Think Globally, Act Locally: On the Optimal Seeding for Nonsubmodular Influence Maximization

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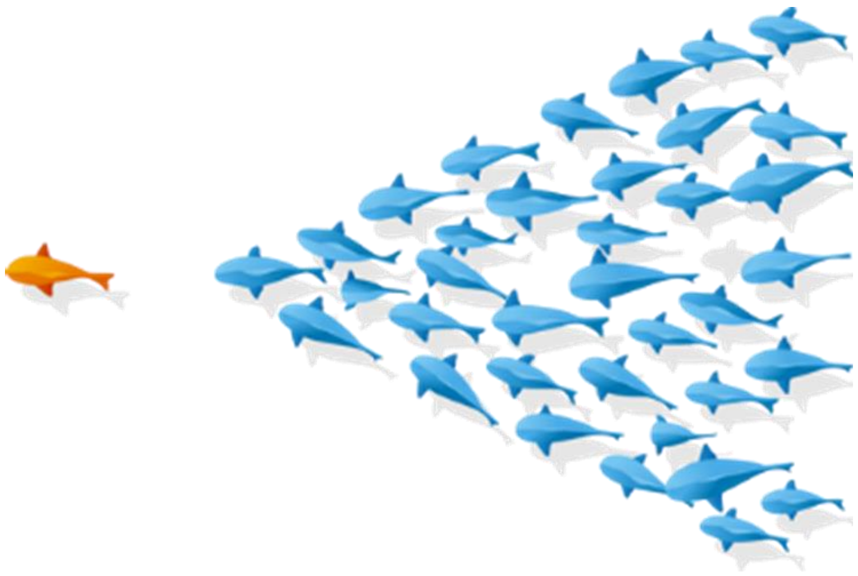
Contagions, Diffusion, Cascade…

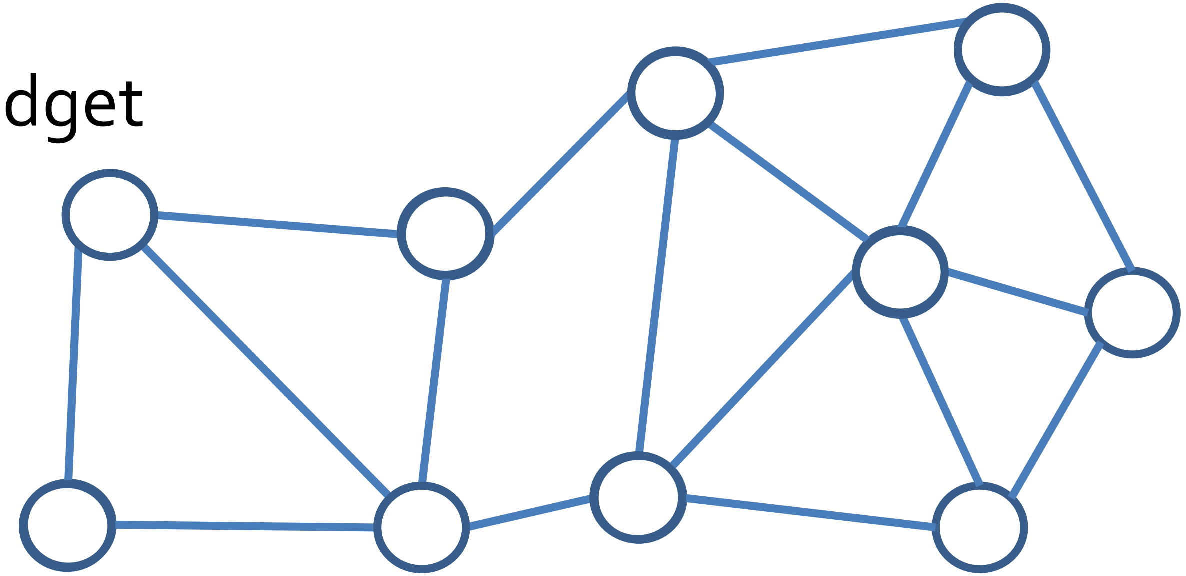
- Ideas, beliefs, behaviors, and technology adoption spread through networks
- Why do we need to study this phenomena?
  - Better Understanding
  - **Promoting good behaviors/beliefs**
  - Stopping bad behavior



Influence Maximization

Find the best K nodes to maximize adoptions [KKT03]

- Input
  - Social network G
  - Model of contagions
  - Total number of seeds K, budget



Influence Maximization

Find the best K nodes to maximize adoptions [KKT03]

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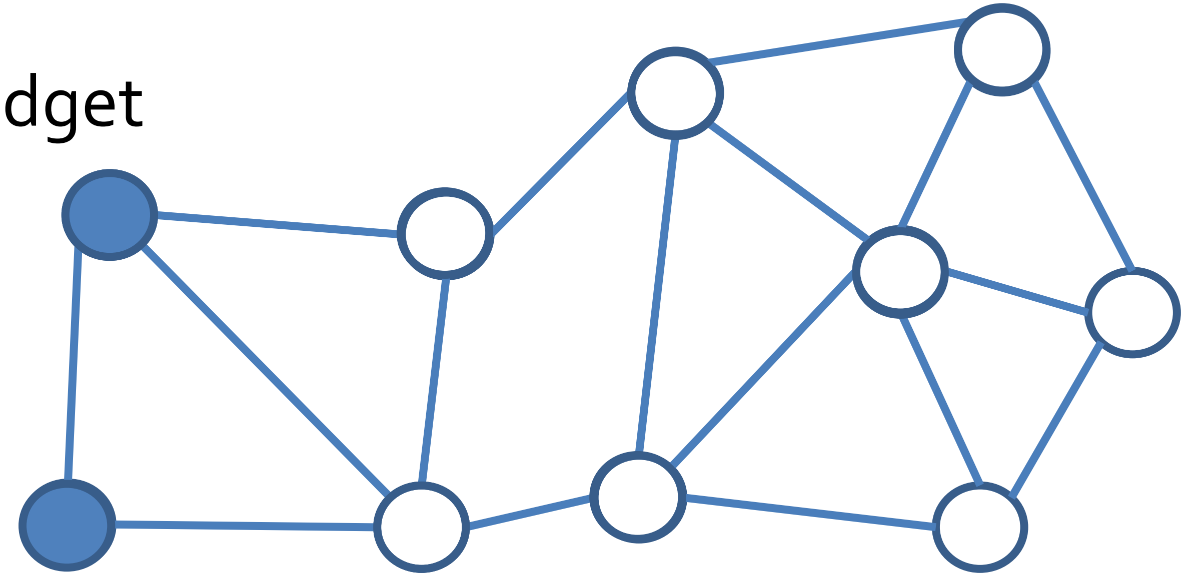
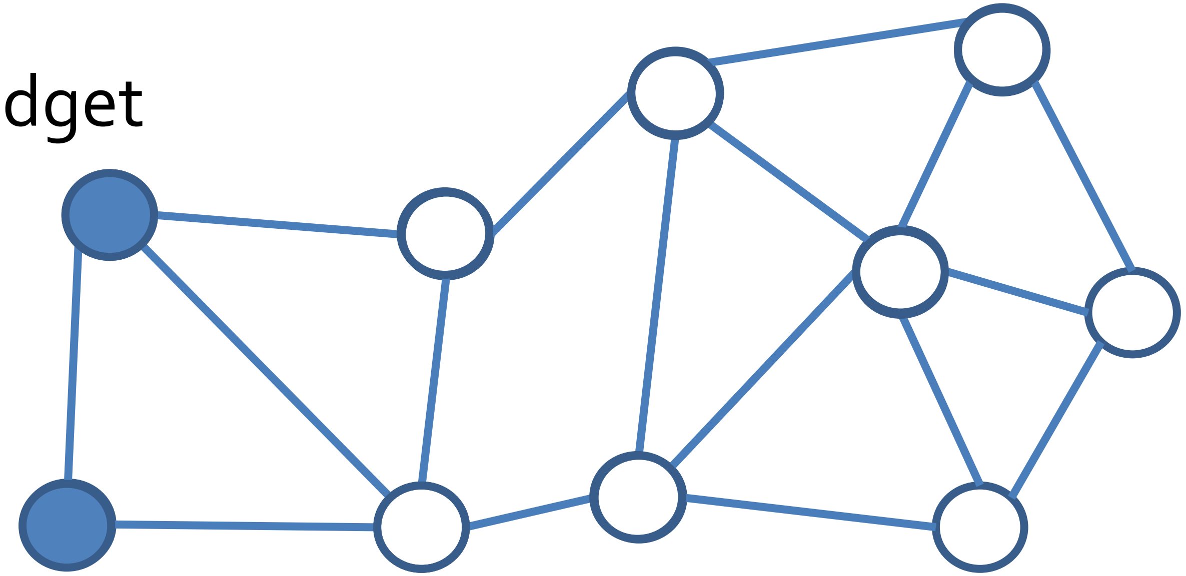


Research Question

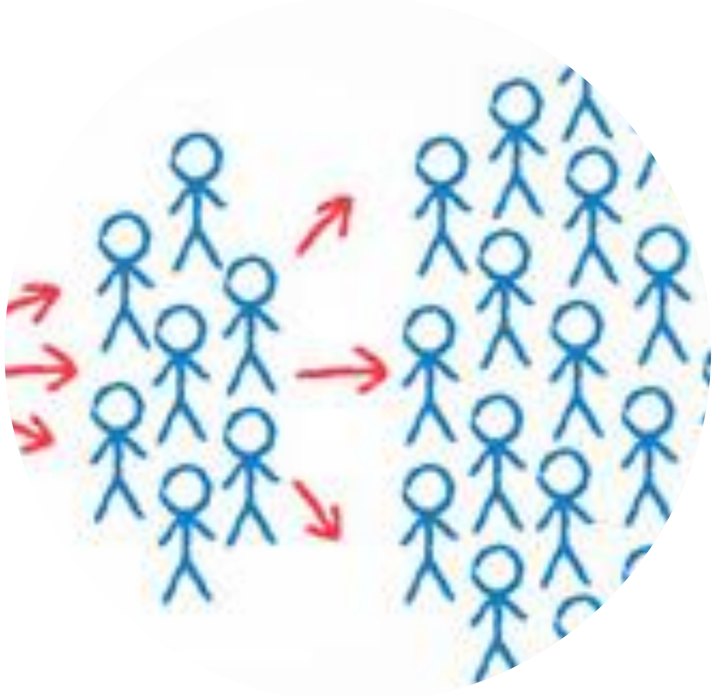
Find the best K nodes to maximize adoptions

- Input
  - Stochastic hierarchical blockmodel (SHBM)
  - r-complex contagion
  - Total number of seeds K, budget
- Output
  - Seed set I, s.t. $|I| = K$



Motivation

Can we promote good behaviors/beliefs on a social network if we only know the community structure of the network?



Outline

- Stochastic Hierarchical Blockmodel
- r-complex contagions
- Main result

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- **Stochastic Hierarchical Blockmodel**
- r-complex contagions
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Possible information about Networks

- Full information

Seattle

Boston

West coast

East coast

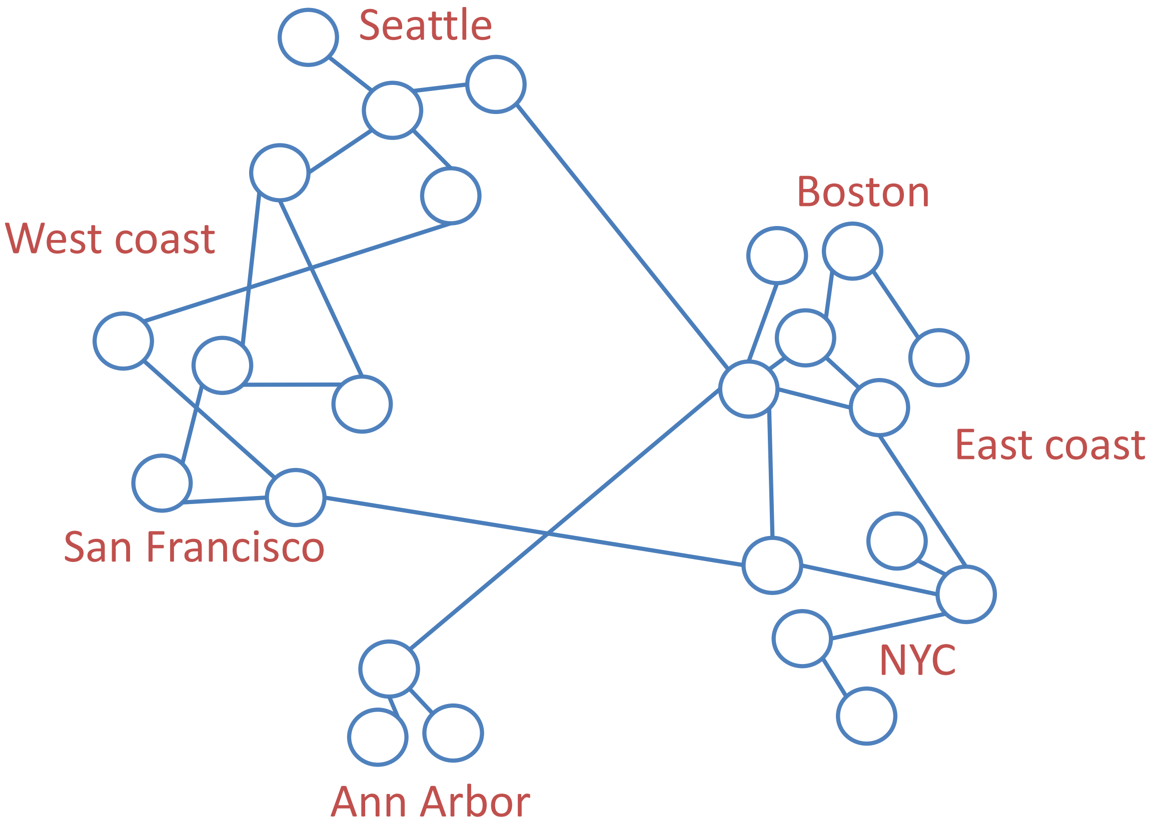
San Francisco

NYC

Ann Arbor

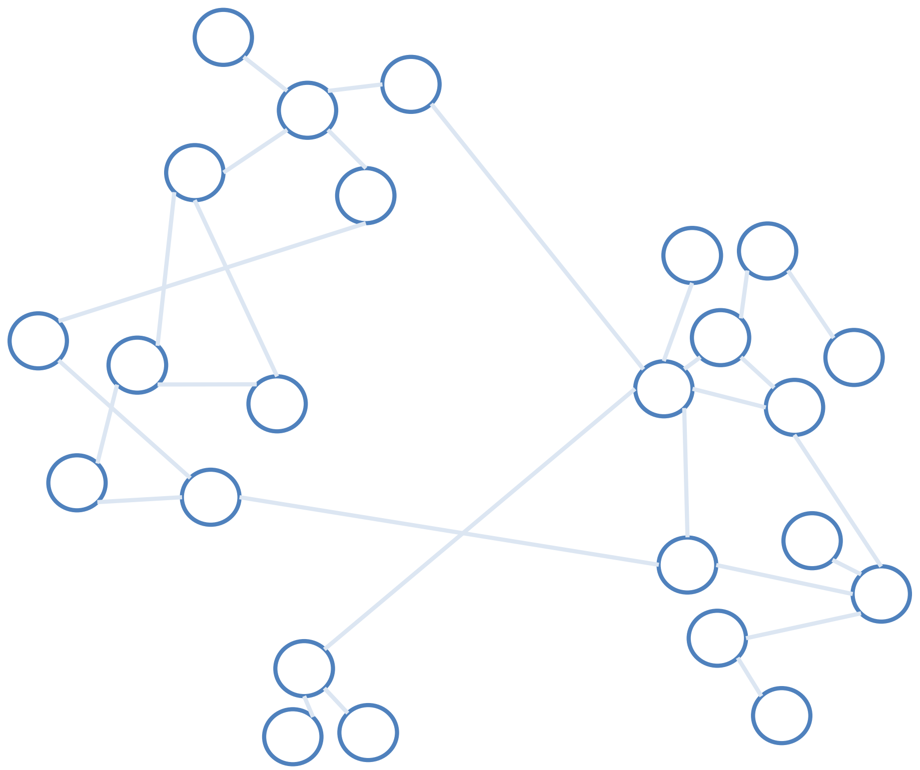
Possible information about Networks

- Full information



Possible information about Networks

- Full information
- Query
  - Edge query, node query, …



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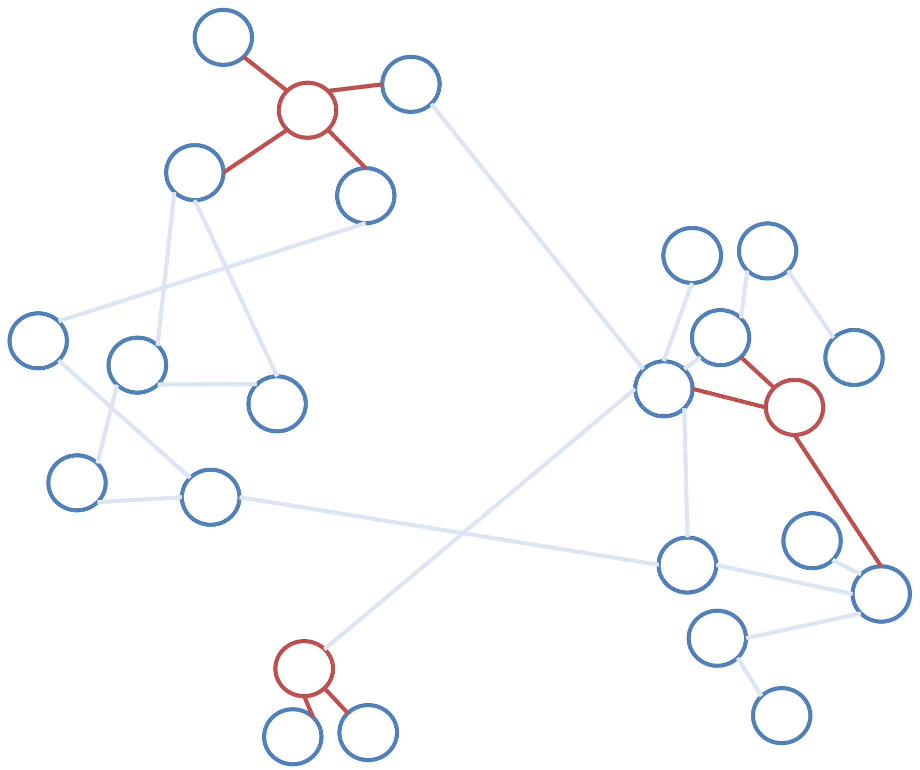
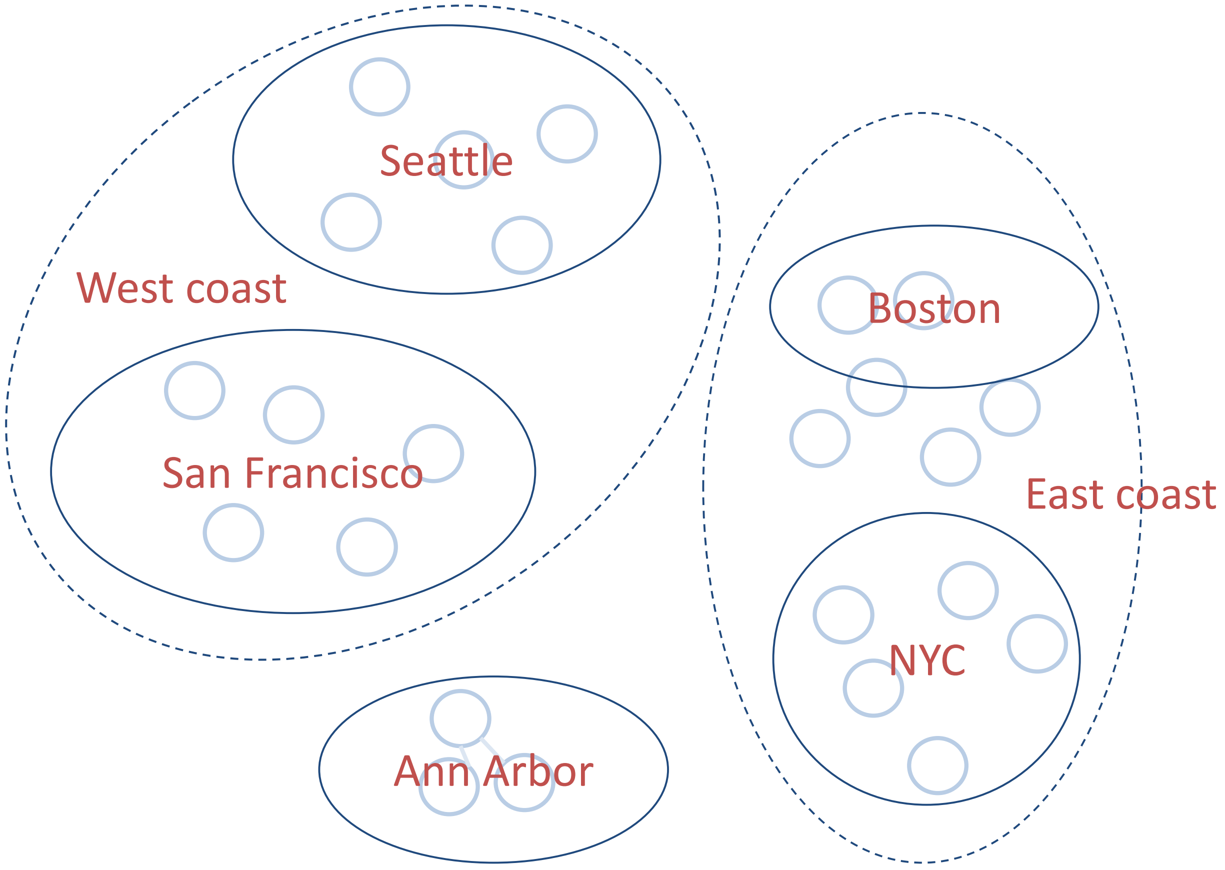


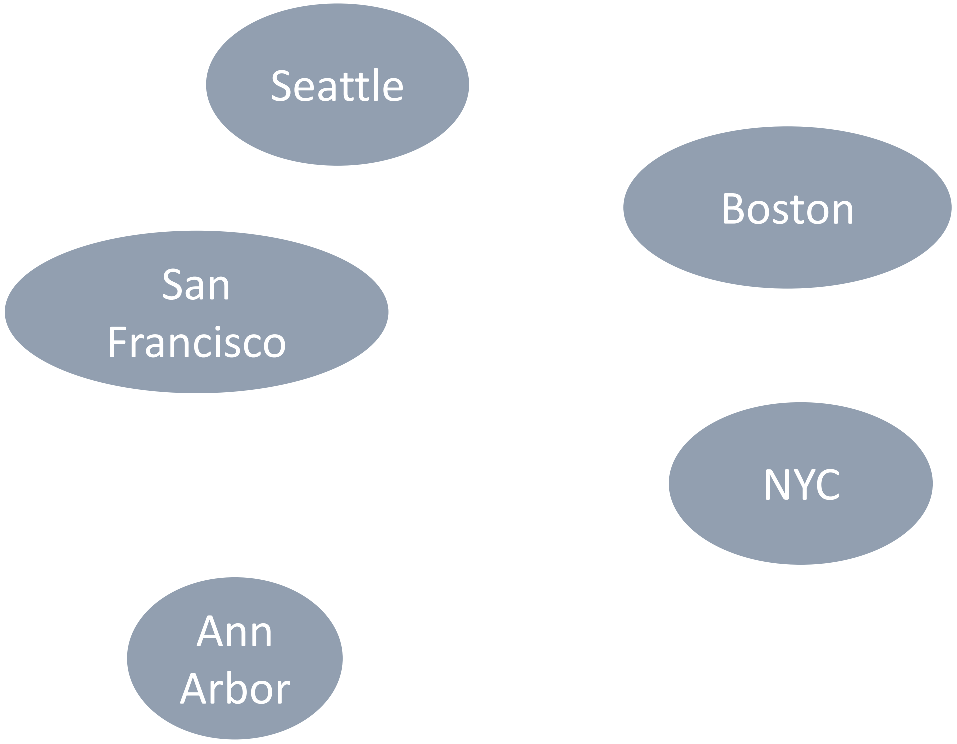
Possible information about Networks

- Full information
- Query
  - Edge query, node query, …
- Coarser information
  - Community structure,
  - Centrality,
  - Betweenness



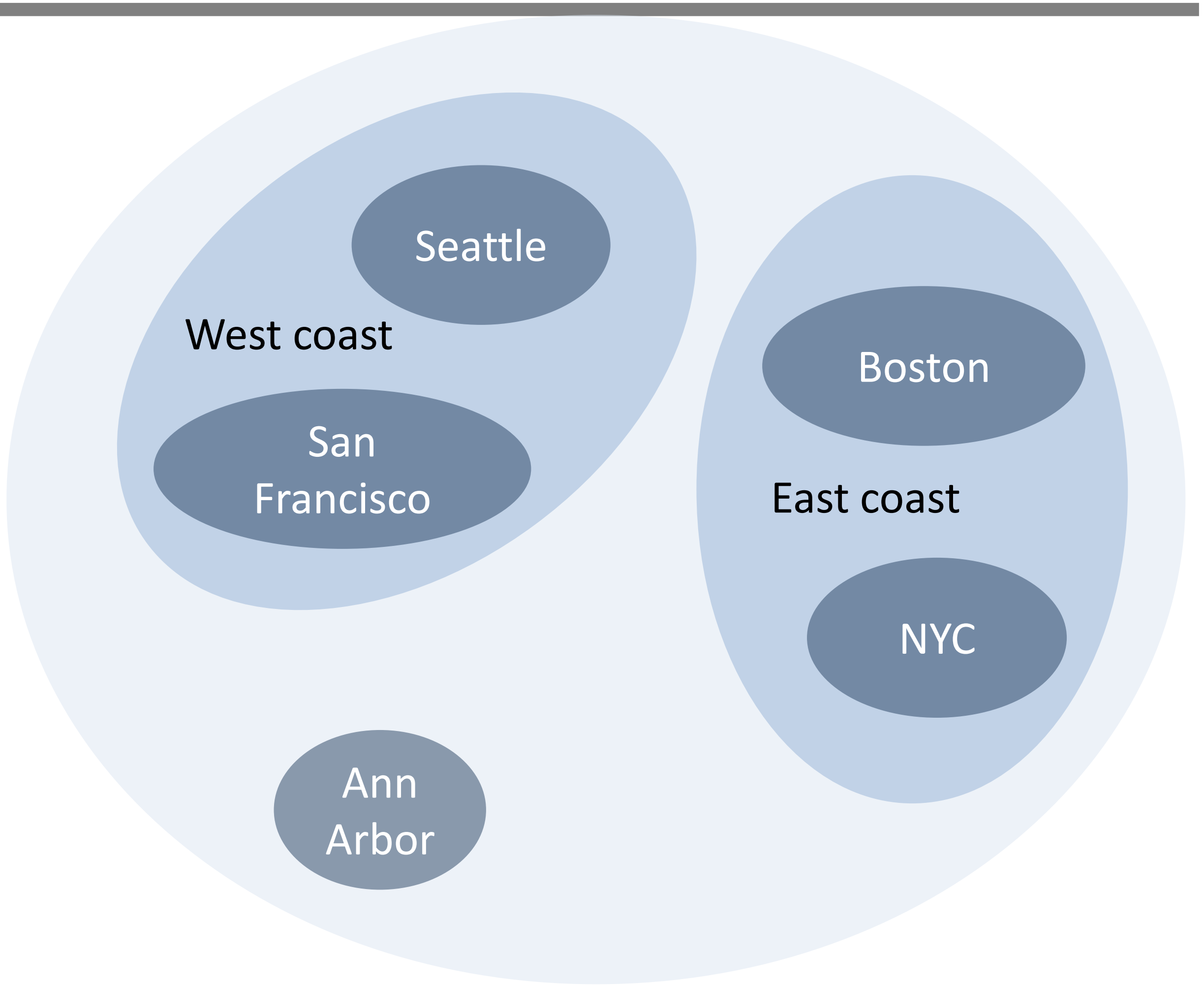
Community Structure

- Social networks often can be easily divided into communities densely connected internally.

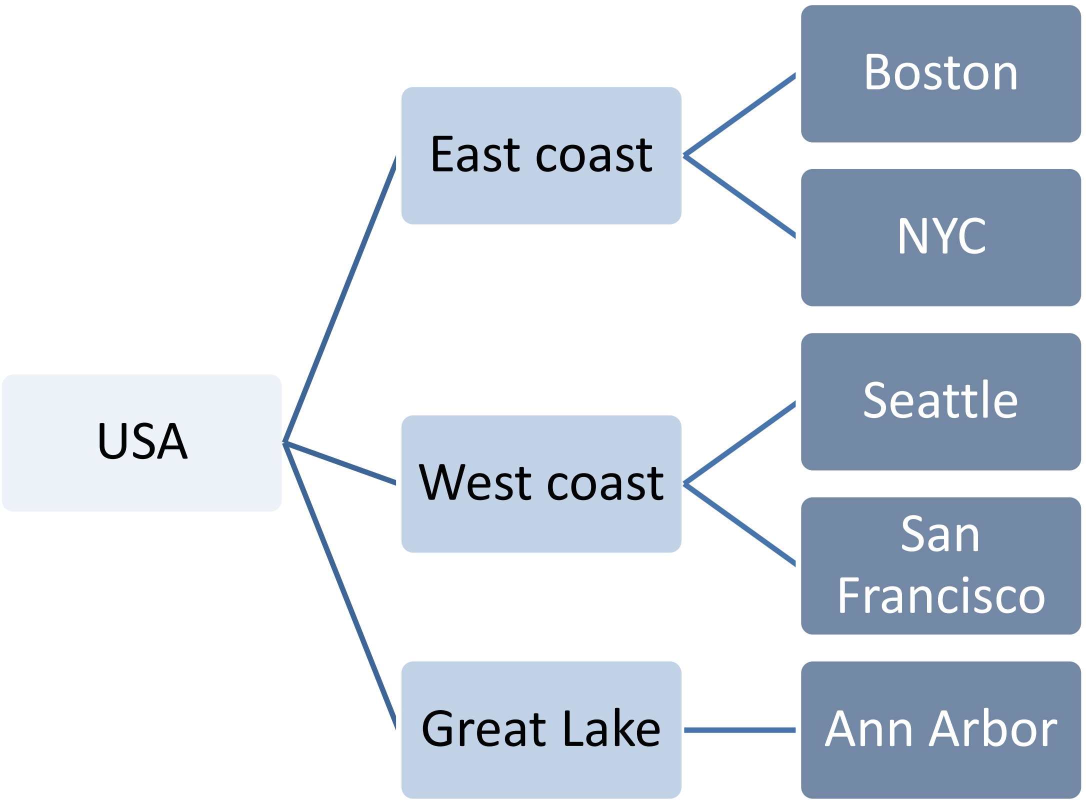


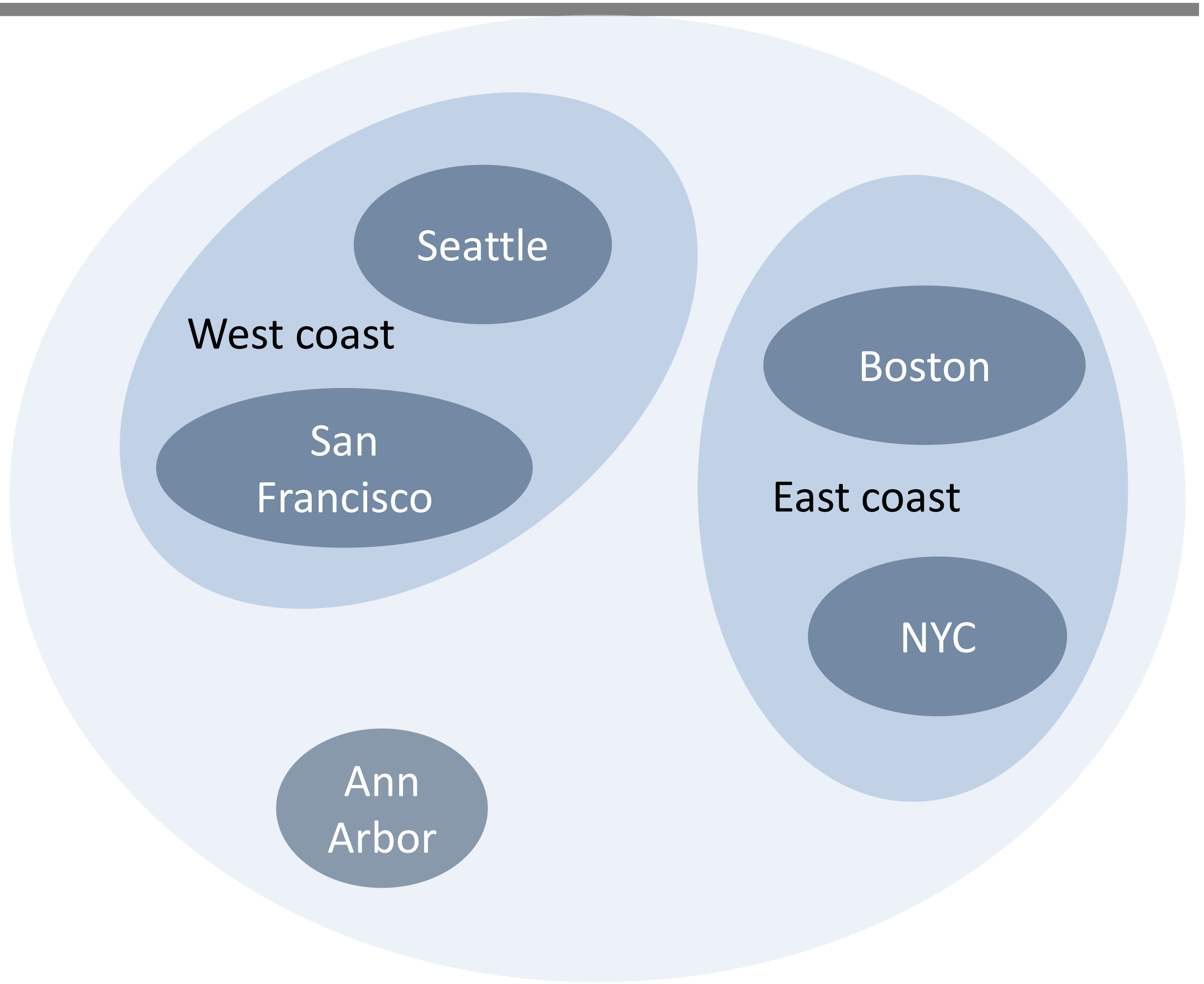
Hierarchical Community Structure

- Social networks often can be easily divided into communities densely connected internally.
- A community can be easily is divided into many sub-communities



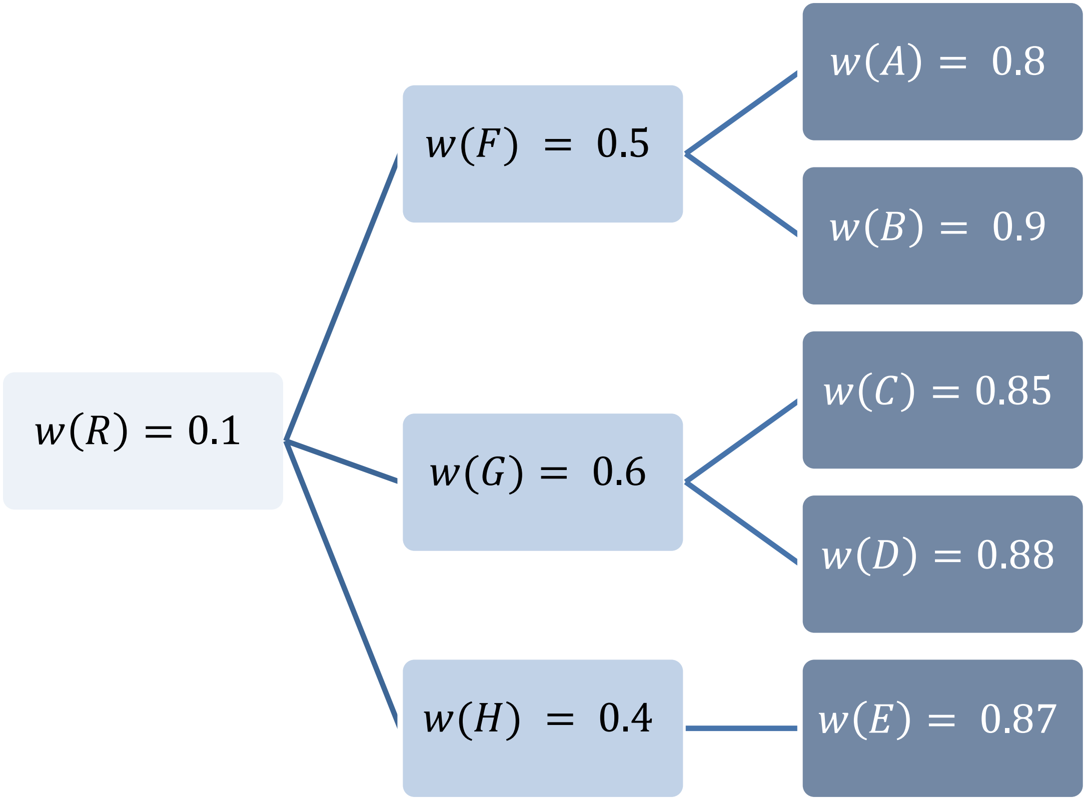
Hierarchical Community Structure



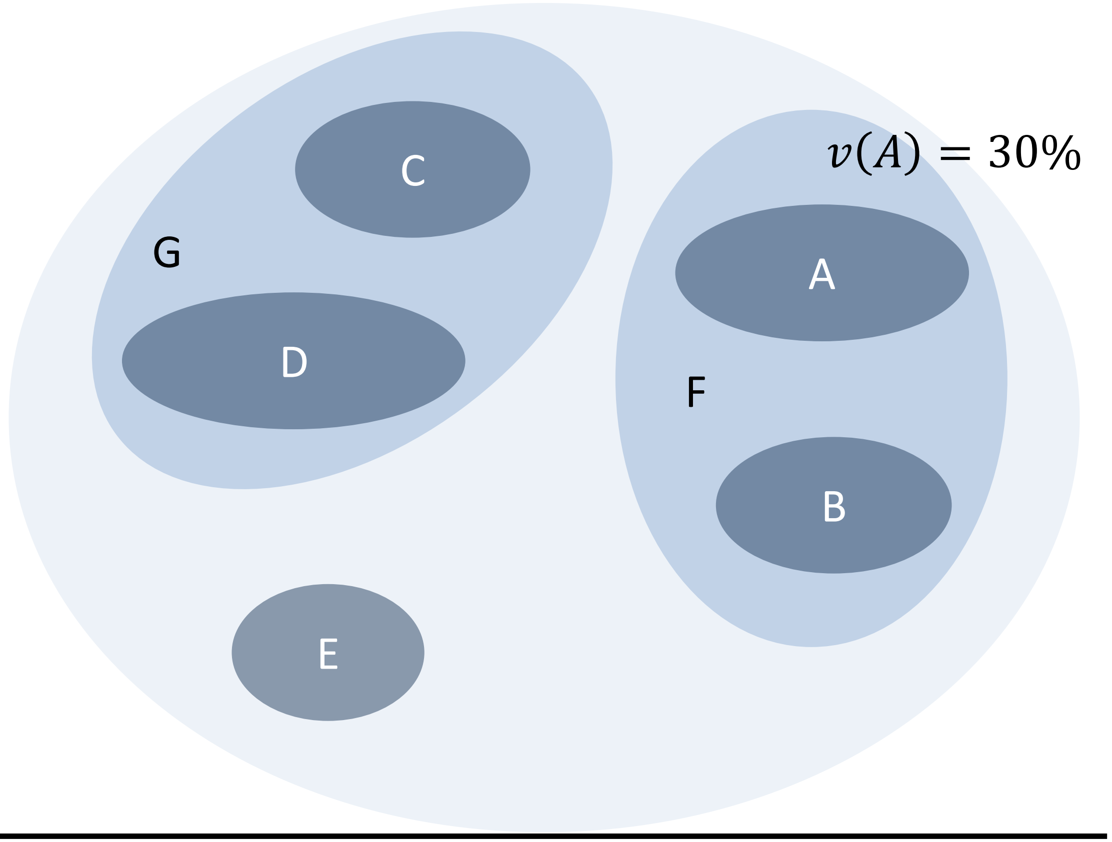


Stochastic Hierarchical Blockmodel (V_T, E_T, w, v)

Connectivity matrix w



Relative population v

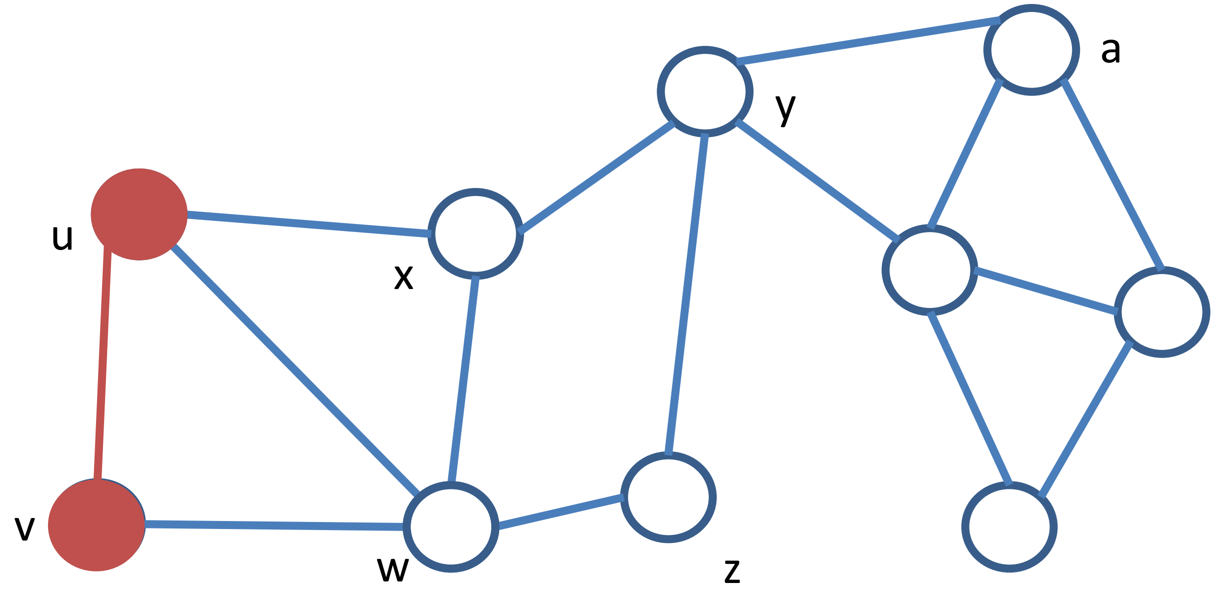


Outline

- Stochastic Hierarchical Blockmodel (SHBM)
- **r-complex contagions**
- Main result

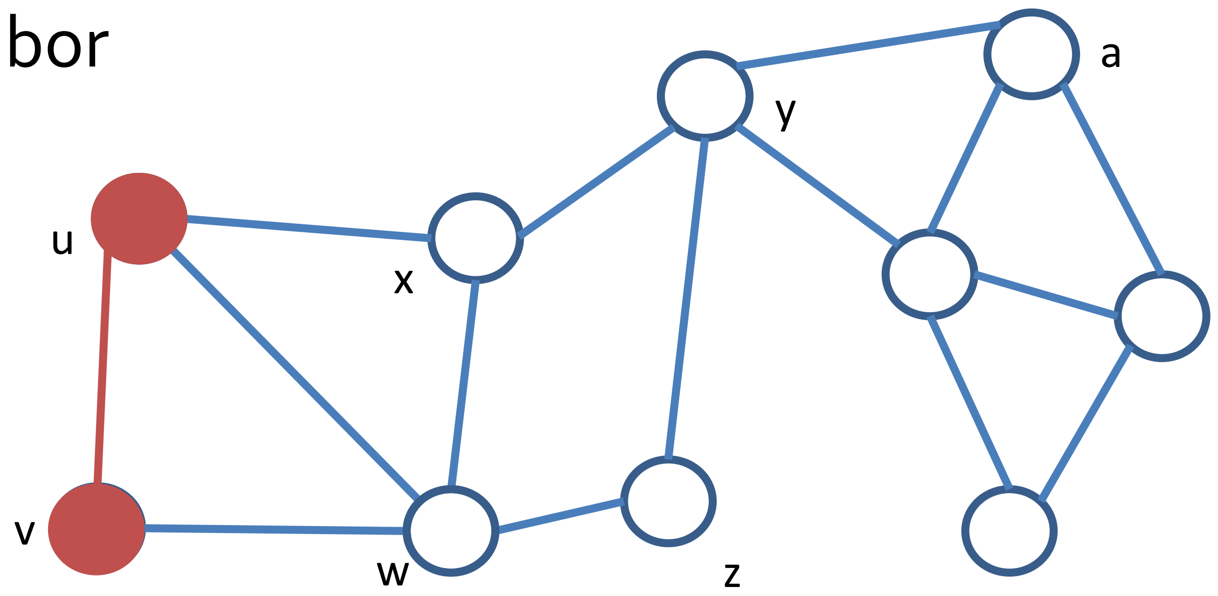
r-Complex Contagions [CLR 79; GEG13]

- Given an initial seed set $I = \{u, v\}$, and a graph G



r-Complex Contagions [CLR 79; GEG13]

- Given an initial seed set $I = \{u, v\}$, and a graph G
- Node becomes infected if it has at least $r(= 2)$infected neighbor



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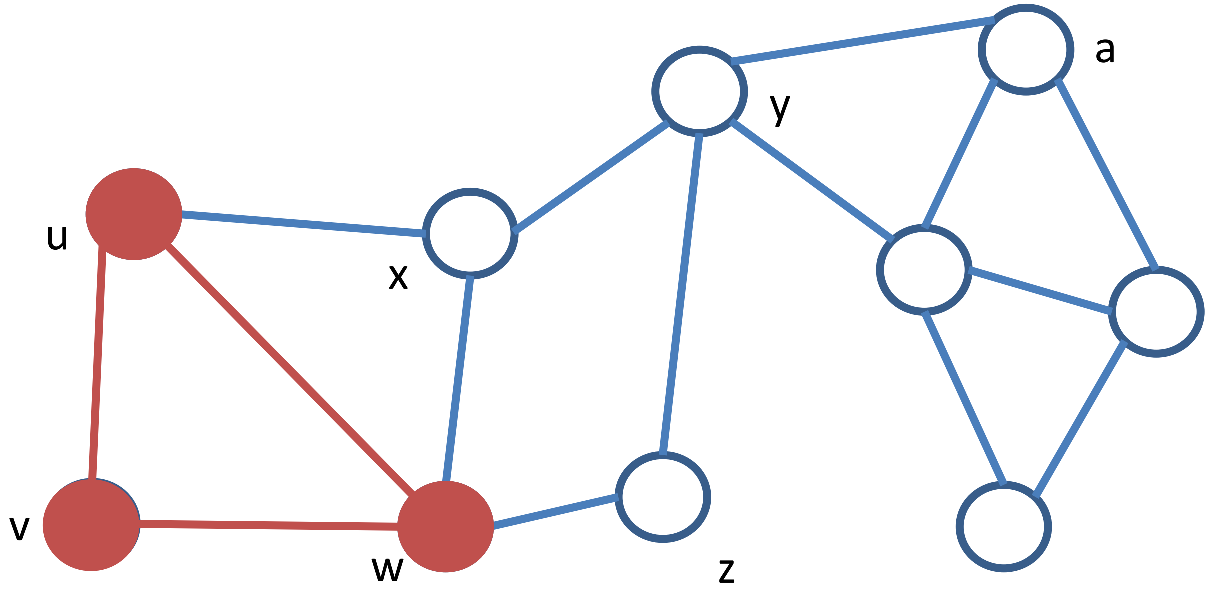

r-Complex Contagions

- Given an initial seed set $I = \{u, v\}$, and a graph G
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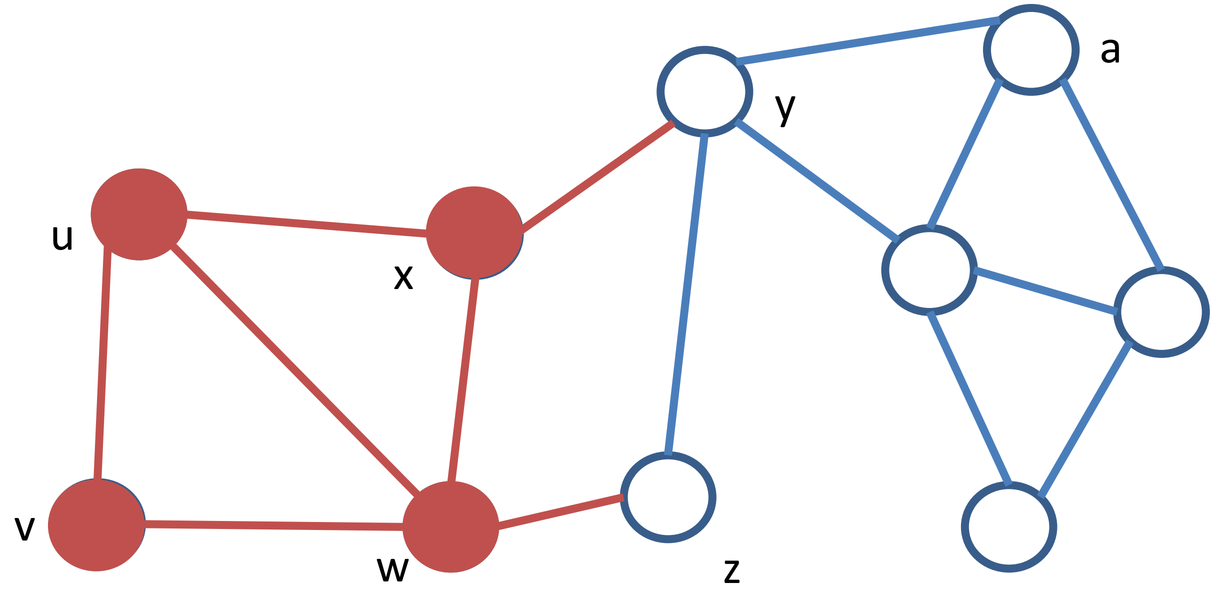
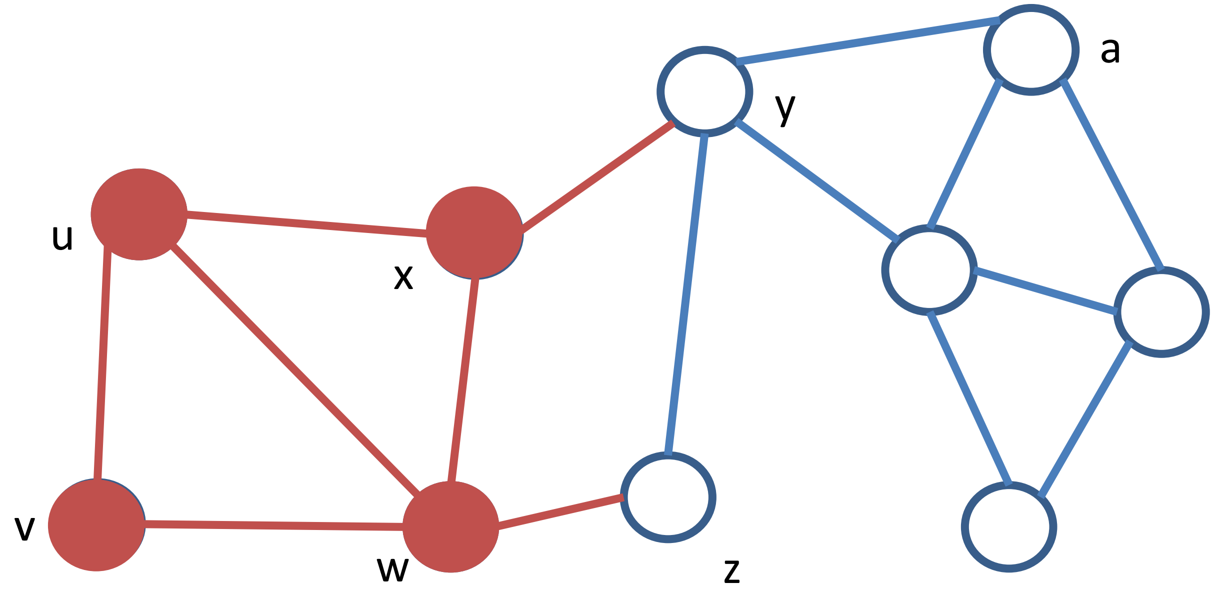
Local activation function $f_v(x) = \mathbb{I}[x \geq r]$



r-Complex Contagions

- Given an initial seed set $I = \{u, v\}$, and a graph G
- Node becomes infected if it has at least r infected neighbor
- The total number of infected vertices $\sigma_{r,G}(I)$

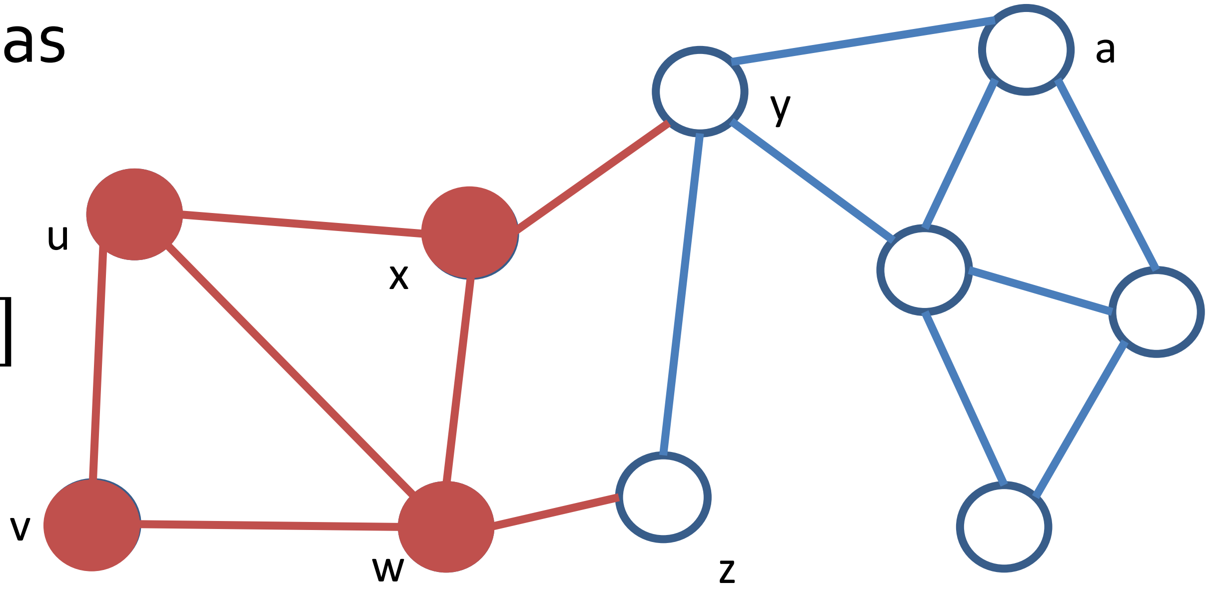
$f_v(x) = \mathbb{I}[x \geq r]$
$\sigma_{r,G}(I)$



r-Complex Contagions

- Given an initial seed set $I = \{u, v\}$, and a distribution over graphs, $\mathcal{g}$, e.g., SHBM.
- Node becomes infected if it has at least r infected neighbor
- The total number of infected vertices $\sigma_{r,\mathcal{g}}(I) = \mathbb{E}_{\mathcal{g}}[\sigma_{r,G}(I)]$

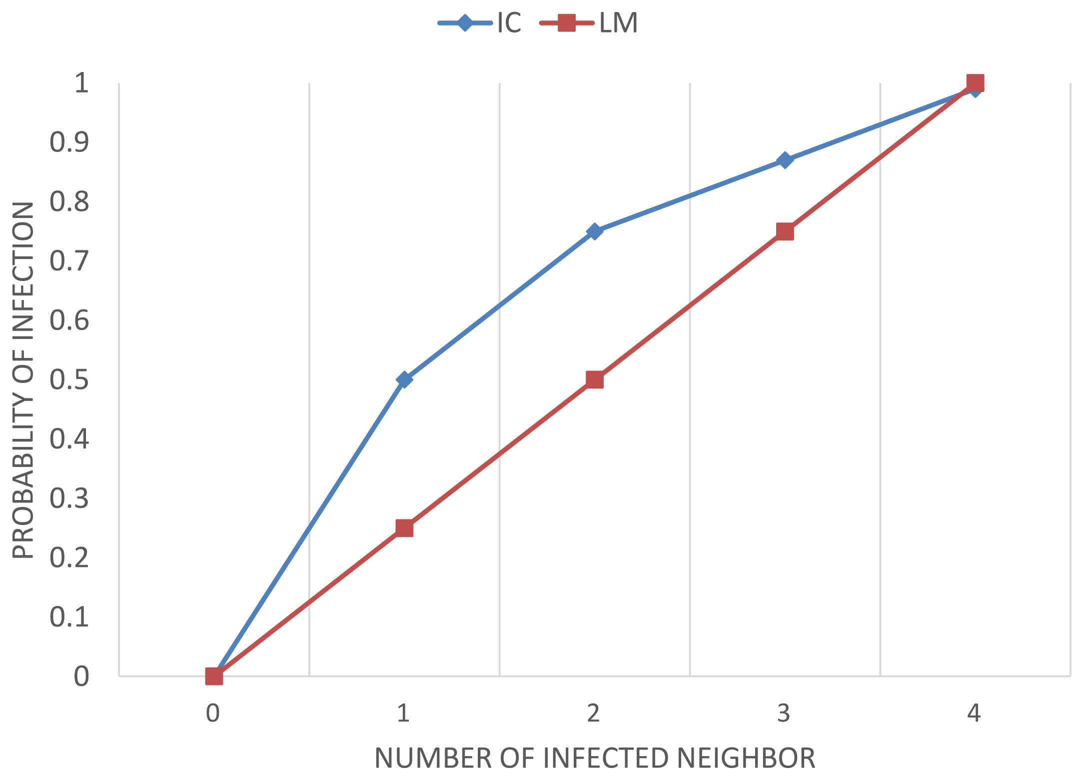
$$(r, G, I) \mapsto \sigma_{r,G}(I)$$



Nonsubmodular vs Submodular InfMax

Submodular InfMax

- linear threshold, independent cascade
- Complexity:
  - $(1 - 1/e)$-approximation



For all $A \subset B \subseteq V$, and $x \in V$
$$f_v(A \cup \{x\}) - f_v(A) \geq f_v(B \cup \{x\}) - f_v(B)$$

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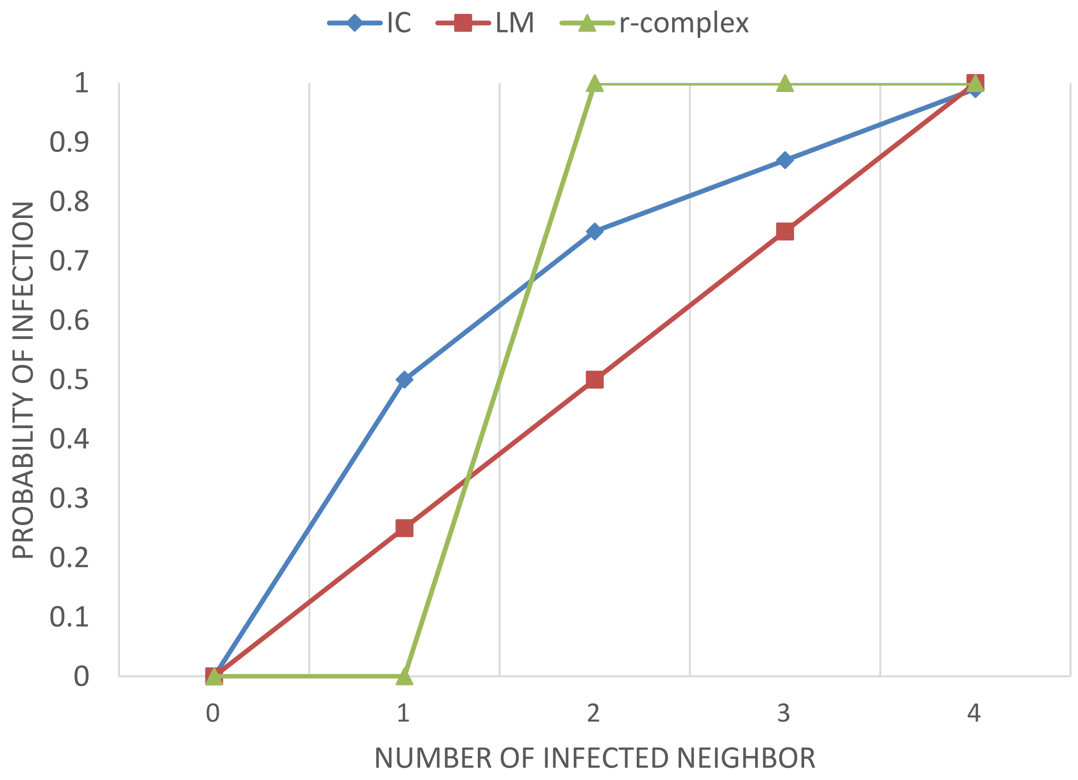

Nonsubmodular vs Submodular InfMax

Submodular InfMax

- linear threshold, independent cascade
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Nonsubmodular InfMax

- r-complex contagions, general threshold model
- Complexity:
  - NP-hard to approximate within $n^{1-\epsilon}$ [KKT03]
  - NP-hard to approximate within $n^{1-\epsilon}$ on SHBM if nodes can have different thresholds r [ST17]

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Find the best K nodes to maximize adoptions

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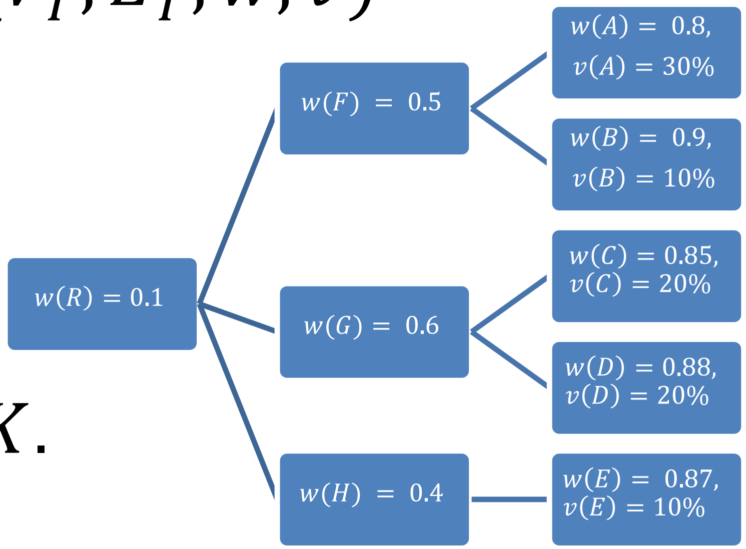

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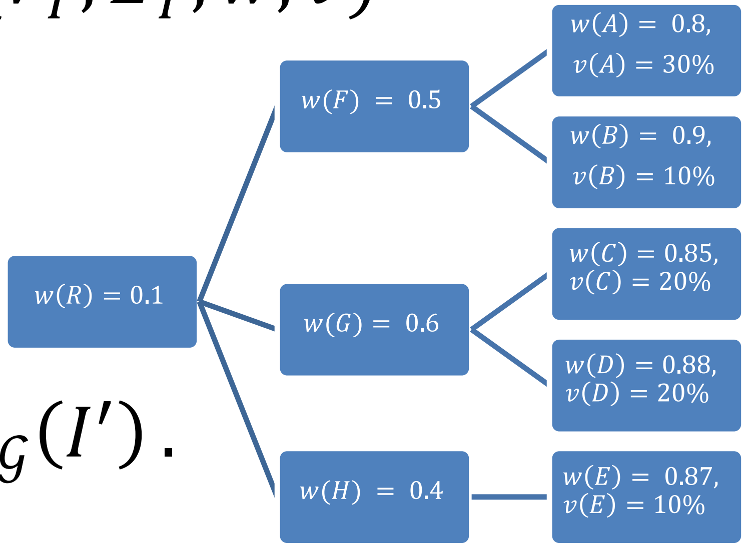
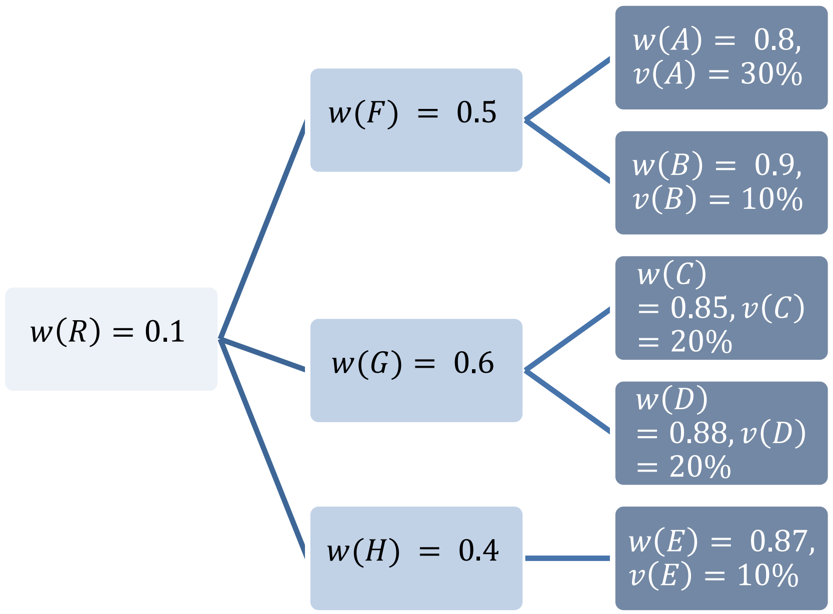


Main result

Given r, budget K, and a SHBM (V_T, E_T, w, v) with $n \to \infty$, we should put all seed into a community

$$t^* = \arg\max v(t)n \cdot w(t)^r$$

- Large communities
- Proper separation
- Dense tree



Observation 1

- Does r-complex contagion spread with constant number on Erdős-Rényi Graph $\mathcal{G}(n,p)$? [JLTV12]

Subcritical	$p = o\left(\frac{1}{n^{\frac{1}{r}}}\right)$	doesn't spread
Critical	$p = \frac{c}{n^{\frac{1}{r}}}$	spread with constant probability
Supercritical	$p = \omega\left(\frac{1}{n^{\frac{1}{r}}}\right)$	spread with high probability

Main Result

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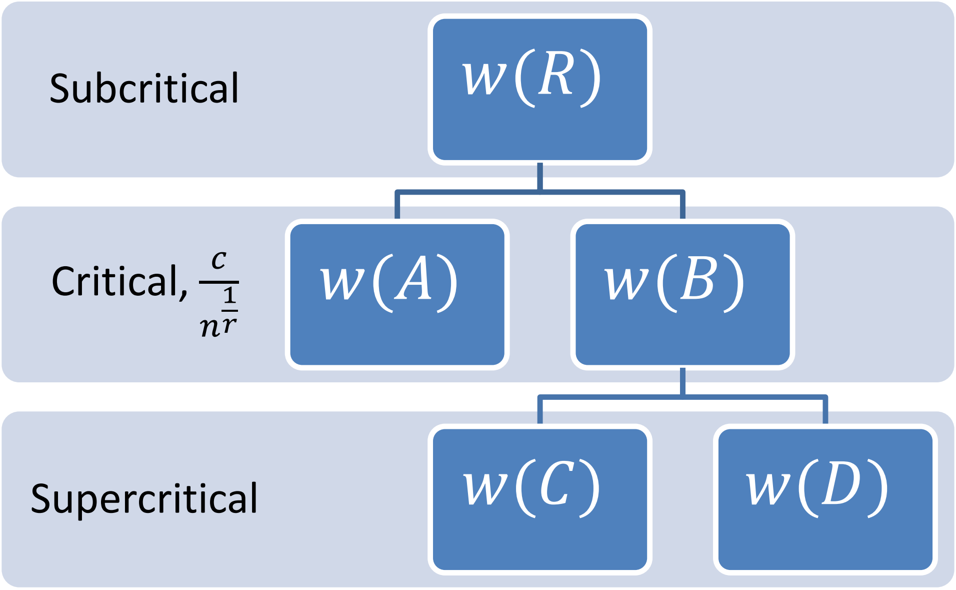

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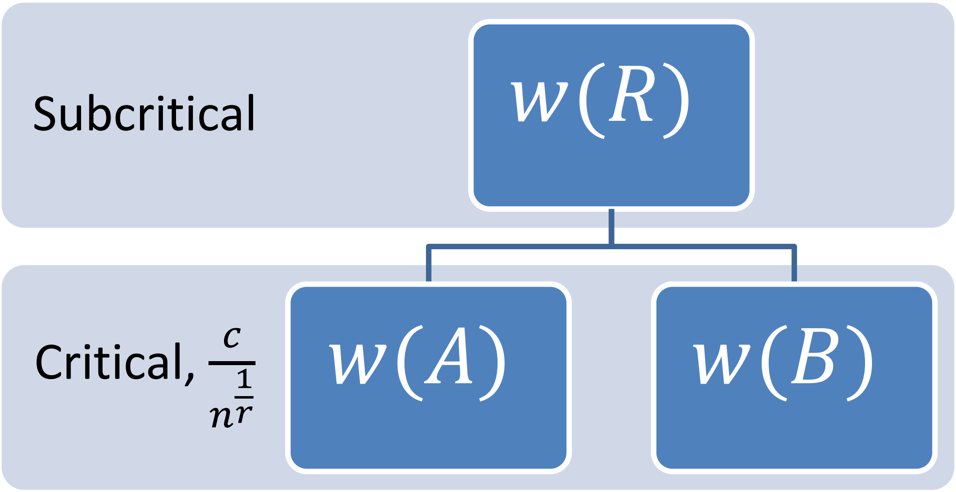


Observation 2

Given two isolated $G(n,p)$ with $p = cn^{-1/r}$, and budget K, to maximize the infection you should:

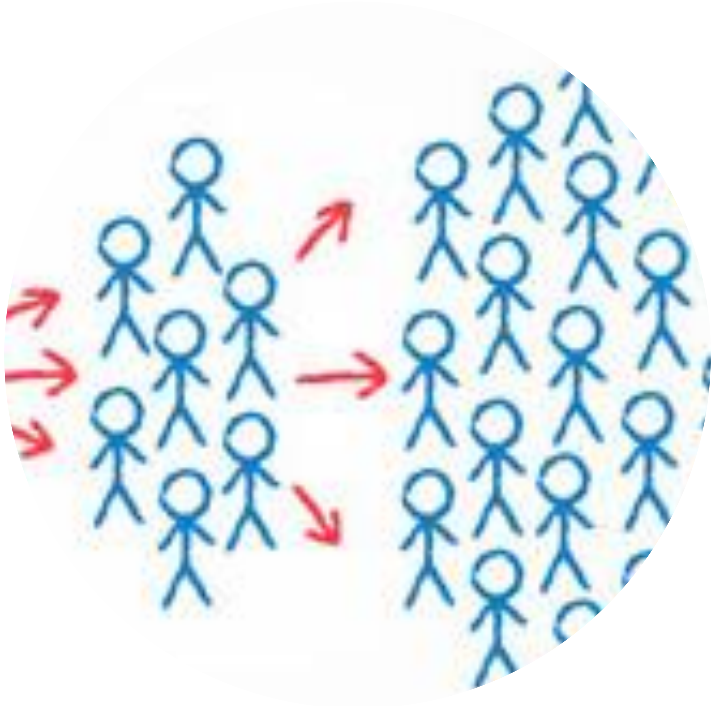
1) Go all in $(K,0)$
2) Hedge your bet: $(K/2, K/2)$

Take-Home Messages

- For nonsubmodular influence maximization (e.g., r-complex contagion), putting seeds together to create synergy is more beneficial.
- In sharp contrast to submodular influence maximization (e.g., Linear Threshold, Independent Cascade) where we should spread the seeds to avoid waste of seeds' power.

Open Problems on Influence Maximization

- Information about graphs
  - Community structure, Centrality, Betweenness
  - Node query, Edge query
- Beyond submodular contagions models
  - r-complex contagions
  - general threshold [GGSY16]
  - 2-quasi-submodular [ST17]

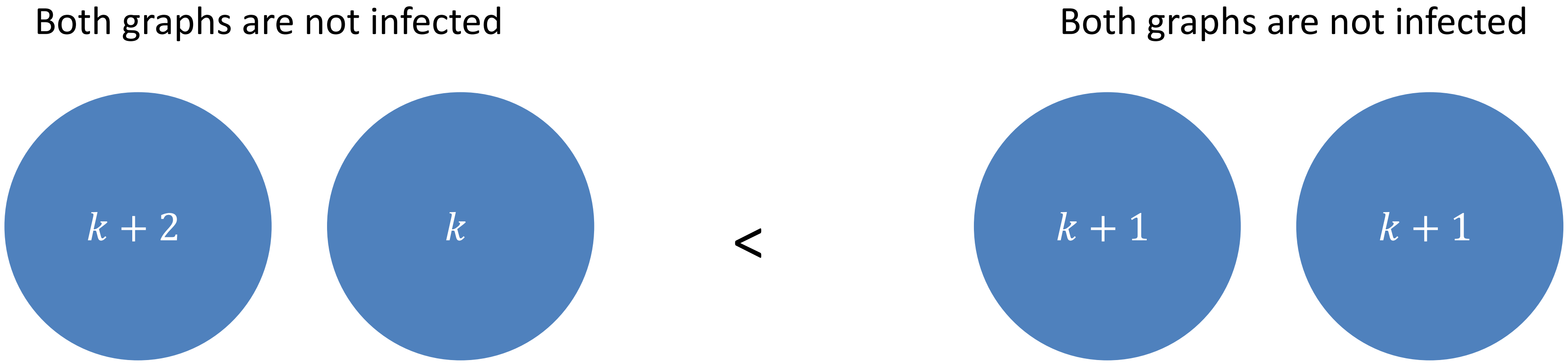


Technical Lemma

Let E_k^n: the event that k seeds *do not* infected the graph $G(n, p)$ with $p = cn^{-1/r}$. For all $k \geq r - 1$

$$\Pr(E_{k+2}^n) \Pr(E_k^n) < \Pr(E_{k+1}^n) \Pr(E_{k+1}^n)$$

as $n \to \infty$.



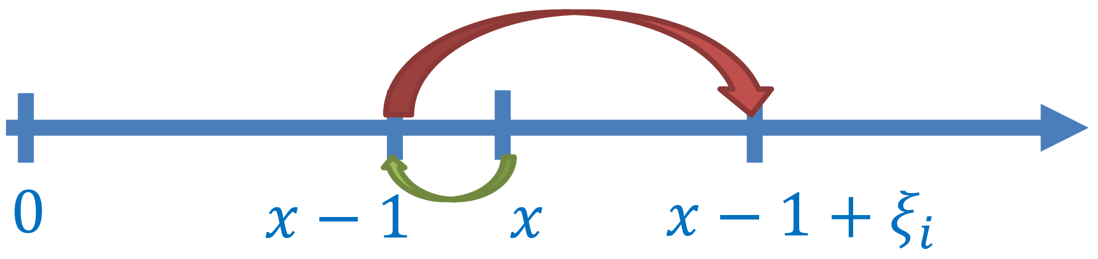
Erdős-Rényi Graphs $\mathcal{G}(n,p)$ with $p = cn^{\frac{-1}{r}}$

Equivalent (when $n \to \infty$)
inhomogeneous random walk on $\mathbb{R}$:

- Start at $x = k$;
- In each iteration i:
  - move to the left by 1 unit;
  - sample $\xi_i \sim \text{Poisson}\left(\binom{i-1}{r-1} \cdot c^r\right)$, move to right by ξ_i units;
- Terminate if hits $x = 0$;

Two cases:

- Hit $x = 0$: not infected, E_k^n
- Go to infinity: infected



Back to our technical lemma

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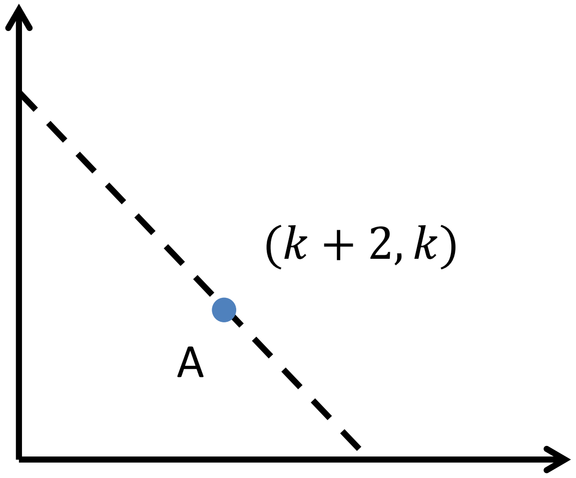
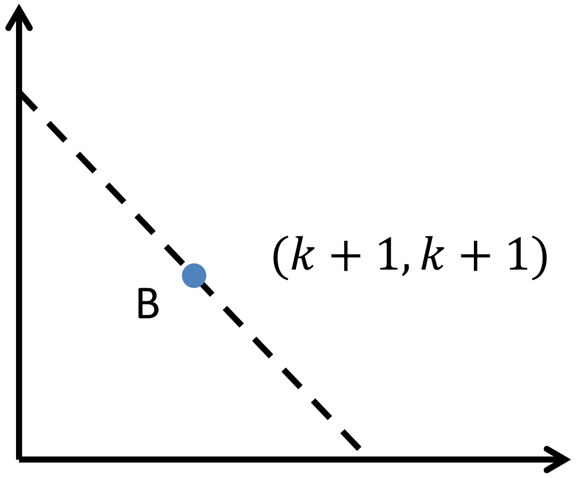
$$\Pr(E_{k+2}^n)\Pr(E_k^n) < \Pr(E_{k+1}^n)\Pr(E_{k+1}^n)$$

Both graphs are not infected

as $n \to \infty$.



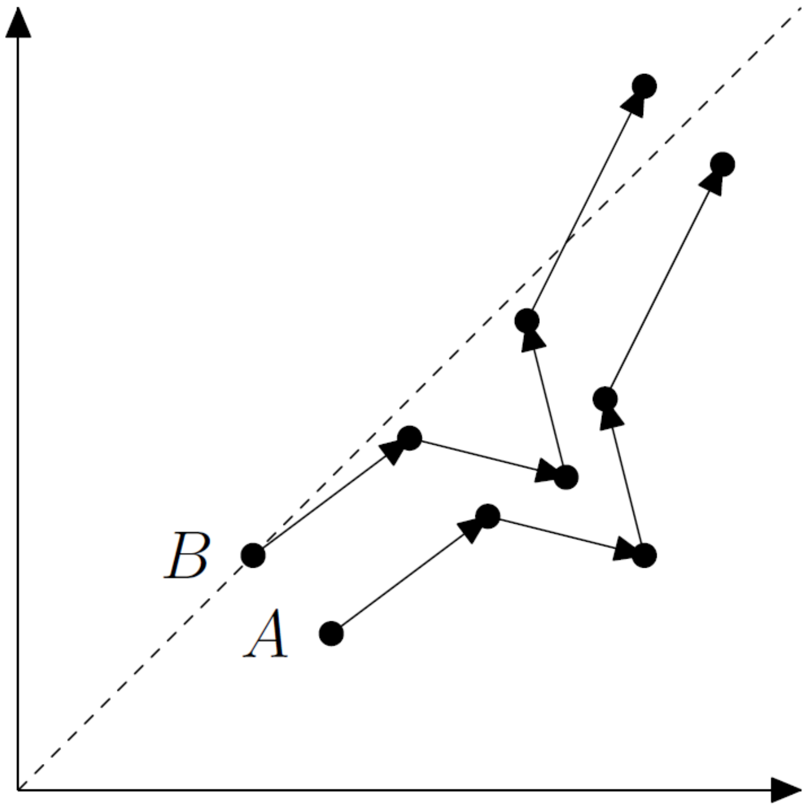


Hit $(0{,}0)$

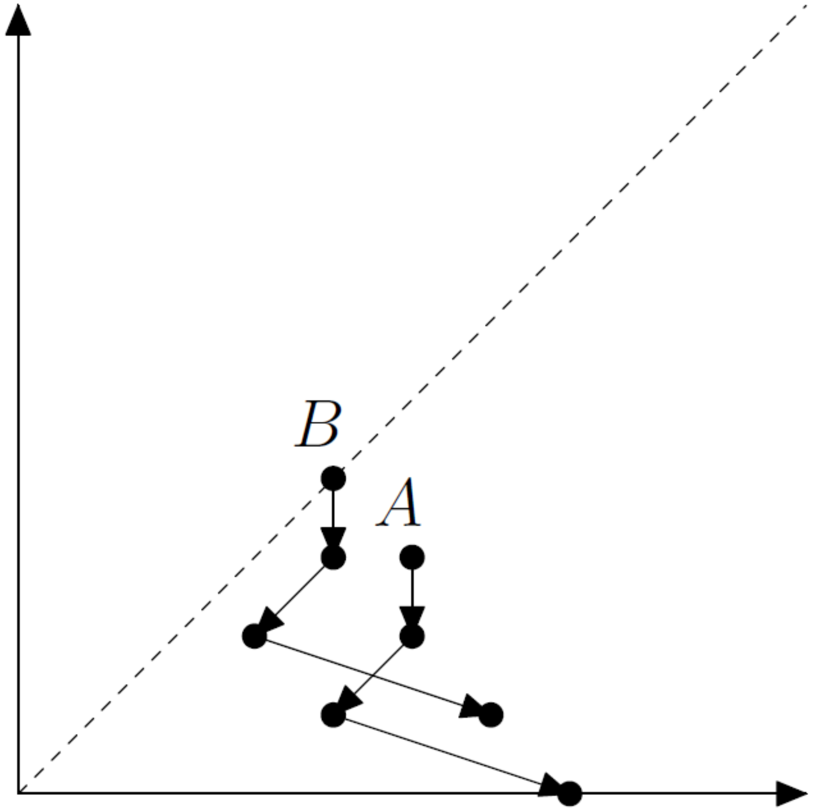
A coupling argument

We couple the two walks A, B in the same way until...

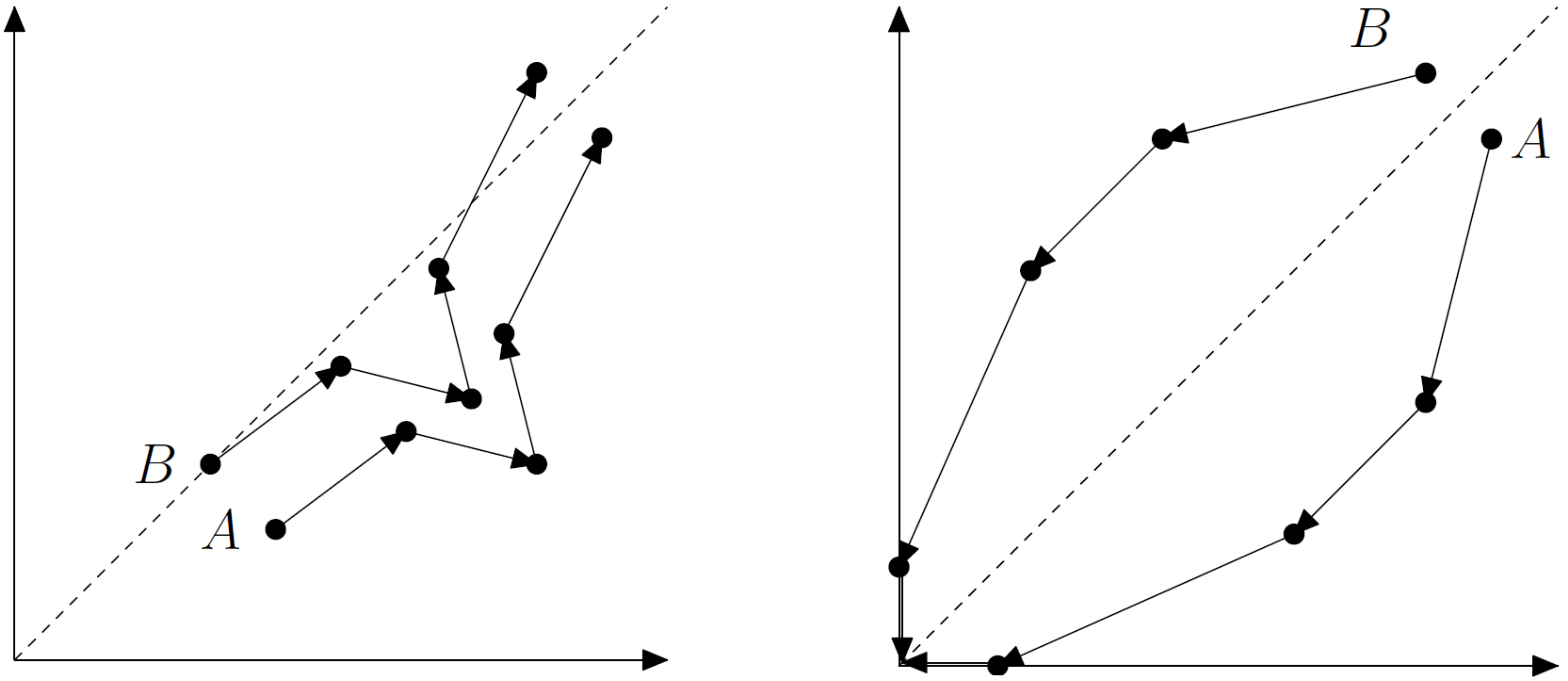
A, B are symmetric, $\mathcal{E}_{symm}$



A hits the x-axis, $\mathcal{E}_{skew}$



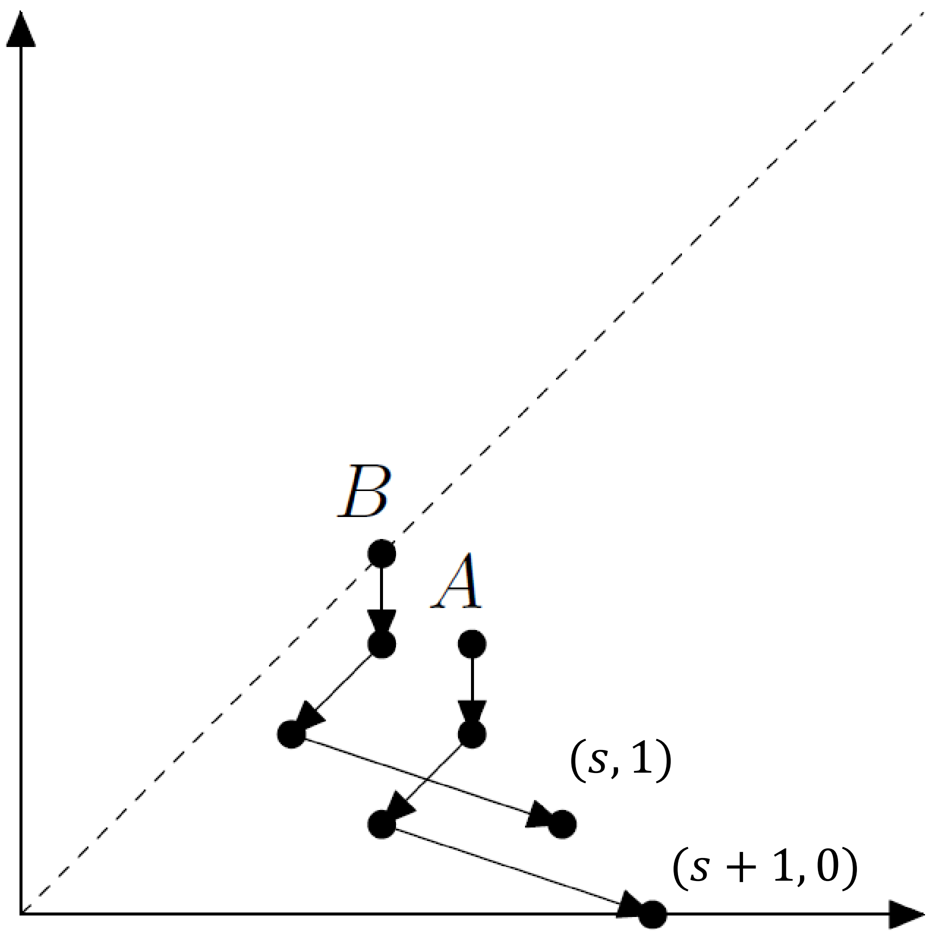
When A, B are symmetric to $y = x$, $\mathcal{E}_{symm}$



When A hits the x-axis, $\mathcal{E}_{skew}$

- Both needs to move $S+1$ units to reach $(0,0)$.
  - A: $S+1$ steps *sequentially*.
  - B: S steps in x-direction and 1 step in y-direction *in parallel*.
- B is easier to reach $(0,0)$, as the Poisson mean is increasing.

$$\xi_i \sim \text{Poisson}\left(\binom{i-1}{r-1} \cdot c^r\right)$$



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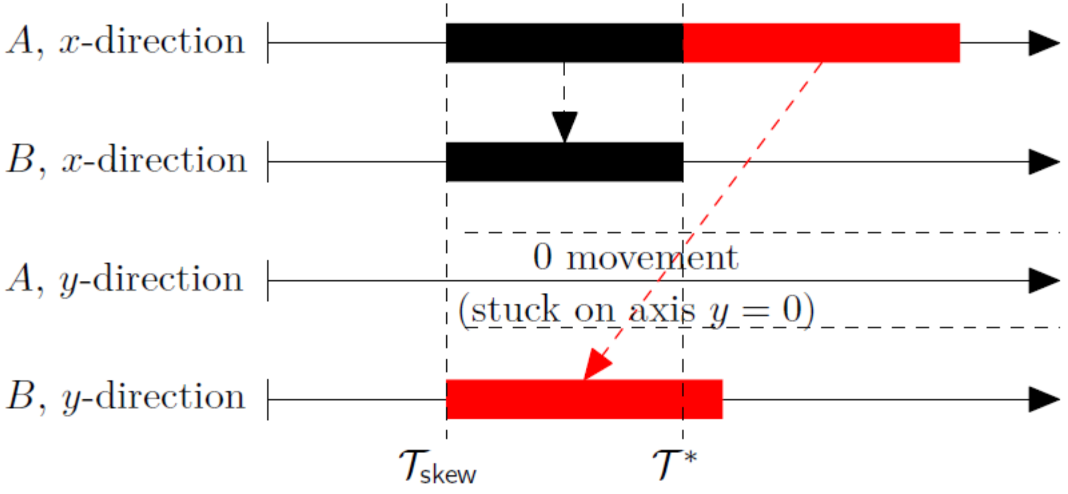
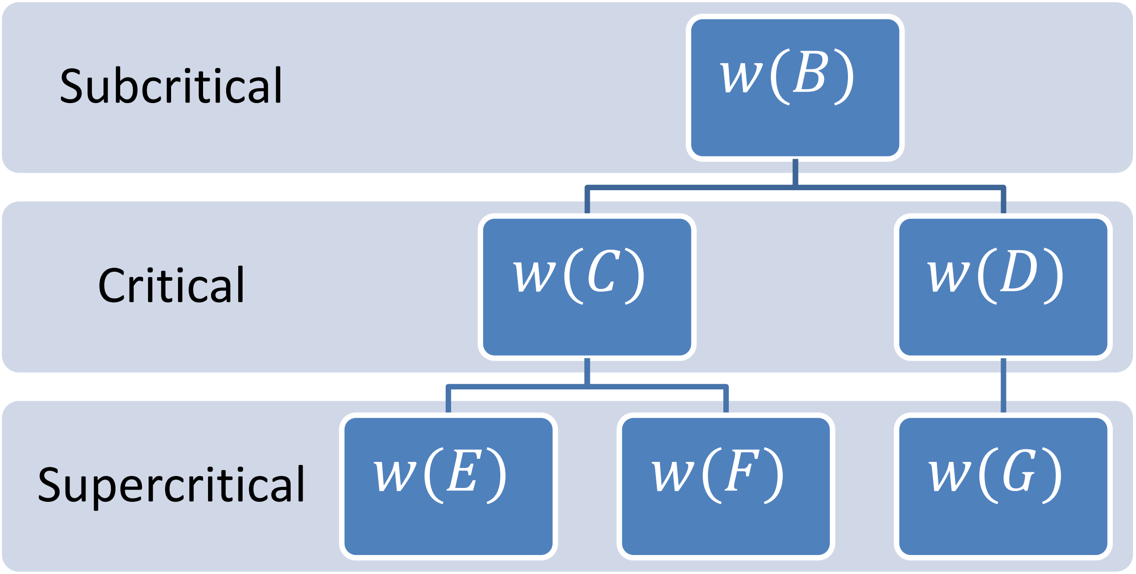


The time line for the coupling after event $\mathcal{E}_{\text{skew}}$ happens.

Beyond Dense Tree

- Find the densest community



Beyond Dense Tree

- Decompose into dense subtree
  - Find the densest community
  - Dynamic programming