Assortativity and Mixing

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Definition

General mixing

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Contag

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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 [5, 6], and Boguñá and Serano. [1].

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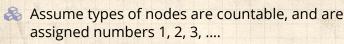
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General mixing between node categories



Consider networks with directed edges.

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

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

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

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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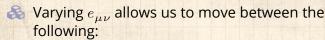
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Notes:



 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.

- $\ref{Disassortative}$ 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 [6]:

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

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

- Tr 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.
- $3 ||E^2||_1$ is a normalization factor so $r_{\text{max}} = 1$.
- $lap{N}$ When Tr $e_{\mu\mu}=1$, we have r=1.
- $\red{\$}$ When $e_{\mu\mu}=a_{\mu}b_{\mu}$, we have r=0. \checkmark

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Correlation coefficient:

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Notes:



Rrightarrow r = -1 is inaccessible if three or more types are present.



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



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



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

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



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Watch your step

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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).

 $\begin{cases} \&a_j \end{case}$ and b_k are defined as before.

Can now measure correlations between nodes based on this scalar quantity using standard Pearson correlation coefficient ☑:

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

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

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Degree-degree correlations

- Natural correlation is between the degrees of connected nodes.
- $\red {\mathbb R}$ Now define e_{jk} with a slight twist:

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

= **Pr** $\left(\begin{array}{c}$ an edge runs between a node of in-degree j and a node of out-degree k

- & Useful for calculations (as per R_k)
- Important: Must separately define P_0 as the $\{e_{jk}\}$ contain no information about isolated nodes.
- $\ \ \,$ Directed networks still fine but we will assume from here on that $e_{jk}=e_{kj}.$

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Degree-degree correlations



Notation reconciliation for undirected networks:

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

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

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

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Degree-degree correlations

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Error estimate for r:



 \mathbb{R} Remove edge i and recompute r to obtain r_i .

Repeat for all edges and compute using the jackknife method [3]

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

Mildly sneaky as variables need to be independent for us to be truly happy and edges are correlated...

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Measurements of degree-degree correlations

	Group	Network	Туре	Size n	Assortativity r	Error σ
	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
Social	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
	g	Power grid	undirected	4 941	-0.003	0.013
Technological	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
	k	Protein interactions	undirected	2 115	-0.156	0.010
	- 1	Metabolic network	undirected	765	-0.240	0.007
Biological	m	Neural network	directed	307	-0.226	0.016
	n	Marine food web	directed	134	-0.263	0.037
	0	Freshwater food web	directed	92	-0.326	0.031



Social networks tend to be assortative (homophily)

Technological and biological networks tend to be disassortative

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"I like it"

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

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activated by one neighbor with probability B_{k1} , we can handle various problems:

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- 1. find the giant component size.
- 2. find the probability and extent of spread for simple disease models.
- 3. find the probability of spreading for simple threshold models.







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 \mathfrak{S} 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} .

 \bigotimes Define $\vec{B}_1 = [B_{k_1}]$.

Plan: Find the generating function $F_i(x; \vec{B}_1) = \sum_{n=0}^{\infty} f_{n,j} x^n$.

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Recursive relationship:

$$\begin{split} F_j(x;\vec{B}_1) &= x^0 \sum_{k=0}^{\infty} \frac{e_{jk}}{R_j} (1 - B_{k+1,1}) \\ &+ x \sum_{k=0}^{\infty} \frac{e_{jk}}{R_j} B_{k+1,1} \left[F_k(x;\vec{B}_1) \right]^k. \end{split}$$

- First term = Pr (that the first node we reach is not in the game).
- Second term involves \mathbf{Pr} (we hit an active node which has k outgoing edges).
- Next: find average size of active components reached by following a link from a degree j+1 node = $F'_j(1; \vec{B}_1)$.

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

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& Rearranging and introducing a sneaky δ_{ik} :

$$\sum_{k=0}^{\infty} \left(\delta_{jk} R_k - k B_{k+1,1} e_{jk} \right) F_k'(1; \vec{B}_1) = \sum_{k=0}^{\infty} e_{jk} B_{k+1,1}.$$





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In matrix form, we have

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

where

$$\begin{split} \left[\mathbf{A}_{\mathbf{E},\vec{B}_1} \right]_{j+1,k+1} &= \delta_{jk} R_k - k B_{k+1,1} e_{jk}, \\ \left[\vec{F}'(1;\vec{B}_1) \right]_{k+1} &= F_k'(1;\vec{B}_1), \\ \left[\mathbf{E} \right]_{j+1,k+1} &= e_{jk}, \text{ and } \left[\vec{B}_1 \right]_{k+1} = B_{k+1,1}. \end{split}$$

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So, in principle at least:

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

- Arr 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:

$$\mathsf{det} \mathbf{A}_{\mathbf{E},\vec{B}_1} = 0$$

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General condition details:

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

The above collapses to our standard contagion condition when $e_{ik} = R_i R_k$ (see next slide). [2]

3 When $\vec{B}_1 = B\vec{1}$, we have the condition for a simple disease model's successful spread

$$\det\left[\delta_{jk} R_{k-1} - B(k-1) e_{j-1,k-1}\right] = 0.$$

 \mathbb{R} When $\vec{B}_1 = \vec{1}$, we have the condition for the existence of a giant component:

$$\det\left[\delta_{jk}R_{k-1} - (k-1)e_{j-1,\,k-1}\right] = 0.$$

Bonusville: We'll find a much better version of this set of conditions later...

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Retrieving the cascade condition for uncorrelated networks

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We'll next find two more pieces:

- 1. P_{trig} , the probability of starting a cascade
- 2. S, the expected extent of activation given a small seed.

Triggering probability:

Generating function:

$$H(x; \vec{B}_1) = x \sum_{k=0}^{\infty} P_k \left[F_{k-1}(x; \vec{B}_1) \right]^k.$$

Generating function for vulnerable component size is more complicated.

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Want probability of not reaching a finite component.

$$\begin{split} P_{\mathrm{trig}} &= S_{\mathrm{trig}} = & 1 - H(1; \vec{B}_1) \\ &= & 1 - \sum_{k=0}^{\infty} P_k \left[F_{k-1}(1; \vec{B}_1) \right]^k. \end{split}$$



 \clubsuit Last piece: we have to compute $F_{k-1}(1; \vec{B}_1)$.



Nastier (nonlinear)—we have to solve the recursive expression we started with when x = 1:

$$\begin{split} F_j(1;\vec{B}_1) &= \sum_{k=0}^{\infty} \frac{e_{jk}}{R_j} (1 - B_{k+1,1}) + \\ &\qquad \qquad \sum_{k=0}^{\infty} \frac{e_{jk}}{R_j} B_{k+1,1} \left[F_k(1;\vec{B}_1) \right]^k. \end{split}$$



Iterative methods should work here.

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Truly final piece: Find final size using approach of Gleeson [4], a generalization of that used for uncorrelated random networks.

Need to compute $\theta_{j,t}$, the probability that an edge leading to a degree j node is infected at time t.

🙈 Evolution of edge activity probability:

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

$$\sum_{k=1}^{\infty} \frac{e_{j-1,k-1}}{R_{j-1}} \sum_{i=0}^{k-1} \binom{k-1}{i} \theta_{k,t}^{i} (1-\theta_{k,t})^{k-1-i} B_{ki}.$$

Overall active fraction's evolution:

$$\phi_{t+1} = \phi_0 + (1 - \phi_0) \sum_{k=0}^{\infty} P_k \sum_{i=0}^k \binom{k}{i} \theta_{k,t}^{\,i} (1 - \theta_{k,t})^{k-i} B_{ki}.$$

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As before, these equations give the actual evolution of ϕ_t for synchronous updates.

 \red Contagion condition follows from $\vec{\theta}_{t+1} = \vec{G}(\vec{\theta}_t)$.

 \Longrightarrow Expand \vec{G} around $\vec{\theta}_0 = \vec{0}$.

$$\theta_{j,t+1} = G_j(\vec{0}) + \sum_{k=1}^{\infty} \frac{\frac{\partial G_j(\vec{0})}{\partial \theta_{k,t}}}{\partial \theta_{k,t}} \theta_{k,t} + \frac{1}{2!} \sum_{k=1}^{\infty} \frac{\partial^2 G_j(\vec{0})}{\partial \theta_{k,t}^2} \theta_{k,t}^2 + \dots \\ \text{Contagion Spreading contriguents produced in the product of the product of$$

A If $G_i(\vec{0}) \neq 0$ for at least one j, always have some infection.

 \Re If $G_j(\vec{0}) = 0 \,\forall j$, want largest eigenvalue $\left[\frac{\partial G_j(\vec{0})}{\partial \theta_{k,t}}\right] > 1.$

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

$$\frac{\partial G_j(\vec{0})}{\partial \theta_{k,t}} = \frac{e_{j-1,k-1}}{R_{j-1}}(k-1)B_{k1}$$

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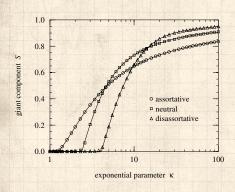
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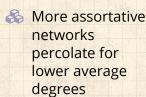




How the giant component changes with assortativity:



from Newman, 2002 [5]



But disassortative networks end up with higher extents of spreading.

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Toy guns don't pretend blow up things ...

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Robust-yet-Fragileness of the Death Star

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