Assortativity and Mixing

Complex Networks, CSYS/MATH 303, Spring, 2010

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Outline

Basic idea:

- ► Random networks with arbitrary degree distributions cover much territory but do not represent all networks.

- ► Moving away from pure random networks was a key first step.

- ► We can extend in many other directions and a natural one is to introduce correlations between different kinds of nodes.

- ► Node attributes may be anything, e.g.:
    1. degree
    2. demographics (age, gender, etc.)
    3. group affiliation

- ► We speak of mixing patterns, correlations, biases...

- ► Networks are still random at base but now have more global structure.

- ► Build on work by Newman [3, 4].

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General mixing between node categories

- ▶ Assume types of nodes are countable, and are assigned numbers 1, 2, 3, ...
- ▶ Consider networks with directed edges.

$$e_{\mu\nu} = \Pr \left(\begin{array}{c} \text{an edge connects a node of type } \mu \\ \text{to a node of type } \nu \end{array} \right)$$

$$a_\mu = \Pr(\text{an edge comes from a node of type } \mu)$$

$$b_\nu = \Pr(\text{an edge leads to a node of type } \nu)$$

- ▶ Write $\mathbf{E} = [e_{\mu\nu}]$, $\vec{a} = [a_\mu]$, and $\vec{b} = [b_\nu]$.
- ▶ Requirements:

$$\sum_{\mu\,\nu} e_{\mu\nu} = 1, \ \sum_\nu e_{\mu\nu} = a_\mu, \ \text{and} \sum_\mu e_{\mu\nu} = b_\nu.$$

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Connection to degree distribution:

Notes:

▶ Varying $e_{\mu\nu}$ allows us to move between the following:

1. Perfectly assortative networks where nodes only connect to like nodes, and the network breaks into subnetworks.
   Requires $e_{\mu\nu} = 0$ if $\mu \neq \nu$ and $\sum_\mu e_{\mu\mu} = 1$.

2. Uncorrelated networks (as we have studied so far)
   For these we must have independence: $e_{\mu\nu} = a_\mu b_\nu$.

3. Disassortative networks where nodes connect to nodes distinct from themselves.

▶ Disassortative networks can be hard to build and may require constraints on the $e_{\mu\nu}$.

▶ Basic story: level of assortativity reflects the degree to which nodes are connected to nodes within their group.

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Correlation coefficient:

- Quantify the level of assortativity with the following assortativity coefficient [4]:

$$r = \frac{\sum_\mu e_{\mu\mu} - \sum_\mu a_\mu b_\mu}{1 - \sum_\mu a_\mu b_\mu} = \frac{\text{Tr}\,\mathbf{E} - ||E^2||_1}{1 - ||E^2||_1}$$

  where $|| \cdot ||_1$ is the 1-norm = sum of a matrix's entries.

- $\text{Tr}\,\mathbf{E}$ is the fraction of edges that are within groups.

- $||E^2||_1$ is the fraction of edges that would be within groups if connections were random.

- $1 - ||E^2||_1$ is a normalization factor so $r_{\max} = 1$.

- When $\text{Tr}\,e_{\mu\mu} = 1$, we have $r = 1$. ✓

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Correlation coefficient:

Notes:

- ▶ $r = -1$ is inaccessible if three or more types are presents.

- ▶ Disassortative networks simply have nodes connected to unlike nodes—no measure of how unlike nodes are.

- ▶ Minimum value of r occurs when all links between non-like nodes: $\text{Tr}\, e_{\mu\mu} = 0$.

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$$r_{\min} = \frac{-||E^2||_1}{1 - ||E^2||_1}$$

where $-1 \leq r_{\min} < 0$.

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Scalar quantities

- ▶ Now consider nodes defined by a scalar integer quantity.

- ▶ Examples: age in years, height in inches, number of friends, ...

- ▶ e_{jk} = **Pr** a randomly chosen edge connects a node with value j to a node with value k.

- ▶ a_j and b_k are defined as before.

- ▶ Can now measure correlations between nodes based on this scalar quantity using standard Pearson correlation coefficient (⊞):

$$r = \frac{\sum_{jk} j\,k\,(e_{jk} - a_j b_k)}{\sigma_a \sigma_b} = \frac{\langle jk \rangle - \langle j \rangle_a \langle k \rangle_b}{\sqrt{\langle j^2 \rangle_a - \langle j \rangle_a^2}\sqrt{\langle k^2 \rangle_b - \langle k \rangle_b^2}}$$

- ▶ This is the observed normalized deviation from randomness in the product jk.

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- e_{jk} = **Pr** a randomly chosen edge connects a node with value j to a node with value k.
- a_j and b_k are defined as before.
- Can now measure correlations between nodes based on this scalar quantity using standard Pearson correlation coefficient (⊞):

$$r = \frac{\sum_{jk} j\,k(e_{jk} - a_j b_k)}{\sigma_a \sigma_b} = \frac{\langle jk \rangle - \langle j \rangle_a \langle k \rangle_b}{\sqrt{\langle j^2 \rangle_a - \langle j \rangle_a^2}\sqrt{\langle k^2 \rangle_b - \langle k \rangle_b^2}}$$

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Degree-degree correlations

- ▶ Natural correlation is between the degrees of connected nodes.

- ▶ Now define e_{jk} with a slight twist:

$$e_{jk} = \mathbf{Pr} \left(\begin{array}{l} \text{an edge connects a degree } j+1 \text{ node} \\ \text{to a degree } k+1 \text{ node} \end{array} \right)$$

$$= \mathbf{Pr} \left(\begin{array}{l} \text{an edge runs between a node of in-degree } j \\ \text{and a node of out-degree } k \end{array} \right)$$

- ▶ Useful for calculations (as per R_k)

- ▶ Important: Must separately define P_0 as the $\{e_{jk}\}$ contain no information about isolated nodes.

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Degree-degree correlations

▶ Notation reconciliation for undirected networks:

$$r = \frac{\sum_{jk} j\,k(e_{jk} - R_j R_k)}{\sigma_R^2}$$

where, as before, R_k is the probability that a randomly chosen edge leads to a node of degree $k + 1$, and

$$\sigma_R^2 = \sum_j j^2 R_j - \left[\sum_j j R_j \right]^2 .$$

Degree-degree correlations

Error estimate for r:

- ▶ Remove edge i and recompute r to obtain r_i.

- ▶ Repeat for all edges and compute using the jackknife method (⊞) [1]

$$\sigma_r^2 = \sum_i (r_i - r)^2.$$

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Measurements of degree-degree correlations

	Group	Network	Type	Size n	Assortativity r	Error σ_r
Social	a	Physics coauthorship	undirected	52 909	0.363	0.002
	a	Biology coauthorship	undirected	1 520 251	0.127	0.0004
	b	Mathematics coauthorship	undirected	253 339	0.120	0.002
	c	Film actor collaborations	undirected	449 913	0.208	0.0002
	d	Company directors	undirected	7 673	0.276	0.004
	e	Student relationships	undirected	573	-0.029	0.037
	f	Email address books	directed	16 881	0.092	0.004
Technological	g	Power grid	undirected	4 941	-0.003	0.013
	h	Internet	undirected	10 697	-0.189	0.002
	i	World Wide Web	directed	269 504	-0.067	0.0002
	j	Software dependencies	directed	3 162	-0.016	0.020
Biological	k	Protein interactions	undirected	2 115	-0.156	0.010
	l	Metabolic network	undirected	765	-0.240	0.007
	m	Neural network	directed	307	-0.226	0.016
	n	Marine food web	directed	134	-0.263	0.037
	o	Freshwater food web	directed	92	-0.326	0.031

▶ Social networks tend to be assortative (homophily)

▶ Technological and biological networks tend to be disassortative

Spreading on degree-correlated networks

▶ Next: Generalize our work for random networks to degree-correlated networks.

▶ As before, by allowing that a node of degree k is activated by one neighbor with probability b_{k1}, we can handle various problems:

1. find the giant component size.

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3. find the probability of spreading for simple threshold models.

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- ▶ Goal: Find $f_{n,j}$ = **Pr** an edge emanating from a degree $j + 1$ node leads to a finite active subcomponent of size n.
- ▶ Repeat: a node of degree k is in the game with probability b_{k1}.
- ▶ Define $\vec{b}_1 = [b_{k1}]$.
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▶ Recursive relationship:

$$F_j(x; \vec{b}_1) = x^0 \sum_{k=0}^{\infty} \frac{e_{jk}}{R_j}(1 - b_{k+1,1})$$
$$+ x \sum_{k=0}^{\infty} \frac{e_{jk}}{R_j} b_{k+1,1} \left[F_k(x; \vec{b}_1) \right]^k.$$

▶ First term = **Pr** that the first node we reach is not in the game.

▶ Second term involves **Pr** we hit an active node which has k outgoing edges.

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- Differentiate $F_j(x; \vec{b}_1)$, set $x = 1$, and rearrange.
- We use $F_k(1; \vec{b}_1) = 1$ which is true when no giant component exists. We find:

$$R_j F_j'(1; \vec{b}_1) = \sum_{k=0}^{\infty} e_{jk} b_{k+1,1} + \sum_{k=0}^{\infty} k e_{jk} b_{k+1,1} F_k'(1; \vec{b}_1)$$

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Spreading on degree-correlated networks

- In matrix form, we have

$$\mathbf{A}_{\mathbf{E}, \vec{b}_1} \vec{F}'(1; \vec{b}_1) = \mathbf{E} \vec{b}_1$$

where

$$\left[\mathbf{A}_{\mathbf{E}, \vec{b}_1}\right]_{j+1, k+1} = \delta_{jk} R_k - k b_{k+1,1} e_{jk},$$

$$\left[\vec{F}'(1; \vec{b}_1)\right]_{k+1} = F_k'(1; \vec{b}_1),$$

$$[\mathbf{E}]_{j+1, k+1} = e_{jk}, \text{ and } \left[\vec{b}_1\right]_{k+1} = b_{k+1,1}.$$

Spreading on degree-correlated networks

- So, in principle at least:

$$\vec{F}'(1; \vec{b}_1) = \mathbf{A}^{-1}_{\mathbf{E}, \vec{b}_1} \, \mathbf{E} \vec{b}_1.$$

- Now: as $\vec{F}'(1; \vec{b}_1)$, the average size of an active component reached along an edge, increases, we move towards a transition to a giant component.

- Right at the transition, the average component size explodes.

- Exploding inverses of matrices occur when their determinants are 0.

- The condition is therefore:

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$$\det \mathbf{A}_{\mathbf{E}, \vec{b}_1} = \det \left[\delta_{jk} R_{k-1} - (k-1) b_{k,1} e_{j-1,k-1} \right] = 0.$$

► The above collapses to our standard contagion condition when $e_{jk} = R_j R_k$.

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We'll next find two more pieces:

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2. S, the expected extent of activation given a small seed.

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- ▶ Truly final piece: Find final size using approach of Gleeson[2], a generalization of that used for uncorrelated random networks.

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$$\theta_{j,t+1} = G_j(\vec{\theta}_t) = \phi_0 + (1 - \phi_0) \times$$

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Assortativity and Mixing

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Assortativity by degree

Contagion

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- ▶ Condition for spreading is therefore dependent on eigenvalues of this matrix:

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How the giant component changes with assortativity
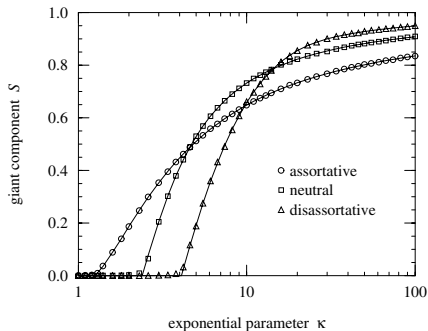
from Newman, 2002 [3]

- ► More assortative networks percolate for lower average degrees
- ► But disassortative networks end up with higher extents of spreading.

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