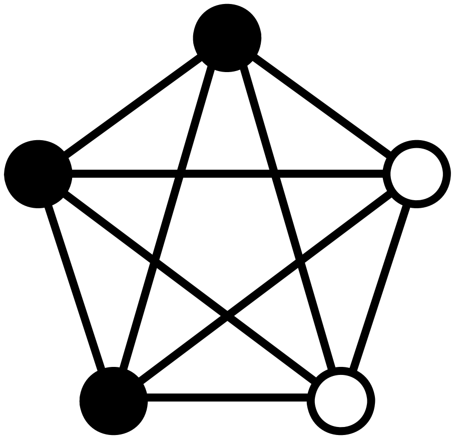
Simulation II: Dynamics on Networks



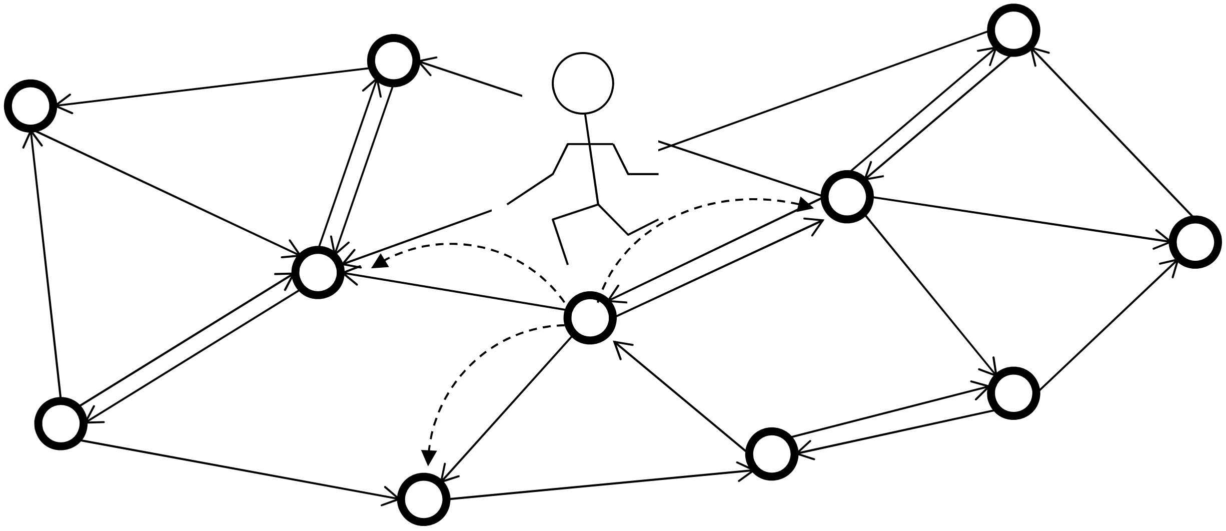
Hiroki Sayama
sayama@binghamton.edu

Dynamics *on* networks

- Dynamic state changes taking place on a static network topology
  - Regulatory dynamics on gene/protein networks
  - Population dynamics on ecological networks
  - Disease infection on social networks
  - Information/culture propagation on organizational/social networks

Simple example: Random walk on a network

- An agent (or a set of agents) moving on a network
- An agent jumps randomly to one of the neighbor nodes at each time step



Exercise

- Simulate random walk of an agent on a directed random network made of 50 nodes

- Count how many times each node was visited by the agent over time

TPM and asymptotic probability distribution (review)

- $|\lambda| <= 1$ for all eigenvalues
- If the original network is strongly connected (with some additional conditions), the TPM has one and only one eigenvalue 1 (no degeneration)

→ This is a unique dominant eigenvalue; the probability vector will converge to its corresponding eigenvector

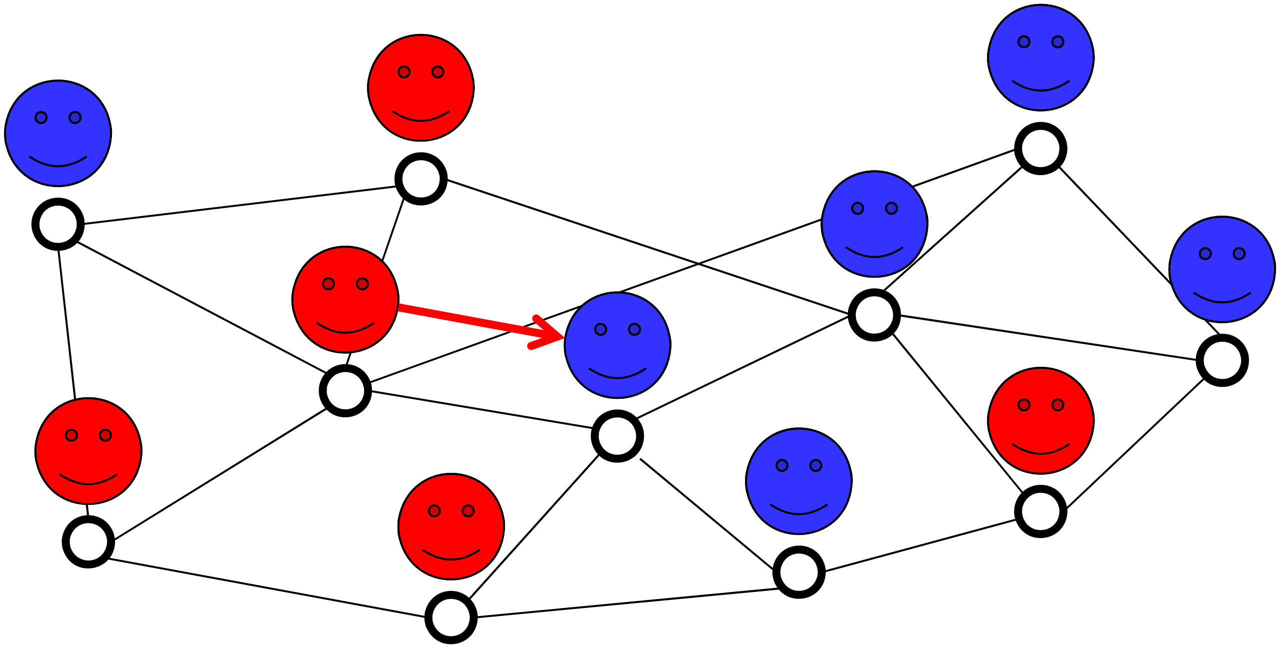
Exercise

- Construct the transition probability matrix of the random network used in the previous exercise
- Find its dominant eigenvector with λ = 1
- Compare the results with the previous "counting" results

Dynamics on Networks with Discrete Node States

Opinion formation (Voter model)

- A simple model of opinion formation in society
  - Opinions = discrete states



Three versions of voter models

- Original voter model
  - A randomly selected node copies the opinion of one of its neighbors
- Reverse voter model
  - A randomly selected node “pushes” its opinion into one of its neighbors
- Link-based voter model
  - An opinion is copied through a randomly selected link

Exercise

- Simulate the three different versions of the voter model (original, reverse and link-based) on a Barabasi-Albert scale-free network

- Compare the speed of opinion homogenization between the three models
  - Why different?

Epidemics (SIS/SIR model)

- Initially, a small fraction of nodes are infected by a disease
- If a susceptible node has an infected neighbor, it will be infected with probability p_i (per infected neighbor)
- An infected node will recover and become susceptible (SIS) or recovered (SIR) with probability p_r

Exercise

- Study the effects of infection/ recovery probabilities on the fixation of a disease on a random social network
  - In what condition will the disease remain within society?
  - In what condition will it go away?
  - Is the transition smooth, or sharp?

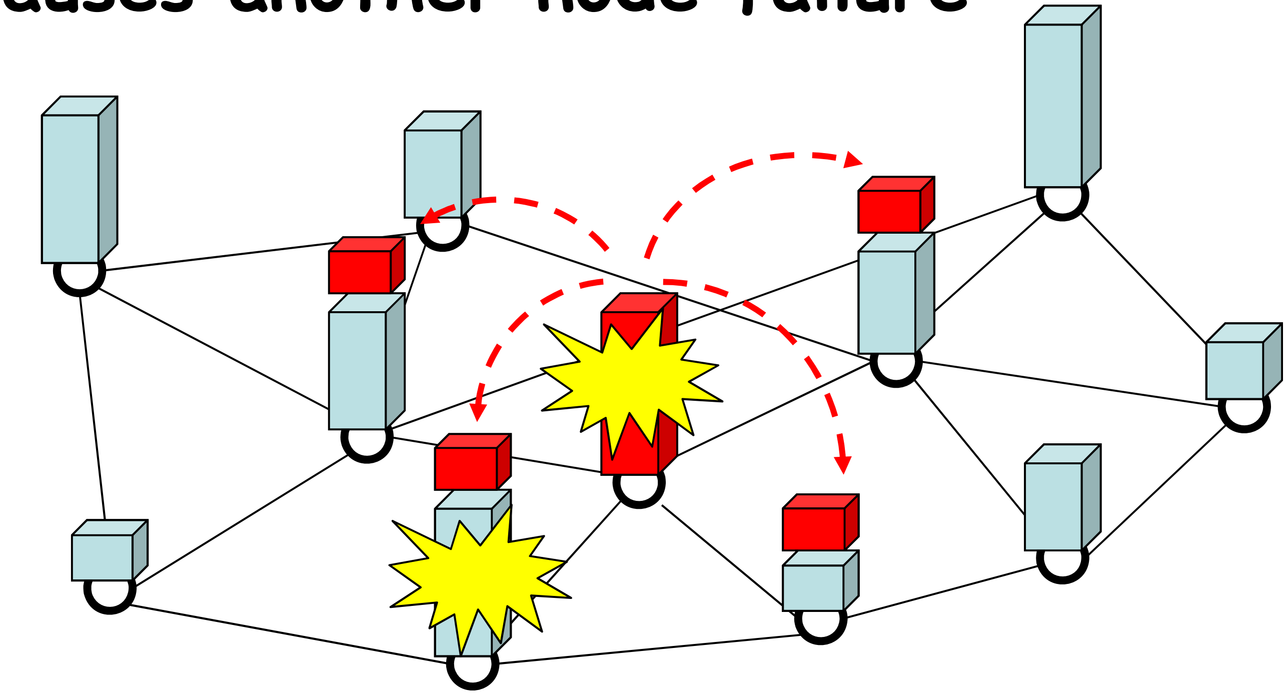
Exercise

- Do the same experiments with WS small-world networks and BA scale-free networks

- Compare their properties

Cascade of failure

- Load on a failing node is divided and distributed to its neighbors
- If the load exceeds capacity of each node, it causes another node failure

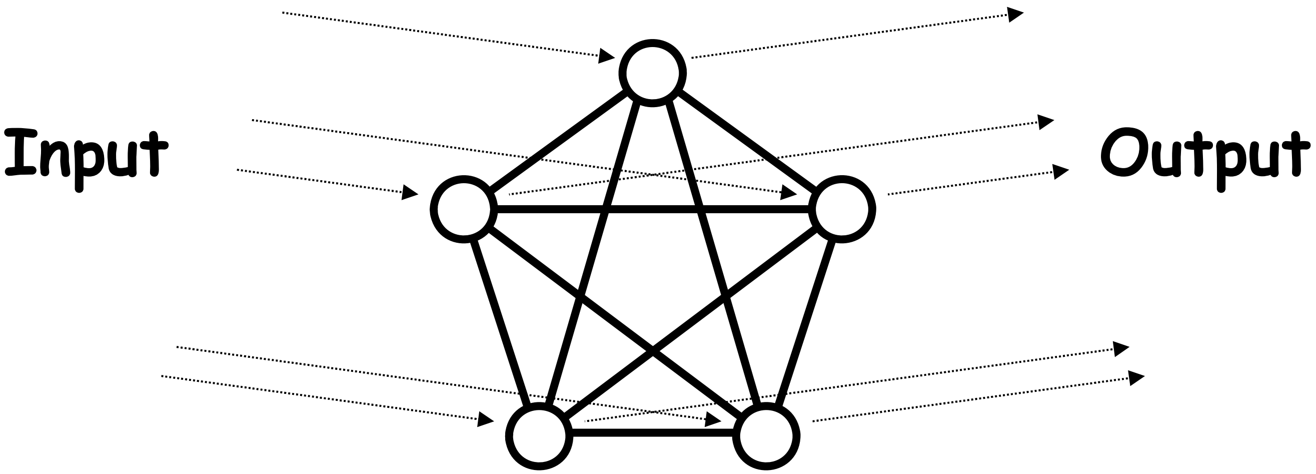


Exercise

- Simulate a cascade of failure on a scale-free network made of 100 nodes with random node capacities and load assignments

- Investigate which node has the most significant impact when it fails

Hopfield network



Input

Output

- A.k.a. "**attractor network**"
- Neurons connected in a shape of an undirected weighted complete graph
- Each neuron takes either 1 or -1, and updates its state in discrete time

State-transition rule

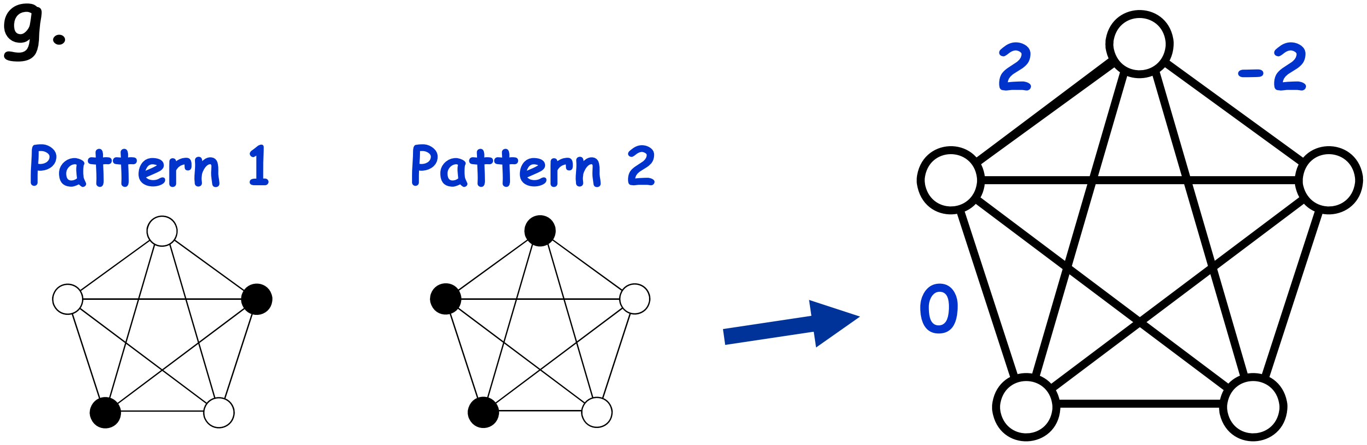
$$s_i(t+1) = \text{sign}\left(\Sigma_j \, w_{ij} \, s_j(t) \right)$$

- w_{ij} : connection weight between neuron i and neuron j
- $w_{ij} = w_{ji}$ (symmetric interaction)
- $w_{ii} = 0$ (no feedback to itself)

Setting weights by "imprinting"

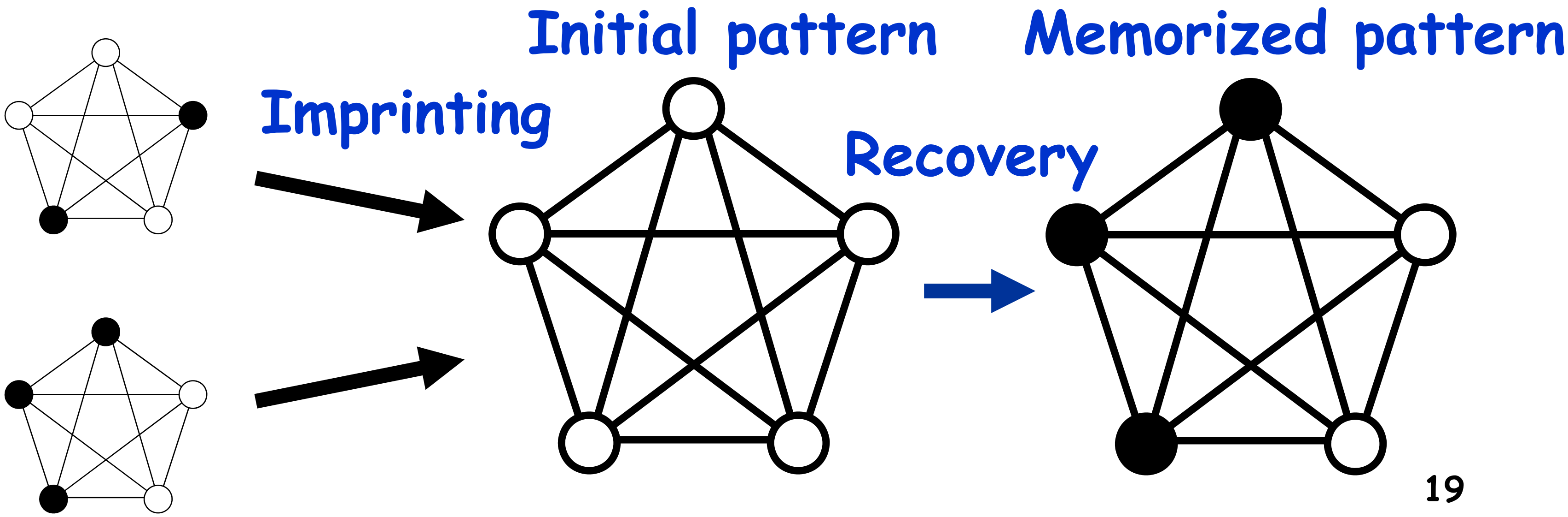
$$w_{ij} = \Sigma_k s^k_i s^k_j$$

- k : index of patterns memorized
- s^k_i : state of neuron i in pattern k
  - e.g.



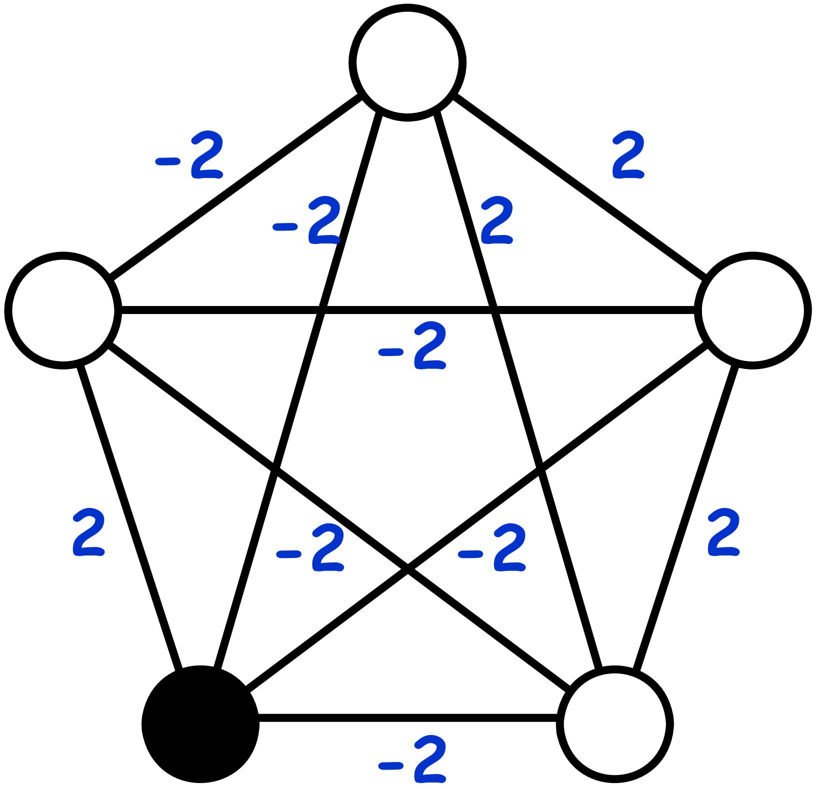
Recovering patterns

- When started with some initial pattern, the network "remembers" the closest pattern in its memory (or its reversal)
  - Can be applied to content addressable memory, pattern recognition, etc.



Exercise

- Simulate the behavior of the following Hopfield network



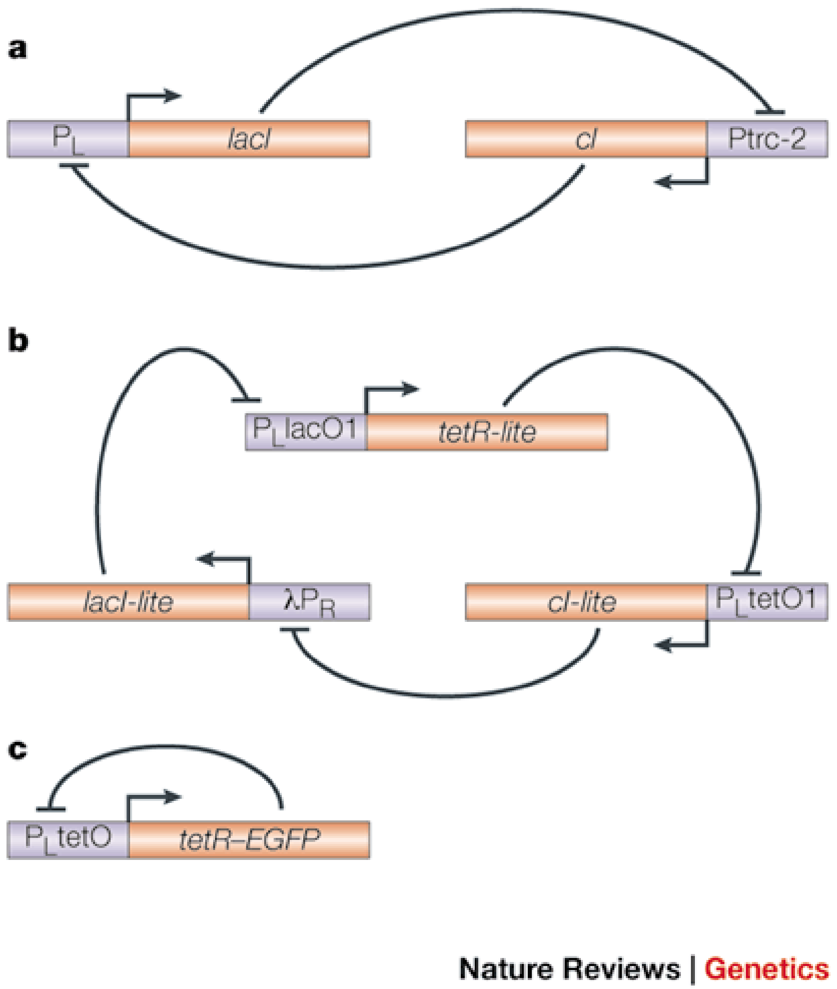
○ : +1

● : -1

2, -2 : weights

Gene regulatory network

- Each gene is activated or inhibited by other genes
  - Forming a network of “logic gates”
  - Each gene takes binary state (on/off)



(from Hasty et al., Nature Reviews Genetics 2, 268-279, 2001)

Boolean network

- Mathematical abstraction of gene regulatory networks
  - Binary node states
  - Each node determines next state using its own Boolean state transition function (referring to neighbors' states)
- Random Boolean network:
  - Network topology and state transition functions are both randomly generated

Example of transition functions

- 2-input functions (2^{2^2}=16 possibilities)

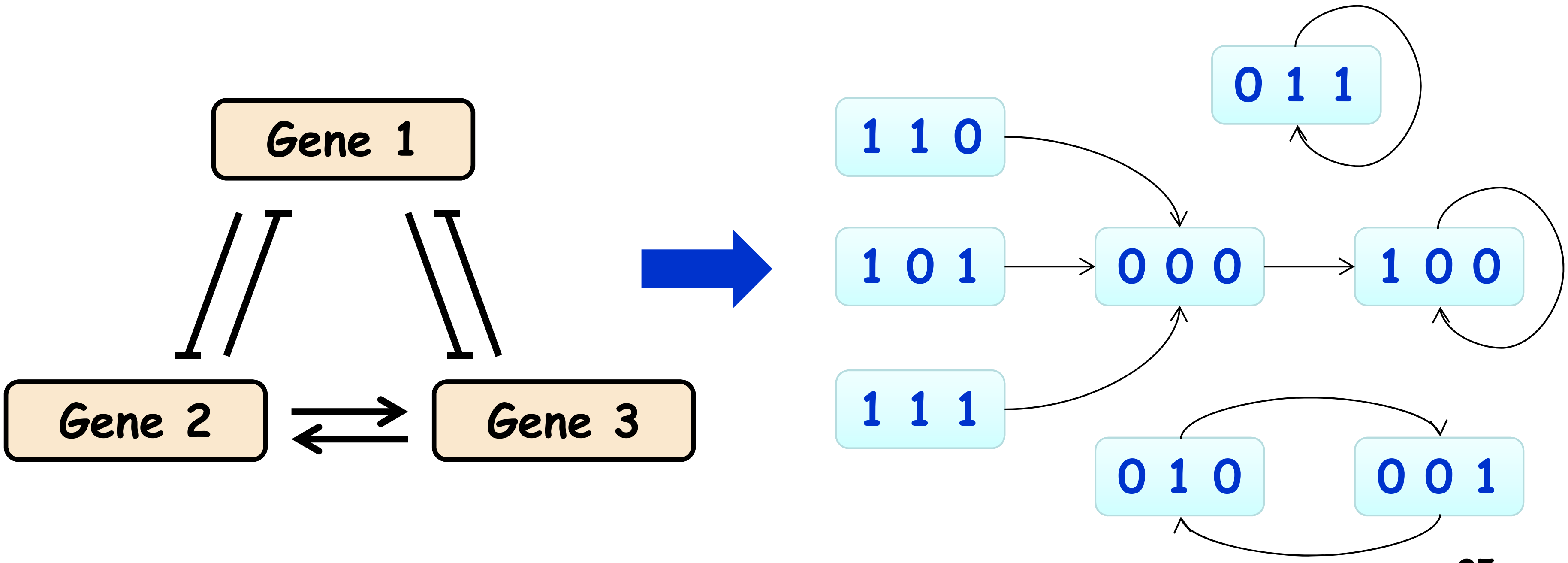
										AND						OR	
X	Y	Z	Z	Z	Z	Z	Z	Z	Z	Z	Z	Z	Z	Z	Z	Z	Z
0	0	0	1	0	1	0	1	0	1	0	1	0	1	0	1	0	1
0	1	0	0	1	1	0	0	1	1	0	0	1	1	0	0	1	1
1	0	0	0	0	0	1	1	1	1	0	0	0	0	1	1	1	1
1	1	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1

Kauffman's NK networks

- N: # of nodes
- K: # of inputs to each node
  - Topologies and state-transition functions are both random
  - Similar to, but not the same as, the NK fitness landscape (NK model) often used in mathematical biology and management sciences

NK network's attractors

- Total # of macro-states: 2^N
- The network eventually falls into one of its "attractors"



Exercise

- Create a Python code that generates the NK network's state-transition diagram (i.e., a directed network whose nodes are the network's macro-states)
- Count how many attractors exist
- Study how # of attractors change when you vary N and K

Dynamics on Networks with Continuous Node States

Simple diffusion

- Individually:

$$\frac{ds_i}{dt} = D \, \Sigma_{j \text{ in } N_i} (s_j - s_i)$$

- Collectively (with Laplacian L):

$$\frac{ds}{dt} = - D \, L \, s$$

Exercise

- Simulate a diffusion process of continuous node states on a Barabasi-Albert scale-free networks with n = 100 and m = 1

Exercise

- Calculate the eigenvalues and eigenvectors of Laplacian matrices of several different network topologies
- Interpret their meanings in the context of diffusion
- Confirm your interpretation by numerical simulation of the diffusion processes

Synchronization

- Linear coupling model:

$$\frac{ds_i}{dt} = F(s_i) + \Sigma_j \left(c_{ij} H(s_j) \right)$$

  - F(s): internal dynamics
  - $C = (c_{ij})$: coupling matrix
  - H(s): output function

- If $s_i(t) = s(t)$ for all i, then the network is synchronized

Synchronization and Laplacian

- If coupling depends only on the difference of outputs across a link:

$$\frac{ds_i}{dt} = F(s_i) + \sigma \Sigma_{j \text{ in } N_i} (H(s_j) - H(s_i))$$

  - I.e., $C = - \sigma L$
  - Laplacian's "spectral gap" (first non-zero eigenvalue) is critical in determining synchronizability of the network

Exercise

- Simulate the following nonlinear Kuramoto model:

$$\frac{ds_i}{dt} = w_i + K/|N_i| \; \Sigma_{j \text{ in } N_i} \sin(s_j - s_i)$$

  - w_i: inherent angular velocity
  - N_i: neighbors of node I

– What kind of networks synchronize most easily?

Exercise

- Measure and plot the following "phase coherence" in the simulation of the Kuramoto model:

$$r = | \Sigma_j e^{i\theta_j} / n |$$

Synchronizability

Synchronizability

- Synchronizability of a simple coupled dynamical network can be studied by conducting stability analysis

$$\frac{dx_i}{dt} = R(x_i) + \alpha \sum_{j \in N_i} (H(x_j) - H(x_i))$$

R(x): Local reaction term (homogeneous)
H(x): Output function

Exercise

- Consider adding a small perturbation to the general solution of the dynamical equation (w/o interactions)

$$\frac{dx}{dt} = R(x) \quad \rightarrow \quad x_s(t)$$

- Conduct stability analysis by assuming:

$$x_i(t) = x_s(t) + \Delta x_i(t)$$

Condition for synchronizability

- Solution $x_s(t)$ is stable (i.e., the network is synchronized) if

$$\alpha \lambda_i H'(x_s(t)) > R'(x_s(t))$$

for all i and t

(you need to consider only λ_2 and λ_n)

Exercise

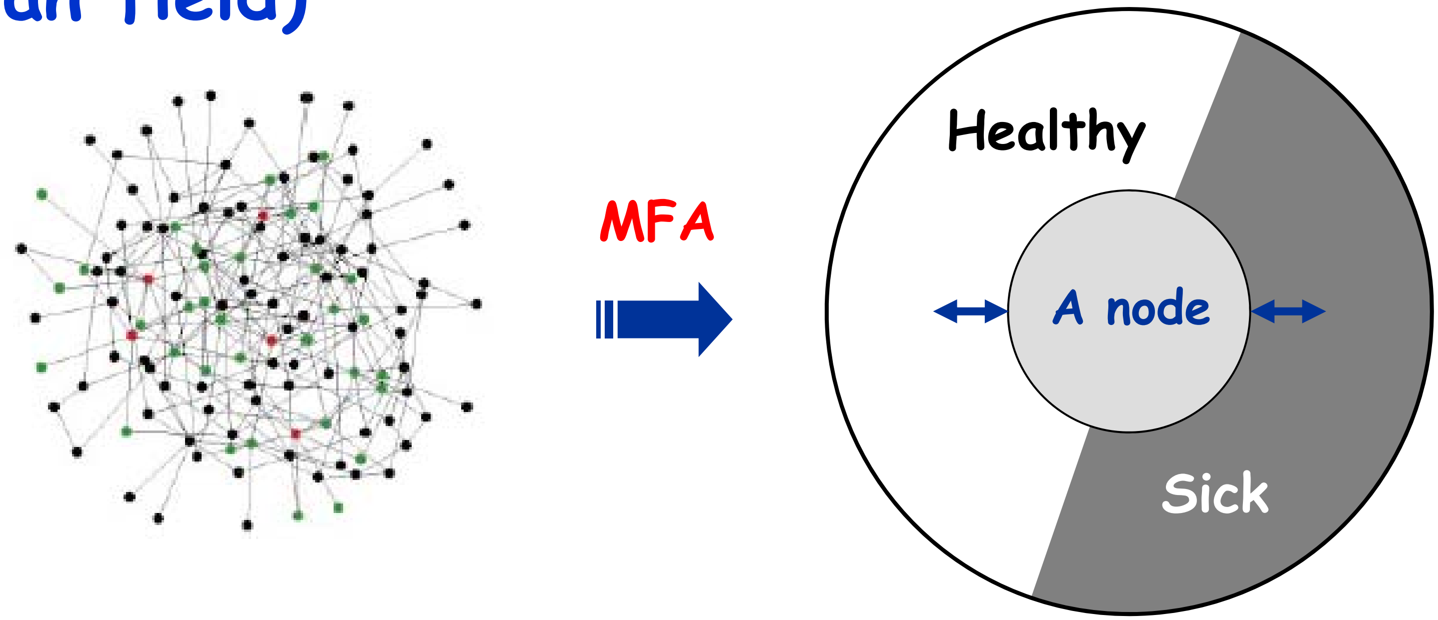
- **Analyze the synchronizability condition of the following coupled oscillator model:**

$$\frac{d\theta_i}{dt} = \beta\theta_i + \alpha \sum_{j \in N_i} (\theta_j - \theta_i)$$

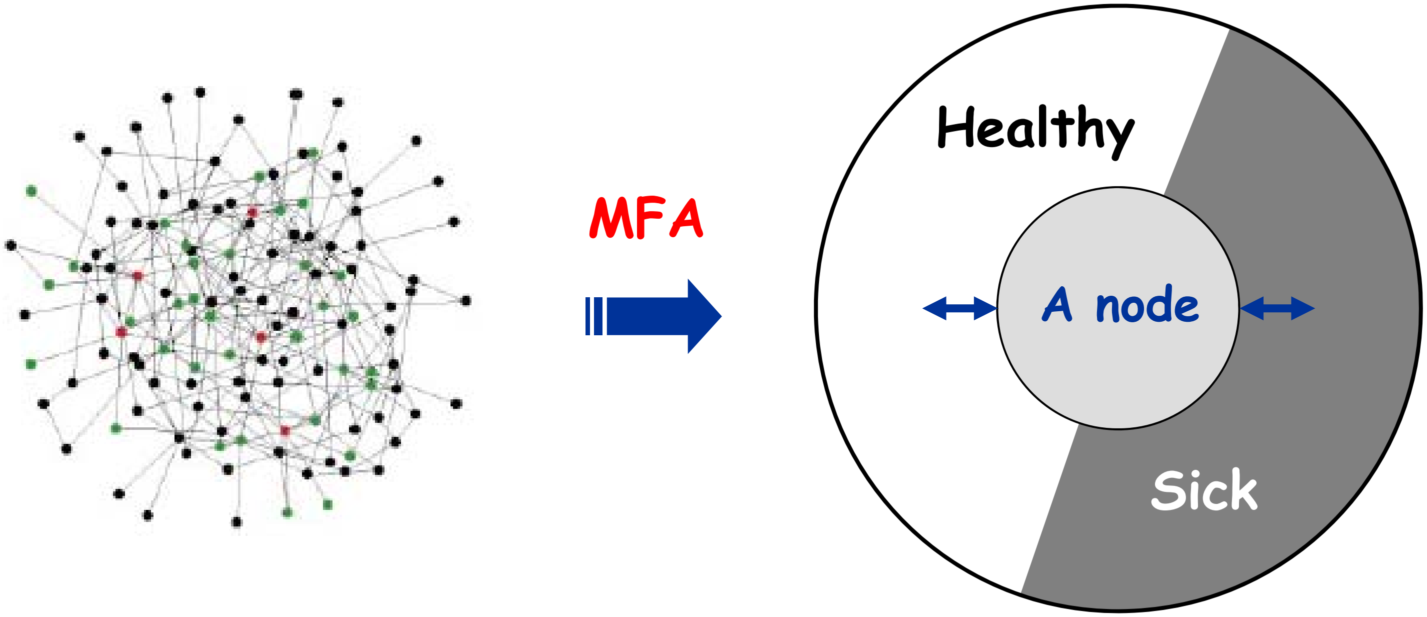
Mean-Field Approximation

Mean-field approximation

- An approximation to drastically reduce the dimensions of the system by reformulating the dynamics in terms of "a state of one node" and "the average of all the rest (= mean field)"



How MFA works



1. Make an approximated description about how one node changes its state through the interaction with the average of all the rest (= mean field)
2. Assume that 1. uniformly applies to all the nodes, and analyze how the mean field itself behaves

Mathematical description of MFA (difference equations)

- Original equations:

$$x^i_t = F^i(\{ x^i_{t-1} \})$$

- Approximate equations with MFA:

$$x^i_t = F'^i(x^i_{t-1}, \langle x \rangle_{t-1})$$

$$\langle x \rangle_t = \Sigma_i x^i_{t-1} / n$$

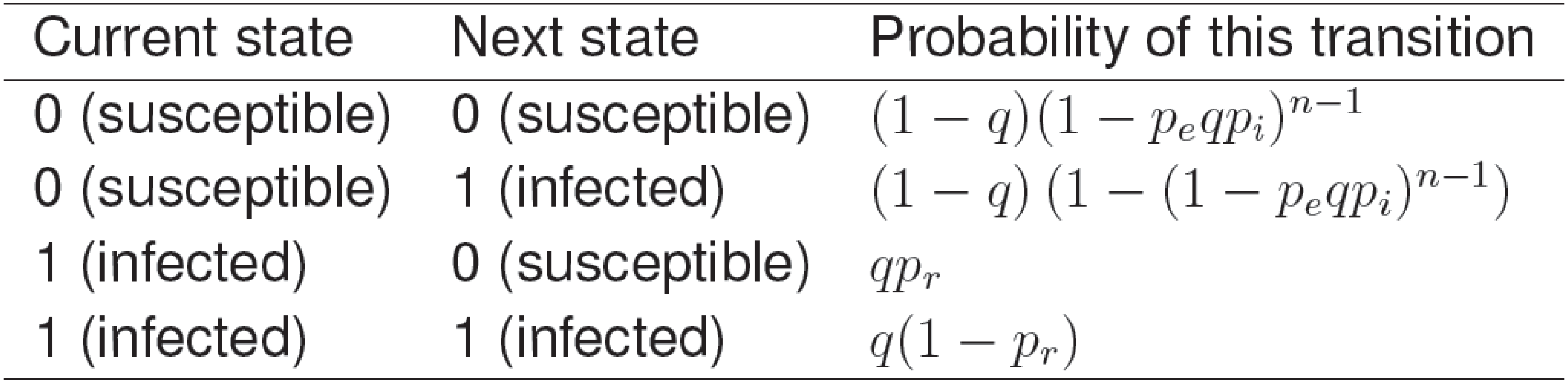
Each state-transition function takes only two arguments: its own state and the “mean field”

Example: SIS on a random network

- Infection probability p_i
- Recovery probability p_r
- Edge probability p_e

- Write down a difference equation that describes how the probability of infected nodes, q_t (mean field), changes over time

Example: SIS on a random network



Current state	Next state	Probability of this transition
0 (susceptible)	0 (susceptible)	$(1-q)(1-p_e q p_i)^{n-1}$
0 (susceptible)	1 (infected)	$(1-q)\left(1-(1-p_e q p_i)^{n-1}\right)$
1 (infected)	0 (susceptible)	$q p_r$
1 (infected)	1 (infected)	$q(1-p_r)$

- Find equilibrium states
- Study the stability of those equilibrium points
  - When does the equilibrium q = 0 become unstable (i.e., epidemic occurs)?

Example: SIS on a SF network

- Infection probability p_i
- Recovery probability p_r
- Degree distribution $P(k)$

- Write down a difference equation that describes how the probability of infected nodes with degree k, $q_t(k)$ (many mean fields), changes over time

Degree-dependent infection

- Probability for a node with degree k to get infected from its neighbor:

$$\sum_{k'} P_n(k'|k)q(k')p_i$$

Pn : neighbor degree probability distribution

If the network is nonassortative:

$$P_n(k') = \frac{k'}{\langle k \rangle} P(k')$$

FYI: Friendship paradox

- “Your friends have more friends than you do, on average”

$$\sum_{k'} k' P_n(k') = \sum_{k'} \frac{k'^2 P(k')}{\langle k \rangle} = \frac{\langle k^2 \rangle}{\langle k \rangle}$$

$$= \frac{\langle k \rangle^2 + \sigma(k)^2}{\langle k \rangle} = \langle k \rangle + \frac{\sigma(k)^2}{\langle k \rangle}$$

Calculation…

Current state	Next state	Probability of this transition
0 (susceptible)	0 (susceptible)	$(1-q(k))\left(1-\sum_{k'}\frac{k'}{\langle k\rangle}P(k')q(k')p_i\right)^k$
0 (susceptible)	1 (infected)	$(1-q(k))\left(1-\left(1-\sum_{k'}\frac{k'}{\langle k\rangle}P(k')q(k')p_i\right)^k\right)$
1 (infected)	0 (susceptible)	$q(k)p_r$
1 (infected)	1 (infected)	$q(k)(1-p_r)$

$$\begin{aligned} q_{t+1}(k) &= (1-q(k))\left(1-\left(1-\sum_{k'}\frac{k'}{\langle k\rangle}P(k')q(k')p_i\right)^k\right)+q(k)(1-p_r) \\ &= (1-q(k))\left(1-(1-q_n p_i)^k\right)+q(k)(1-p_r), \end{aligned}$$

$$q_n = \frac{\sum_{k'} k' P(k')q(k')}{\langle k\rangle}$$

Calculation...

$$\begin{aligned} q_{t+1}(k) &= (1-q(k))\,(1-(1-kq_np_i)) + q(k)(1-p_r) \\ &= (1-q(k))kq_np_i + q(k) - q(k)p_r = f(q(k)) \end{aligned}$$

$$q_{\text{eq}}(k) = \frac{kq_np_i}{kq_np_i + p_r}$$

With this:

$$q_n = \frac{1}{\langle k\rangle}\sum_{k'} k'P(k')\frac{k'q_np_i}{k'q_np_i + p_r}$$

Calculation…

$$q_n = \frac{1}{\langle k \rangle} \sum_{k'} k' P(k') \frac{k' q_n p_i}{k' q_n p_i + p_r}$$

- For BA SF networks, this becomes:

$$q_n = \frac{1}{2m} \sum_{k'=m}^{\infty} k' \cdot 2m^2 k'^{-3} \frac{k' q_n p_i}{k' q_n p_i + p_r},$$

$$1 = m p_i \sum_{k'=m}^{\infty} \frac{1}{k'(k' q_n p_i + p_r)}.$$

$$q_n \approx \frac{p_r}{(e^{\frac{p_r}{m p_i}} - 1) m p_i}$$

Calculation...

- Final stability analysis:

$$\frac{df(q(k))}{dq(k)}\bigg|_{q(k)=\frac{kq_np_i}{kq_np_i+p_r}} = -kq_np_i + \frac{p_r}{kq_np_i+p_r}\frac{k^2P(k)p_i}{\langle k\rangle} + 1 - p_r = r(k)$$

$$\begin{aligned} r(k) &= -k\frac{p_r}{(e^{\frac{p_r}{mp_i}}-1)mp_i}p_i + \frac{p_r}{k\frac{p_r}{(e^{\frac{p_r}{mp_i}}-1)mp_i}p_i+p_r}\frac{k^2\cdot 2m^2k^{-3}p_i}{2m} + 1 - p_r \\ &= -\frac{kp_r}{(e^{\frac{p_r}{mp_i}}-1)m} + \frac{mp_i}{\frac{k^2}{(e^{\frac{p_r}{mp_i}}-1)m}+k} + 1 - p_r \end{aligned}$$

Conclusion

- If $p_i \rightarrow 0$:

$$\lim_{p_i \to 0} r(k) = -\frac{kp_r}{\left(\left[e^{\frac{p_r}{mp_i}} \to \infty\right] - 1\right) m} + \frac{m\,[p_i \to 0]}{\frac{k^2}{\left(\left[e^{\frac{p_r}{mp_i}} \to \infty\right] - 1\right) m} + k} + 1 - p_r$$

$$= 1 - p_r$$

- Since $0 < 1 - p_r < 1$, the non-zero equilibrium state (i.e., epidemic) is still stable even if $p_i \rightarrow 0$ on scale-free networks!!

Take-home lesson

- Dynamics on networks can be influenced significantly by network topology