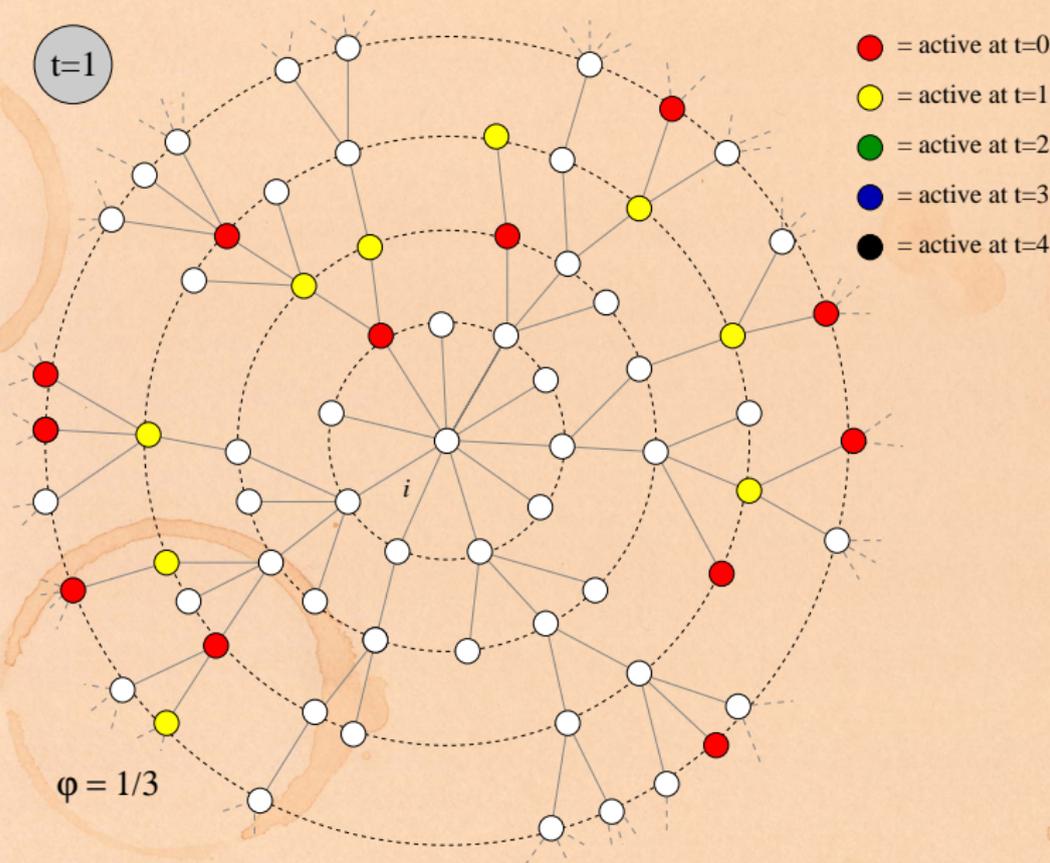
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Expected size of spread



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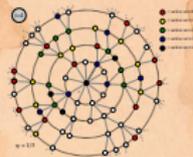
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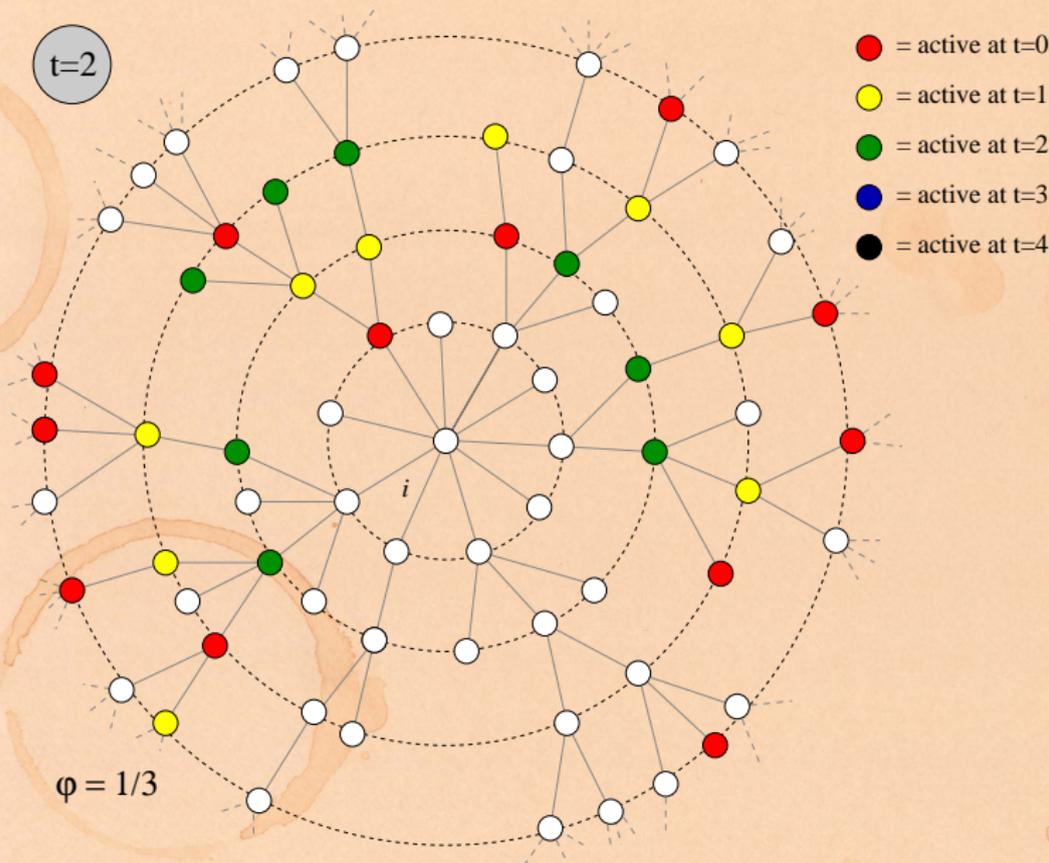
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Expected size of spread



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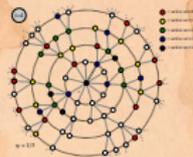
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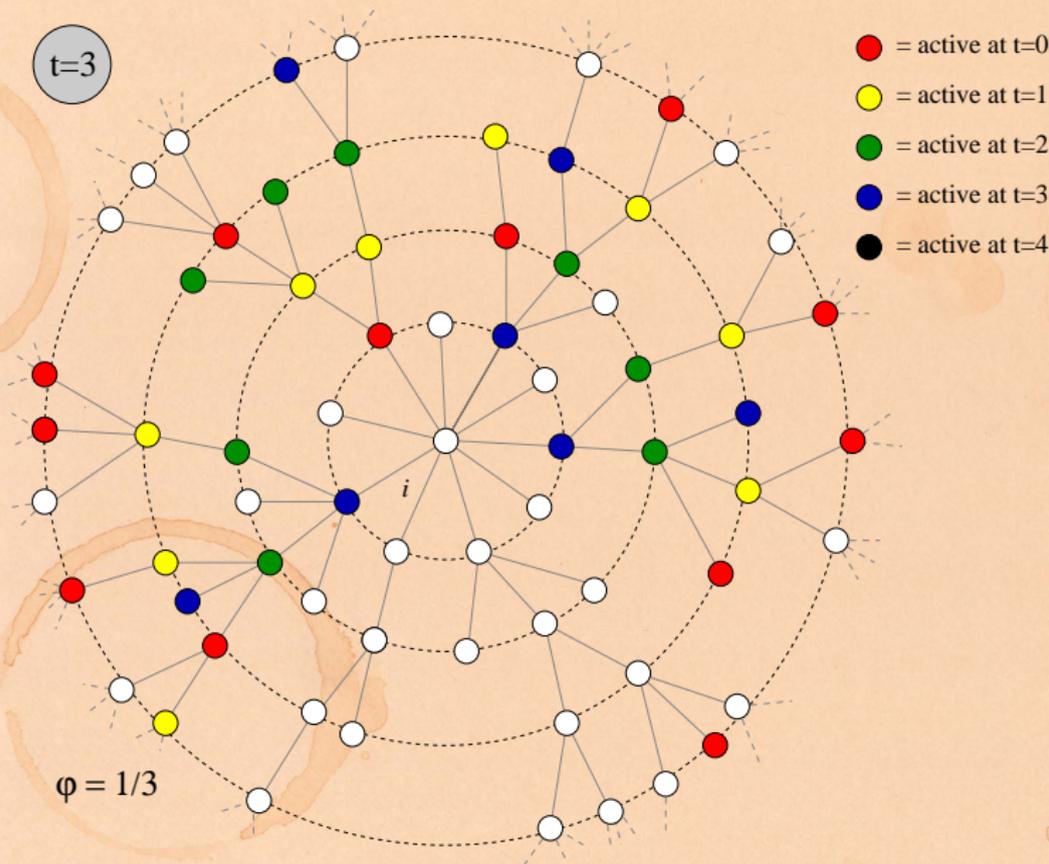
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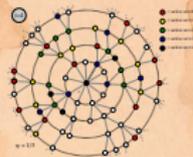
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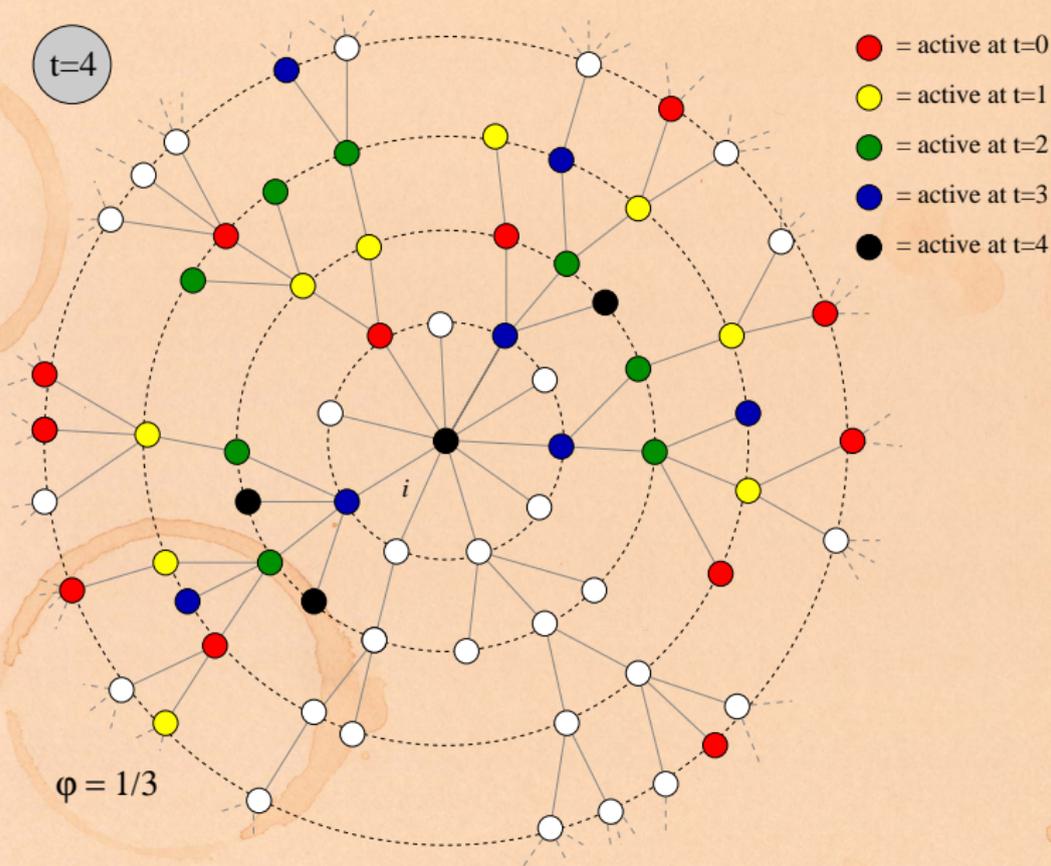
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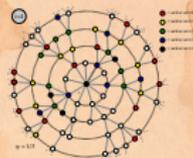
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Expected size of spread

Notes:

- ▶ Calculations are possible nodes do not become inactive (strong restriction).
- ▶ 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.
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Contagion

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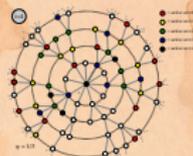
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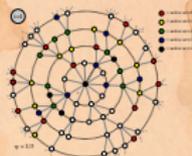
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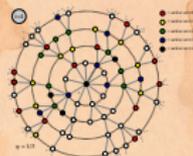
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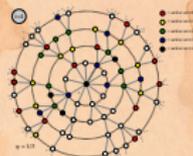
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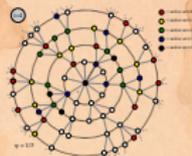
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Expected size of spread

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.

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Global spreading condition

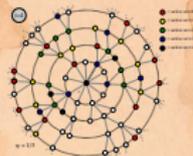
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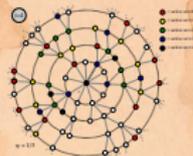
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► Notation:

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

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

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

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

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

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► Combining everything, we have:

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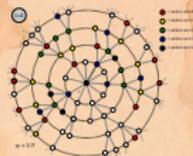
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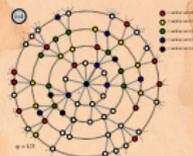
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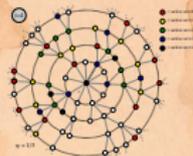
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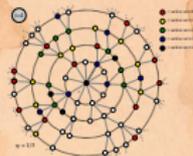
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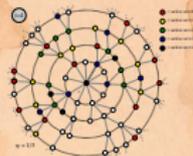
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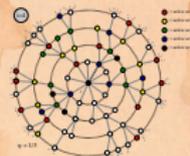
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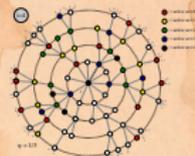
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Expected size of spread

- ▶ For general t , we need to know the probability an edge coming into a degree k node at time t is active.
- ▶ **Notation:** call this probability θ_t .
- ▶ We already know $\theta_0 = \phi_0$.
- ▶ Story analogous to $t = 1$ case:

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

- ▶ Average over all nodes to obtain expression for $\phi_{t,t+1}$:

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

- ▶ So we need to compute θ_t, \dots

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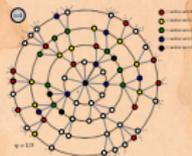
Global spreading
condition

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All-to-all networks

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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.
- ▶ **Notation:** call this probability θ_t .
- ▶ We already know $\theta_0 = \phi_0$.
- ▶ Story analogous to $t = 1$ case:

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

- ▶ Average over all nodes to obtain expression for $\phi_{t,t+1}$:

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- ▶ So we need to compute θ_t, \dots

Contagion

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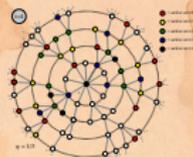
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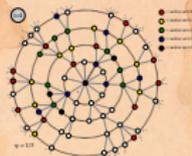
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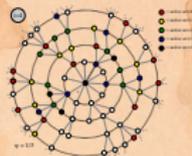
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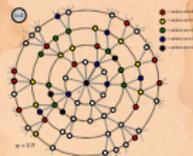
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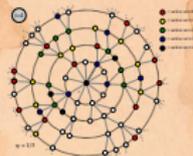
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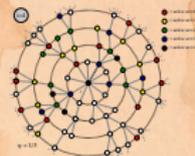
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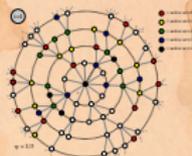
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- ▶ ϕ_0 and $(1 - \phi_0)$ terms account for state of node at time $t = 0$.
- ▶ See this all generalizes to give θ_{t+1} in terms of θ_t, \dots



Expected size of spread

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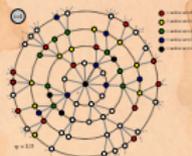
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- ▶ See this all generalizes to give θ_{t+1} in terms of $\theta_t \dots$



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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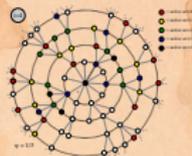
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Comparison between theory and simulations

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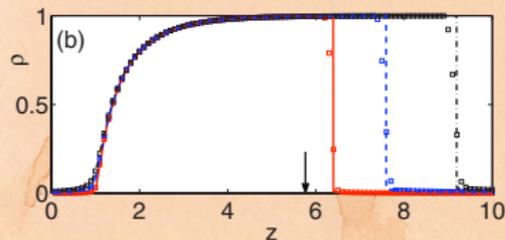
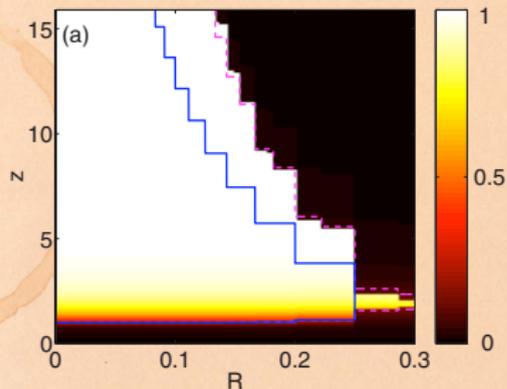
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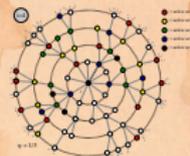
► Pure random networks with simple threshold responses

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

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

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

► Sensible expansion of cascade window as ϕ_0 increases.



From Gleeson and Cahalane [7]

Notes:

- ▶ Retrieve cascade condition for spreading from a single seed in limit $\phi_0 \rightarrow 0$.
- ▶ Depends on map $\theta_{t+1} = G(\theta_t; \phi_0)$.
- ▶ First: if self-starters are present, some activation is assured:

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

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 if

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

Insert question from assignment 8 (田)

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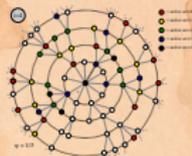
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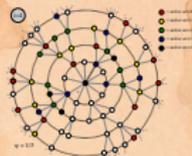
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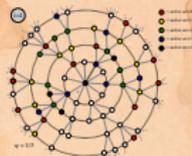
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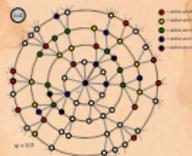
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In words:

- ▶ If $G(0; \phi_0) > 0$, spreading must occur because some nodes turn on for free.
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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 $0 < \theta_* < 1$, then for $\theta_0 > \theta_*$, spreading takes off.
- ▶ Tricky point: G depends on ϕ_0 , so as we change ϕ_0 , we also change G .

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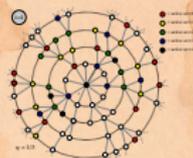
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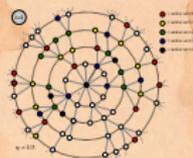
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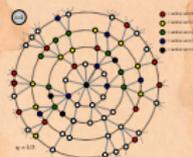
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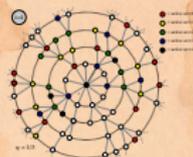
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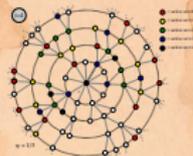
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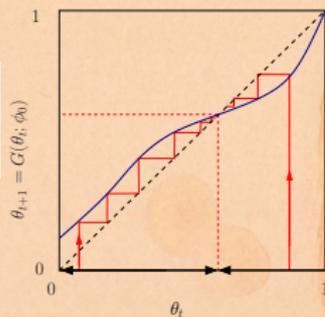
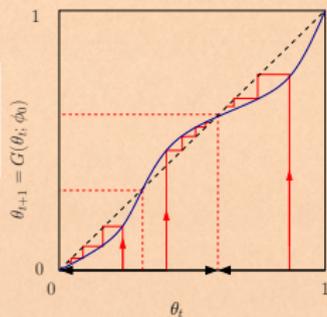
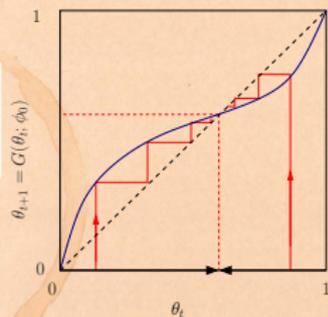
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General fixed point story:



- ▶ Given $\theta_0 (= \phi_0)$, 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 .
- ▶ So choice of ϕ_0 dictates both G and starting point—can't start anywhere for a given G .

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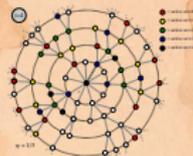
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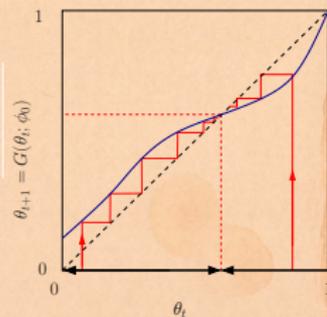
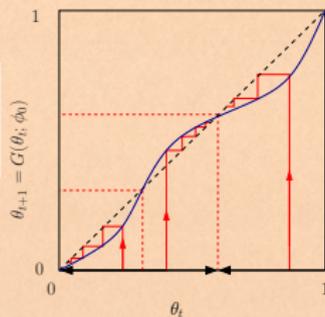
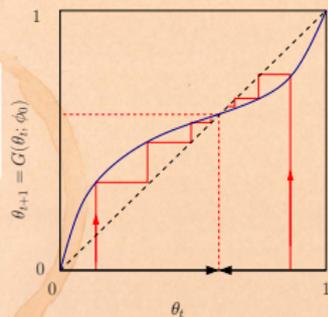
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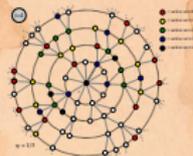
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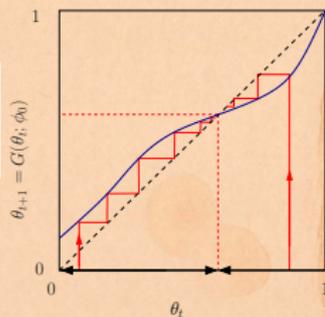
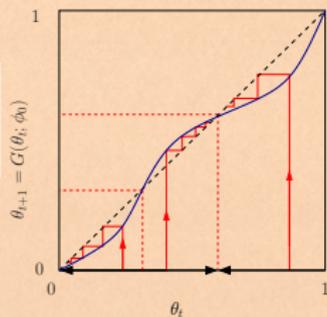
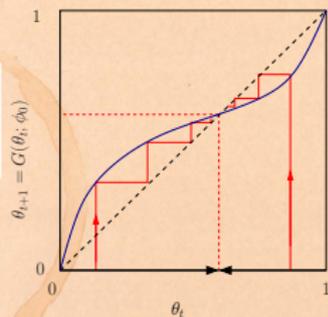
All-to-all networks

Theory

References



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 .
- ▶ So choice of ϕ_0 dictates both G and starting point—can't start anywhere for a given G .

Contagion

Basic Contagion Models

Global spreading condition

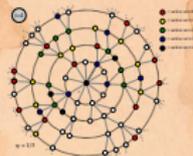
Social Contagion Models

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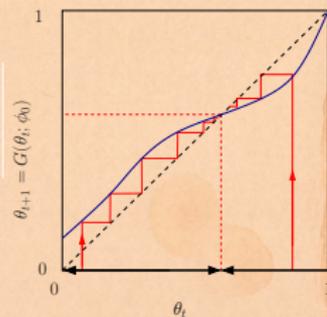
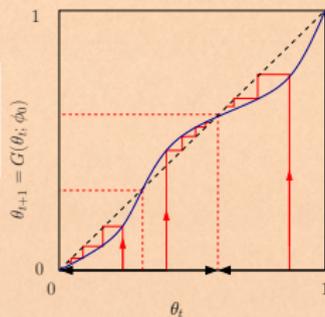
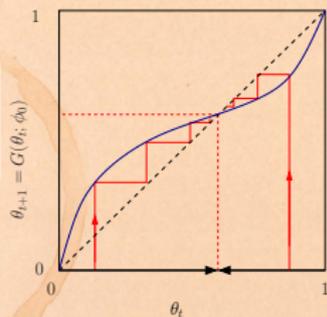
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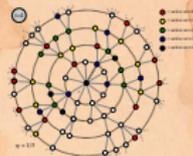
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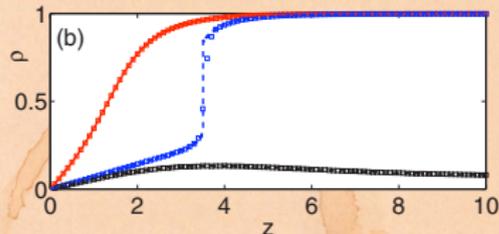
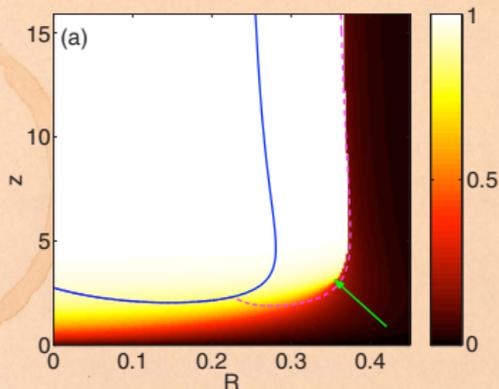
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Comparison between theory and simulations



- ▶ 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 $\langle k \rangle$.

Contagion

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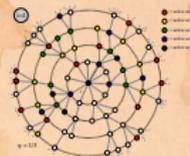
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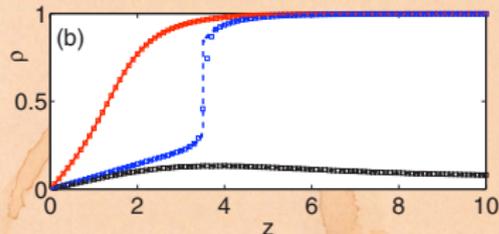
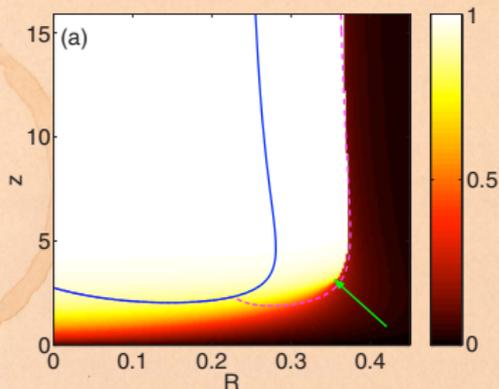
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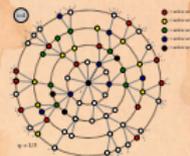
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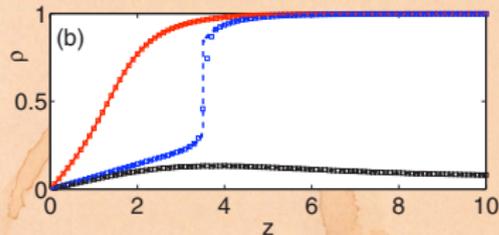
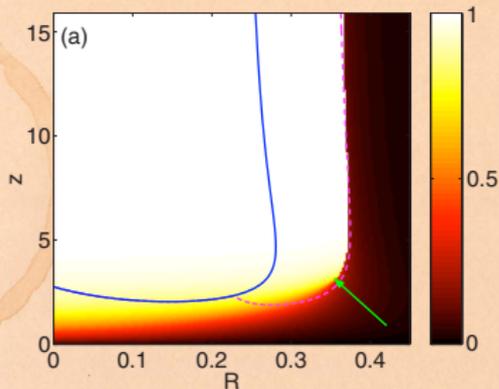
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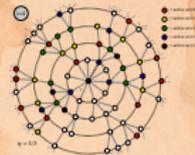
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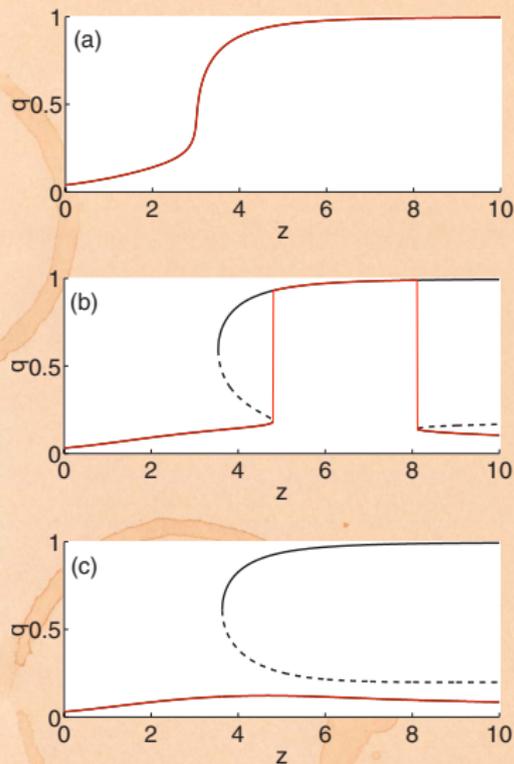
Network version
All-to-all networks

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- ▶ 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: $R = 0.35, 0.371, \text{ and } 0.375$.
- ▶ n.b.: higher values of θ_0 for (b) and (c) lead to higher fixed points of G .
- ▶ Saddle node bifurcations appear and merge (b and c).

Contagion

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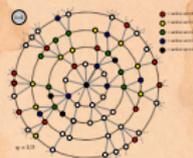
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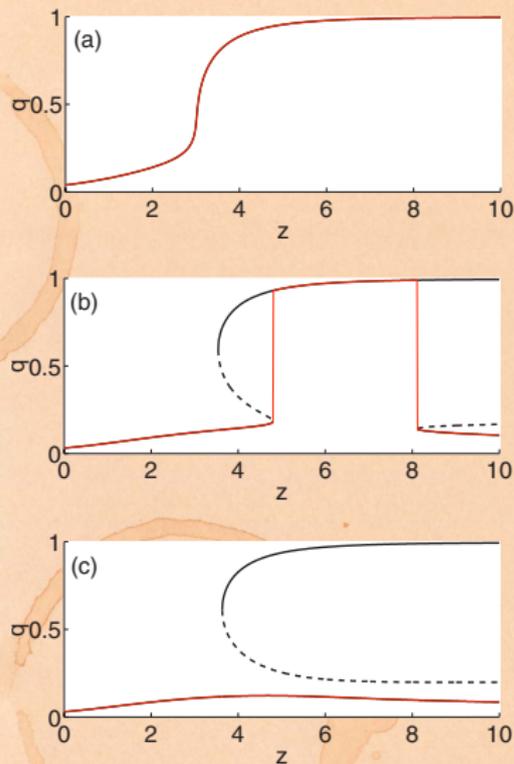
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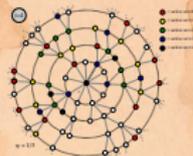
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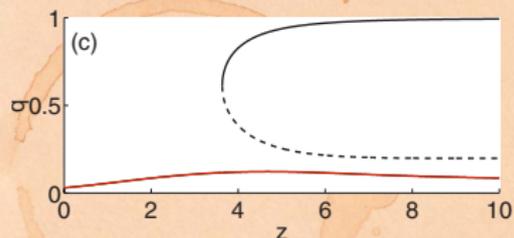
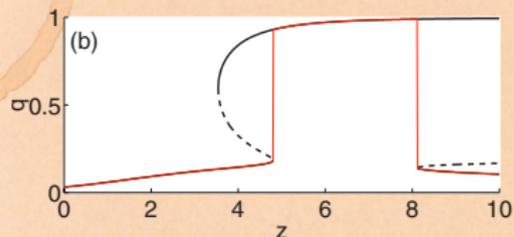
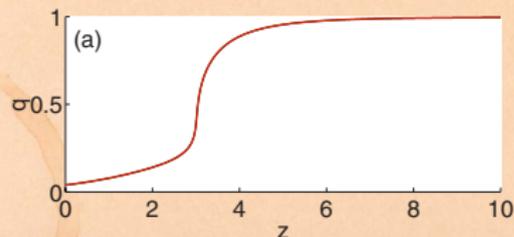
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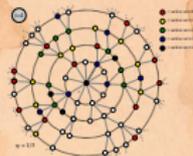
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Spreadarama

Bridging to single seed case:

- ▶ Consider largest vulnerable component as initial set of seeds.
- ▶ Not quite right as spreading must move through vulnerables.
- ▶ But we can usefully think of the vulnerable component as activating at time $t = 0$ because order doesn't matter.
- ▶ Rebuild ϕ_t and θ_t expressions...

Contagion

Basic Contagion Models

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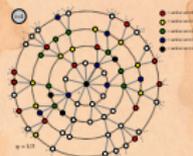
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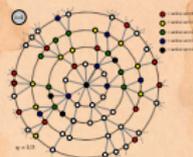
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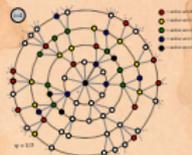
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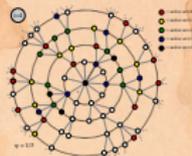
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Spreadarama

Two pieces modified for single seed:

1. $\theta_{t+1} = \theta_{\text{vuln}} +$

$$(1 - \theta_{\text{vuln}}) \sum_{k=1}^{\infty} \frac{kP_k}{\langle k \rangle} \sum_{j=0}^{k-1} \binom{k-1}{j} \theta_t^j (1 - \theta_t)^{k-1-j} B_{kj}$$

with $\theta_0 = \theta_{\text{vuln}} = \mathbf{Pr}$ an edge leads to the giant vulnerable component (if it exists).

2. $\phi_{t+1} = S_{\text{vuln}} +$

$$(1 - S_{\text{vuln}}) \sum_{k=0}^{\infty} P_k \sum_{j=0}^k \binom{k}{j} \theta_t^j (1 - \theta_t)^{k-j} B_{kj}.$$

Contagion

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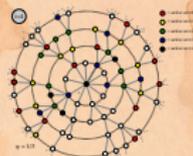
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Time-dependent solutions

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 $\phi(t)$ and $\theta(t)$.

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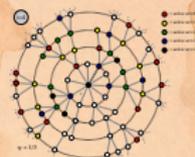
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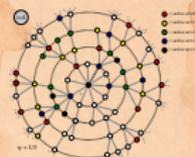
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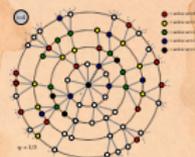
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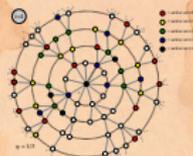
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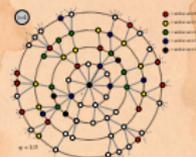
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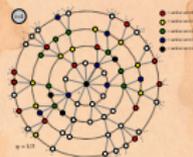
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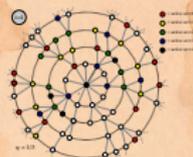
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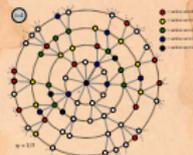
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