# Assortativity and Mixing

Complex Networks
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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 [4, 5], and Boguñá and Serano. [1].





## 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:

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





## 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.





## Correlation coefficient:

- Quantify the level of assortativity with the following assortativity coefficient [5]:

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

where $||\cdot||_1$ is the 1-norm = sum of a matrix's entries.
- $\mathrm{Tr}\,\mathbf{E}$ 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 $\mathrm{Tr}\, e_{\mu\mu} = 1$, we have $r = 1$. ✓
- When $e_{\mu\mu} = a_\mu b_\mu$, we have $r = 0$. ✓

## 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: $\mathrm{Tr}\, \mathbf{e}_{\mu\mu} = 0$.
- $$r_{\min} = \frac{-||E^2||_1}{1 - ||E^2||_1}$$
  where $-1 \le r_{\min} < 0$.




## 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 (⊞):

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

- 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:

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

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

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




## 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

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




## 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 (⊞) [2]

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

- 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 |

- 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.
  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



- 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:

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

- 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.
- Next: find average size of active components reached by following a link from a degree $j+1$ node $= F_j'(1;\vec{B}_1)$.



## Spreading on degree-correlated networks



- 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 $\delta_{jk}$:

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



## 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:

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

- 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:

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

.

## 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 $e_{jk} = R_j R_k$.
- When $\vec{B}_1 = B\vec{1}$, we have the condition for a simple disease model's successful spread

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

- 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...



## Spreading on degree-correlated networks



### We'll next find two more pieces:

1. $P_{\mathrm{trig}}$, 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.



## Spreading on degree-correlated networks



- Want probability of not reaching a finite component.

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

- 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.



## Spreading on degree-correlated networks



- Truly final piece: Find final size using approach of Gleeson [3], 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:

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



## 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 $\vec{\theta}_0 = \vec{0}$.

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

- 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:

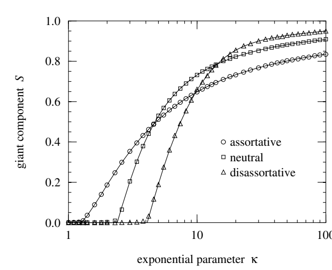
$$\frac{\partial G_j(\vec{0})}{\partial \theta_{k,t}} = \frac{e_{j-1,k-1}}{R_{j-1}}(k-1)B_{k1}$$

Insert question from assignment 9 (⊞)



## How the giant component changes with assortativity:






from Newman, 2002 [4]

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

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