

# Assortativity and Mixing

Last updated: 2018/03/23, 20:59:06

Complex Networks | @networksvox  
CSYS/MATH 303, Spring, 2018

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Definition

General mixing

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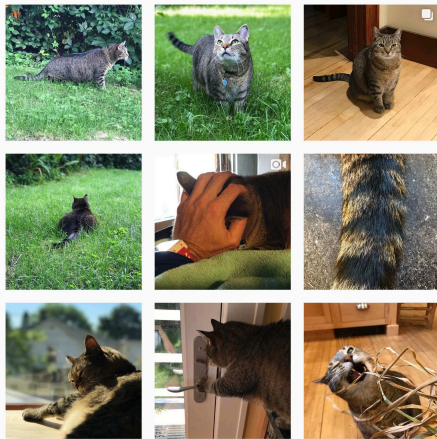
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## Special Guest Executive Producer



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 On Instagram at [pratchett\\_the\\_cat](https://www.instagram.com/pratchett_the_cat) 



# Outline

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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 <sup>[5, 6]</sup>, and Boguñá and Serano. <sup>[1]</sup>.

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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.

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

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

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

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

 Requirements:

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

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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** [6]:

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

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  $r = 1$ . ✓
-  When  $e_{\mu\mu} = a_{\mu} b_{\mu}$ , we have  $r = 0$ . ✓

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# Correlation coefficient:

## Notes:

-   $r = -1$  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.
-  Minimum value of  $r$  occurs when all links between non-like nodes:  $\text{Tr } e_{\mu\mu} = 0$ .


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

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

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# Watch your step

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zzzhhhhwoooommmmm

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NuhnuhNuhnuhNuhnuhNuhnuhNuhnuhNuhnuh

...

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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, ...
-   $e_{jk} = \mathbf{Pr}$  (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 

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

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


# Degree-degree correlations


 Natural correlation is between the degrees of connected nodes.

 Now define  $e_{jk}$  with a slight twist:

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

 Useful for calculations (as per  $R_k$ )

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

 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:

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

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

## Error estimate for $r$ :

-  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...





# Measurements of degree-degree correlations

	Group	Network	Type	Size $n$	Assortativity $r$	Error $\sigma_r$
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

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 Social networks tend to be assortative (homophily)

 Technological and biological networks tend to be disassortative



# Hot lava

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"I like it" ↗

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# Spreading on degree-correlated networks

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 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  $B_{k,1}$ , we can handle various problems:

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.



# Spreading on degree-correlated networks

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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  $\vec{B}_1 = [B_{k1}]$ .

 **Plan:** Find the generating function


$$F_j(x; \vec{B}_1) = \sum_{n=0}^{\infty} f_{n,j} x^n.$$





# Spreading on degree-correlated networks

 Recursive relationship:

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

 **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).

 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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 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:

$$R_j F'_j(1; \vec{B}_1) = \sum_{k=0}^{\infty} e_{jk} B_{k+1,1} + \sum_{k=0}^{\infty} k e_{jk} B_{k+1,1} F'_k(1; \vec{B}_1).$$

 Rearranging and introducing a sneaky  $\delta_{jk}$ :

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

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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

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

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# Spreading on degree-correlated networks

 So, in principle at least:

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

 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:

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

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# Spreading on degree-correlated networks

General condition details:

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

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

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

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

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

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

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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# Spreading on degree-correlated networks


We'll next find two more pieces:

1.  $P_{\text{trig}}$ , 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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# Spreading on degree-correlated networks


-  Want probability of **not reaching** a finite component.

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

-  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  $x = 1$ :

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

-  Iterative methods should work here.

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# Spreading on degree-correlated networks

-  **Truly final piece:** Find final size using approach of Gleeson<sup>[4]</sup>, 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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# Spreading on degree-correlated networks

- As before, these equations give the actual evolution of  $\phi_t$  for synchronous updates.
- Contagion condition follows from  $\vec{\theta}_{t+1} = \vec{G}(\vec{\theta}_t)$ .
- Expand  $\vec{G}$  around  $\vec{\theta}_0 = \vec{0}$ .

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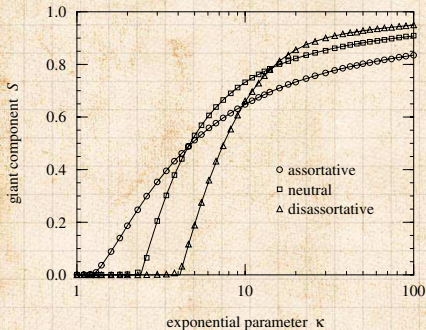
$$\theta_{j,t+1} = G_j(\vec{0}) + \sum_{k=1}^{\infty} \frac{\partial G_j(\vec{0})}{\partial \theta_{k,t}} \theta_{k,t} + \frac{1}{2!} \sum_{k=1}^{\infty} \frac{\partial^2 G_j(\vec{0})}{\partial \theta_{k,t}^2} \theta_{k,t}^2 + \dots$$

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

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



# How the giant component changes with assortativity:



from Newman, 2002 [5]



More assortative networks percolate for lower average degrees



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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# Splsshht

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# Robust-yet-Fragileness of the Death Star

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