# Assortativity and Mixing

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Definition

General mixing

Assortativity by degree

Contagion Spreading condition Triggering probability Expected size



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# Outline

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Random networks with arbitrary degree distributions cover much territory but do not represent all networks. The PoCSverse Assortativity and Mixing 5 of 40

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- 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.

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- 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.

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

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

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- 🛞 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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Assume types of nodes are countable, and are assigned numbers 1, 2, 3, ....

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

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

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

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

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- Solution Varying  $e_{\mu\nu}$  allows us to move between the following:
  - Perfectly assortative networks where nodes only connect to like nodes, and the network breaks into subnetworks.

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#### $\Im$ 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  $\sum_{\mu} e_{\mu\mu} = 1$ .

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- 2. Uncorrelated networks (as we have studied so far)

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 $e_{\mu\nu} = a_{\mu}b_{\nu}.$ 

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

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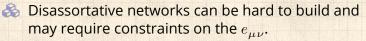
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2. Uncorrelated networks (as we have studied so far) For these we must have independence:

 $e_{\mu\nu} = a_{\mu}b_{\nu}.$ 

- 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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Quantify the level of assortativity with the following assortativity coefficient<sup>[6]</sup>:

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

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

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Tr E is the fraction of edges that are within groups.

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3  $1 - ||E^2||_1$  is a normalization factor so  $r_{max} = 1$ .

 $\Im$  When Tr  $e_{\mu\mu} = 1$ , we have r = 1.

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



#### Notes:

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

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#### 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.

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# Correlation coefficient:

## Notes:

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- 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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## zzzhhhhwoooommmmmm

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## NuhnuhNuhnuhNuhnuhNuhnuhNuhnuh

...

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Now consider nodes defined by a scalar integer quantity. The PoCSverse Assortativity and Mixing 13 of 40

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- Now consider nodes defined by a scalar integer quantity.
- Examples: age in years, height in inches, number of friends, ...

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- Now consider nodes defined by a scalar integer quantity.
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- e<sub>jk</sub> = Pr (a randomly chosen edge connects a node with value j to a node with value k).

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- Can now measure correlations between nodes based on this scalar quantity using standard Pearson correlation coefficient <sup>C</sup>:

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

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

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Natural correlation is between the degrees of connected nodes. The PoCSverse Assortativity and Mixing 14 of 40

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Natural correlation is between the degrees of connected nodes.

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

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

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 $\bigotimes$  Useful for calculations (as per  $R_k$ )

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   Important: Must separately define P<sub>0</sub> as the {e<sub>jk</sub>} contain no information about isolated nodes.



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& Useful for calculations (as per R<sub>k</sub>)
 & Important: Must separately define P<sub>0</sub> as the {e<sub>jk</sub>} contain no information about isolated nodes.
 & Directed networks still fine but we will assume from here on that e<sub>jk</sub> = e<sub>kj</sub>.

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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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## Error estimate for *r*:

 $\mathfrak{R}$  Remove edge *i* and recompute *r* to obtain  $r_i$ .

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## Error estimate for *r*:

 $\Re$  Remove edge *i* and recompute *r* to obtain  $r_i$ .

Repeat for all edges and compute using the jackknife method <sup>[3]</sup>

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

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## Error estimate for r:

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Repeat for all edges and compute using the jackknife method <sup>[3]</sup>

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

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 $\sigma$
	а	Physics coauthorship	undirected	52 909	0.363	0.002
	а	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
	е	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

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Social networks tend to be assortative (homophily)
 Technological and biological networks tend to be disassortative





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## Next: Generalize our work for random networks to 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  $B_{k1}$ , we can handle various problems:



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References

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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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References

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.
- 2. find the probability and extent of spread for simple disease models.



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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  $B_{k1}$ , 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.



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Solution Goal: Find  $f_{n,j} = \mathbf{Pr}$  an edge emanating from a degree j + 1 node leads to a finite active subcomponent of size n.

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References

Solution Goal: Find  $f_{n,j} = \mathbf{Pr}$  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  $B_{k1}$ .



#### The PoCSverse Assortativity and Mixing 22 of 40

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References

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Repeat: a node of degree k is in the game with probability  $B_{k1}$ .

 $\bigotimes$  Define  $\vec{B}_1 = [B_{k,1}].$ 



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References

Solution Goal: Find  $f_{n,j} = \mathbf{Pr}$  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  $\vec{B}_1 = [B_{k1}]$ .

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



🚳 Recursive relationship:

$$\begin{split} F_{j}(x;\vec{B}_{1}) &= x^{0}\sum_{k=0}^{\infty}\frac{e_{jk}}{R_{j}}(1-B_{k+1,1}) \\ &+ x\sum_{k=0}^{\infty}\frac{e_{jk}}{R_{j}}B_{k+1,1}\left[F_{k}(x;\vec{B}_{1})\right]^{k} \end{split}$$

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🚳 Recursive relationship:

$$\begin{split} F_{j}(x;\vec{B}_{1}) &= x^{0}\sum_{k=0}^{\infty}\frac{e_{jk}}{R_{j}}(1-B_{k+1,1}) \\ &+ x\sum_{k=0}^{\infty}\frac{e_{jk}}{R_{j}}B_{k+1,1}\left[F_{k}(x;\vec{B}_{1})\right]^{k} \end{split}$$

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#### First term = Pr (that the first node we reach is not in the game).



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- 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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- 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 + 1node =  $F'_{j}(1; \vec{B}_{1})$ .



 $\Im$  Differentiate  $F_i(x; \vec{B}_1)$ , set x = 1, and rearrange.

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Differentiate F<sub>j</sub>(x; B<sub>1</sub>), set x = 1, and rearrange.
 We use F<sub>k</sub>(1; B<sub>1</sub>) = 1 which is true when no giant component exists.

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Differentiate F<sub>j</sub>(x; B<sub>1</sub>), set x = 1, and rearrange.
We use F<sub>k</sub>(1; B<sub>1</sub>) = 1 which is true when no giant component exists. We find:

$$R_{j}F_{j}'(1;\vec{B}_{1}) = \sum_{k=0}^{\infty} e_{jk}B_{k+1,1} + \sum_{k=0}^{\infty} ke_{jk}B_{k+1,1}F_{k}'(1;\vec{B}_{1})^{\mathbb{R}}$$

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Differentiate F<sub>j</sub>(x; B<sub>1</sub>), set x = 1, and rearrange.
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 $\mathfrak{S}$  Rearranging and introducing a sneaky  $\delta_{ik}$ :

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



🚳 In matrix form, we have

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

where

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

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🚳 So, in principle at least:

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

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🙈 So, in principle at least:

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

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.

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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.

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Right at the transition, the average component size explodes.

Exploding inverses of matrices occur when their determinants are 0.

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🙈 So, in principle at least:

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

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

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## Spreading on degree-correlated networks & General condition details:

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

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

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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  $e_{jk} = R_j R_k$  (see next slide).<sup>[2]</sup>

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

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

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

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

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

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

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

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. $P_{\text{trig}}$ , the probability of starting a cascade

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#### 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.

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#### 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:

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

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#### 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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🚳 Want probability of not reaching a finite component.

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

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Want probability of not reaching a finite component.

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

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

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Want probability of not reaching a finite component.

> $P_{\rm trig} = S_{\rm trig} = \! 1 - H(1; \vec{B}_1)$  $= 1 - \sum_{l=0}^{\infty} P_k \left[ F_{k-1}(1; \vec{B}_1) \right]^k.$

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 $\bigotimes$  Last piece: we have to compute  $F_{k-1}(1; \vec{B}_1)$ . Astier (nonlinear)—we have to solve the recursive expression we started with when x = 1:  $F_j(1; \vec{B}_1) = \sum_{k=0}^{\infty} \frac{e_{jk}}{R_i} (1 - B_{k+1,1}) +$  $\sum_{k=0}^{\infty} \frac{e_{jk}}{R_{j}} B_{k+1,1} \left[ F_{k}(1;\vec{B}_{1}) \right]^{k}.$ 





Want probability of not reaching a finite component.

> $P_{\rm trig} = S_{\rm trig} = \! 1 - H(1; \vec{B}_1)$  $= 1 - \sum_{k=0}^{\infty} P_k \left[ F_{k-1}(1; \vec{B}_1) \right]^k.$

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lterative methods should work here.

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Truly final piece: Find final size using approach of Gleeson<sup>[4]</sup>, a generalization of that used for uncorrelated random networks. The PoCSverse Assortativity and Mixing 33 of 40

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- 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.

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- 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 θ<sub>j,t</sub>, the probability that an edge leading to a degree j node is infected at time t.
   Evolution of edge activity probability:

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

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

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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  $\phi_t$  for synchronous updates.

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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  $\vec{\theta}_0 = \vec{0}$ . The PoCSverse Assortativity and Mixing 34 of 40

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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  $\vec{\theta}_0 = \vec{0}$ . The PoCSverse Assortativity and Mixing 34 of 40

Definition

General mixing

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

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  $\vec{\theta}_0 = \vec{0}$ . The PoCSverse Assortativity and Mixing 34 of 40

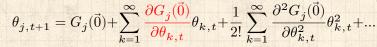
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If G<sub>j</sub>(0) ≠ 0 for at least one j, always have some infection.
 If G<sub>j</sub>(0) = 0 ∀ j, want largest eigenvalue

 $\left[\frac{\partial G_j(\vec{0})}{\partial \theta_{k,t}}\right] > 1.$ 



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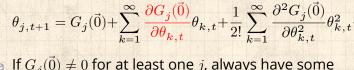
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Solution If  $G_j(\vec{0}) \neq 0$  for at least one j, always have some infection.

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

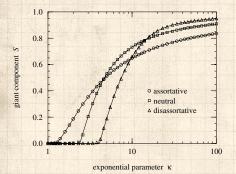
Condition for spreading is therefore dependent on eigenvalues of this matrix:

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

Insert question from assignment 9 🖸



# How the giant component changes with assortativity:



from Newman, 2002<sup>[5]</sup>

🚳 More assortative networks percolate for lower average degrees 3 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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