

# Models of Influence

Introduction to Network Science

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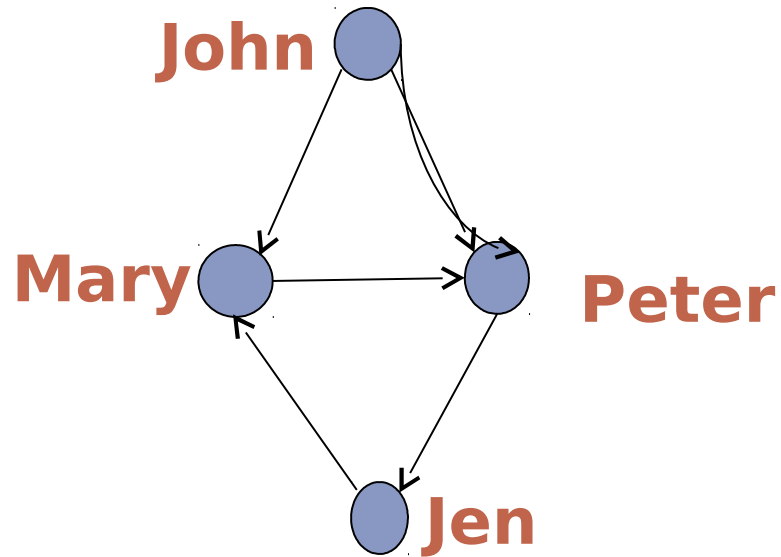
Topic 25

# Sources

- Easley and Kleinberg (2010): Networks, Crowds, and Markets [Ch 19](#)
- Carlos Castillo, Wei Chen, Laks V. S. Lakshmanan (2012): Information and Influence Spread in Social Networks, [KDD Tutorial](#).
- Carlos Castillo (2017): [Social influence](#) slides

# What are our observables?

**Graph**: users,  
links/ties



**Log**: user, action,  
time

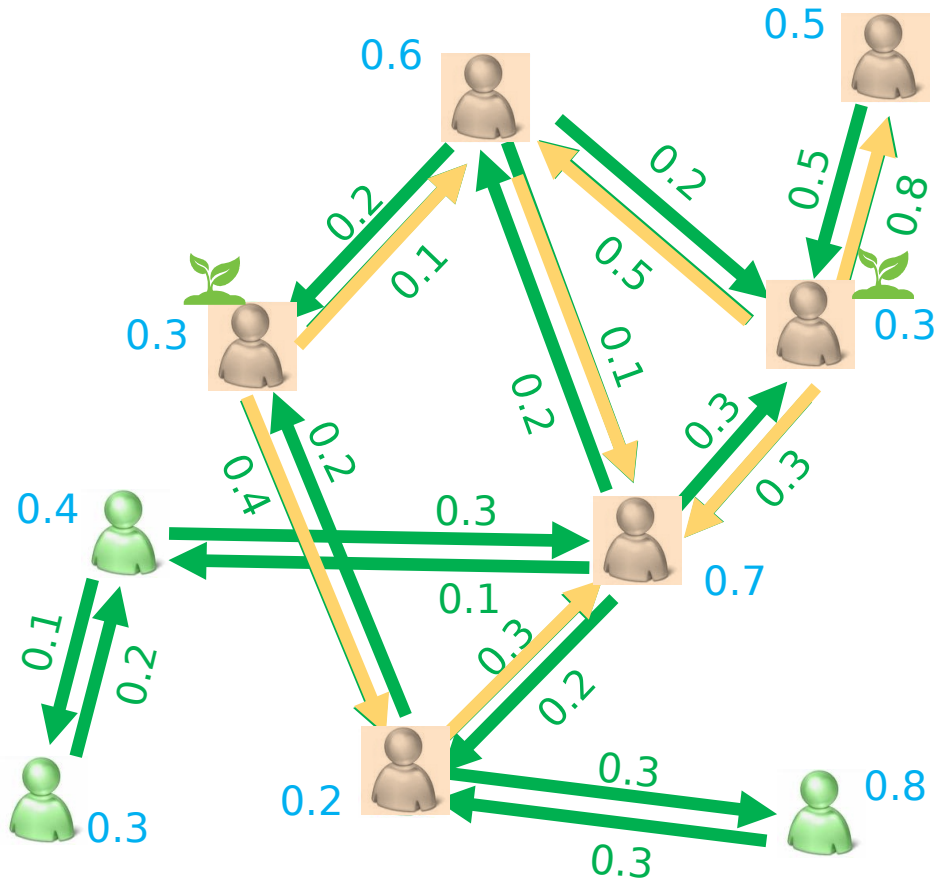
User	Action	Time
John	Rates with 5 stars <i>"The Artist"</i>	June 3 <sup>rd</sup>
Peter	Watches <i>"The Artist"</i>	June 5 <sup>th</sup>
Jen	...	...

# Two main models

- Linear threshold model
- Independent cascade model

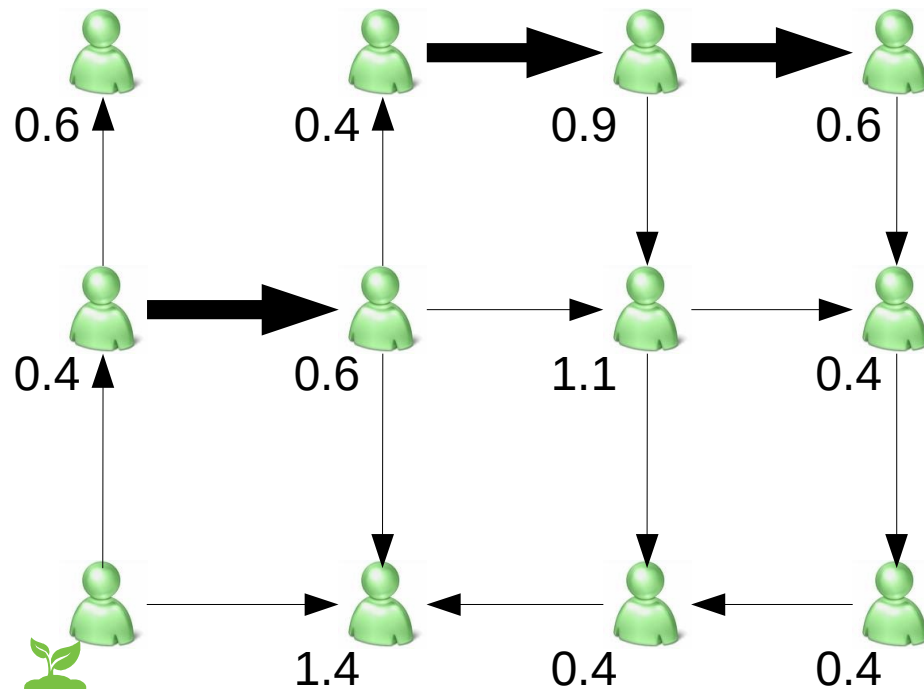
# Linear threshold model

- Nodes have thresholds
- Arcs have weights
- Nodes that receive weighted influence equal or above their threshold become active



# Exercise

Add your results to this  
[Google Spreadsheet](#)  
(Sheet: Linear Threshold)



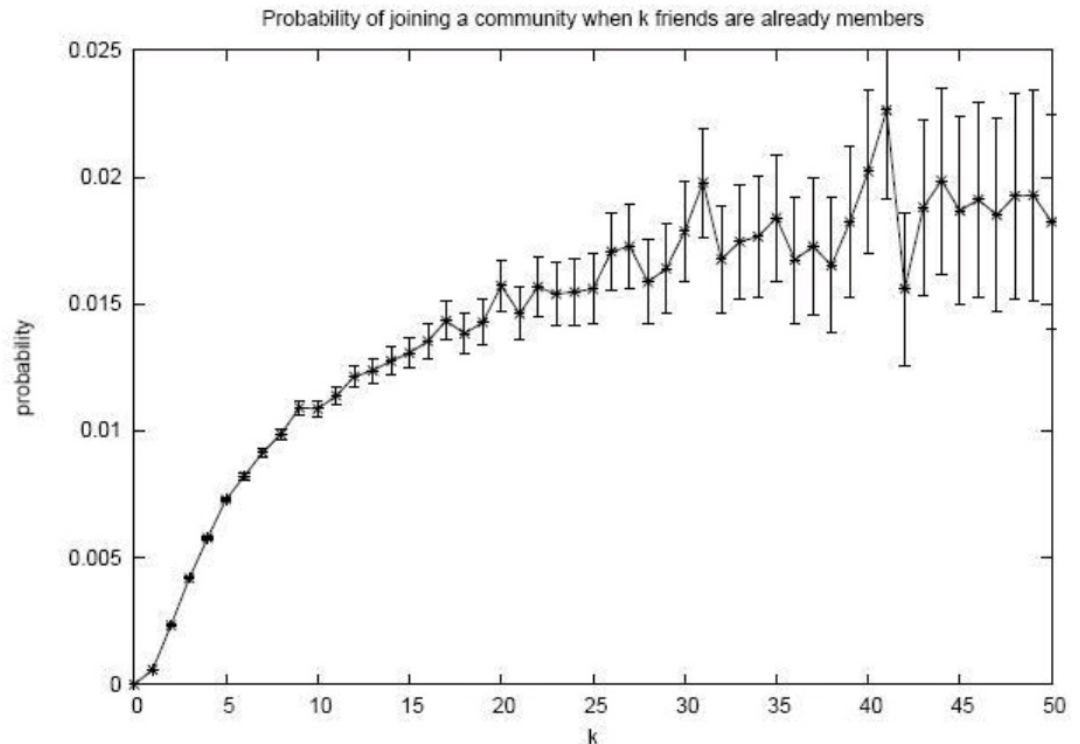
*Thick arrows have weight 1.0*

*Thin arrows have weight 0.5*

*Execute linear threshold model starting from seed node*

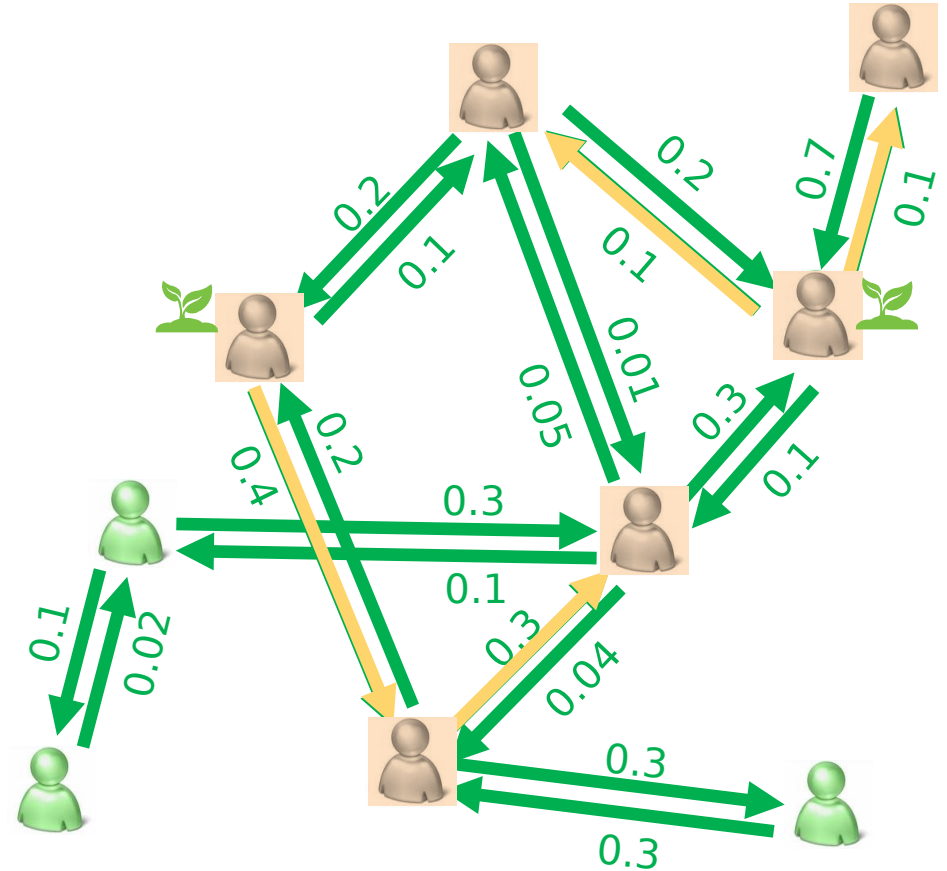
# Linear threshold model

Is the linear threshold model compatible with this observation?



# Independent cascade model

- No thresholds
- Each node, when activating, has one chance of activating each of their neighbors
- Probability of succeeding represented by arc weights



**[Kempe, Kleinberg and Tardos, KDD 2003]**



## Exercise

# Google Spreadsheet



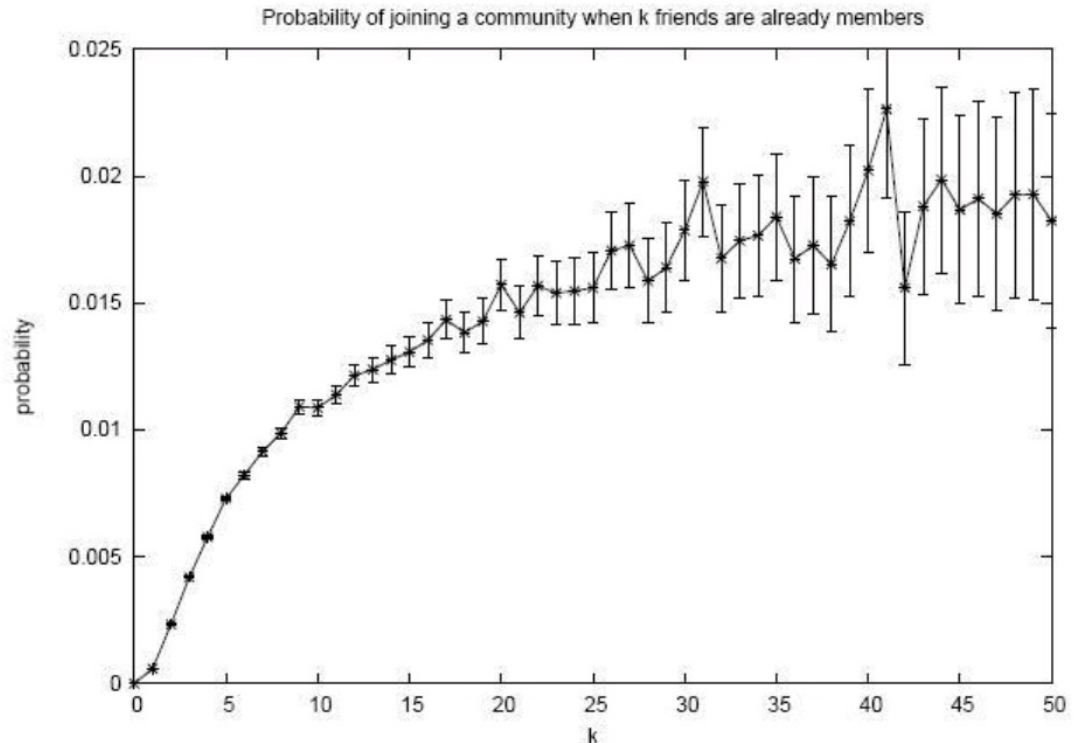
*Thick arrows have probability 0.75*

*Thin arrows have probability 0.5*

*Execute independent  
cascade model starting  
from seed node*

# Independent cascade model

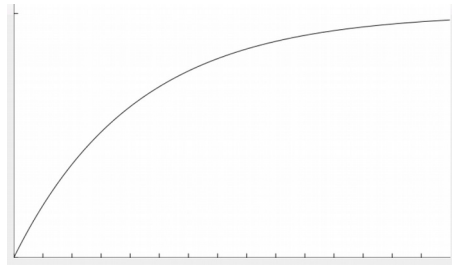
Is the  
independent  
cascade model  
compatible with  
this observation?



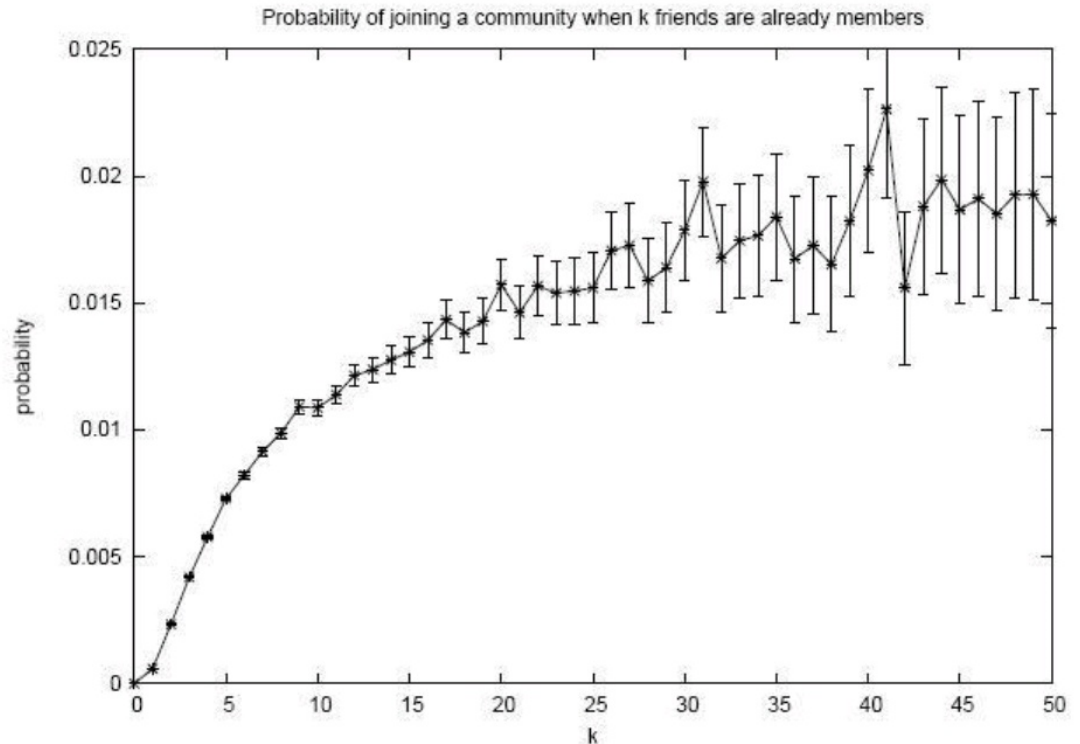
# Independent cascade model

Is the independent cascade model compatible with this observation?

Hint:



$$1 - q^k \text{ for } 0 < q < 1$$



# What are these models assuming?

(List as many assumptions as you can)

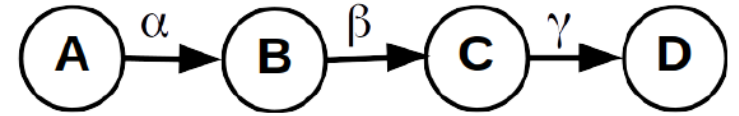
Answer in Nearpod Collaborate  
<https://nearpod.com/student/>  
Code to be given during class

# Summary

# Things to remember

- Influence phenomena exist, they can be modeled, they are hard to create/engineer
- Linear threshold model
- Independent cascade model
- Practice executing these models in small graphs by hand
- Practice writing code implementing them

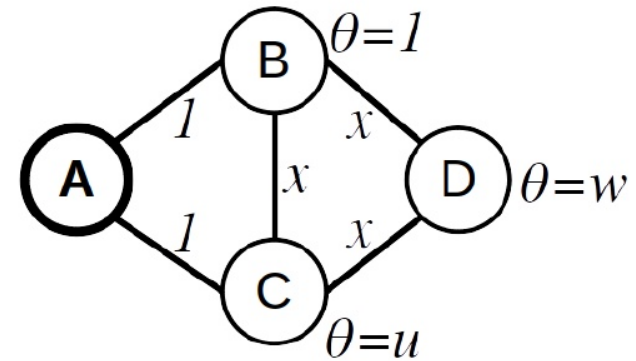
# Practice on your own



- Consider the graph on the top-right, including the infection probabilities indicated in the edges:  $\alpha$ ,  $\beta$  and  $\gamma$ . Let  $X_i$  be the expected number of nodes infected under the Independent Cascade Model for an infection starting at node  $i$ , including the node initially infected.
- For instance, if an infection starts from node B, the probability that the number of nodes infected is 2 is  $P(X_B = 2) = \beta \cdot (1 - \gamma)$ . This is because for the infected to be 2 we need the infection from B to C to succeed and the infection from C to D to fail.
- Remember that the expectation of a variable  $X$  is  $E[X] = \sum x \cdot P(X = x)$ , where the summation is done over the possible values  $x$  that the variable can take.
- 1. What is  $E[X_C]$  as a function of  $\gamma$ ?
- 2. What is  $E[X_A]$  as a function of  $\alpha$ ,  $\beta$ ,  $\gamma$ ?

# Practice on your own (cont.)

- Consider this graph and the Linear Threshold model executed on it, starting from seed node A.
- The influence weights are written next to the edges, and the thresholds  $\theta$  are written next to the nodes.
- Indicate what is the range of values of  $x$  for node C to be infected, but not node D. Justify briefly your answer.



1.  $\underline{\hspace{1cm}} \leq x < \underline{\hspace{1cm}}$

2. Justification:



# Practice on your own (cont.)

- Consider the graph on the right as the Independent Cascade model executed on it, starting from seed node A.
- The contagion probability of all edges is  $p$
- Indicate what is the probability that at the end of the process:
  1. Only node A is infected:
  2. Only nodes A, B are infected:
  3. Only nodes A, B, C are infected:
  4. Only nodes A, B, D are infected:

