



# CptS 591: Elements of Network Science

**Epidemics** 



#### Proposed Project Titles (CptS 591, Spring 2021)

- **Team 5**: Adversarial aspects of social interaction: MMO Eve Online data
- **Team 1**: Probabilistic synthesis of temporal graphs
- **Team 6**: Graph clustering for product recommendation
- **Team 8**: Information flow analysis on Bitcoin data
- **Team 7:** Core-Periphery structure analysis on Bitcoin data
- **Team 11**: Community detection for analysis of Bitcoin OTC and Bitcoin Alpha networks

- **Team 3**: Analysis of hospital transfer networks
- **Team 4**: Semi-supervised learning using graph signals
- **Team 2**: Analysis of subreddits wit a view on conflicts and attacks
- **Team 13**: Analysis of information campaigns on Twitter networks
- **Team 9**: *Graph similarity*
- **Team 10**: Analysis of geographic networks of Covid data
- **Team 12**: Improving collaborative filtering recommender system using optimization

April 27

April 29





# Models of cascading behavior

- Diffusion of ideas and behaviors (last two lectures)
  - Payoff driven
  - Deterministic
  - Node-to-node level analysis
  - Requires detailed information about the data

#### • Epidemics

- No decision making
- Complex process
- Unobservable on node-to-node level
- Modeled as a random process





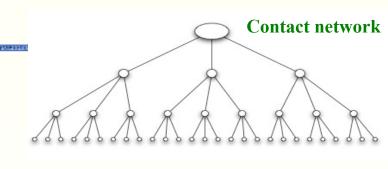
### **Branching Processes**

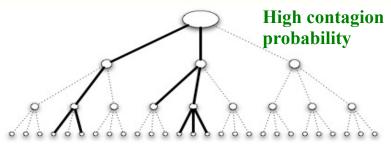
#### • First wave:

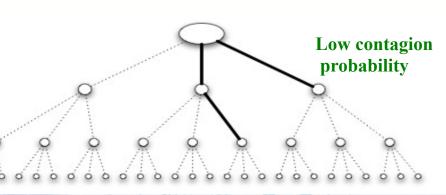
- A person carrying a disease enters a population and transmits it to each person he meets independently with probability p.
- He meets k people while he is contagious.
- Second wave:
  - Each person in the first wave meets k different people, resulting in a second wave of  $k^2$  people.
  - Each infected person in the first wave passes the disease independently with probability p.
- Subsequent waves formed in similar way.

#### **Question:**

For which values of p and k does the epidemic die-out/run forever?











### The basic reproductive number, R<sub>0</sub>

- $R_0$  = expected number of new cases of the disease caused by a single individual.
- $R_0 = pk$
- If R<sub>0</sub> < 1, then with probability 1, the disease dies out after a finite number of waves. If R<sub>0</sub> > 1, then with probability > 0, the disease persists by infecting at least one person in each wave.
- Reducing  $R_0$  (in the vicinity of the critical value 1): public-health measures
  - Reduce k (quarantine)
  - Reduce p (improved behavioral measures)





### The branching process

- Is an oversimplified model for disease spread (structure has no triangles)
- Will consider models that can handle more complex structures





# The SIR Epidemic Model

- At each individual node, still branching process model
- But contact structure is much more general.
- An individual node goes through three potential stages:
  - Susceptible
  - Infectious
  - Removed
- Contact network represented as a directed graph: an edge from v to w means, if v becomes infected, the disease has the potential to spread directly to w.
- Progress of epidemic controlled by:
  - Structure of contact network
  - Parameters p (probability of cotagion) and t<sub>I</sub> (length of infection)





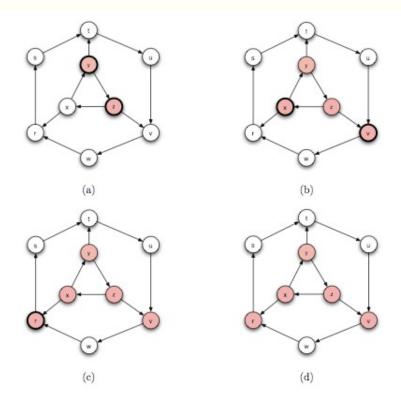
## The SIR model process

- Initially, some nodes are in the state I, all others are in S
- $\bullet$  Each node v that enters I remains infectious for a fixed number of steps  $t_{\rm I}$
- During each of the t<sub>I</sub> steps, node v has probability p of passing the disease to each of its susceptible neighbors
- After t<sub>I</sub> steps, node v is no longer infectious or susceptible (it is Removed)





# SIR: Example $(t_I = 1)$







### Extensions to the SIR model

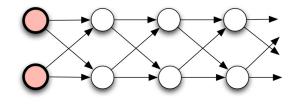
- Heterogenous contagion probability
  - Separate probability p(v,w) to each directed edge (v,w)
- Infectious period random in length
  - An infected node has probability q of recovering in each step while it is infected
- More elaborate extensions:
  - Separate I into a sequence of several states (e.g. early, middle and late periods of the infection) and allow the contagion probabilities to vary across the states.





# The Role of Basic Reproduction Number in the SIR model

- In networks that do not have a tree structure, the simple dichotomy in epidemic behavior determined by R<sub>0</sub> does not necessarily hold.
- Example: consider the highly structured (double-chain, with four outgoing edges joining layers) network shown at the right. Consider the parameters t\_1 = 1, infection probability p=2/3, and assume the left most two nodes are initially infected.
- For this example, the expected number of new cases caused by a node is  $2 \times 2/3 = 4/3$ . So R\_0 > 1. Despite this, the disease will die out almost surely after reaching only a finite number of steps. (Note that the "failure" rate per each step is  $(1/3)^4 = 1/81$ .)







### SIR Epidemics and Percolation

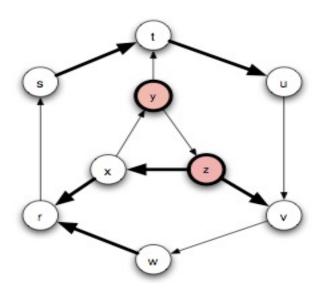
- Epidemics can alternatively be viewed as a *static* process!
- Suppose in the SIR model  $t_I = 1$ .
- Consider a point when node v has just become infectious, and it has a susceptible neighbor w.
- Node v has one chance to infect w (since  $t_I = 1$ ), and it succeeds with probability p.
- The outcome of this random event can be viewed as if it were determined by flipping a coin that has probability p of coming up "heads".
- Continuing this reasoning, we can assume that a coin was flipped for each edge of the contact network at the beginning and the result stored. This divides edges into *open* and *closed*.





### SIR Epidemics and Percolation

• A node v will become infected during the epidemic if and only if there is a path to v from one of the initially infected nodes that consists entirely of open edges.







### The SIS Epidemic model

- Models epidemics in which nodes can be reinfected multiple times.
- Nodes simply alternate between two possible states: Susceptible and Infectious. No Removed state.
- Mechanics of the SIS model:
  - Initially some nodes are in I, all others in S
  - Each node that enters I remains infectious for a fixed number of steps t<sub>I</sub>
  - During each of the t<sub>I</sub> steps, node v has probability p of passing the disease to each of its susceptible neighbors
  - After t<sub>I</sub> steps, node v is no longer infectious, it returns to S



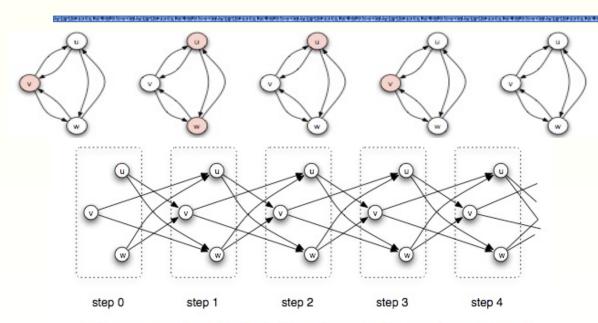


### Life Cycles of SIR and SIS Epidmics

- Overall trajectories of SIR and SIS epidemics are qualitatively quite different
  - SIR epidemic on a finite graph comes to an end after a relatively small number of steps. (Since it burns through a bounded supply of nodes.)
  - SIS epidemics can run for an extremely long time as it cycles through the nodes potentially multiple times.
- A key research question in SIS epidemic on a given contact network is to understand how long the outbreak will last and how many individuals will be affected at different points in time.
- Some progress has been made on this question for network structures that are mathematically tractable. Much work remains to be done.

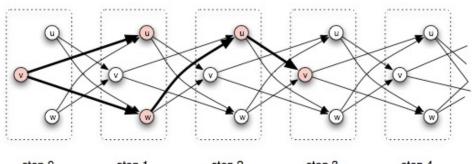


#### Connection between SIR and SIS model



Despite the differences, certain SIS models can also be formulated as special cases of SIR.

(a) To represent the SIS epidemic using the SIR model, we use a "time-expanded" contact network









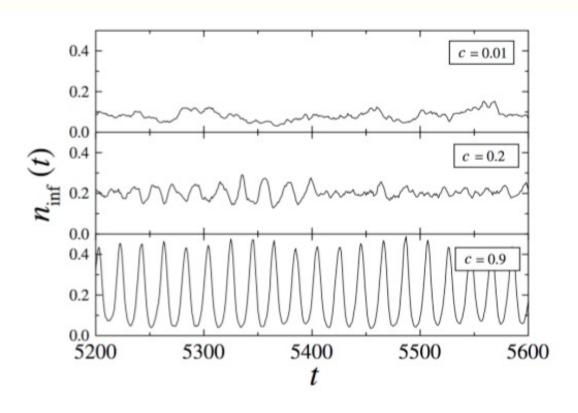
# Synchronization: SIRS model, small-world contact networks

- Synchronization, ingredients
  - Temporary immunity
  - Long-range links in the contact network
- SIRS (combination of SIR and SIS) epidemic model:
  - Initially, some nodes are in the I state and all others are in the S state
  - $\bullet$  Each node v that enters the I state remains infections for a fixed number of steps  $t_I$
  - $\bullet$  During each of these  $t_I$  steps, node v has probability p of passing the disease to each of its susceptible neighbors
  - (New feature of the model): after  $t_I$  steps, node v is no longer infectious. It then enters the R state for a fixed number of steps  $t_R$ . During this time, it can not be infected with the disease, nor does it transmit the disease to other nodes. After  $t_R$  steps in the R state, node v returns to the S state.





# Synchronization: SIRS model, small-world contact networks







# Synchronization in epidemics: some interesting research directions

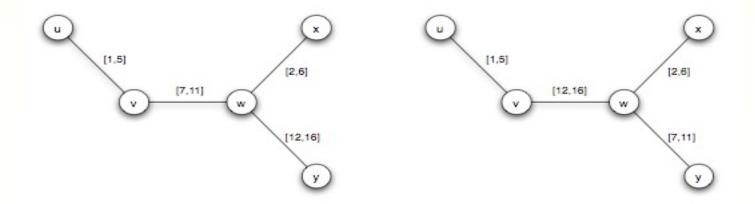
- Results shown in previous slide are based on simulations; analyzing the onset of synchronization mathematically in the SIRS (or similar) model is unexplored.
- Synchronization in Epidemic Data
  - Empirical study and evaluation of proposed models
- Modeling more complex temporal phenomena. E.g. some data sets show epidemics in different cities can synchronize in the sense of being "out of phase".
- How do interventions interplay with synchronization?





# Transient contacts and the dangers of concurrency

• Each edge is annotated with the period of time during which it existed

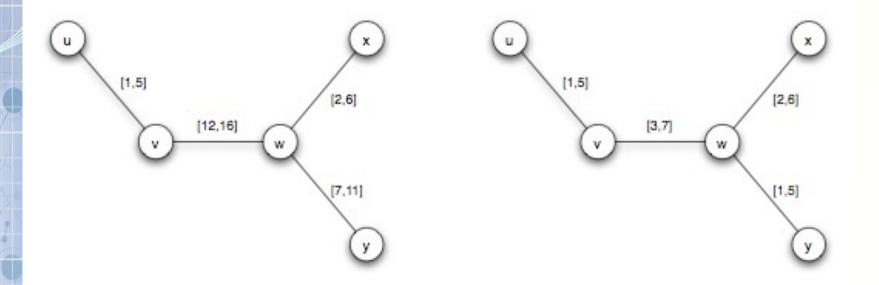


Temporal edges are important models in many areas, including sociology, epidemiology, mathematics, and computer science





## The dangers of concurrency







# Further Readings (Besides Chapter 21 of Easley-Kleinberg)

- Romero, B. Meeder, J. Kleinberg. Differences in the Mechanics of Information Diffusion Across Topics: Idioms, Political Hashtags, and Complex Contagion on Twitter. In Proc. WWW, 2011.
- J. Ugander, L. Backstrom, C. Marlow, J. Kleinberg. Structural Diversity in Social Contagion. In Proc. National Academy of Sciences, 2012.
- D. Cosley, D. Huttenlocher, J. Kleinberg, X. Lan, S. Suri. Sequential Influence Models in Social Networks. In Proc. ICWSM, 2010.
- S. Myers, C. Zhu, J. Leskovec. Information diffusion and external influence in Networks. In Proc. KDD, 2012.
- L. Backstrom, D. Huttenlocher, J. Kleinberg, X. Lan. Group Formation in Large Social Networks: Membership, Growth, and Evolution. In Proc. KDD, 2006.

- M. Miller, C. Sathi, D. Wiesenthal, J. Leskovec, C. Potts. Sentiment Flow Through Hyperlink Networks. In Proc. ICWSM, 2011.
- A. Ganesh , L. Massoulie , D. Towsley. The effect of network topology on the spread of epidemics. In IEEE INFOCOM, 2005.
- S. Myers, J. Leskovec. Clash of the Contagions: Cooperation and Competition in Information Diffusion. In Proc. ICDM 2012.
- H. Kwak, C. Lee, H. Park, S. Moon. What is Twitter, a social network or a news media? In Proc. WWW, 2010.
- E. Adar, L. Adamic. Tracking information epidemics in blogspace. In Proc. Web intelligence, 2005.

