Cascading Behavior in Networks

Thanks to Jure Leskovec, Stanford and Panayiotis Tsaparas, Univ. of Ioannina for slides

Agenda

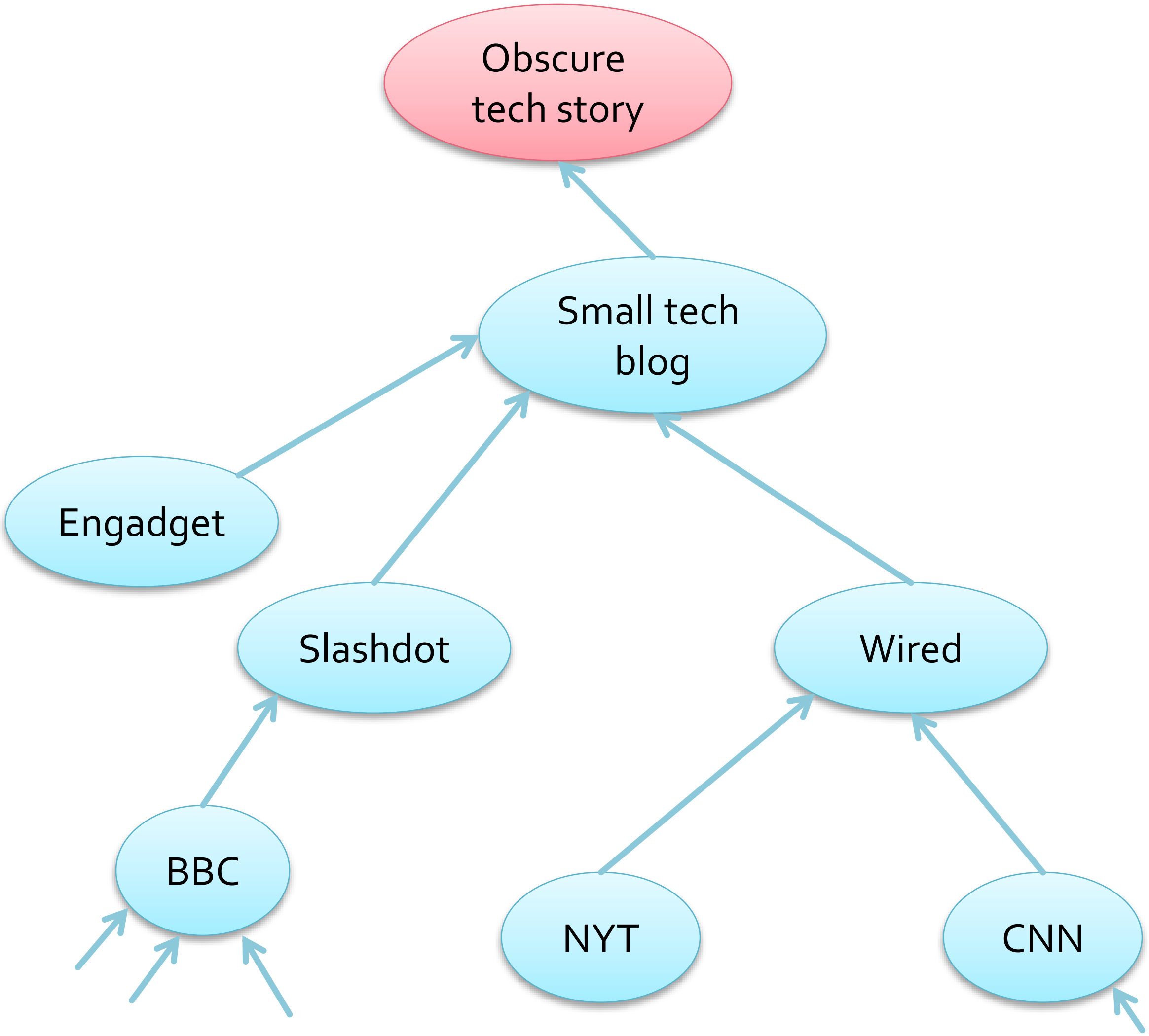
- Spreading Through Networks
- Decision Based Model of Diffusion
  - Granovetter’s Model of Collective Action
  - Threshold Model of Diffusion
  - Game Theoretic Model of Diffusion
  - Extending the Model: Allow People to Adopt A & B (skipped)
- Probabilistic Models of Diffusion
  - Epidemic Model Based on Trees
  - Models of Disease Spreading
  - Independent Cascade Model
  - Modeling Interactions Between Contagions (skipped)

Spreading Through Networks

- **Spreading through networks:**
  - Cascading behavior
  - Diffusion of innovations
  - Network effects
  - Epidemics
- **Behaviors that cascade from node to node like an epidemic**

- **Examples:**
  - **Biological:**
    - Diseases via contagion
  - **Technological:**
    - Cascading failures
    - Spread of information
  - **Social:**
    - Rumors, news, new technology
    - Viral marketing

Information Diffusion: Media



Obscure tech story

Small tech blog

Engadget

Slashdot

Wired

BBC

NYT

CNN

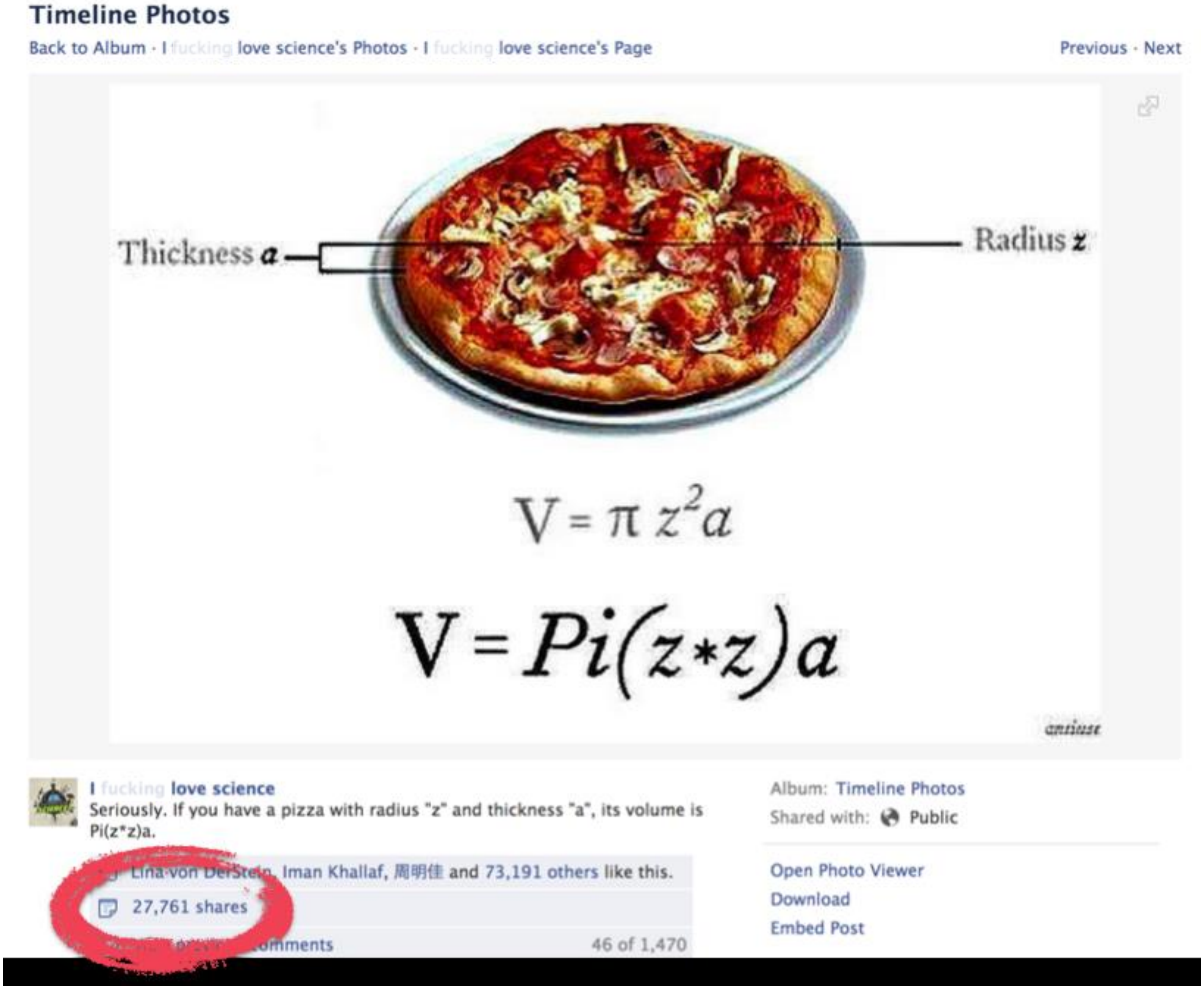
Twitter & Facebook post sharing

Lada Adamic shared a link via Erik Johnston.
January 16, 2013

When life gives you an almost empty jar of nutella, add some ice cream... (and other useful tips)

50 Life Hacks to Simplify your World
twistedsifter.com

Life hacks are little ways to make our lives easier. These low-budget tips and trick can help you organize and de-clutter space; prolong and preserve your products; or teach you...



Timeline Photos

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$$V = \pi z^2 a$$

$$V = Pi(z*z)a$$

I fucking love science

Seriously. If you have a pizza with radius "z" and thickness "a", its volume is Pi(z*z)a.

Lina von DerStein, Iman Khallaf, 周明佳 and 73,191 others like this.

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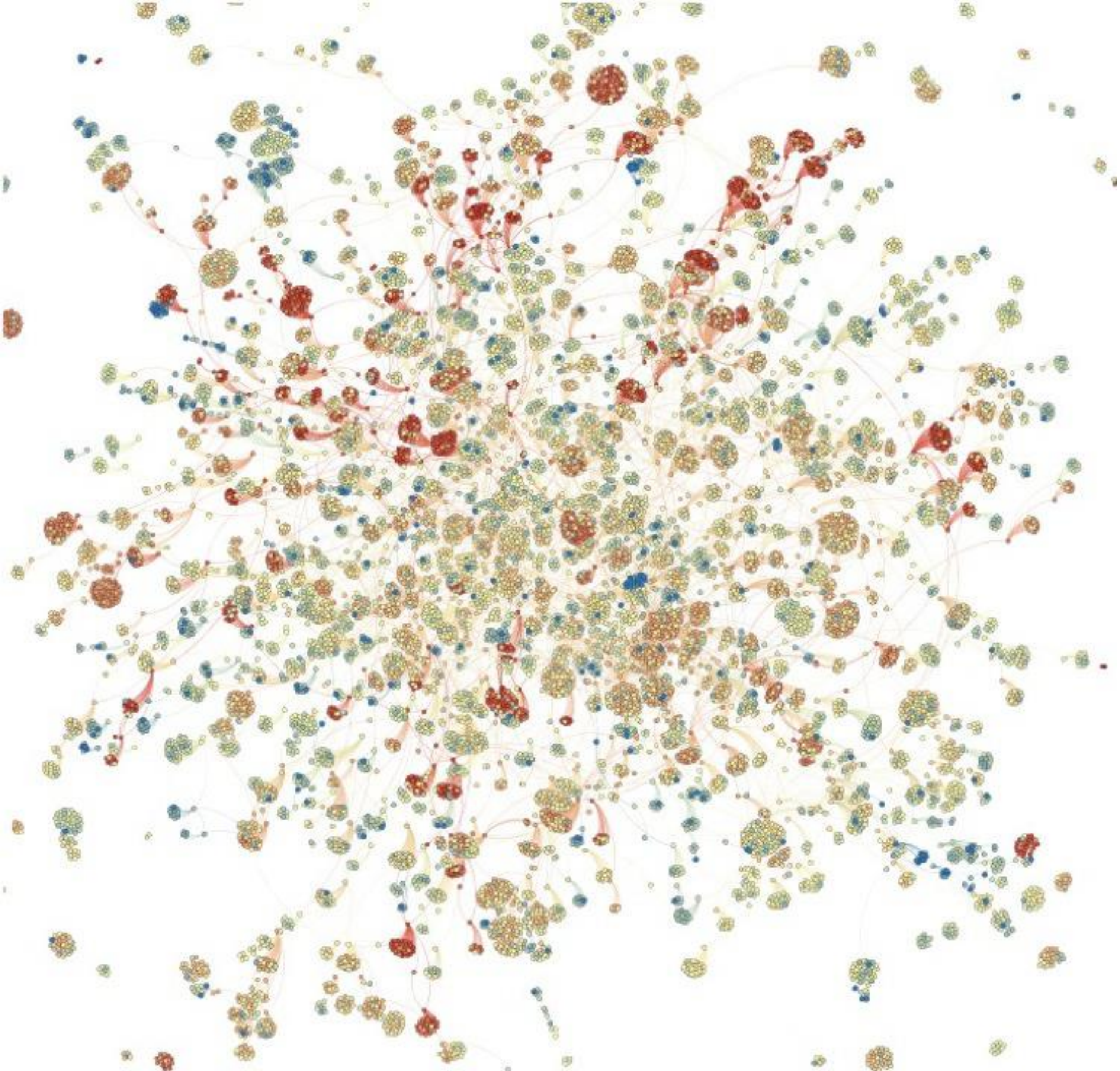
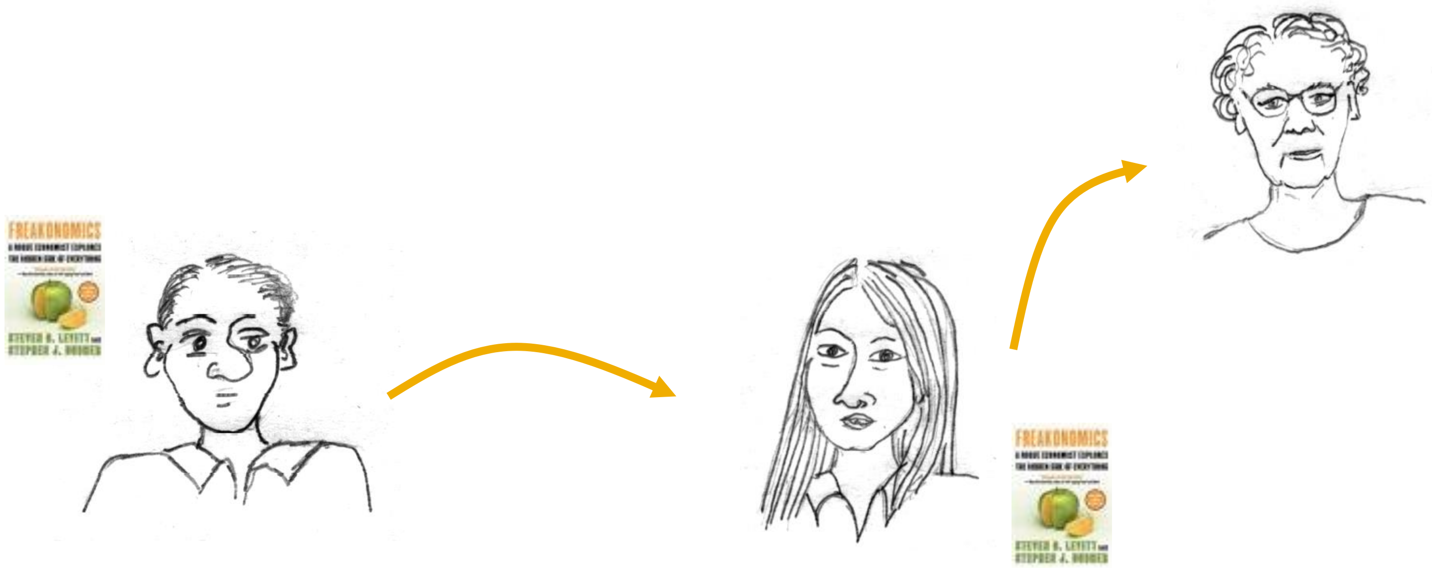
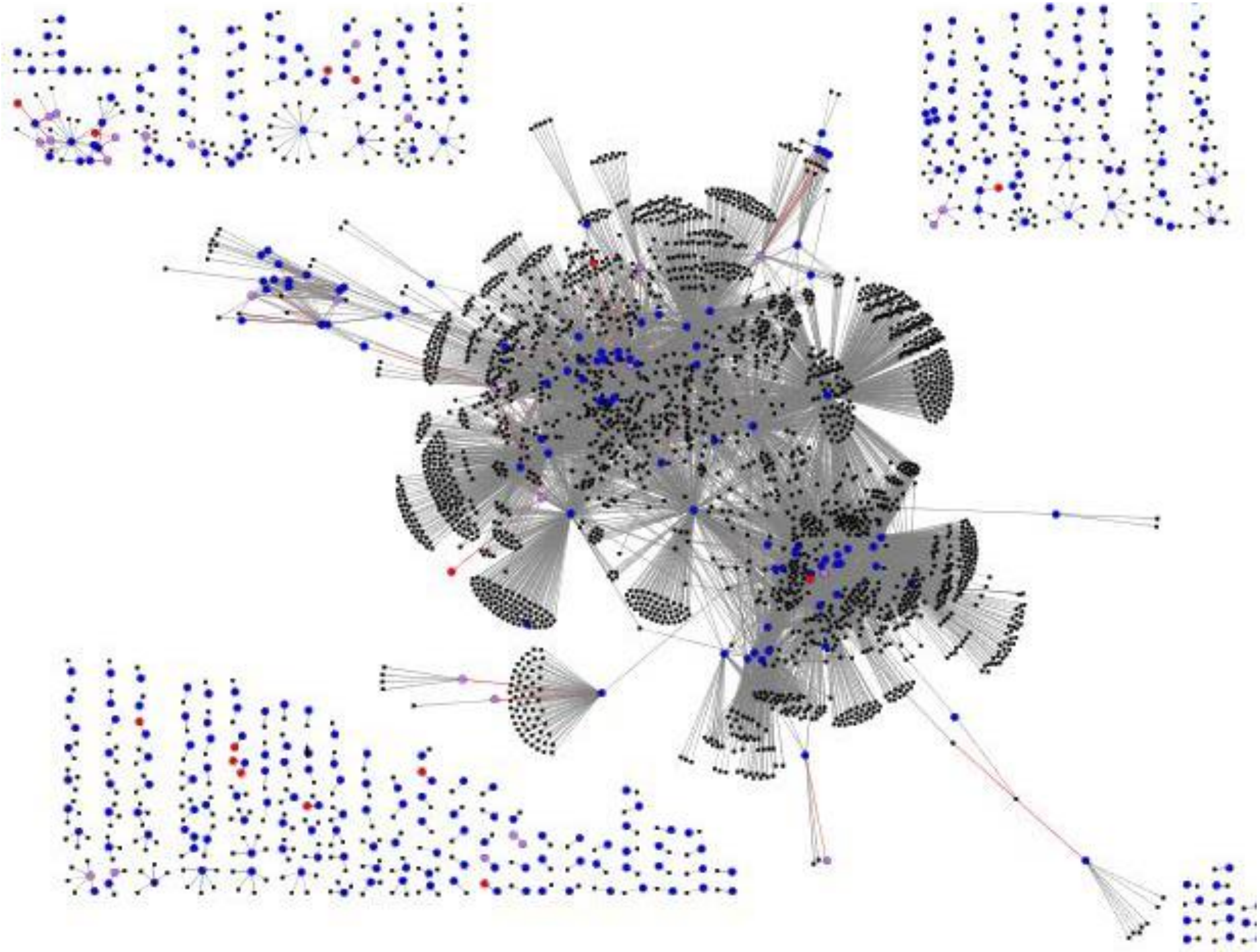


Diffusion in Viral Marketing

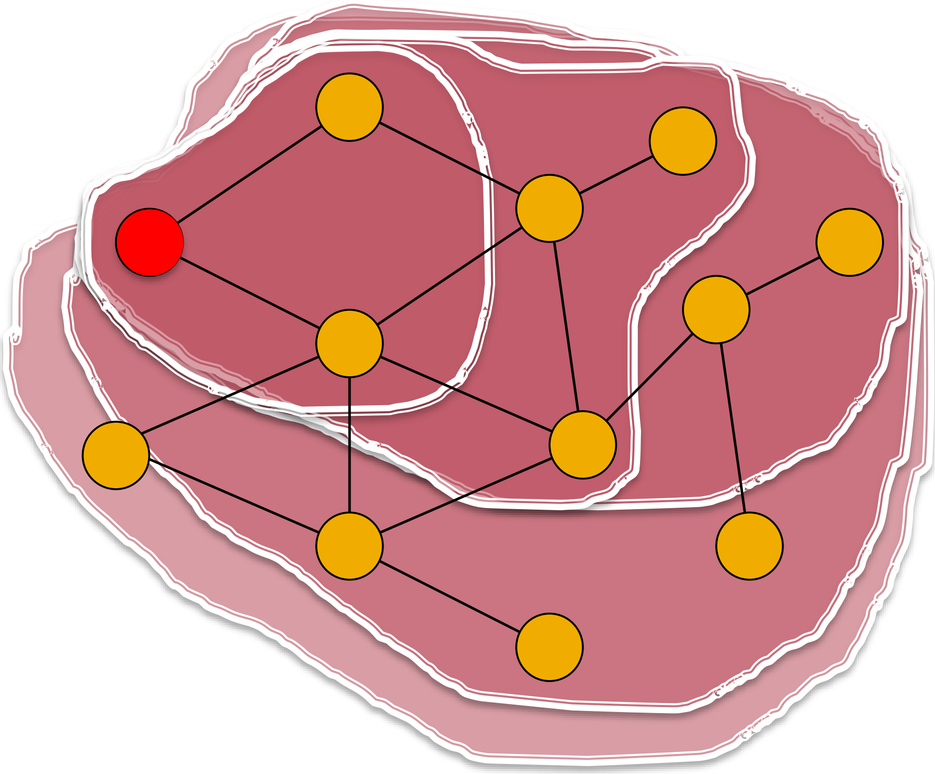
- **Product adoption:**
  - Senders and followers of recommendations



Diffusion in Viral Marketing

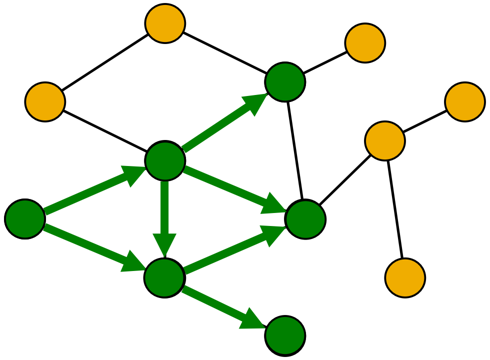


Spread of Diseases (e.g., Ebola)

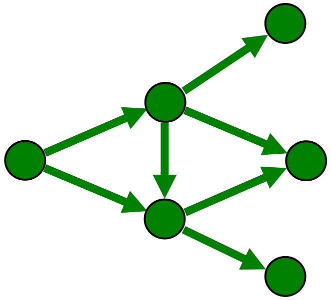


Network Cascades

- **Contagion that spreads over the edges of the network**
- It creates a propagation tree, i.e., **cascade**



Network



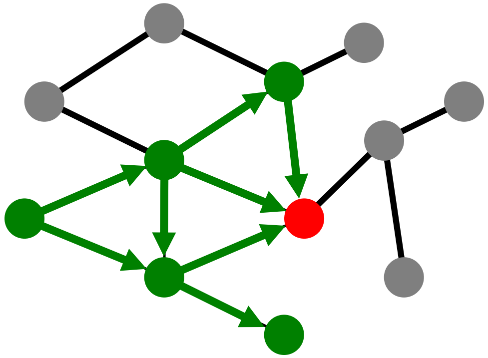
Cascade
(propagation graph)

Terminology:

- Stuff that spreads: Contagion
- “Infection” event: Adoption, infection, activation
- We have: Infected/active nodes, adoptors

How Do We Model Diffusion?

- **Decision based models (Threshold Model):**
  - Models of product adoption, decision making
    - A node observes decisions of its neighbors and makes its own decision
  - **Example:**
    - You join demonstrations if *k* of your friends do so too
- **Probabilistic models:**
  - **Models of influence or disease spreading**
    - An infected node tries to "push" the contagion to an uninfected node
  - **Example:**
    - You "catch" a disease with some prob. from each active neighbor in the network



Decision Based Models of Diffusion

Agenda

- Decision Based Model of Diffusion
  - Granovetter’s Model of Collective Action
  - Threshold Model of Diffusion
  - Game Theoretic Model of Diffusion
  - Extending the Model: Allow People to Adopt A & B (skipped)

Granovetter’s Model of Collective Action

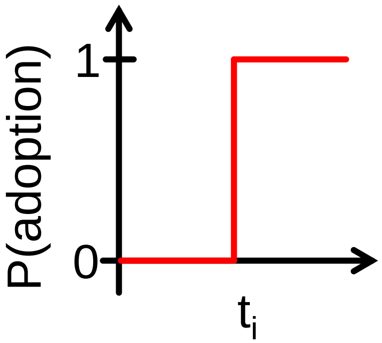
[Granovetter '78]

Decision Based Models

- **Collective Action** [Granovetter, '78]
  - **Model where everyone sees everyone else's behavior (that is, we assume a complete graph)**
  - **Examples:**
    - Clapping or getting up and leaving in a theater
    - Keeping your money or not in a stock market
    - Neighborhoods in cities changing ethnic composition
    - Riots, protests, strikes
- **How does the number of people participating in a given activity grow or shrink over time?**

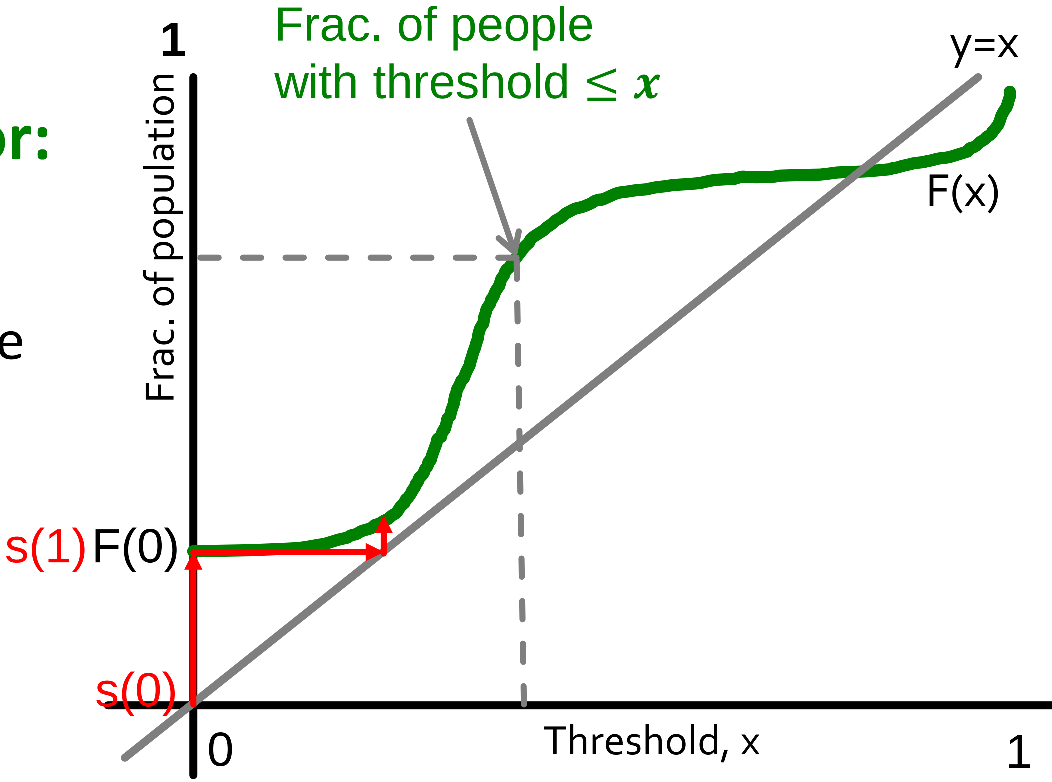
Collective Action: The Model

- ***n* people – everyone observes all actions**
- Each person ***i*** has a threshold t_i $(0 \leq t_i \leq 1)$
  - Node ***i*** will adopt the behavior iff at least t_i fraction of people have already adopted:
    - **Small t_i**: early adopter
    - **Large t_i**: late adopter
  - Time moves in discrete steps
- **The population is described by $\{t_1,\ldots,t_n\}$**
  - **F(x)** … fraction of people with threshold $t_i \leq x$
    - F(x) is a property of the contagion given to us. F(x) is the **c.d.f.** of *x*



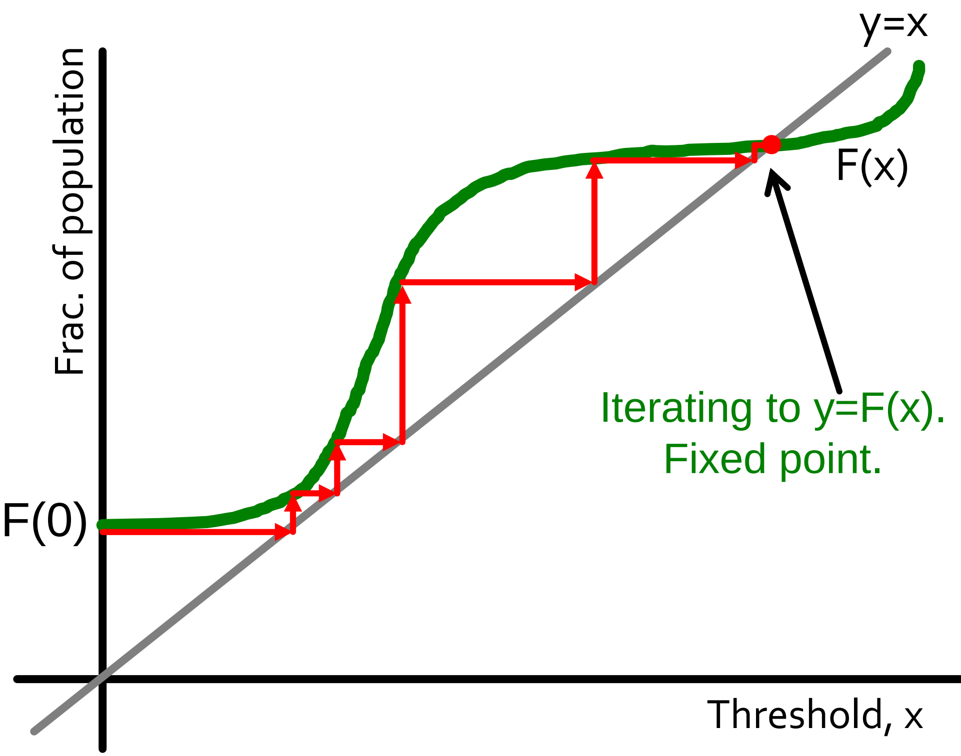
Collective Action: Dynamics

- **F(x)** … fraction of people with threshold $t_i \leq x$
  - **F(x) is non-decreasing:** $F(x+\varepsilon) \geq F(x)$
- **The model is dynamic:**
  - **Step-by-step change in number of people adopting the behavior:**
    - **F(x)** … frac. of people with threshold ≤ **x**
    - **s(t)** … number of people participating at time **t**
  - **Simulate:**
    - s(0) = 0
    - s(1) = F(0)
    - s(2) = F(s(1)) = F(F(0))



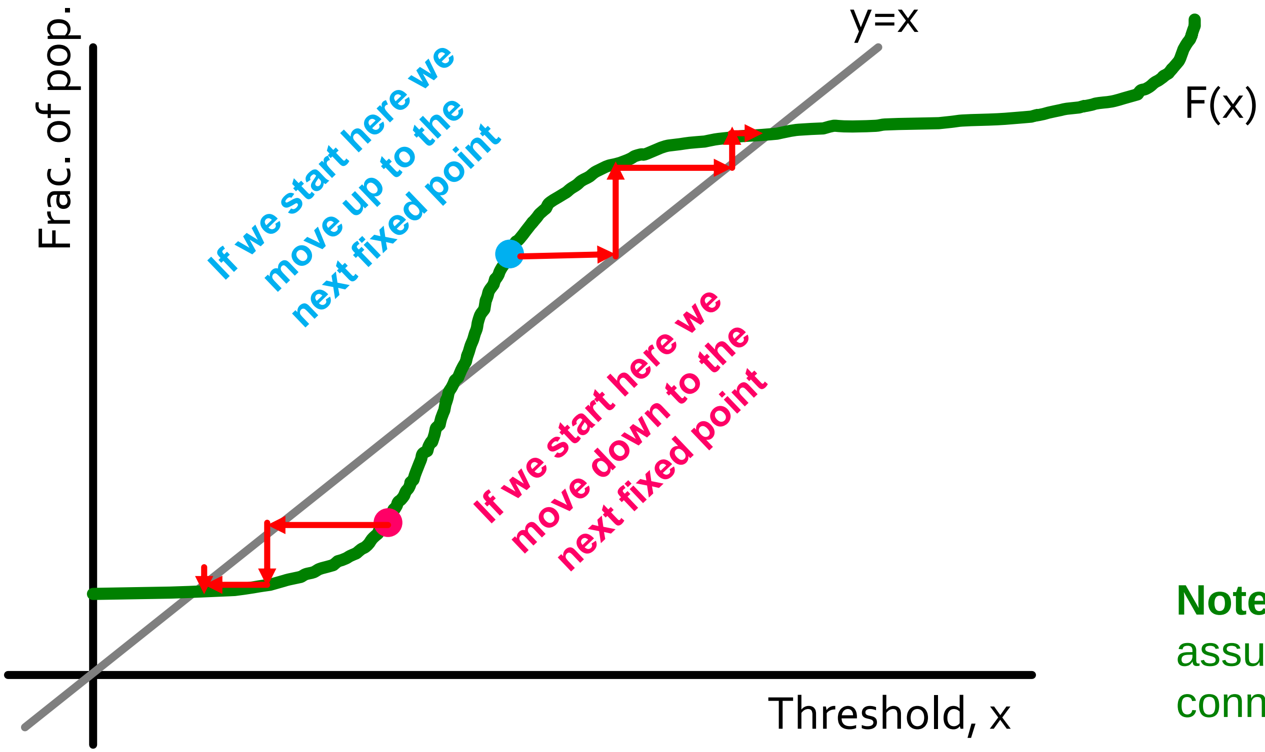
Collective Action: Dynamics

- **Step-by-step change in number of people :**
  - **F(x)** … fraction of people with threshold ≤ **x**
  - **s(t)** … number of participants at time **t**
- **Easy to simulate:**
  - s(0) = 0
  - s(1) = F(0)
  - s(2) = F(s(1)) = F(F(0))
  - s(t+1) = F(s(t)) = $F^{t+1}(0)$
- **Fixed point: F(x)=x**
  - Updates to **s(t)** to converge to a stable fixed point
  - There could be other fixed points but starting from **0** we only reach the first one



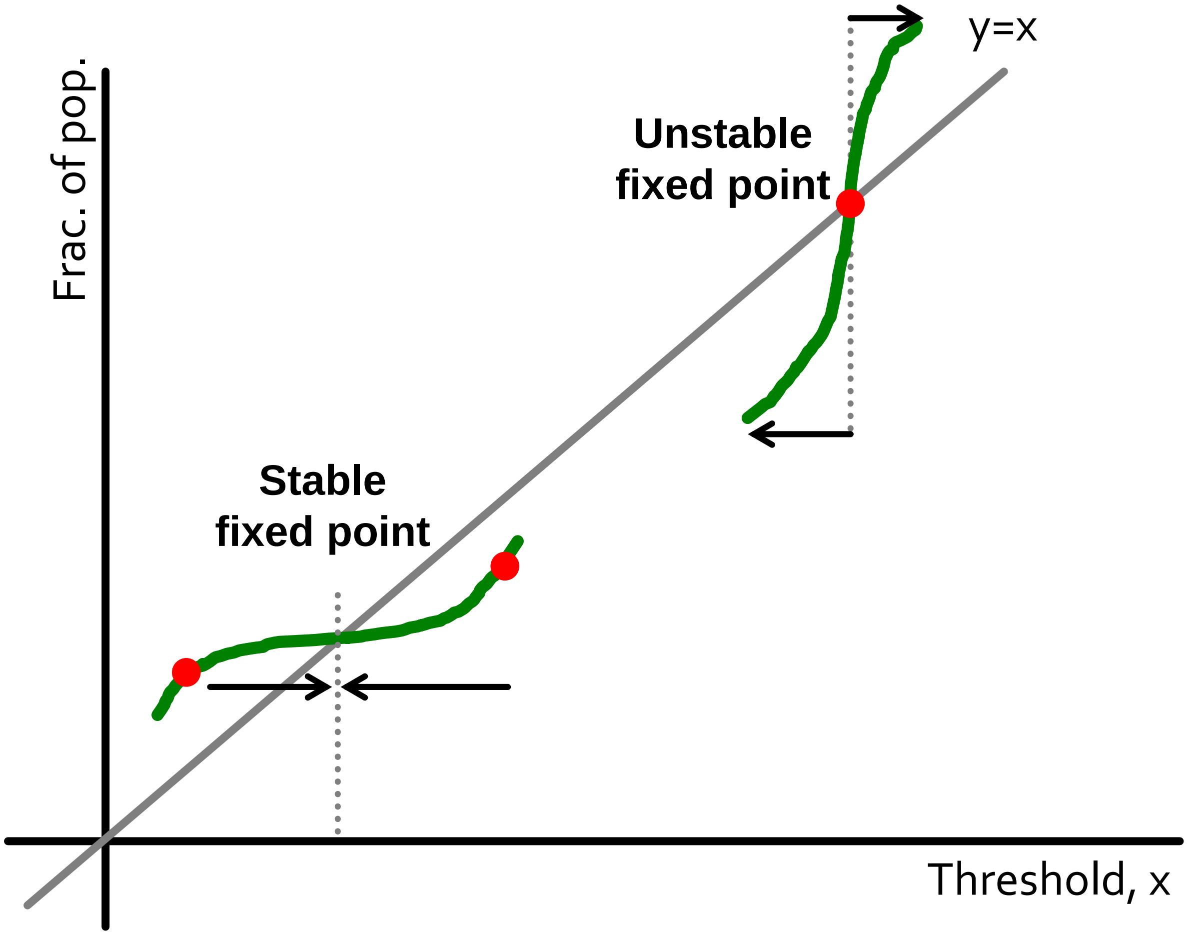
Starting Elsewhere

- **What if we start the process somewhere else?**
  - We move up/down to the next fixed point
  - **How is market going to change?**



Note: we are assuming a fully connected graph

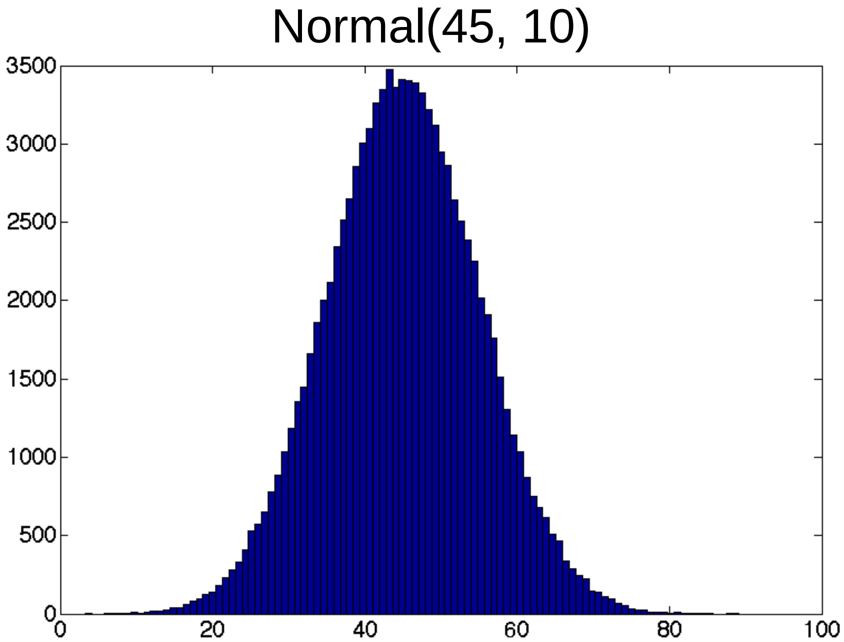
Stable vs. Unstable Fixed Point



Discontinuous Transition

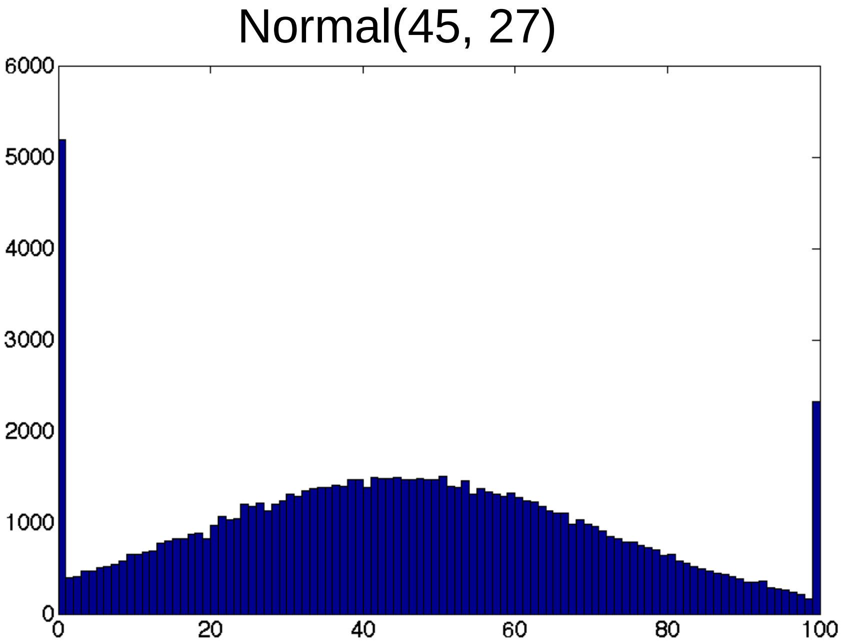
- Each threshold ***t_i*** is drawn independently from some distribution ***$F(x) = Pr[thresh \leq x]$***
  - **Suppose:** Normal with **μ=n/2**, variance **σ**

Small σ:



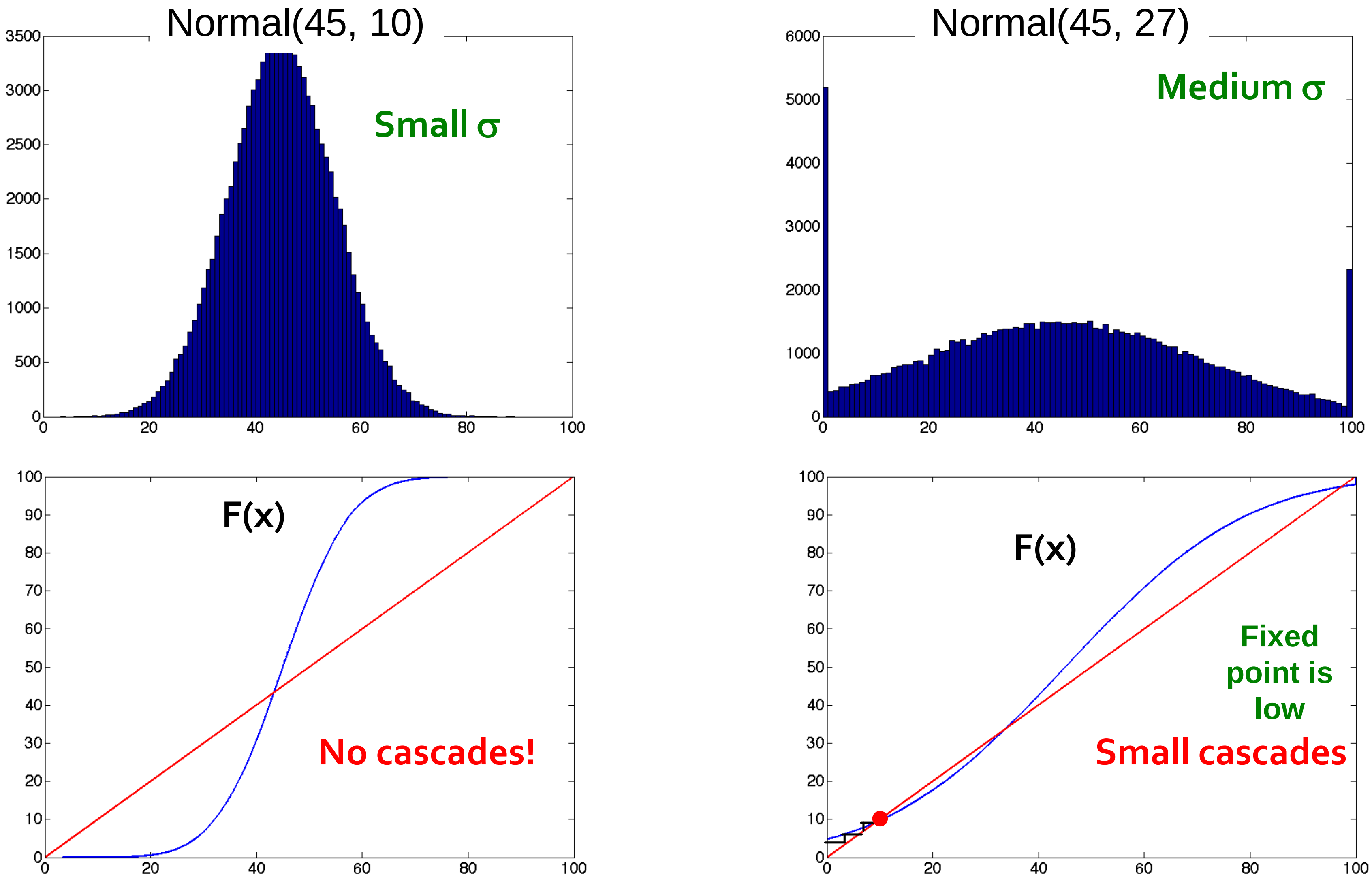
Normal(45, 10)

Medium σ:



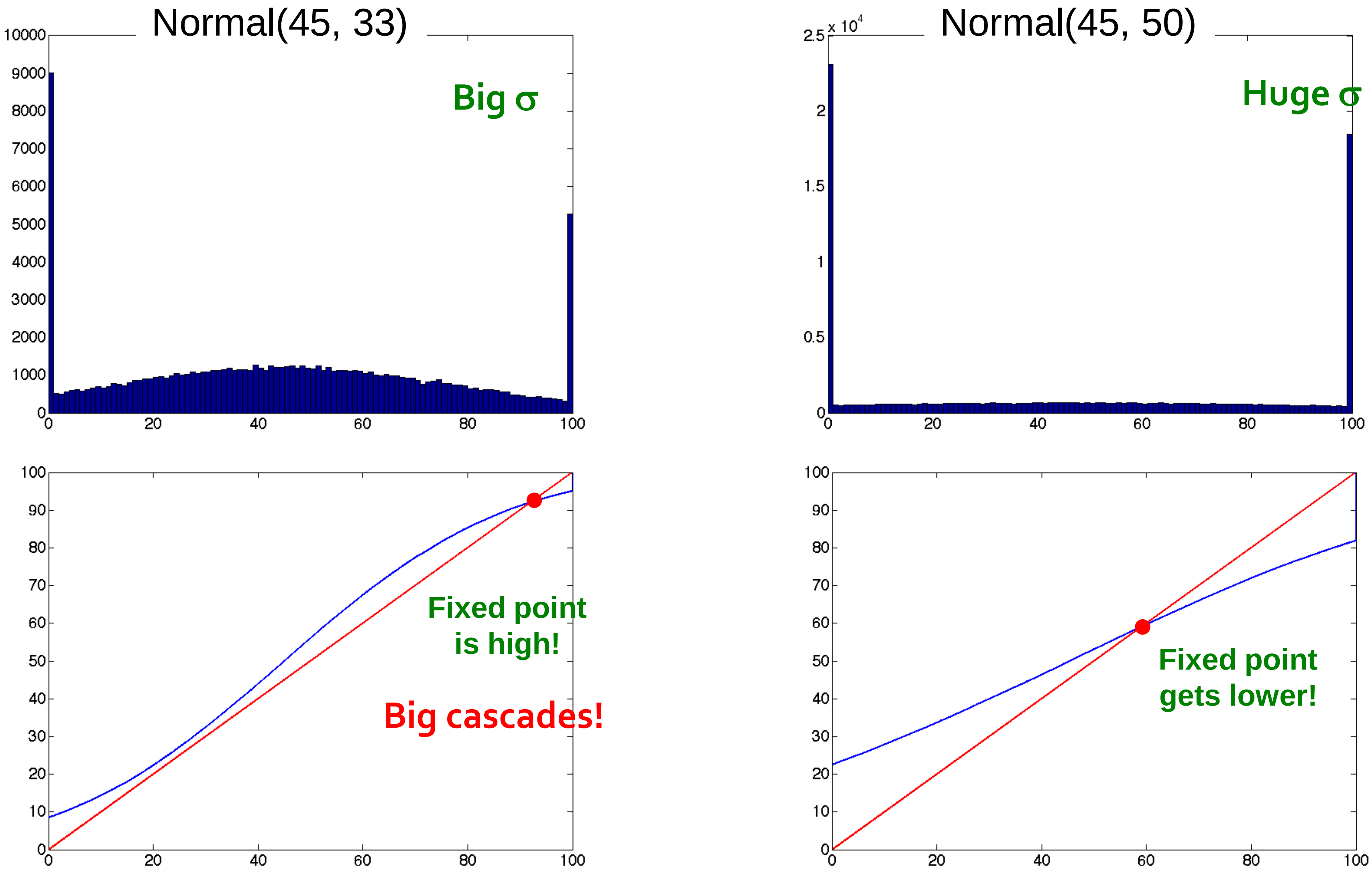
Normal(45, 27)

Discontinuous Transition



Bigger variance let's you build a bridge from early adopters to mainstream

Discontinuous Transition


Normal(45, 33)

Normal(45, 50)

Big σ

Huge σ

Fixed point
is high!

Big cascades!

Fixed point
gets lower!

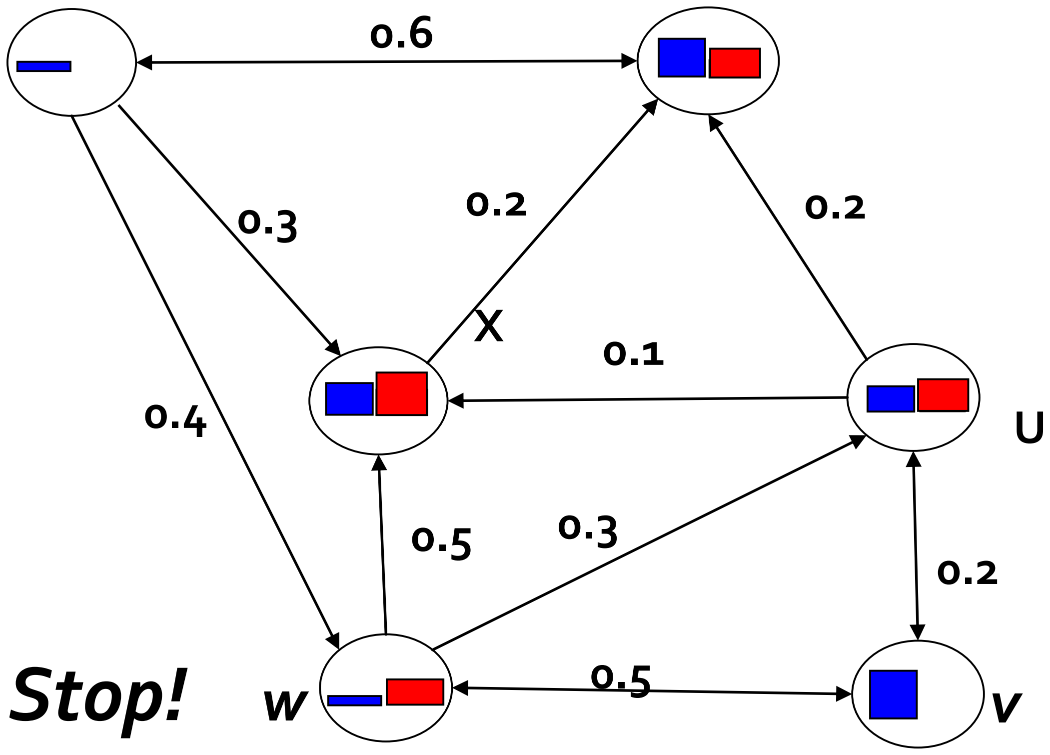
But if we increase the variance the fixed point starts going down

Weaknesses of the Model

- **No notion of social network:**
  - Some people are more influential
  - It matters who the early adopters are, not just how many
- **Models people's awareness** of size of participation **not just actual number of people participating**
  - Modeling perceptions of who is adopting the behavior vs. who you believe is adopting
  - Non-monotone behavior – dropping out if too many people adopt
  - People get "locked in" to certain choice over a period of time
- **Modeling thresholds**
  - Richer distributions
  - Deriving thresholds from more basic assumptions
    - game theoretic models

Threshold Model of Diffusion

Linear Threshold Model



Example

○ Inactive Node

🟢 Active Node

🟦 Threshold

🟥 Active neighbors

Thresholds:

$$\vartheta_v \sim U[0,1]$$

Influenced when:

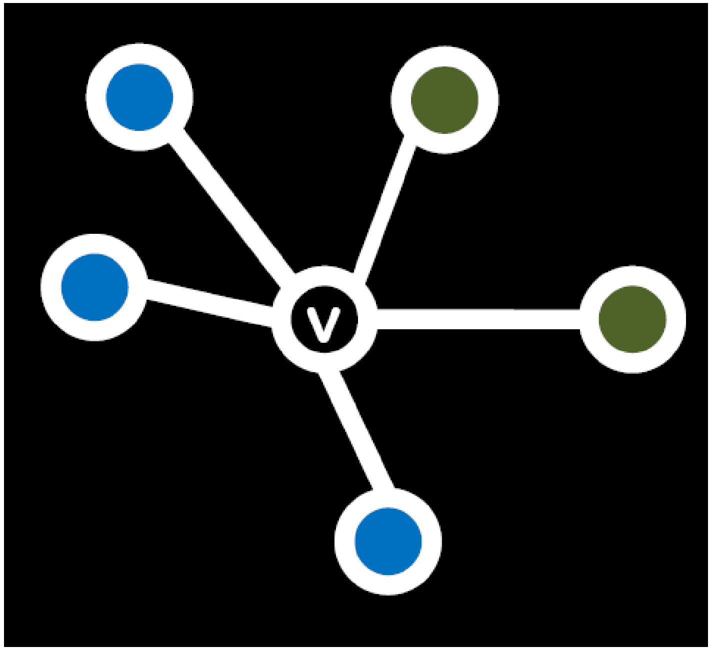
$$\sum_{w \text{ active neighbor of } v} b_{v,w} \ge \theta_v$$

Game-theoretic Model of Cascades

[Morris 2000]

Game Theoretic Model of Cascades

- **Based on 2 player coordination game**
  - 2 players – each chooses technology A or B
  - Each person can only adopt **one** "behavior", **A** or **B**
  - You gain more payoff if your friend has adopted the **same** behavior as you



Local view of the network of node **v**

Example: VHS vs. BetaMax

Example: BlueRay vs. HD DVD

Blu-ray Disc

HD DVD ™

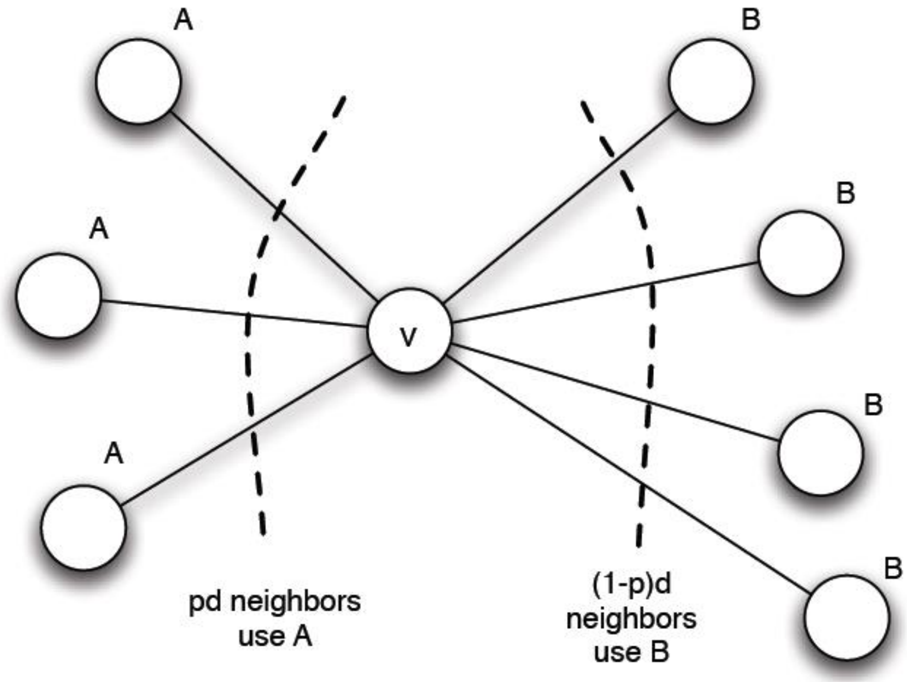
The Model for Two Nodes

- ***Payoff matrix:***
  - If both **v** and **w** adopt behavior **A**, they each get payoff ***a > 0***
  - If ***v*** and ***w*** adopt behavior ***B***, they each get payoff ***b > 0***
  - If ***v*** and ***w*** adopt the opposite behaviors, they each get ***0***

- **In some large network:**
  - Each node ***v*** is playing a copy of the game with each of its neighbors
  - **Payoff**: sum of node payoffs per game

		w	
		A	**B**
v	**A**	a, a	o,o
	B	o,o	b,b

Calculation of Node v



Threshold:
v chooses ***A*** if

$$p > \frac{b}{a+b} = q$$

p… frac. v's nbrs. with A
q… payoff threshold

- Let **v** have ***d*** neighbors
- Assume fraction ***p*** of ***v***'s neighbors adopt ***A***
  - *Payoff*$_v$ = $a \cdot p \cdot d$, if *v* chooses A
    = $b \cdot (1-p) \cdot d$, if *v* chooses B
- **Thus: *v* chooses A if: $a \cdot p \cdot d > b \cdot (1-p) \cdot d$**

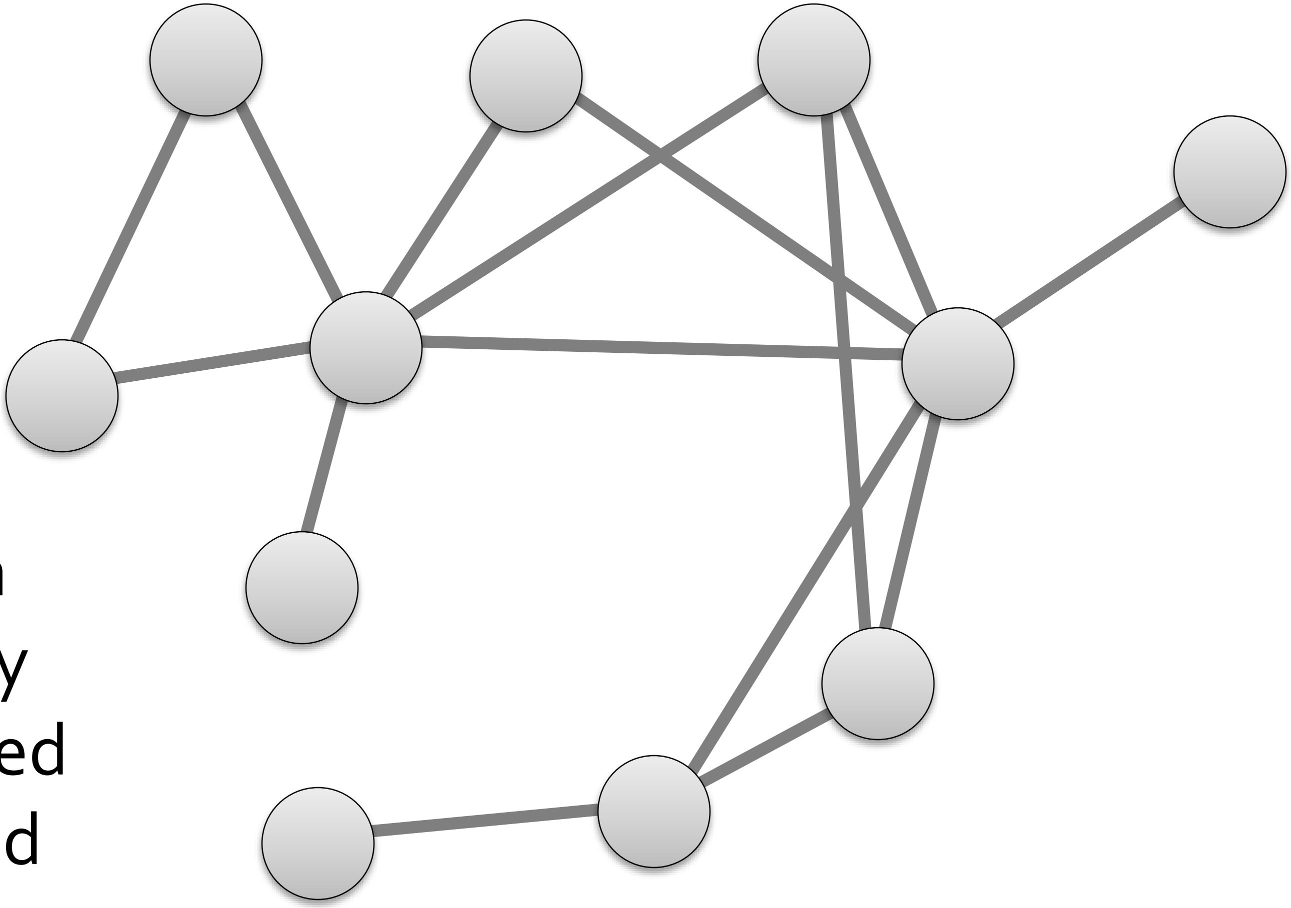
Example Scenario

- Scenario:
  Graph where everyone starts with ***B***
  Small set ***S*** of early adopters of ***A***
  - Hard-wire ***S*** – they keep using ***A*** no matter what payoffs tell them to do
- **Assume payoffs are set in such a way that nodes say:**
  If more than 50% of my friends take A
  I'll also take A

  (this means: **a = b-ε** and **q>1/2**)

Example Scenario

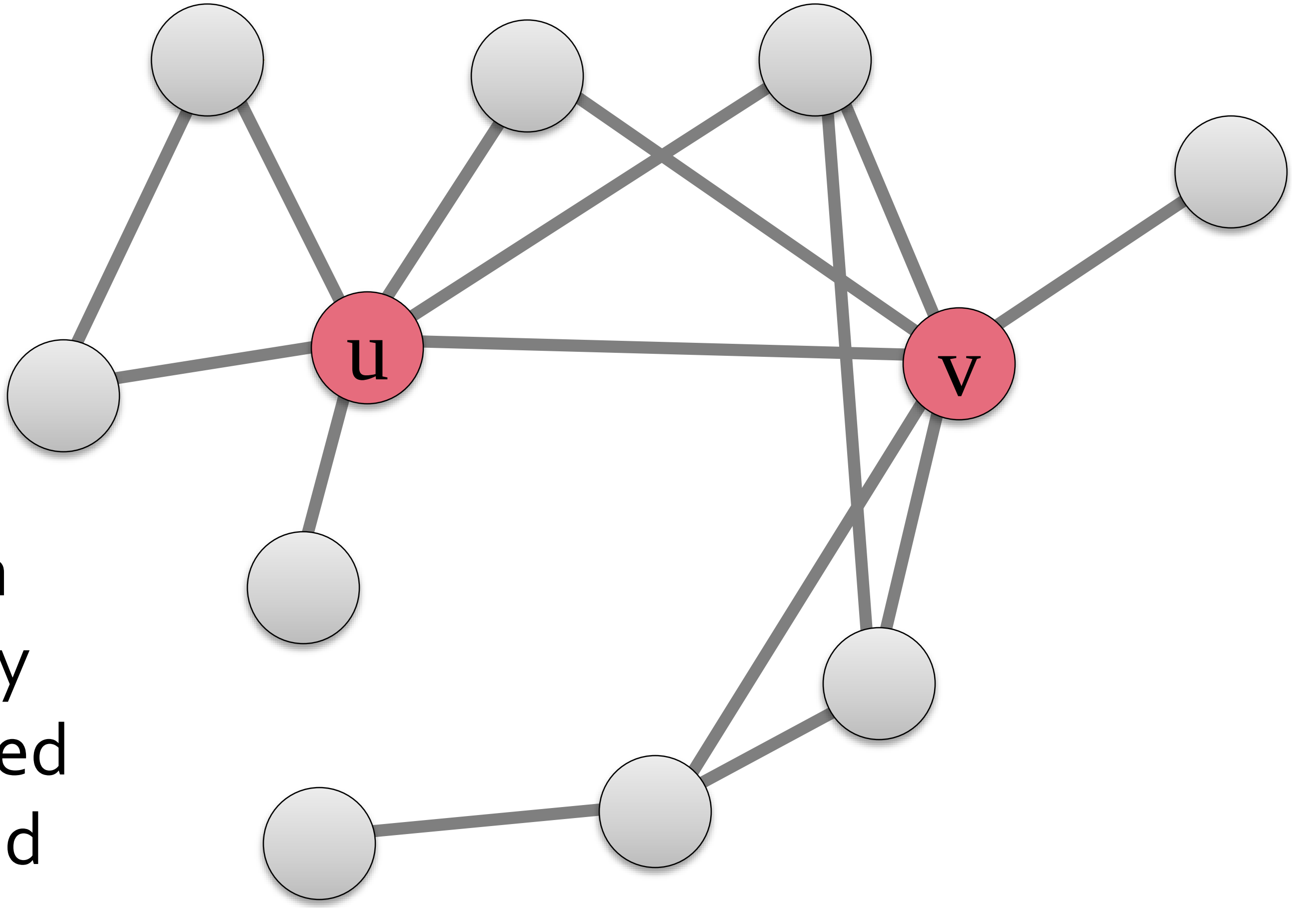
$S = \{u, v\}$



If **more** than **q=**50% of my friends are red I'll also be red

Example Scenario

$S = \{u, v\}$



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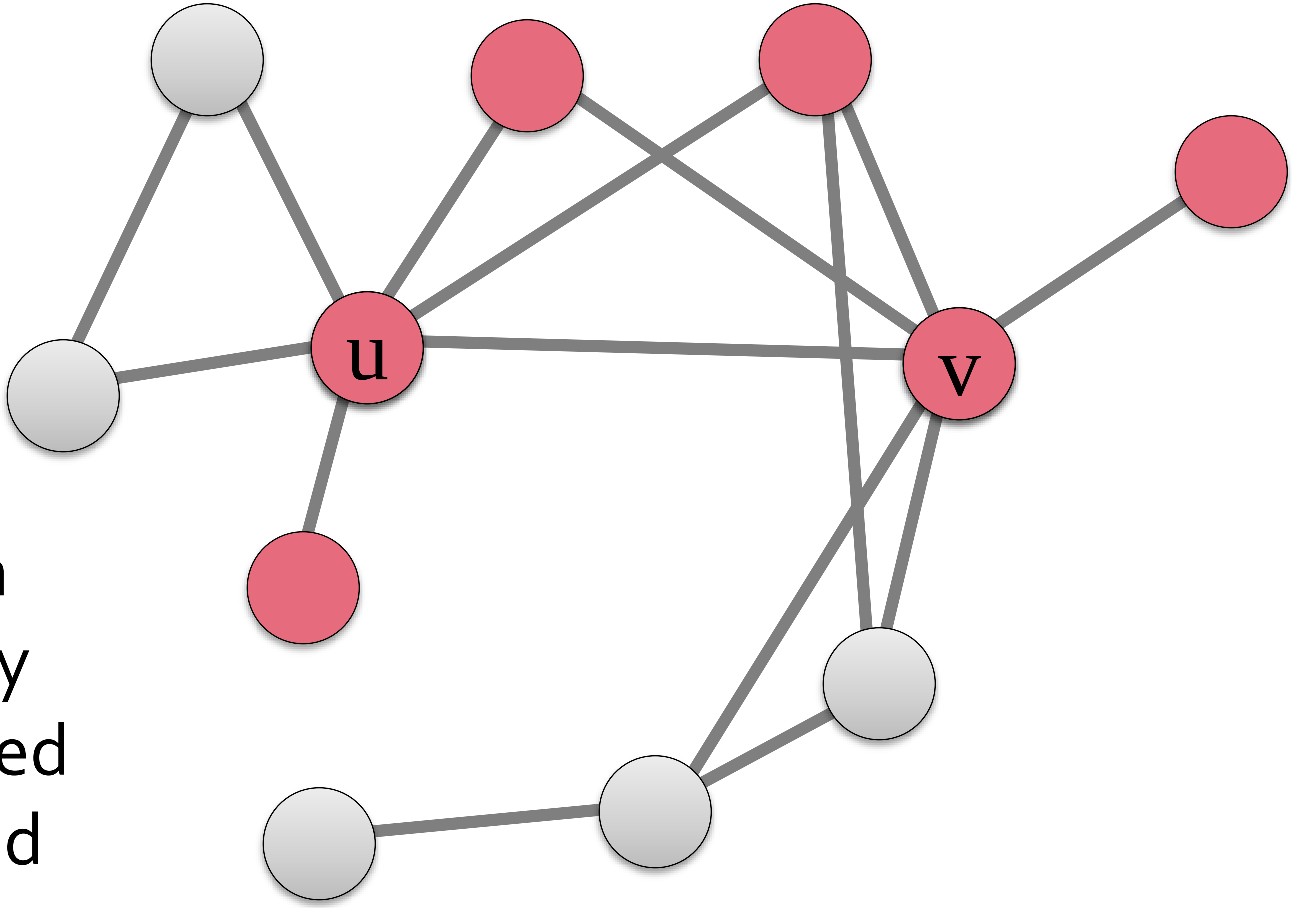

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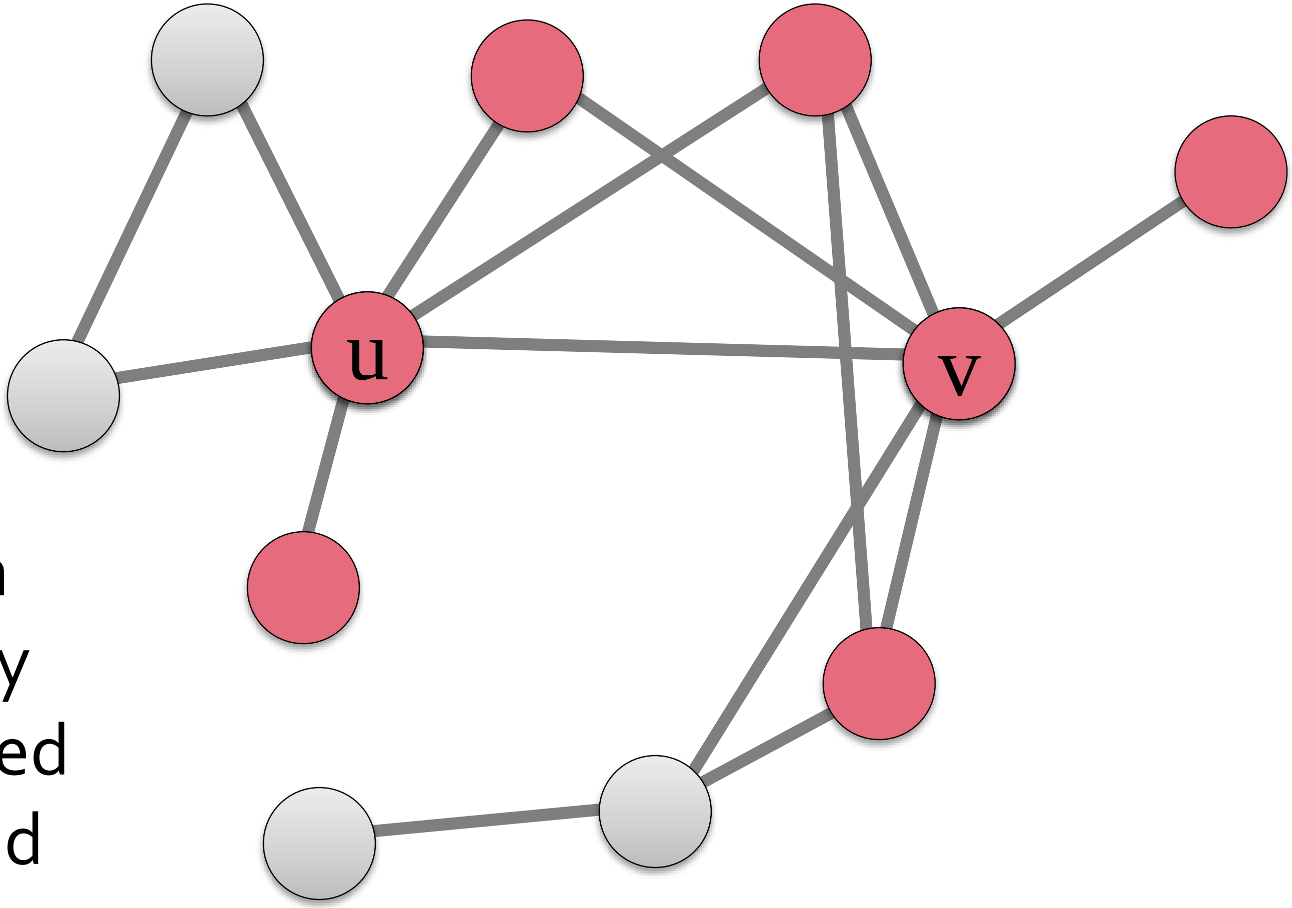

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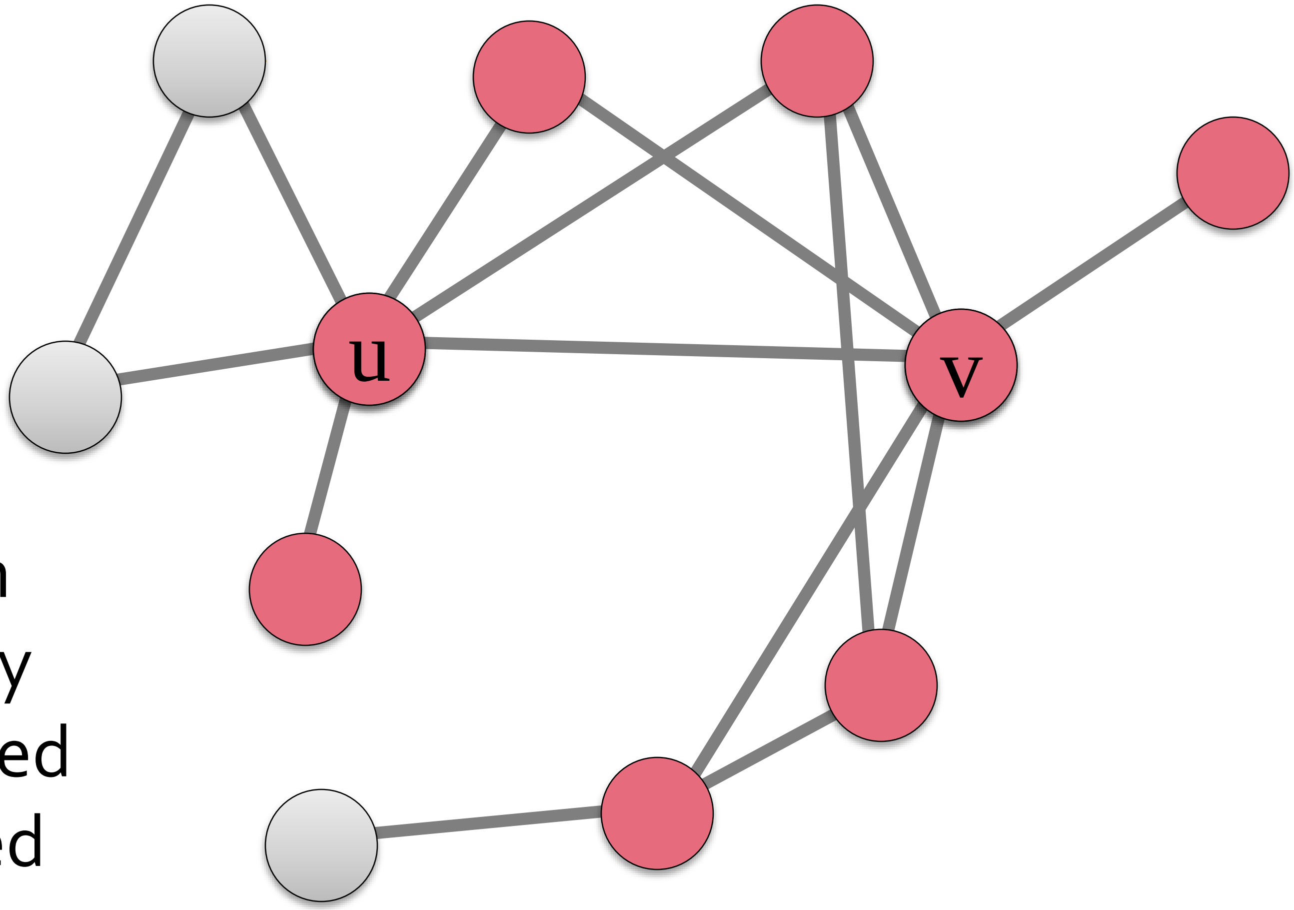

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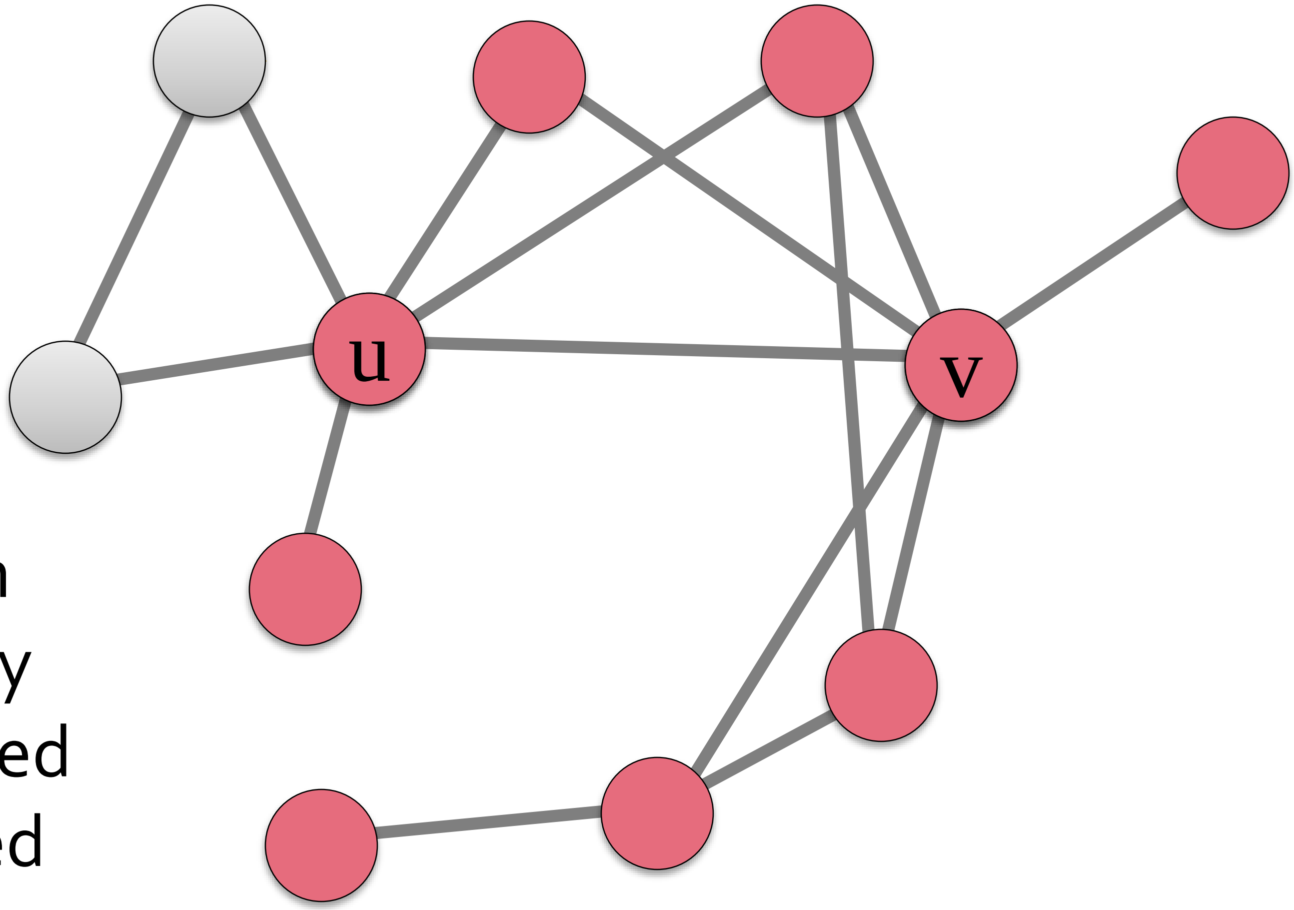


If **more** than **q=**50% of my friends are red I'll also be red

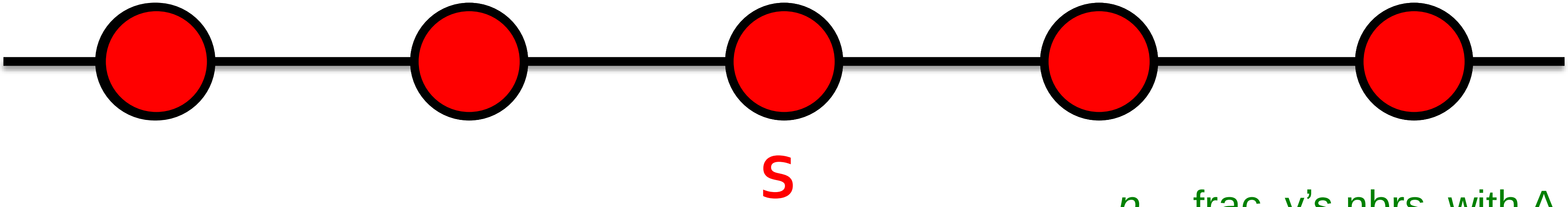
Infinite Graphs

v chooses ***A*** if ***p>q***

$$q = \frac{b}{a+b}$$

- **Consider infinite graph *G***
  - (but each node has finite number of neighbors!)
- We say that a finite set ***S*** causes a cascade in *G* with **threshold *q*** if, when ***S*** adopts ***A***, eventually **every node in G adopts *A***
- Example: **Path**

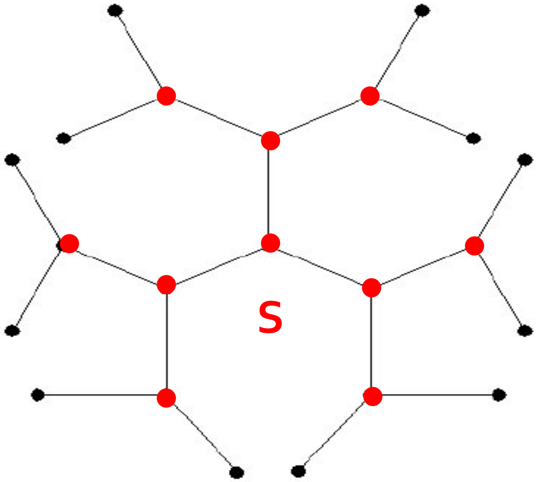
If ***q<1/2*** then cascade occurs



p… frac. v's nbrs. with A
q… payoff threshold

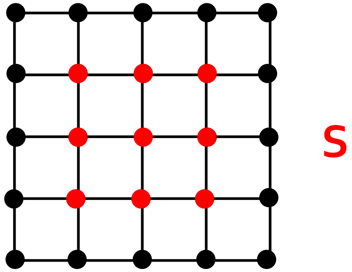
Infinite Graphs

- **Infinite Tree:**



If *q<1/3* then cascade occurs

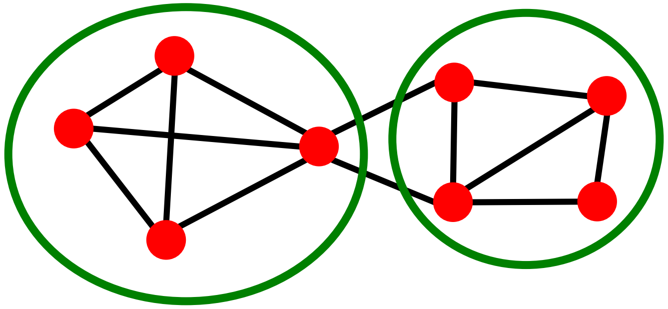
- **Infinite Grid:**



If *q<1/4* then cascade occurs

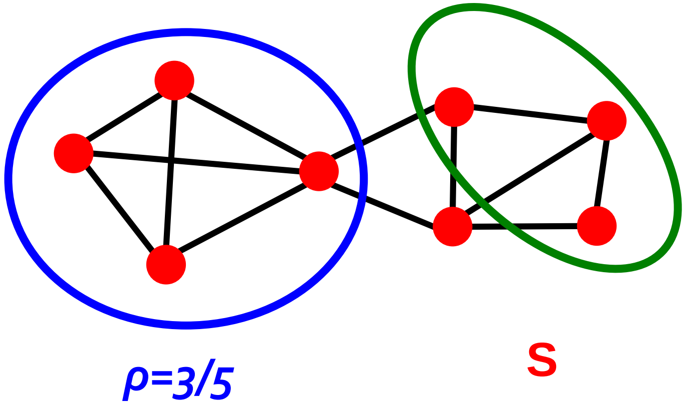
Stopping Cascades

- **What prevents cascades from spreading?**
- Def: **Cluster of density *ρ*** is a **set of nodes *C*** where each node in the set has at least ***ρ*** fraction of edges in ***C***



Stopping Cascades

- **Let S be an initial set of adopters of A**
- All nodes apply threshold ***q*** to decide whether to switch to **A**
- **Two facts:**
  - 1) If ***G\S*** contains a cluster of density ***>(1-q)*** then ***S*** can not cause a cascade
  - 2) If **S** fails to create a cascade, then there is a cluster of density ***>(1-q)*** in **G\S**



No cascade if q>2/5

Extending the Model: Allow People to Adopt A and B

Cascades & Compatibility

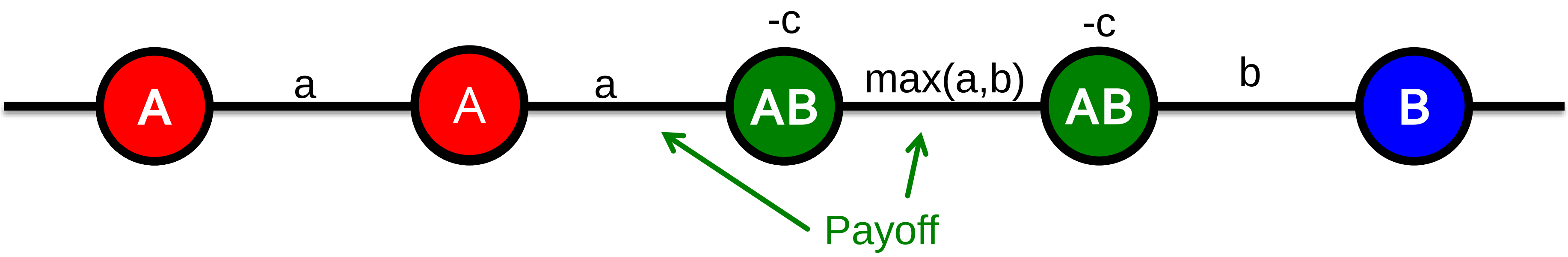
- **So far:**
  - Behaviors ***A*** and ***B*** compete
  - Can only get utility from neighbors of same behavior: ***A*-*A* get a, *B*-*B* get *b*, *A*-*B* get *0***
- **Let an extra strategy "*AB*"**
  - ***AB*-*A*** : gets ***a***
  - ***AB*-*B*** : gets ***b***
  - ***AB*-*AB*** : gets **max(*a*, *b*)**
  - **Also:** Some **cost *c*** for the effort of maintaining both strategies (summed over all interactions)
    - Note: a given node can receive *a* from one neighbor and *b* from another by playing AB, which is why it could be worth the cost *c*

w

		A	B	AB
	A	a, a	o,o	a, a
v	B	o,o	b,b	b,b
	AB	a, a	b,b	max(a,b), max(a,b)

Cascades & Compatibility: Model

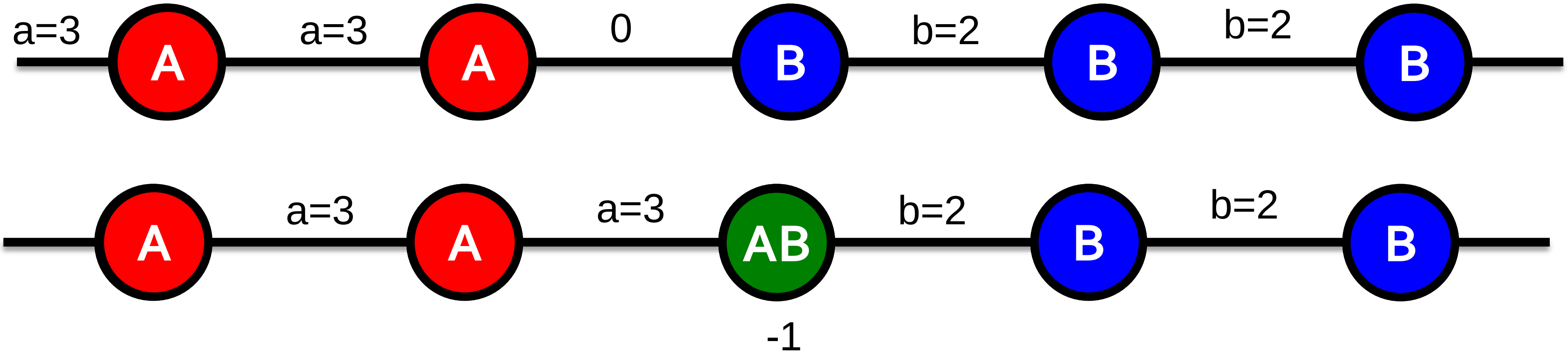
- Every node in an infinite network starts with ***B***
- Then a finite set ***S*** initially adopts ***A***
- Run the model for ***t=1,2,3,…***
  - Each node selects behavior that will optimize payoff (given what its neighbors did in at time ***t-1***)



- **How will nodes switch from *B* to *A* or *AB*?**

Example: Path Graph (1)

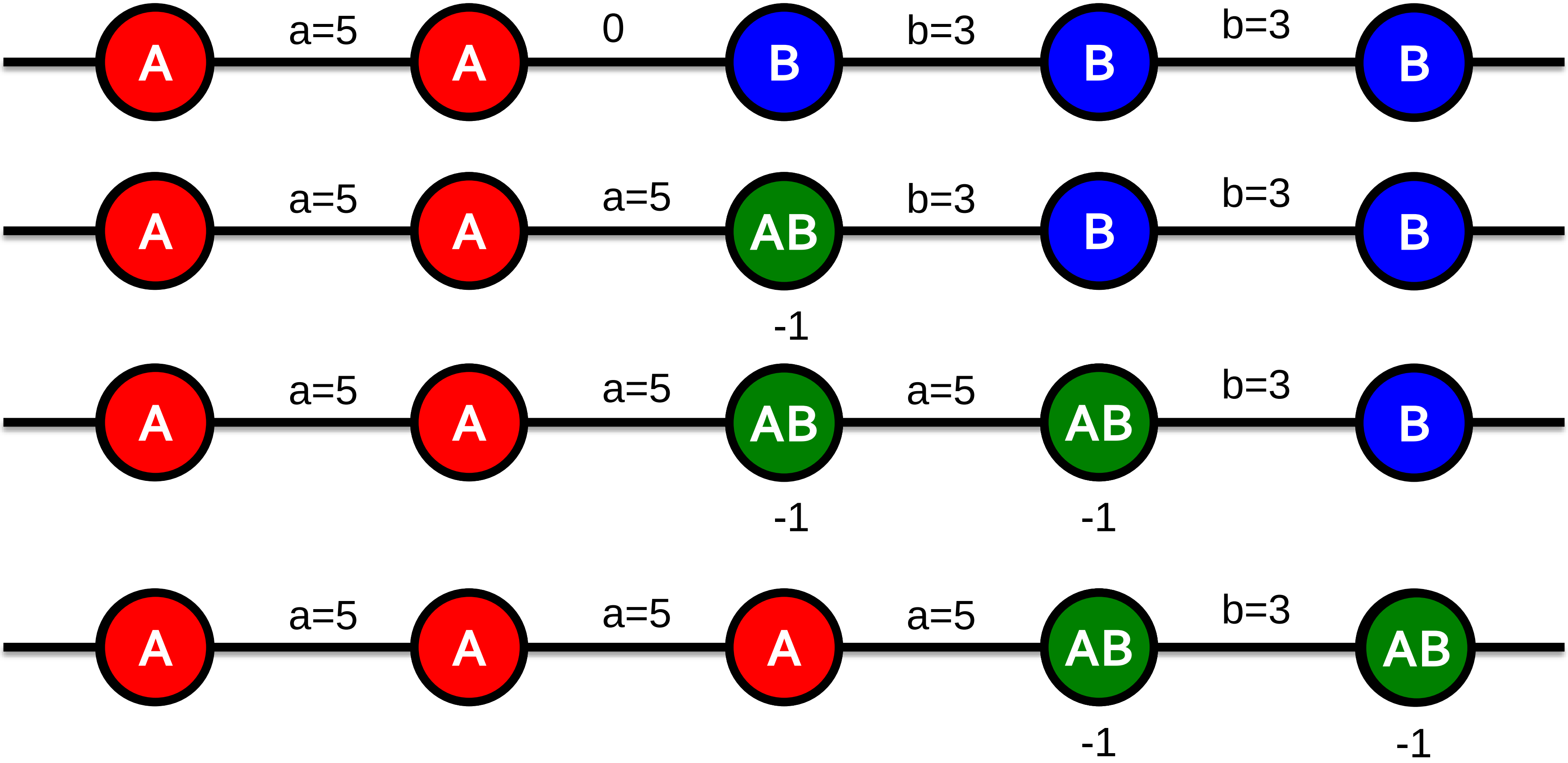
- **Path graph:** Start with all **B**s, **a** > **b** (**A** is better)
- **One node switches to A – what happens?**
  - **With just A, B:** **A** spreads if ***a*** **>** ***b***
  - **With A, B, AB: Does A spread?**
- **Example: a=3, b=2, c=1**



Cascade stops

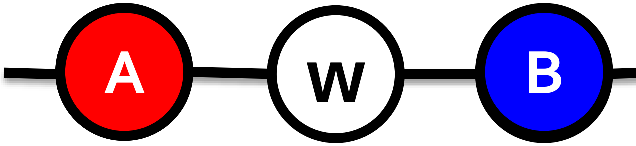
Example: Path Graph (2)

- Example: a=5, b=3, c=1

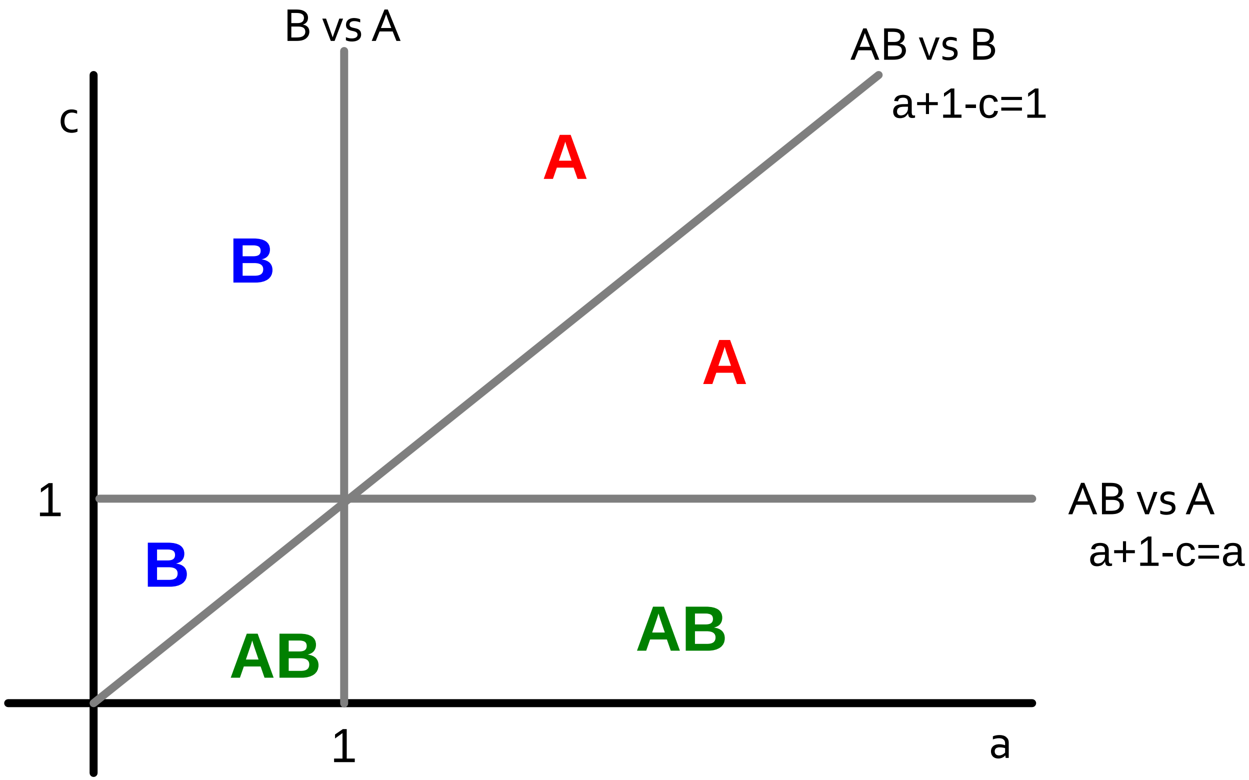


Cascade never stops!

For what pairs (c,a) does A spread?



- **Infinite path, start with all Bs**
- **Payoffs for *w*: A**:a, **B**:1, **AB**:a+1-c
- What does node ***w*** in **A-*w*-B** do?



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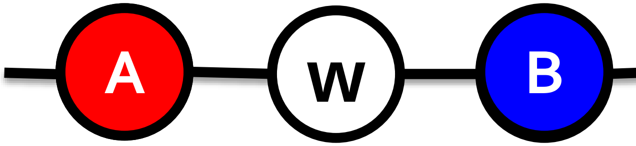

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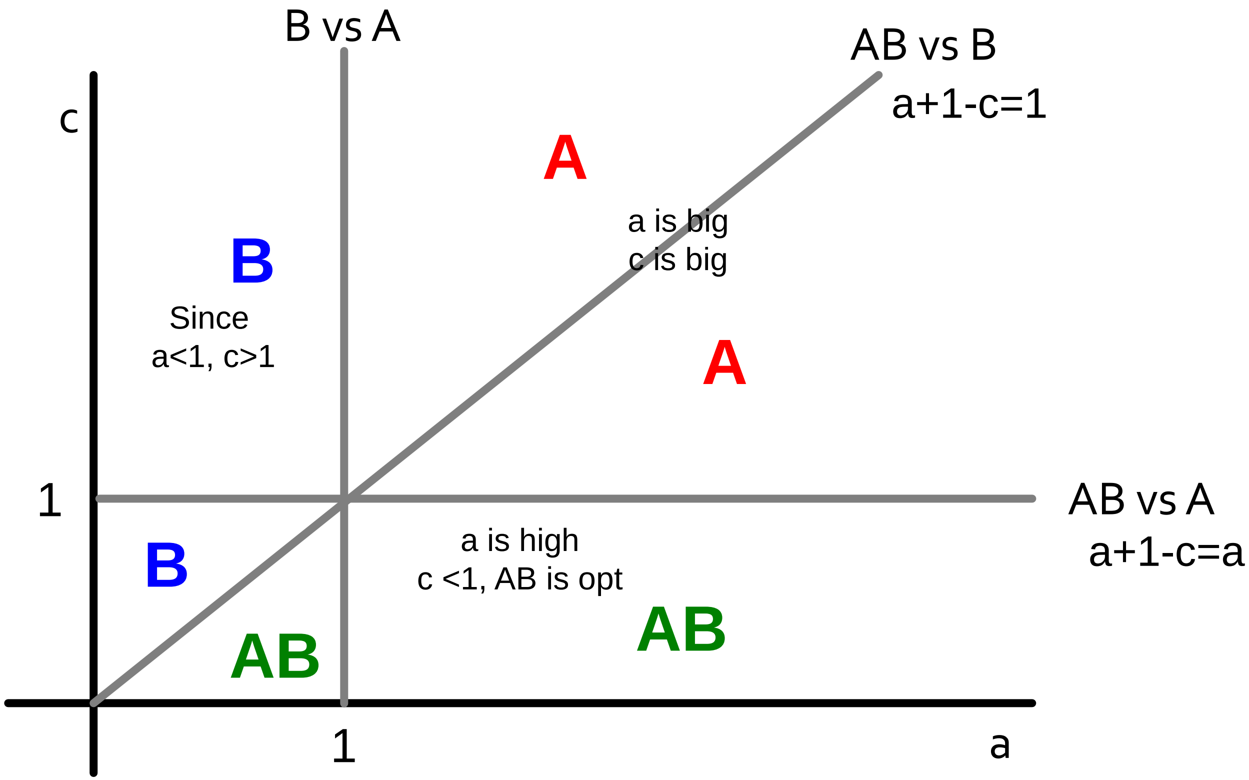
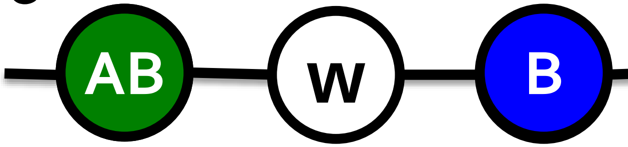
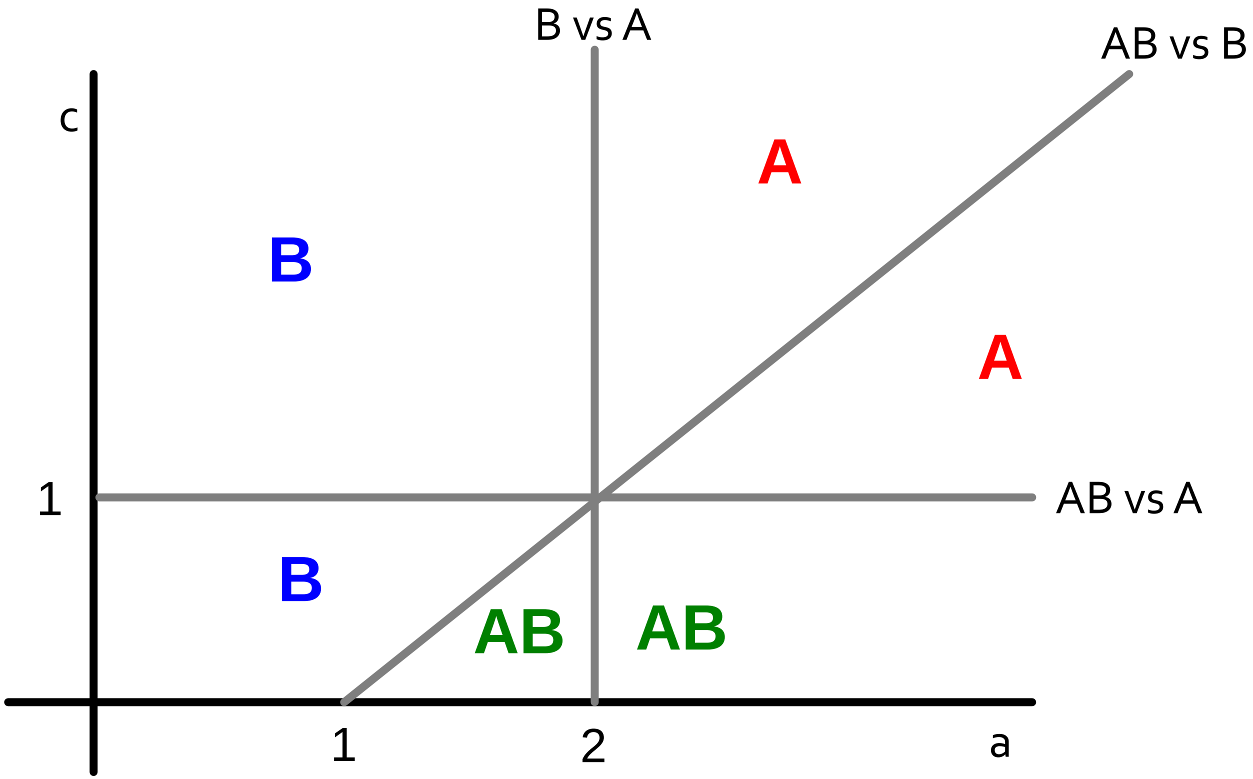
- **Payoffs for *w*: A**:a, **B**:1, **AB**:a+1-c
- What does node ***w*** in **A-*w*-B** do?



For what pairs (c,a) does A spread?

- **Same reward structure as before but now payoffs for *w* change:** **A**:a, **B**:1+1, **AB**:a+1-c
- **Notice: Now also AB spreads**
- What does node ***w*** in **AB-*w*-B** do?





For what pairs (c,a) does A spread?

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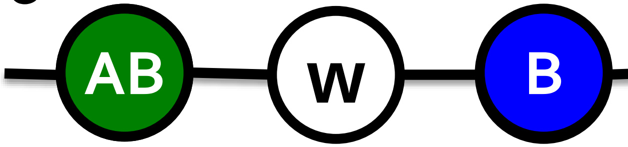
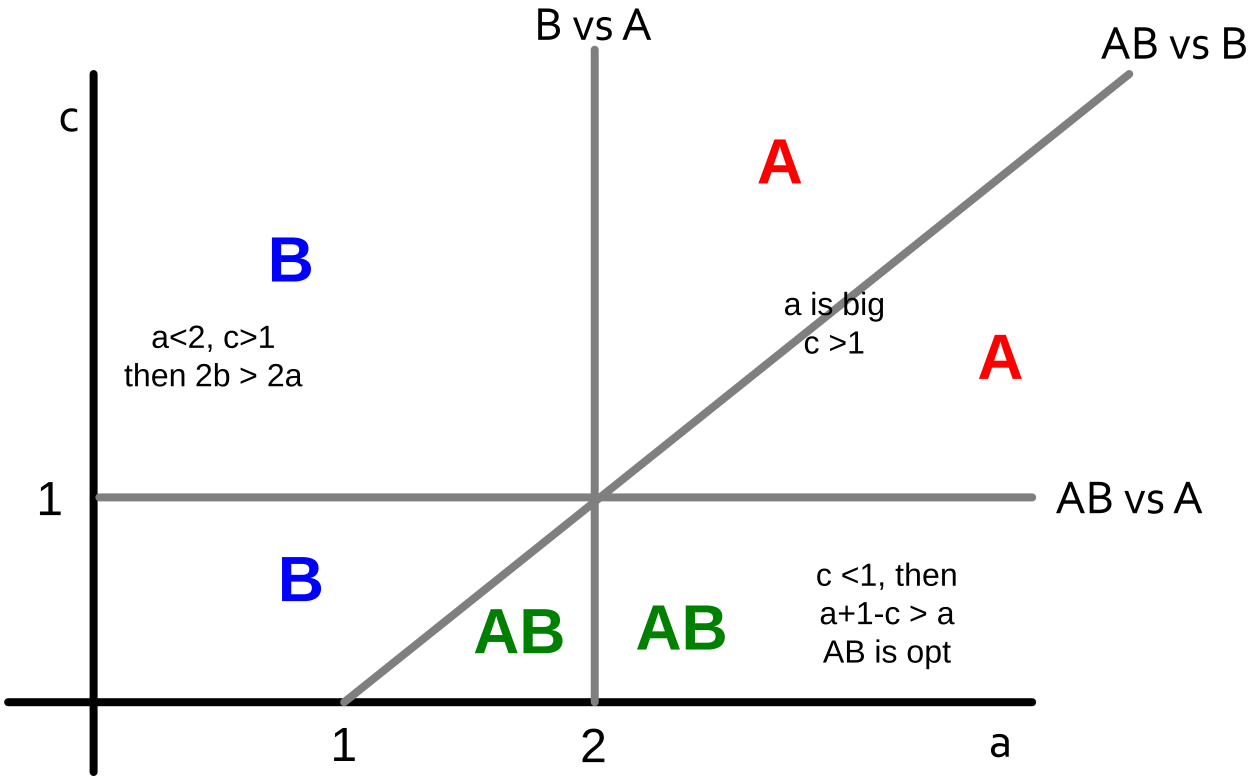
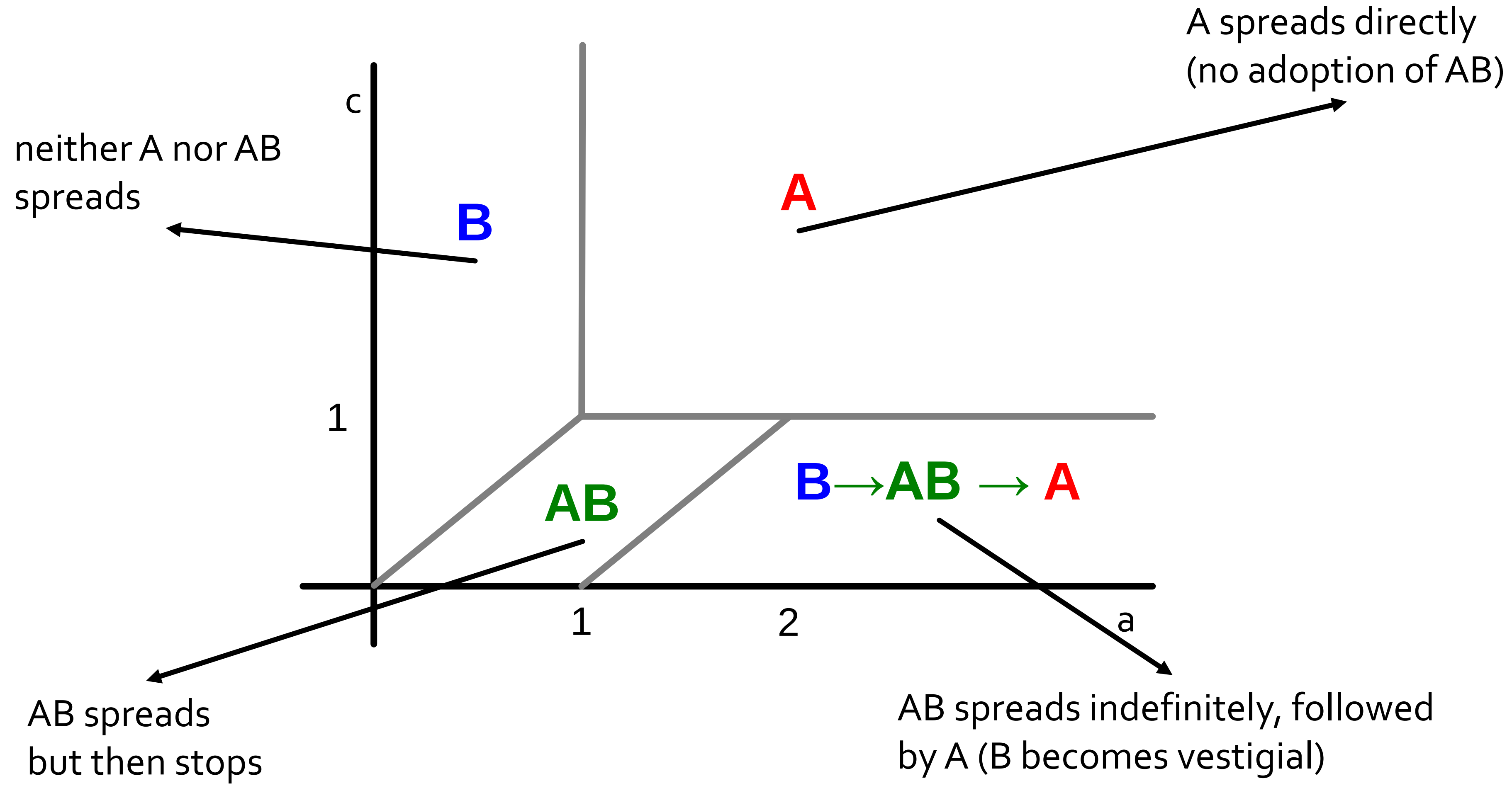




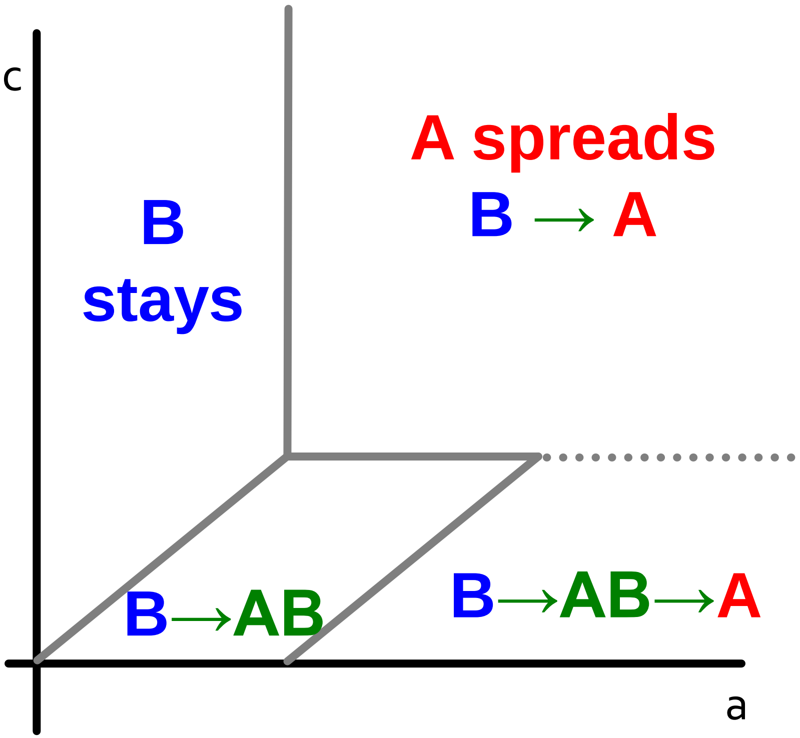
For what pairs (c,a) does A spread?

- **Joining the two pictures:**

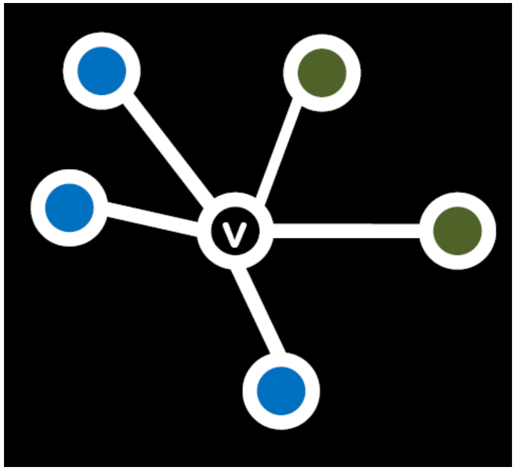


Lesson

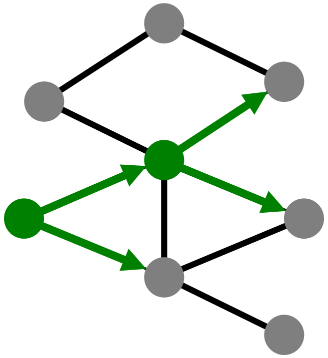
- ***B* is the default throughout the network until new/better *A* comes along. What happens?**
  - **Infiltration:** If **B** is too compatible then people will take on both and then drop the worse one **(B)**
  - **Direct conquest:** If **A** makes itself not compatible – people on the border must choose. They pick the better one (**A**)
  - **Buffer zone:** If you choose an optimal level then you keep a static "buffer" between **A** and **B**



Models of Cascading Behavior



- **So far:**
  Decision Based Models
  - Utility based
  - Deterministic
  - “Node” centric: A node observes decisions of its neighbors and makes its own decision
  - Require us to know too much about the data
- **Next: Probabilistic Models**
  - Let’s you do things by observing data
  - We lose “why people do things”



Probabilistic Contagion and Models of Influence

Agenda

- Epidemic Model Based on Trees
- Models of Disease Spreading
- Independent Cascade Model
- Modeling Interactions Between Contagions (Optional)

Epidemics

Understanding the spread of viruses and epidemics is of great interest to

- Health officials
- Sociologists
- Mathematicians
- Hollywood

The underlying contact network clearly affects the spread of an epidemic

Epidemics

- Model epidemic spread as a random process on the graph and study its properties
- Questions that we can answer:
  - What is the projected growth of the infected population?
  - Will the epidemic take over most of the network?
  - How can we contain the epidemic spread?

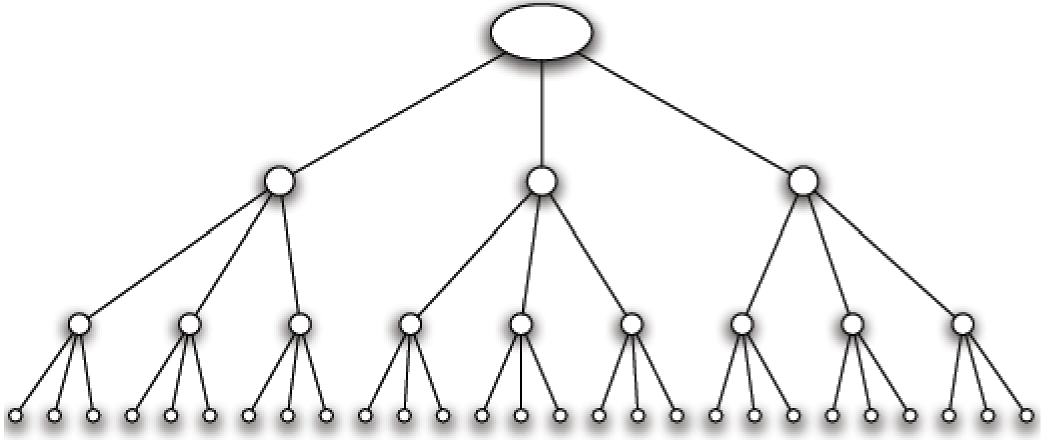
Diffusion of ideas and the spread of influence can also be modeled as epidemics

Epidemic Model Based on Trees

Simple probabilistic model of cascades where we will learn about the **reproductive number**

A Simple Model

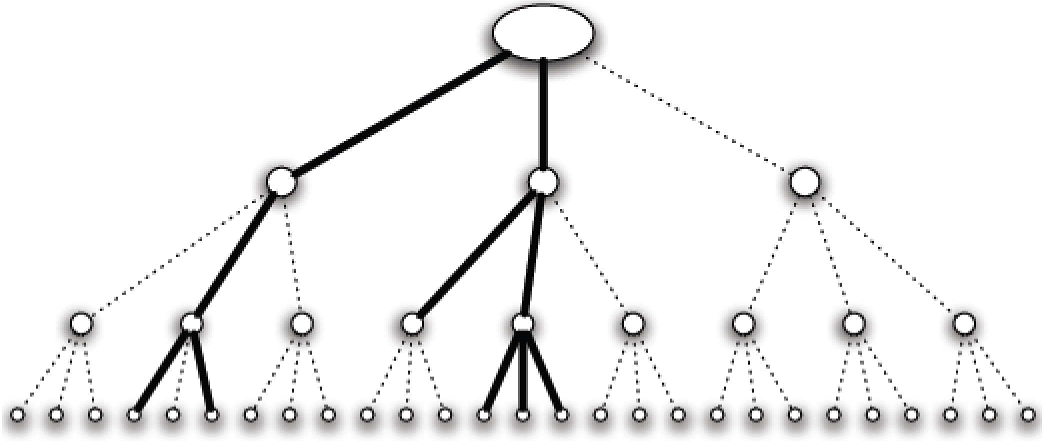
- **Branching process**: A person transmits the disease to each people she meets independently with a probability ***p***
- An infected person meets ***k*** (new) people while she is contagious
- Infection proceeds in **waves**



Contact network is a tree with branching factor *k*

Infection Spread

- We are interested in the number of people infected (spread) and the duration of the infection
- This depends on the infection probability ***p*** and the branching factor ***k***

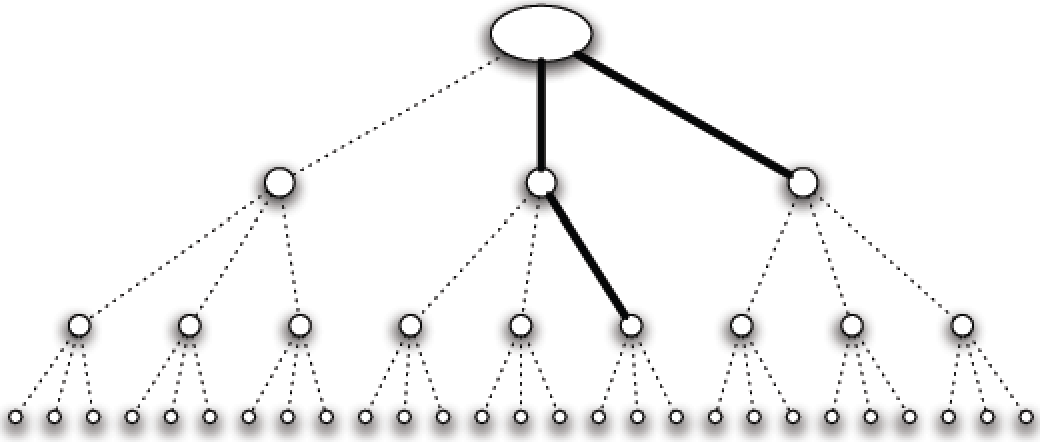


An aggressive epidemic with high infection probability

The epidemic survives after three steps

Infection Spread

- We are interested in the number of people infected (spread) and the duration of the infection
- This depends on the infection probability ***p*** and the branching factor ***k***



A mild epidemic with low infection probability

The epidemic dies out after two steps

Basic Reproductive Number

- Basic Reproductive Number ($\boldsymbol{R_0}$): the expected number of new cases of the disease caused by a single individual

$$\boldsymbol{R_0 = kp}$$

- Claim: (a) If $R_0 < 1$, then with probability 1, the disease dies out after a finite number of waves. (b) If $R_0 > 1$, then with probability greater than 0 the disease persists by infecting at least one person in each wave

1. If $\boldsymbol{R_0 < 1}$ each person infects less than one person in expectation. The infection eventually ***dies out***
2. If $\boldsymbol{R_0 > 1}$ each person infects more than one person in expectation. The infection ***persists***

Analysis

- X_n: random variable indicating the number of infected nodes after ***n*** steps
- $q_n = \Pr[X_n \geq 1]$: probability that there exists at least 1 infected node after ***n*** steps
- $q^* = \lim q_n$: the probability of having infected nodes as $n \rightarrow \infty$

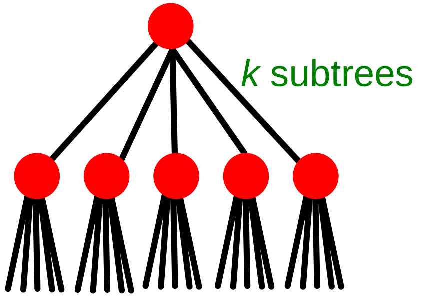
It can be shown that

(a)$R_0 < 1 \Rightarrow q^* = 0$

(b) $R_0 > 1$=> $q^* > 0$.

Probabilistic Spreading Models

- **Epidemic Model based on Random Trees**
  - **(a variant of branching processes)**
  - A patient meets ***k*** other people
  - With probability ***p* > *0*** infects each of them
- **Q: For which values of *k* and *p* does the epidemic run forever?**
  - **Run forever:** $\lim_{n\to\infty} P\left[\begin{array}{l}\text{At least 1 infected}\\ \text{node at depth n}\end{array}\right] > 0$
  - **Die out:** -- || -- $= 0$



Probabilistic Spreading Models

- **q_{nj} = prob. there is an infected node at depth n *starting from a specific child node***

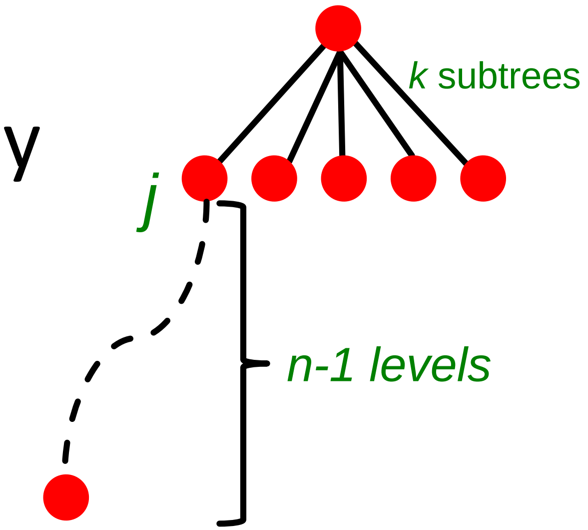
$$q_{nj} = p \cdot q_{n-1}$$

- Fails with probability (the complementary view)

$$1 - p \cdot q_{n-1}$$

- All **k** subtrees fail with probability

$$(1 - p \cdot q_{n-1})^k$$



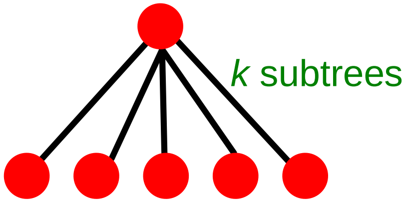
Probabilistic Spreading Models

- q_n **= prob. there is an infected node at depth** n
- **We need:** $\lim_{n\to\infty} q_n = ?$ (based on p and k)
- All **k** subtrees fail with probability

$$(1 - p \cdot q_{n-1})^k$$

- **Taking the complement:**

$$q_n = 1 - \underbrace{(1 - p \cdot q_{n-1})^k}_{\text{No infected node at depth } n \text{ from the root}}$$



- $\lim_{n\to\infty} q_n$ **= result of iterating**

$$\mathrm{f(x)} = 1 - (1 - p \cdot x)^k$$

  - Starting at $x = 1$ (since $q_1 = 1$)

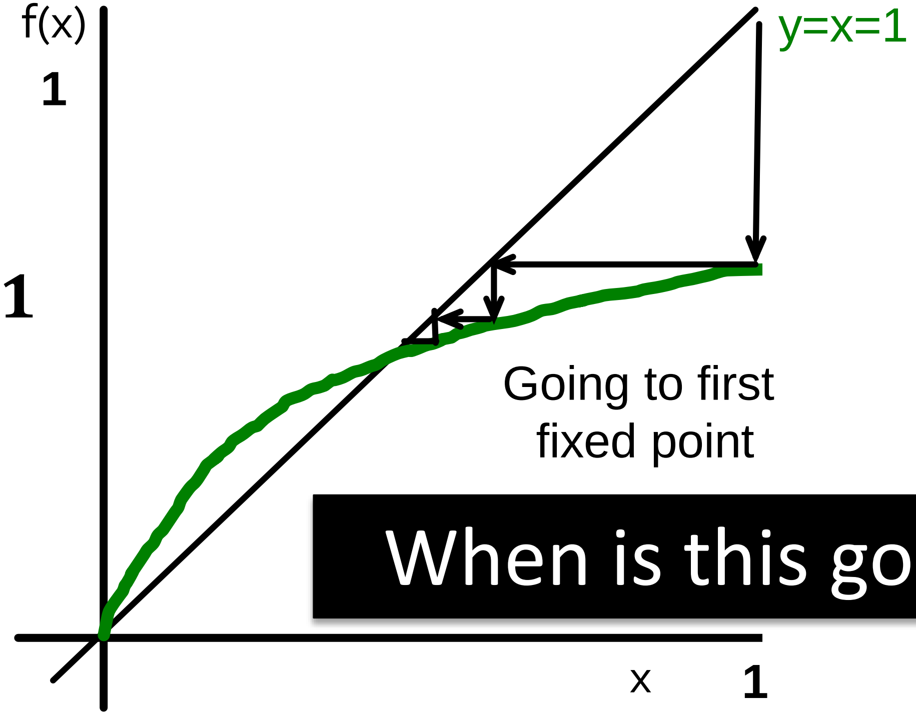
Properties of $f(x) = 1 - (1 - px)^k$

- $f(0) = 0$, *so intercepts at point (0,0)*
- $f(1) = 1 - (1 - p)^k < 1$, *so at x=1, f(1) is below the y=x line*
- $f'(x) = p \cdot k(1 - px)^{k-1}$, positive and f' monotonically decreasing on [0,1], so concave curve
- $f'(0) = p \cdot k = R_0$, so
  - for $\boldsymbol{R_0 > 1}$ f starts above the y=x line
  - for $\boldsymbol{R_0 < 1}$ f starts below the y=x line

Fixed Point: $f(x) = 1 - (1 - px)^k$

Case 1:

$\boldsymbol{R_0 = pk > 1}$



y = f(x)

Going to first fixed point

When is this going to 0?

What do we know about f(x)?

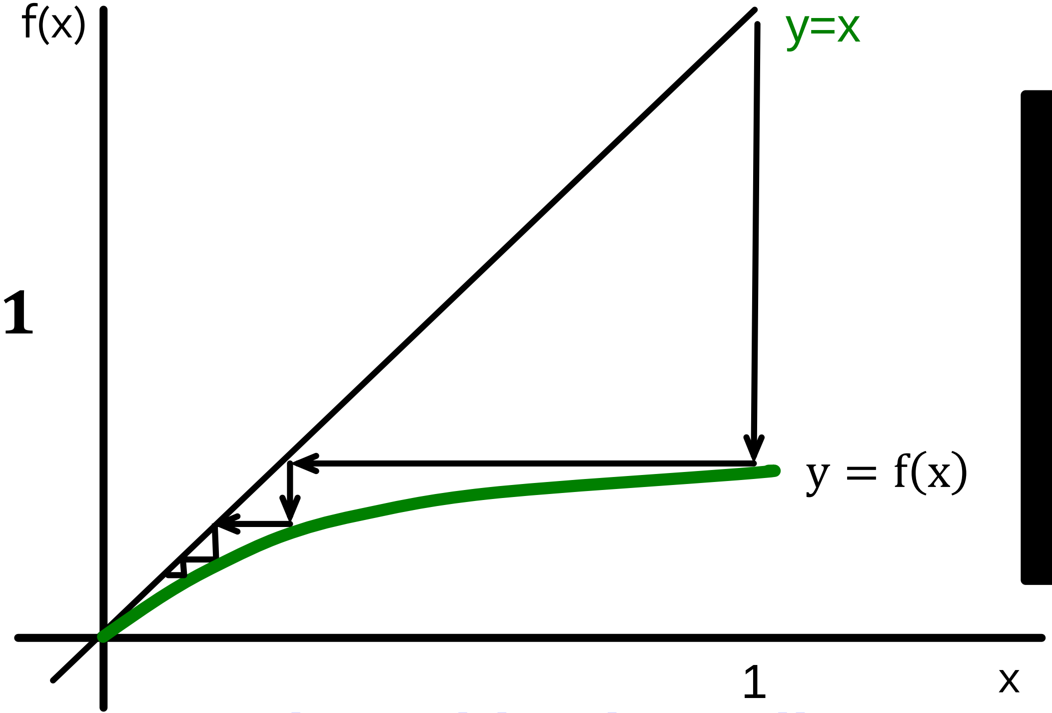
$f(0) = 0, f(1) = 1 - (1-p)^k < 1$, *so at x=1, f(1) is below the y=x line*

$f'(x) = p \cdot k(1-px)^{k-1}$, so concave on [0,1]

$f'(0) = p \cdot k = R_0$, so for $R_0 > 1$ f starts above the y=x line

Fixed Point: When is this zero?

Case 2:
$R_0 = pk < 1$



Reproductive number $R_0 = p \cdot k$:
There is an epidemic if $R_0 \geq 1$

For the epidemic to die out we need *f(x)* to be below *y=x*!

So: $f'(0) = p \cdot k < 1$

$$\lim_{n \to \infty} q_n = 0 \ \ when \ \ \boldsymbol{p \cdot k < 1}$$

$p \cdot k$ = expected # of people that we infect

Branching process

- Assumes no network structure, no triangles or shared neighbors

Models of Disease Spreading

The SIR model

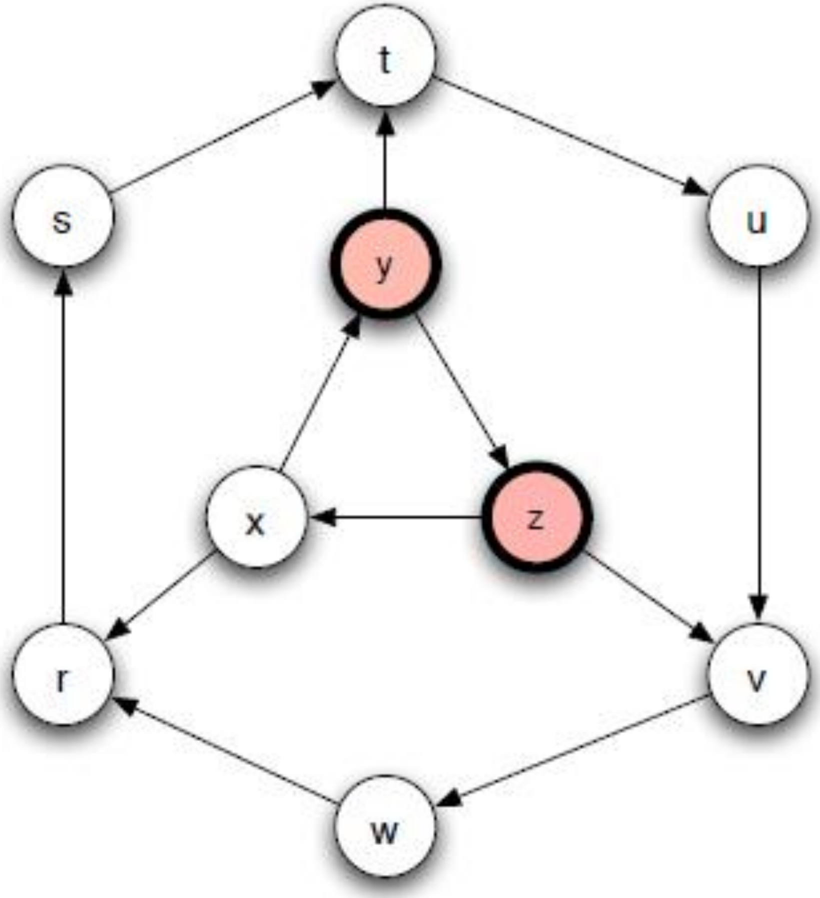
- Each node may be in the following states
  - Susceptible: healthy but not immune
  - Infected: has the virus and can actively propagate it
  - Removed: (Immune or Dead) had the virus but it is no longer active

- Parameter *p*: the probability of an Infected node to infect a Susceptible neighbor

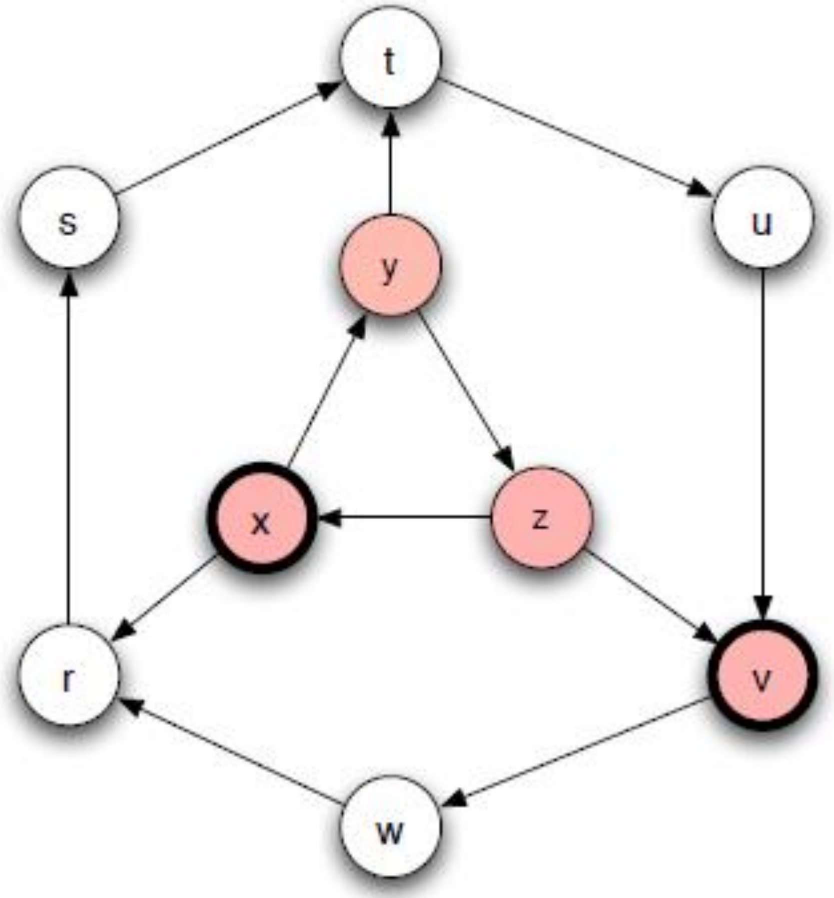
The SIR process

- Initially all nodes are in state S(usceptible), except for a few nodes in state I(nfected).
- An infected node stays infected for t_I steps.
  - Simplest case: $t_I = 1$
- At each of the t_I steps the infected node has probability *p* of infecting any of its susceptible neighbors
  - *p*: Infection probability
- After t_I steps the node is Removed

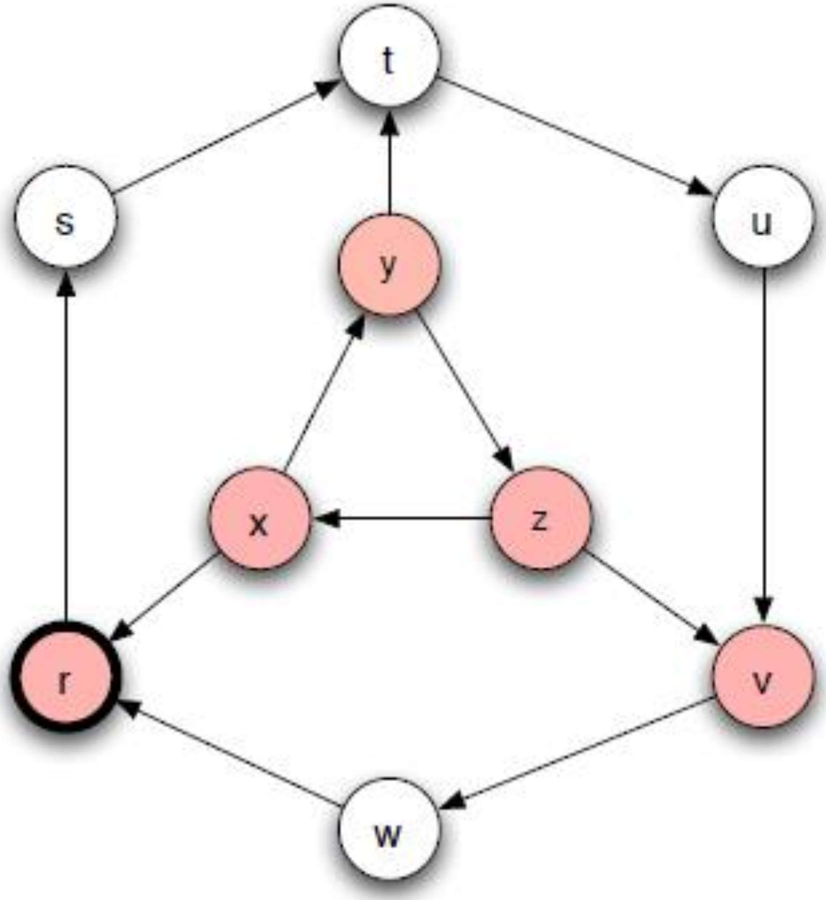
Example



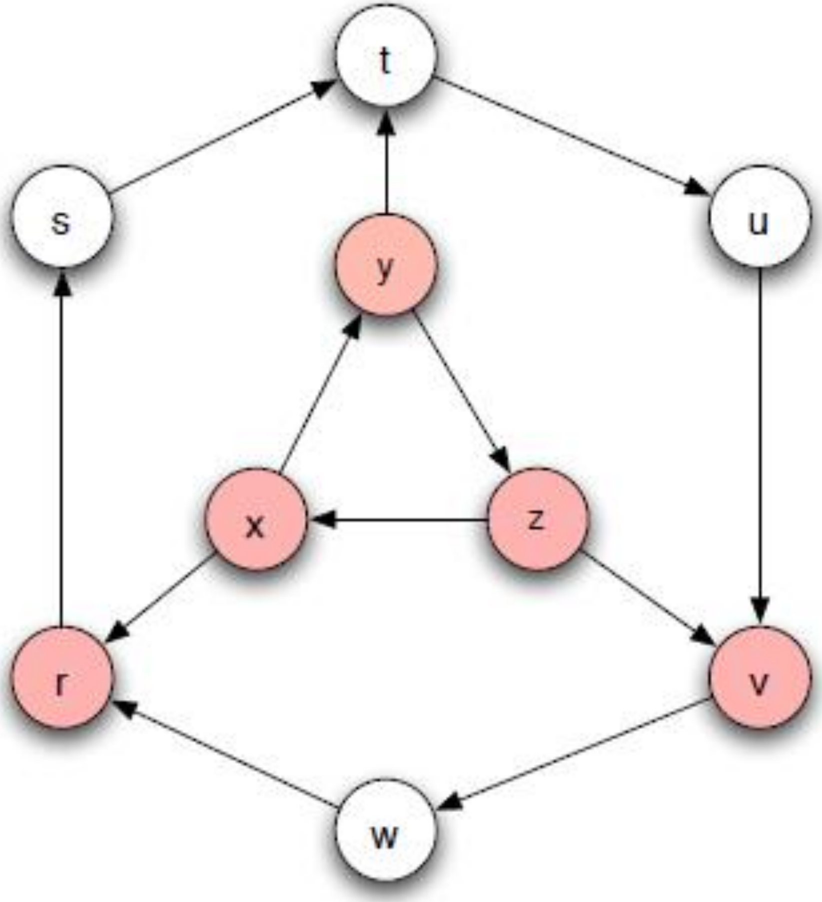
Example



Example



Example



Example SIR Epidemic

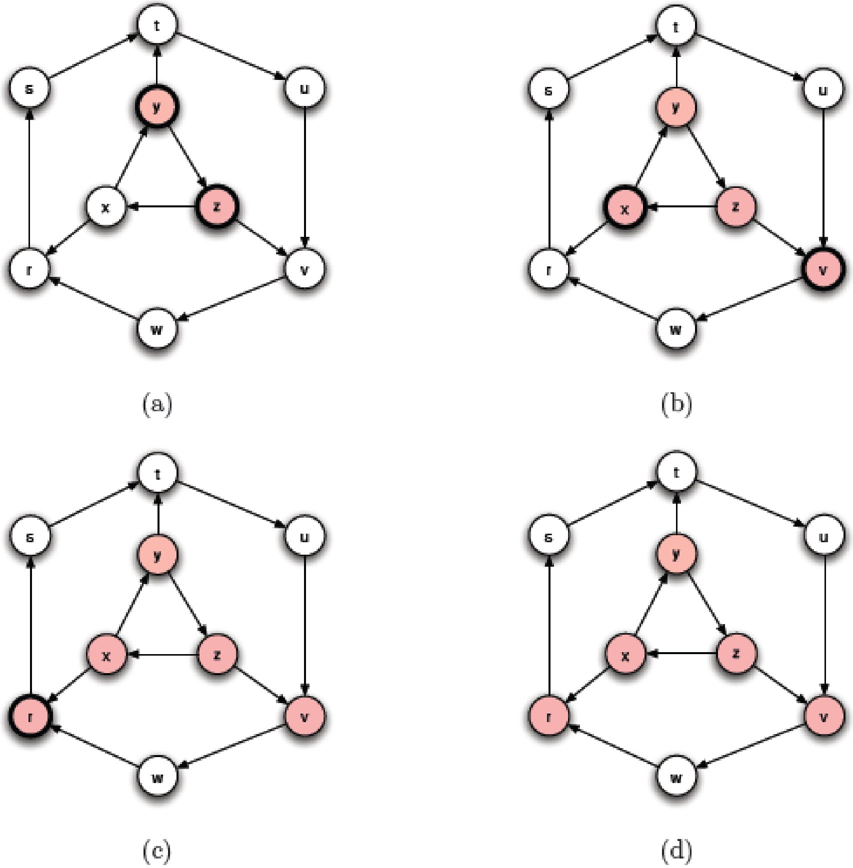


Figure 21.2: The course of an SIR epidemic in which each node remains infectious for a number of steps equal to $t_I = 1$. Starting with nodes y and z initially infected, the epidemic spreads to some but not all of the remaining nodes. In each step, shaded nodes with dark borders are in the Infectious (I) state and shaded nodes with thin borders are in the Removed (R) state.

Percolation

- Percolation: we have a network of “pipes” which can carry liquids, and they can be either open, or closed
  - The pipes can be pathways within a material
- If liquid enters the network from some nodes, does it reach most of the network?
  - The network percolates

SIR and Percolation

- There is a connection between SIR model and percolation
- When a virus is transmitted from u to v, the edge (u,v) is activated with probability p
- We can assume that all edge activations have happened in advance, and the input graph has only the active edges
- Which nodes will be infected?
  - The nodes reachable from the initial infected nodes
- In this way we transformed the dynamic SIR process into a static one
  - This is essentially percolation in the graph

Example

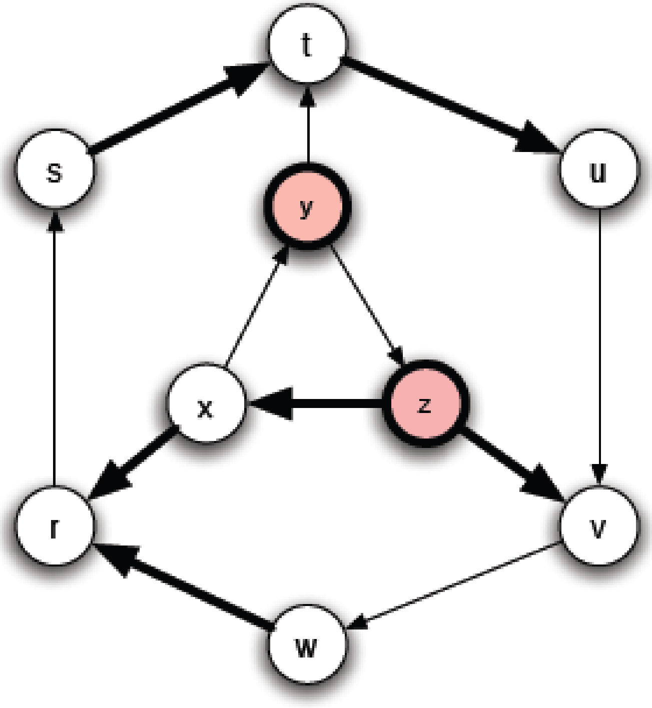


Figure 21.4: An equivalent way to view an SIR epidemic is in terms of *percolation*, where we decide in advance which edges will transmit infection (should the opportunity arise) and which will not.

The SIS model

- Susceptible-Infected-Susceptible
  - Susceptible: healthy but not immune
  - Infected: has the virus and can actively propagate it
- An Infected node infects a Susceptible neighbor with probability ***p***
- An Infected node becomes Susceptible again with probability ***q*** (or after t_I steps)
  - In a simplified version of the model q = 1
- Nodes alternate between Susceptible and Infected status

Example

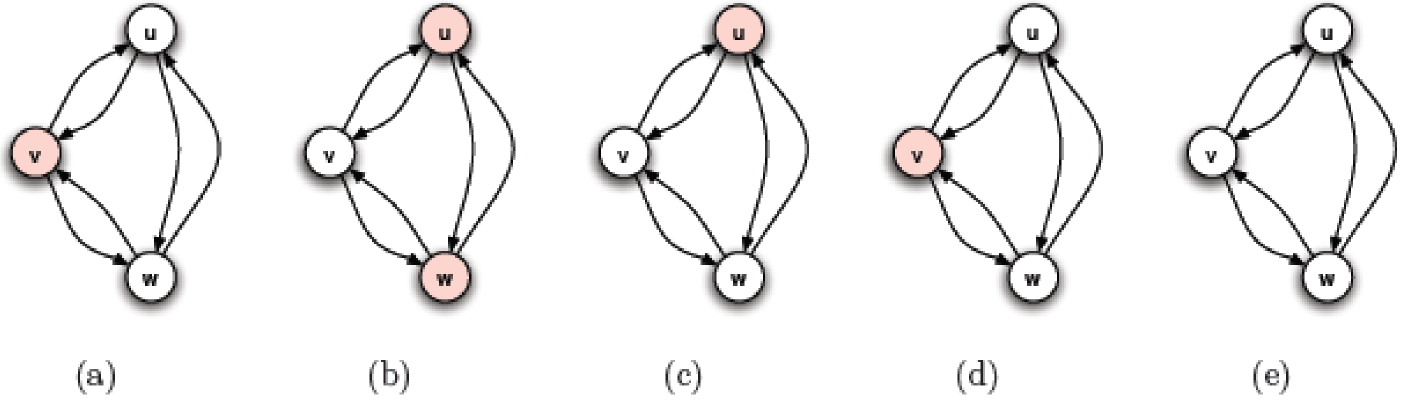


Figure 21.5: In an SIS epidemic, nodes can be infected, recover, and then be infected again. In each step, the nodes in the Infectious state are shaded.

- When no Infected nodes, virus dies out
- Question: will the virus die out?

An eigenvalue point of view

- If A is the adjacency matrix of the network, then the virus dies out if

$$\lambda_1(A) \leq \frac{q}{p}$$

- Where $\lambda_1(A)$ is the first eigenvalue of A

Y. Wang, D. Chakrabarti, C. Wang, C. Faloutsos. *Epidemic Spreading in Real Networks: An Eigenvalue Viewpoint*. SRDS 2003

SIRS

- Initially, some nodes e in the ***I*** state and all others in the ***S*** state
- Each node ***u*** that enters the ***I*** state remains infectious for a fixed number of steps t_I. During each of these t_I steps, ***u*** has a probability ***p*** of infecting each of its susceptible neighbors
- After t_I steps, ***u*** is no longer infectious. Enters the ***R*** state for a fixed number of steps t_R. During each of these t_R steps, ***u*** cannot be infected nor transmit the disease
- After $\mathbf{t}_\mathrm{R}$ steps in the ***R*** state, node ***u*** returns to the ***S*** state

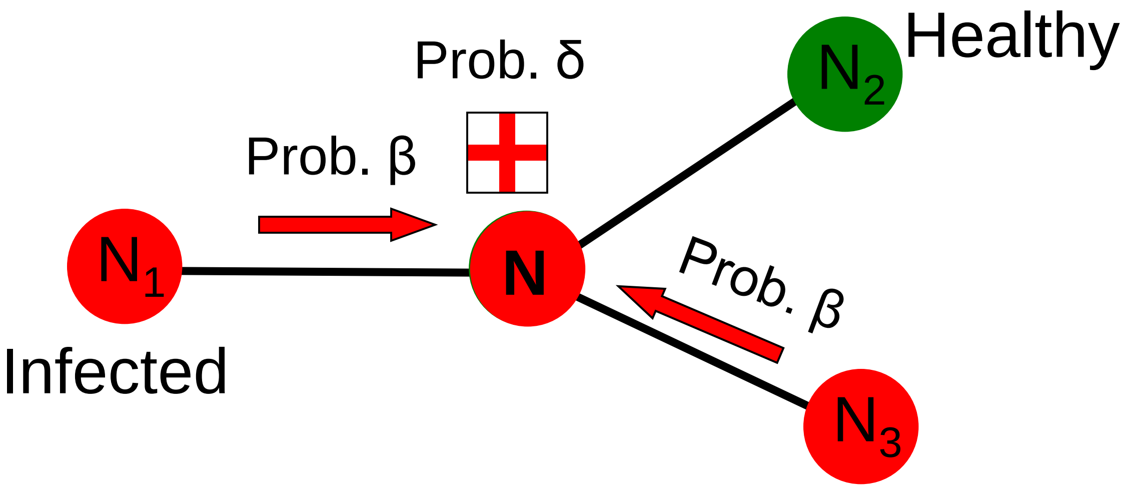
Models of Disease Spreading

We will learn about the **epidemic threshold**

Spreading Models of Viruses

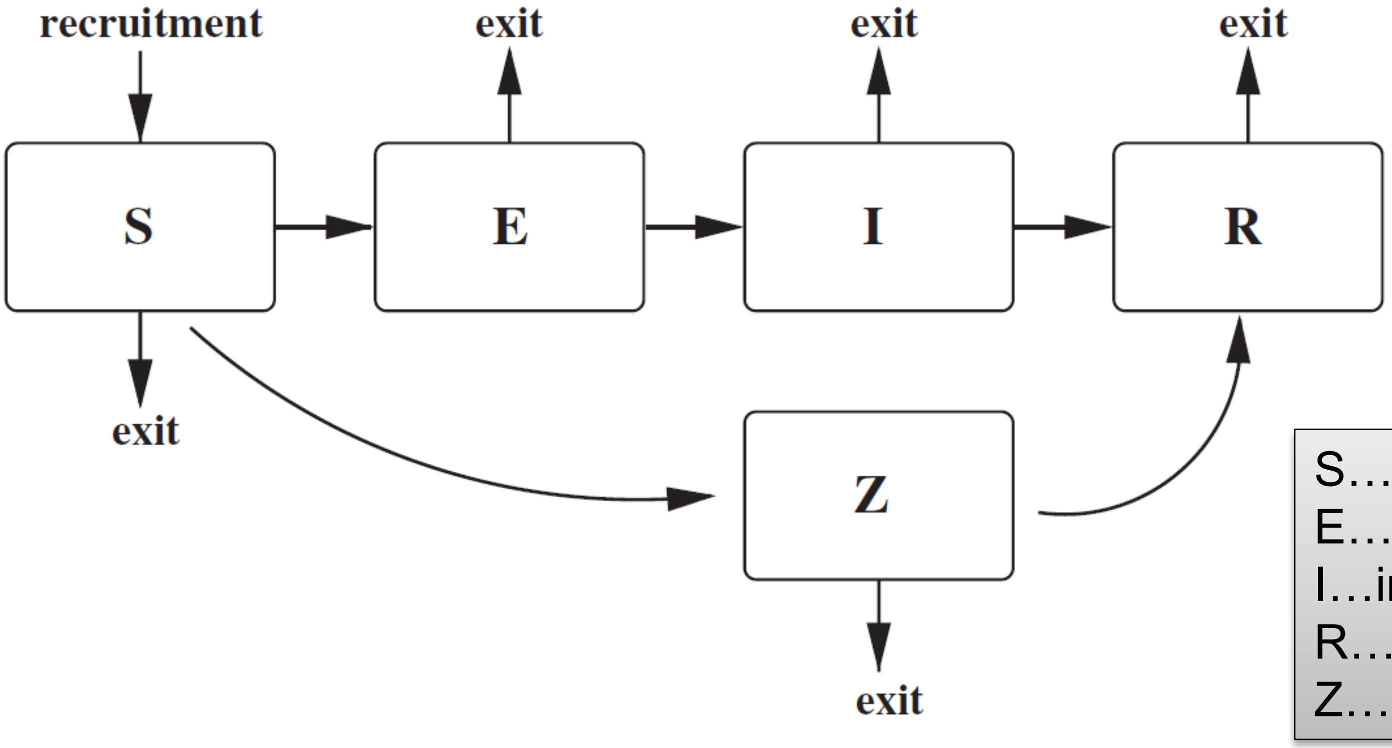
Virus Propagation: 2 Parameters:

- **(Virus) Birth rate β:**
  - probability that an infected neighbor attacks
- **(Virus) Death rate δ:**
  - Probability that an infected node heals



More Generally: S+E+I+R Models

- **General scheme for epidemic models:**
  - **Each node can go through phases:**
    - Transition probs. are governed by the model parameters



S…susceptible
E…exposed
I…infected
R…recovered
Z…immune

SIR Model

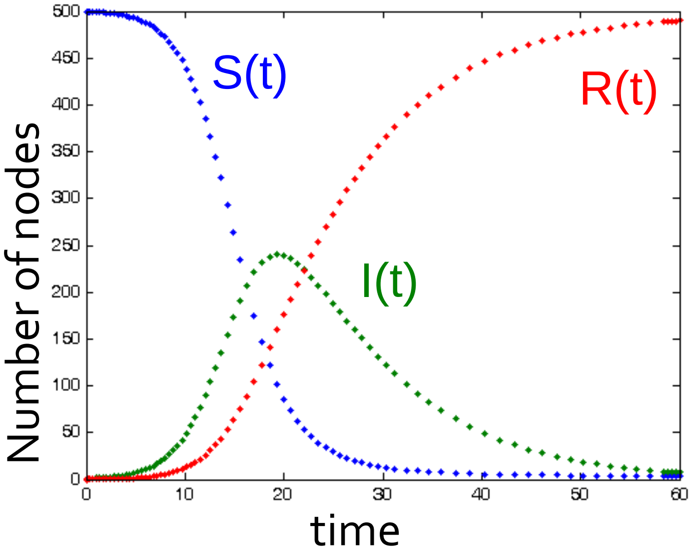
- **SIR model:** Node goes through phases

$$\text{Susceptible} \xrightarrow{\beta} \text{Infected} \xrightarrow{\delta} \text{Recovered}$$

  - Models chickenpox or plague:
    - Once you heal, you can never get infected again
- **Assuming perfect mixing** (The network is a complete graph) **the model dynamics are:**

$$\frac{dS}{dt} = - bSI \qquad \frac{dR}{dt} = dI$$

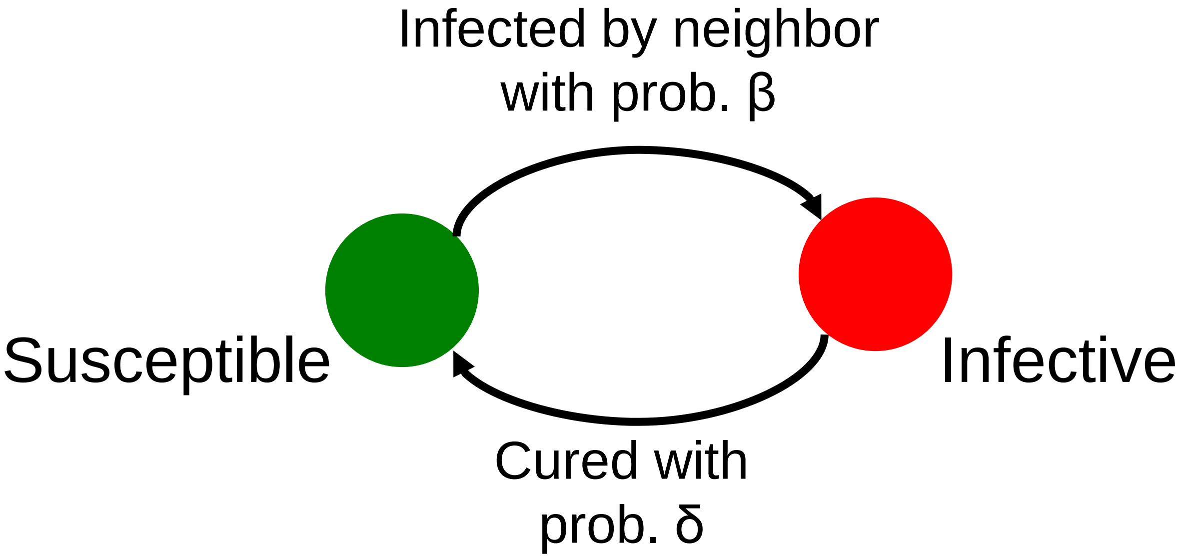
$$\frac{dI}{dt} = bSI - dI$$



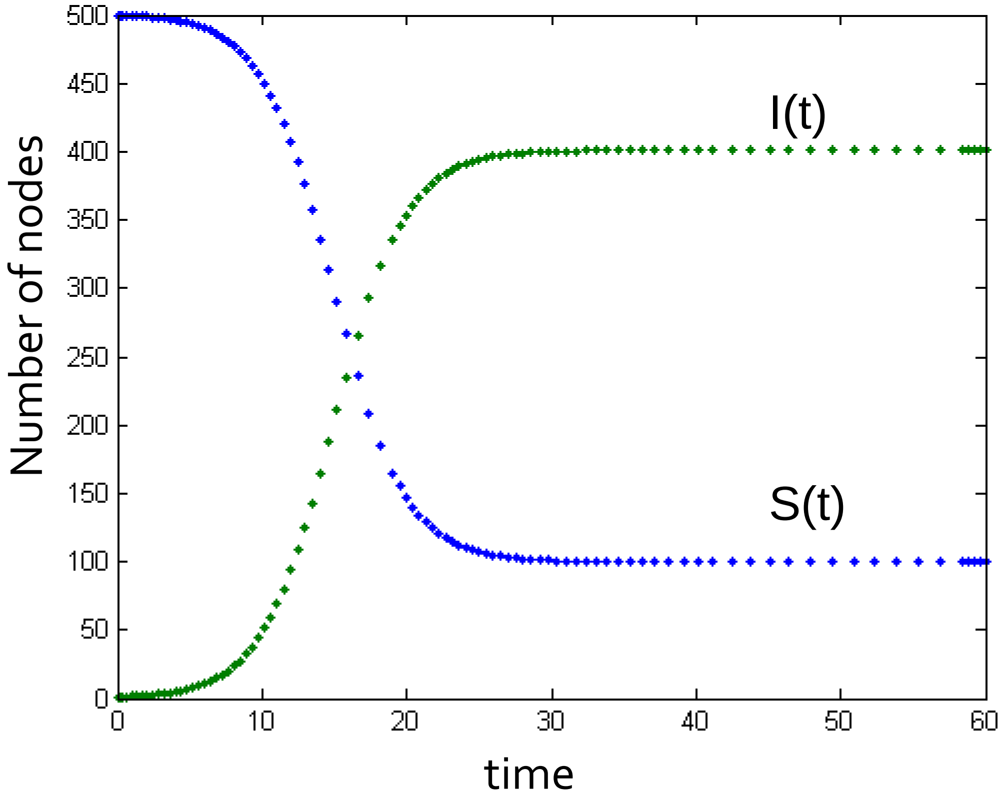
Kermack-McKendrick Model: http://mathworld.wolfram.com/Kermack-McKendrickModel.html

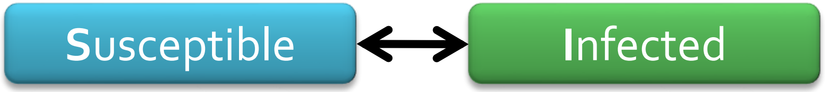
SIS Model

- Susceptible-Infective-Susceptible (SIS) model
- Cured nodes immediately become susceptible
- Virus “strength”: s = β / δ
- Node state transition diagram:



SIS Model





- **Models flu:**
  - Susceptible node becomes infected
  - The node then heals and become susceptible again
- **Assuming perfect mixing (complete graph):**

$$\frac{dS}{dt} = -\beta SI + \delta I$$

$$\frac{dI}{dt} = \beta SI - \delta I$$

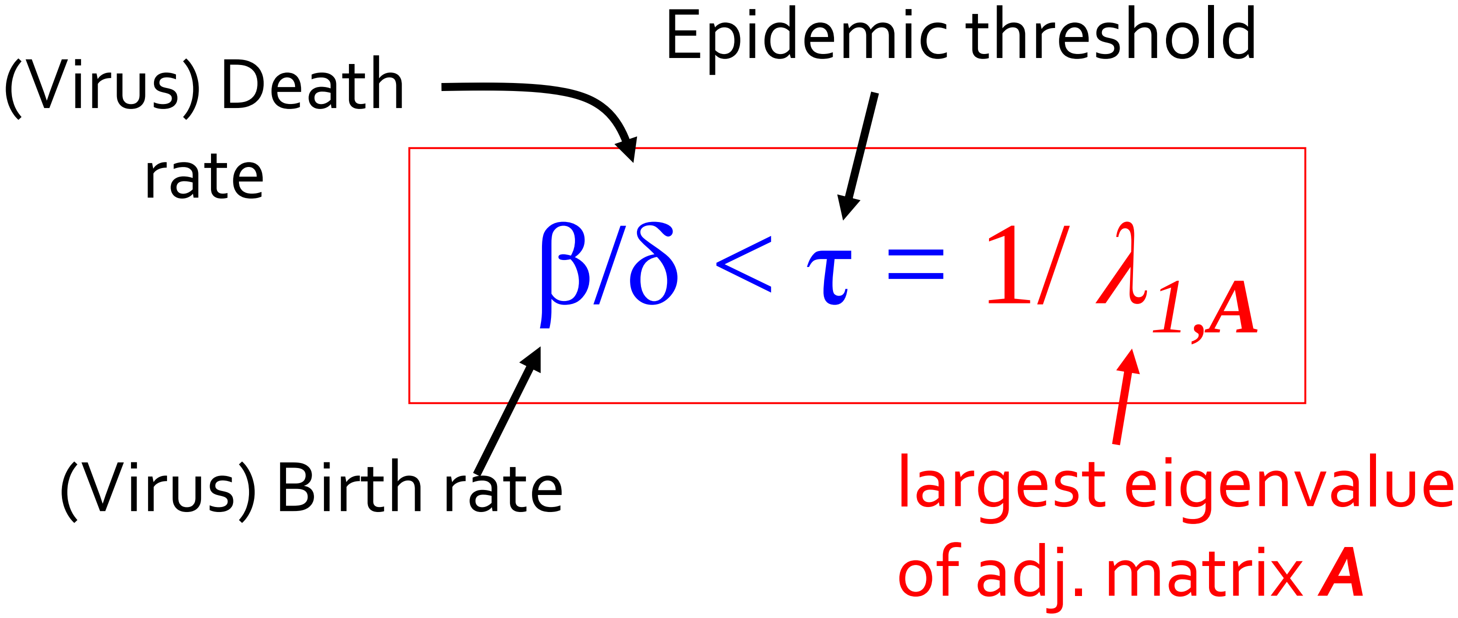
Question: Epidemic threshold *t*

- SIS Model:
  Epidemic threshold of an arbitrary graph *G* is τ, such that:
  - If virus strength $s = \beta / \delta < \tau$
    the epidemic can not happen
    (it eventually dies out)
- Given a graph what is its epidemic threshold?

[Wang et al. 2003]

Epidemic Threshold in SIS Model

- **We have no epidemic if:**



Epidemic threshold

(Virus) Death rate

$$\boxed{\beta/\delta < \tau = 1/\lambda_{1,A}}$$

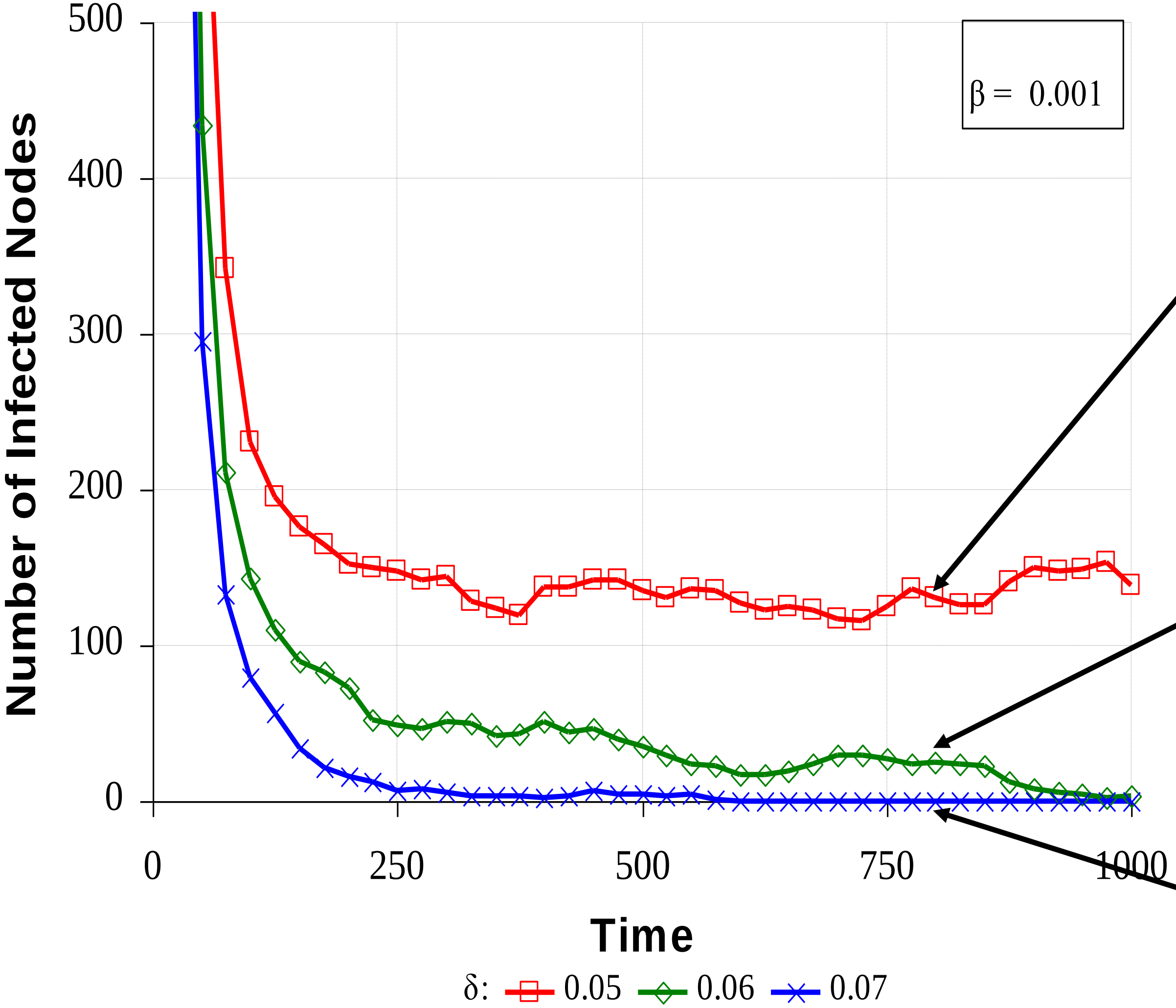
(Virus) Birth rate

largest eigenvalue of adj. matrix ***A***

► $\lambda_{1,A}$ ***alone captures the property of the graph!***

[Wang et al. 2003]

Experiments (AS graph)



10,900 nodes and
31,180 edges

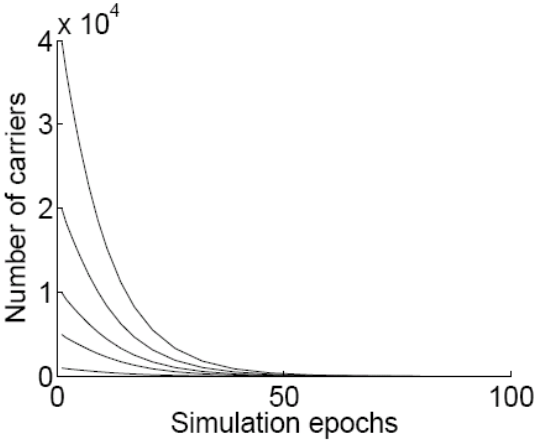
$s=\beta/\delta > \tau$
(above threshold)

$s=\beta/\delta = \tau$
(at the threshold)

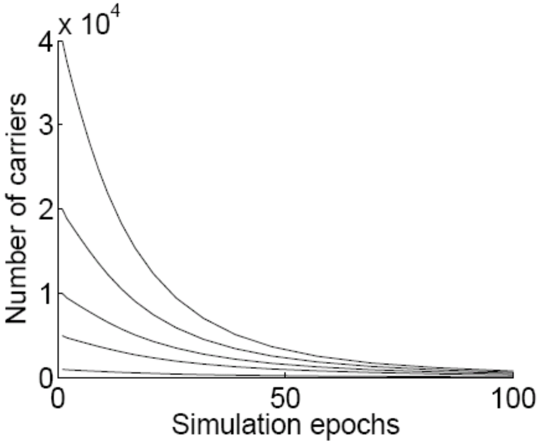
$s=\beta/\delta < \tau$
(below threshold)

Experiments

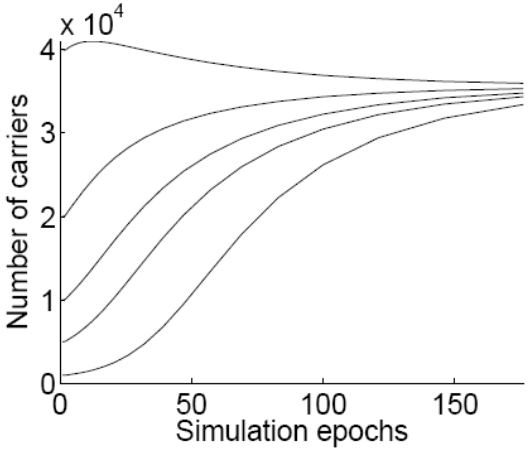
- **Does it matter how many people are initially infected?**



(a) Below the threshold, s=0.912

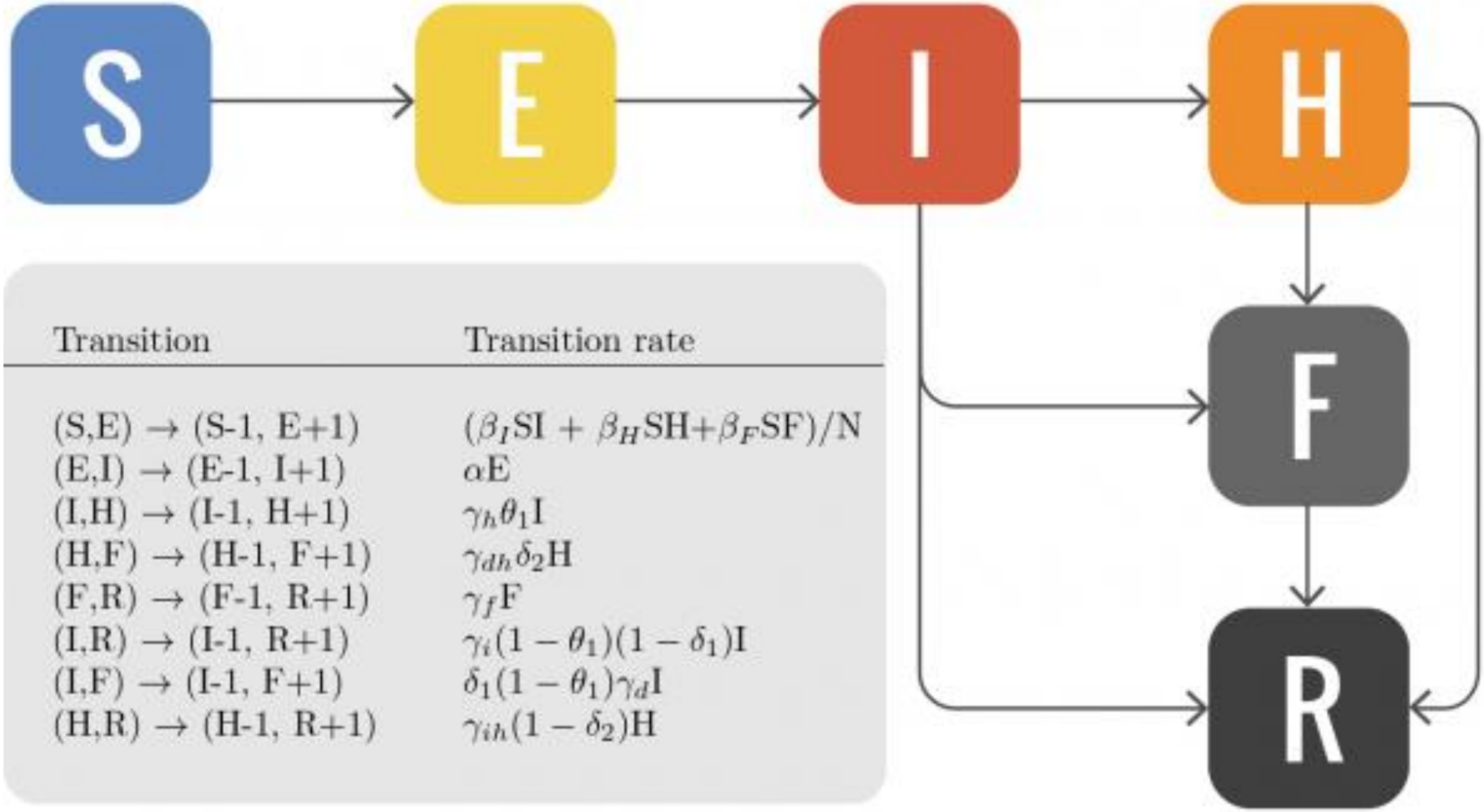


(b) At the threshold, s=1.003



(c) Above the threshold, s=1.1

Example: Ebola



Transition	Transition rate
$(S,E) \rightarrow (S-1, E+1)$	$(\beta_I SI + \beta_H SH+\beta_F SF)/N$
$(E,I) \rightarrow (E-1, I+1)$	αE
$(I,H) \rightarrow (I-1, H+1)$	$\gamma_h \theta_1 I$
$(H,F) \rightarrow (H-1, F+1)$	$\gamma_{dh} \delta_2 H$
$(F,R) \rightarrow (F-1, R+1)$	$\gamma_f F$
$(I,R) \rightarrow (I-1, R+1)$	$\gamma_i (1-\theta_1)(1-\delta_1) I$
$(I,F) \rightarrow (I-1, F+1)$	$\delta_1 (1-\theta_1) \gamma_d I$
$(H,R) \rightarrow (H-1, R+1)$	$\gamma_{ih} (1-\delta_2) H$

[Gomes et al., Assessing the International Spreading Risk Associated with the 2014 West African Ebola Outbreak, *PLOS Current Outbreaks*, 2014]
http://currents.plos.org/outbreaks/article/assessing-the-international-spreading-risk-associated-with-the-2014-west-african-ebola-outbreak/

Ebola: Model States & Parameters

Model States

S: susceptible individuals

E: exposed individuals

I: infectious cases in the community

H: hospitalized cases

F: dead but not yet buried

R: individuals no longer transmitting the disease

Model Parameters

$\boldsymbol{\beta_I}$: transmission coefficient in the community

$\boldsymbol{\beta_H}$: transmission coefficient at the hospital

$\boldsymbol{\beta_F}$: transmission coefficient during funerals

$\boldsymbol{\theta_1}$: computed so that **θ%** of infectious cases are hospitalized

δ: Compartment specific $\boldsymbol{\delta_1}$ and $\boldsymbol{\delta_2}$ so that overall case-fatality ratio is **δ**

$\boldsymbol{\alpha^{-1}}$: the mean incubation period

$\boldsymbol{\gamma_h^{-1}}$: the mean duration from symptom onset to hospitalization

$\boldsymbol{\gamma_{dh}^{-1}}$: the mean duration from hospitalization to death

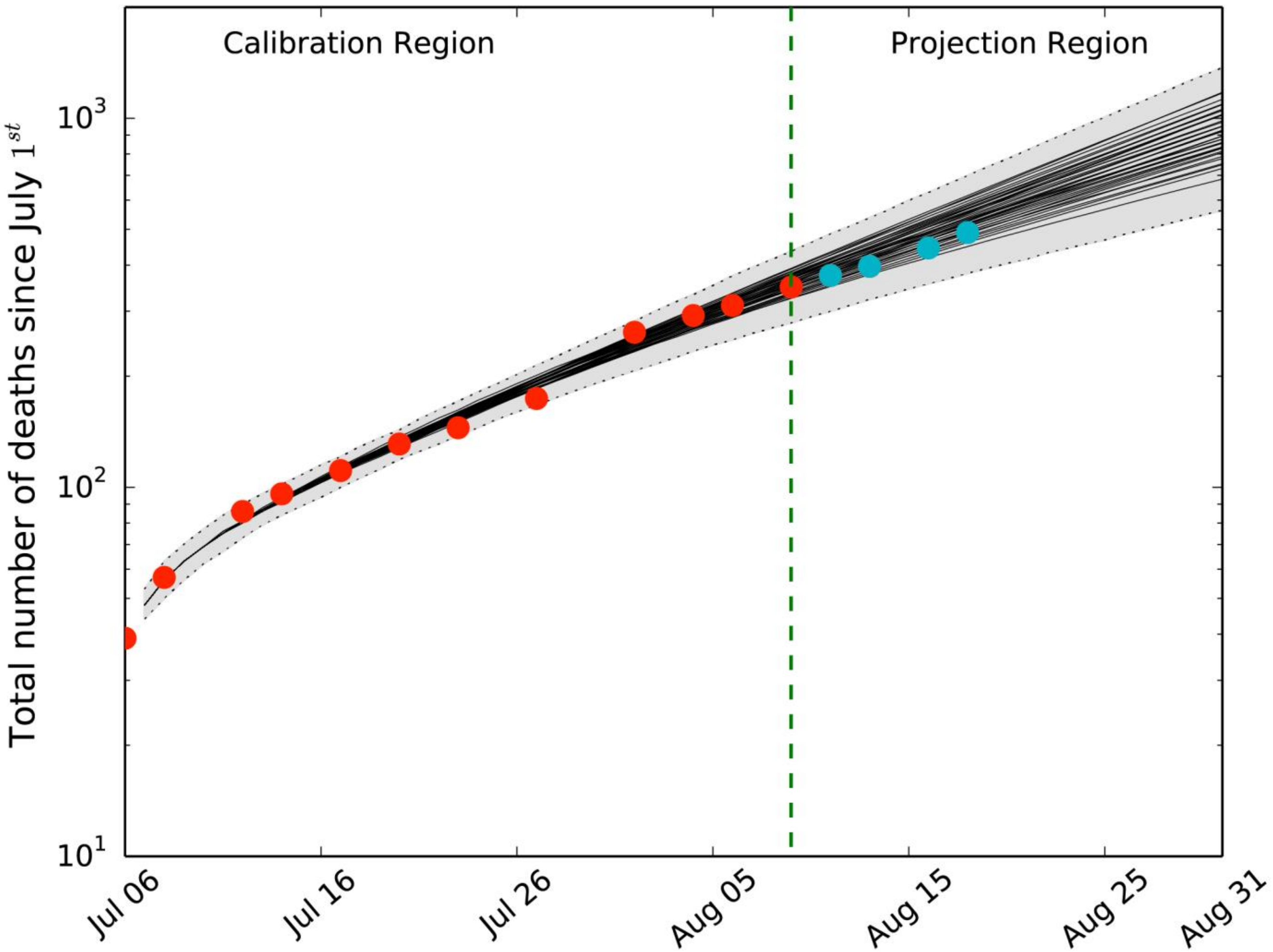
$\boldsymbol{\gamma_i^{-1}}$: the mean duration of the infectious period for survivors

$\boldsymbol{\gamma_{ih}^{-1}}$: the mean duration from hospitalization to end of infectiousness for survivors

$\boldsymbol{\gamma_f^{-1}}$: the mean duration from death to burial

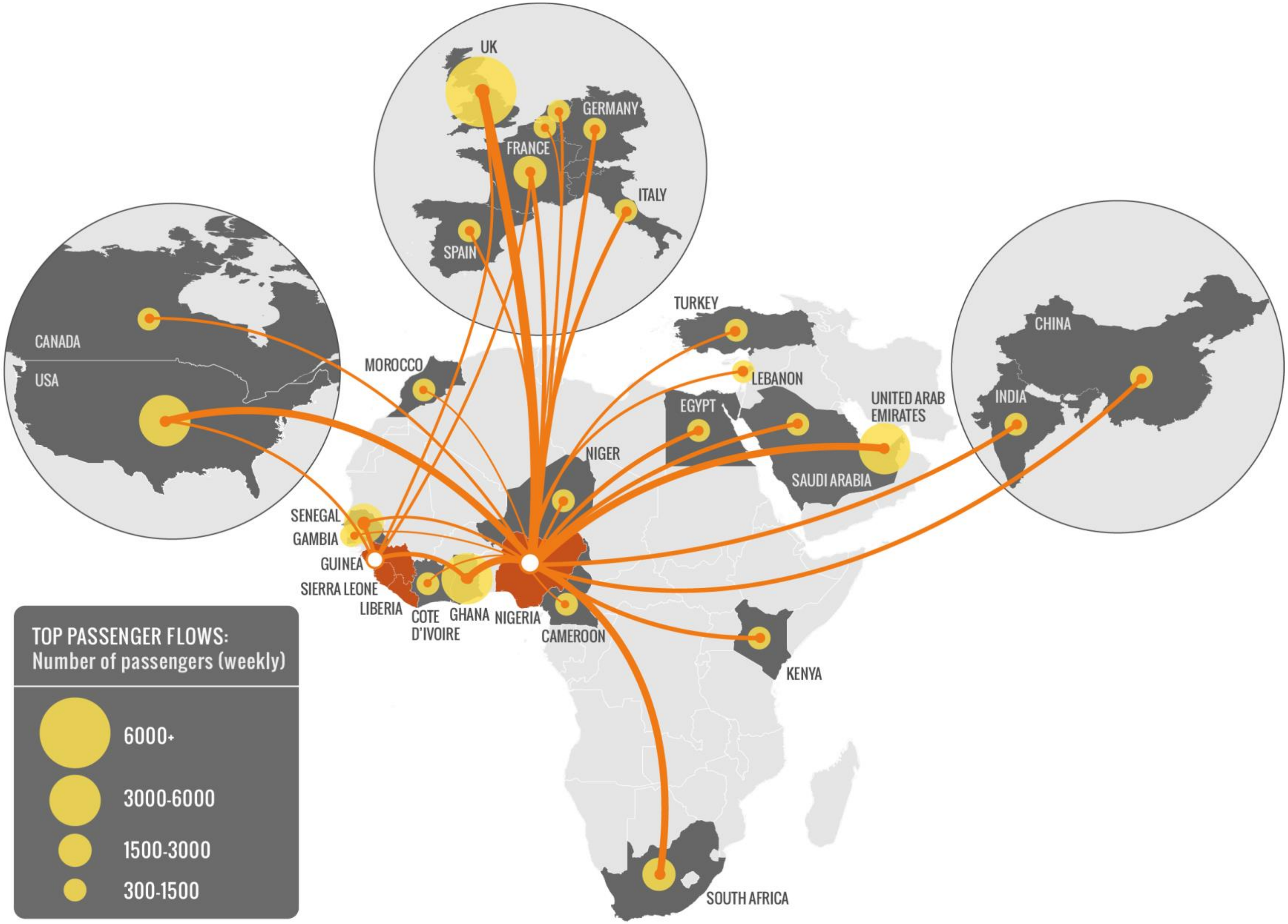
Gomes et al., 2014]

Example: Ebola



Gomes et al., 2014]

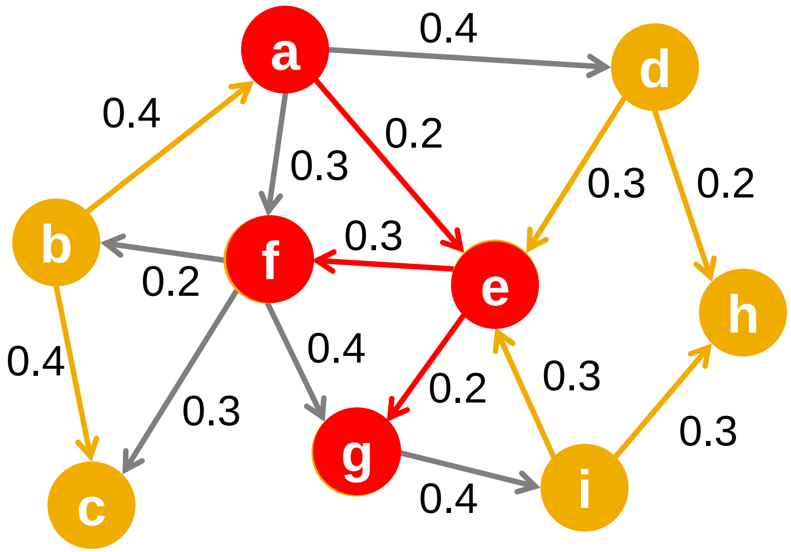
Example: Ebola



Independent Cascade Model

Independent Cascade Model

- **Initially some nodes *S* are active**
- Each edge ***(u,v)*** has probability (weight) p_{uv}



- **When node *u* becomes active/infected:**
  - It activates each out-neighbor ***v*** with prob. p_{uv}
- **Activations spread through the network!**