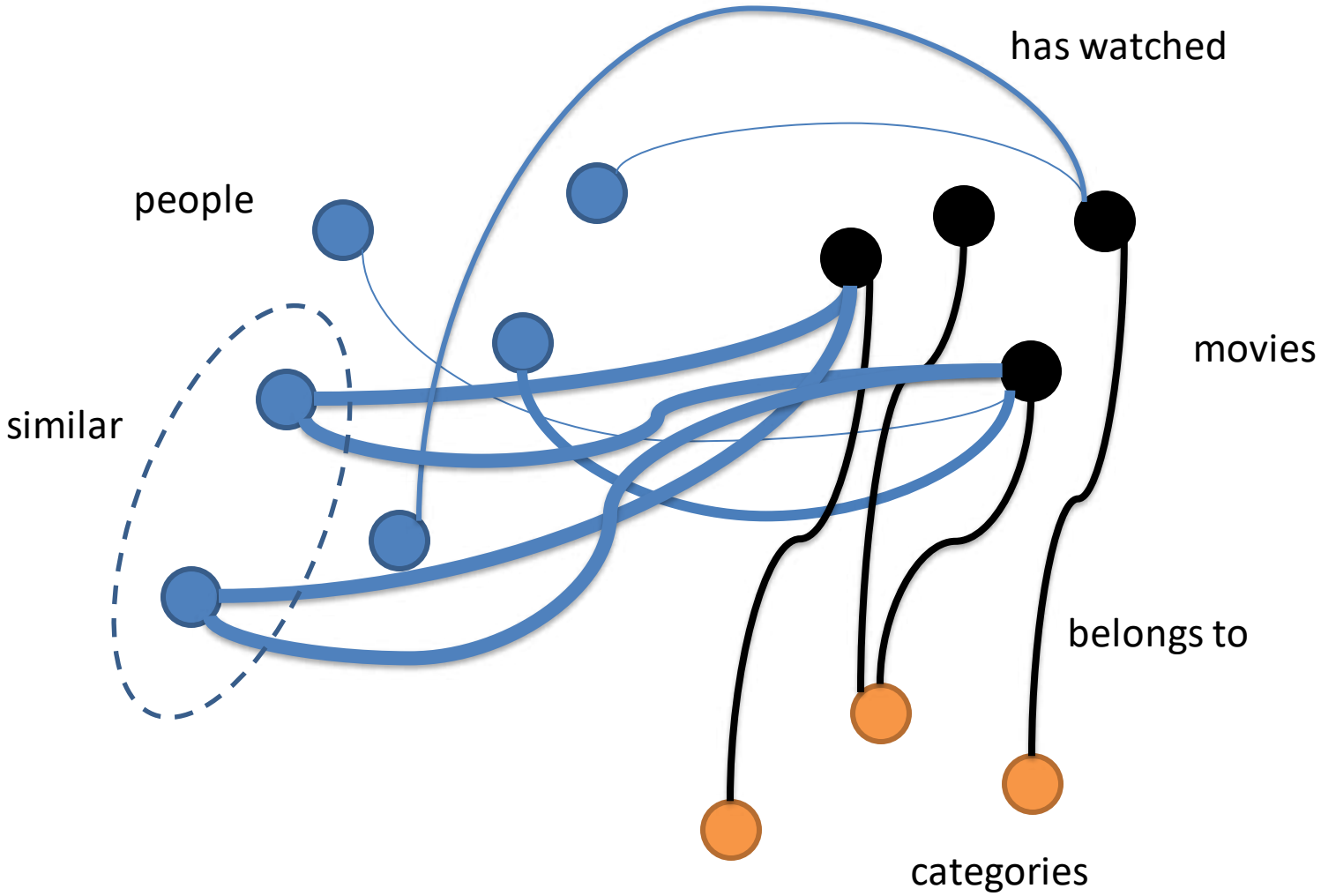
Random walk based similarities



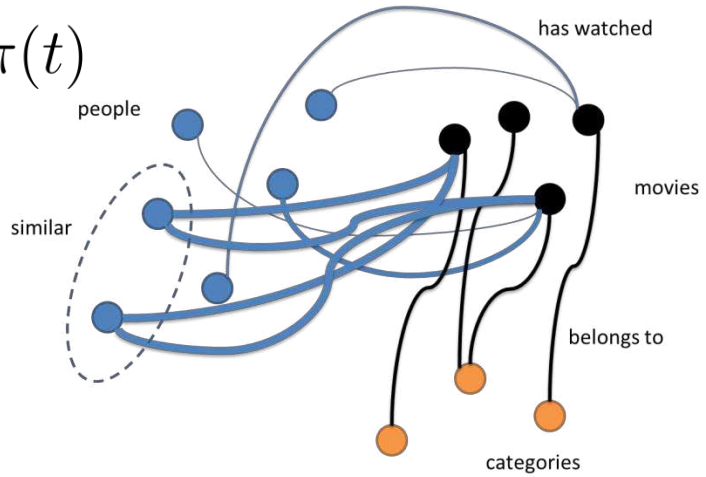
Random walk based similarities

The Markov chain (t - step, $s(t)$ - state at t) describing the sequence of nodes visited by a random walker is called a random walk. The random walk is defined with the following single-step transition probabilities of jumping from any state or node $i = s(t)$ to an adjacent node

$$j = s(t+1) : Pr(s(t+1) = j | s(t) = i) = a_{ij}/a_{ii} = p_{ij},$$

where $a_{ii} = \sum_{j=1}^{n} a_{ij}$. The probability of being in state i at time t is $\pi_i(t) = Pr(s(t) = i)$ and P is the transition matrix with entries p_{ij}. The evolution of Markov chain is given by

$$\pi(t+1) = P^T \pi(t)$$

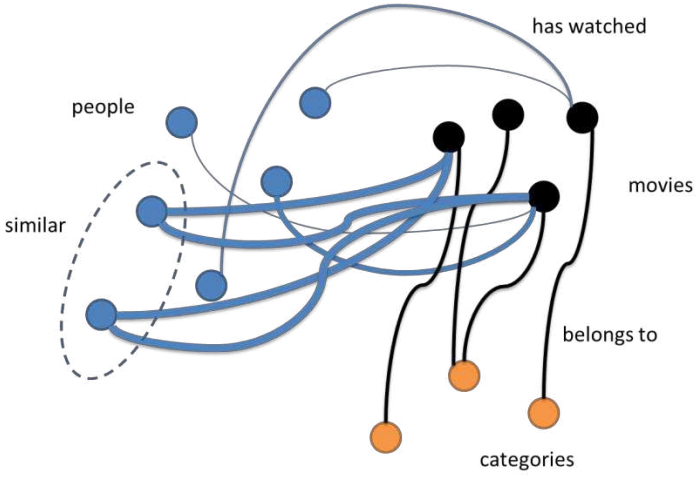


Random walk based similarities

The average first-passage time $m(k|i)$ is the average number of steps that a random walker, starting in (random) state $i \neq k$, will take to enter state k for the first time, i.e.,

$$m(k|i) = E[T_{ik}|s(0) = i], \text{ where } T_{ik} = \min(t \geq 0|s(t) = k,\ s(0) = i).$$

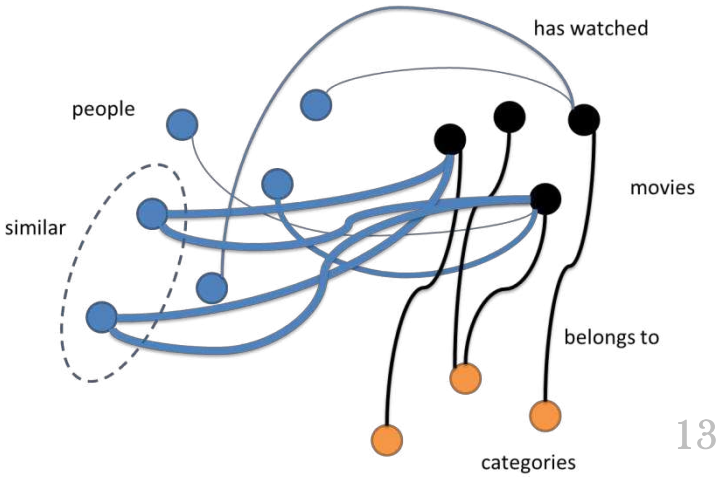
$$\begin{cases} m(k|k) = 0 \\ m(k|i) = 1 + \sum_{j=1}^{n} p_{ij}\, m(k|j), \quad \text{for } i \neq k, \end{cases}$$



Random walk based similarities

The average first-passage cost $o(k|i)$ is the average cost incurred by the random walker starting from state i to reach state k for the first time. The cost of each transition is given by $c(j|i)$.

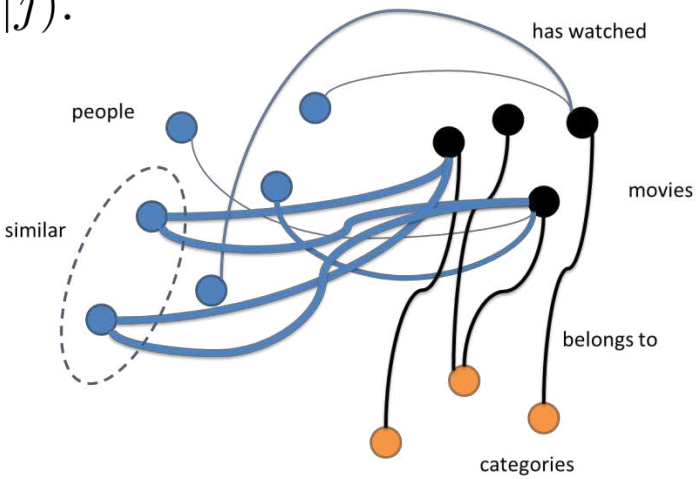
$$\begin{cases} o(k|k) = 0 \\ o(k|i) = \sum_{j=1}^{n} p_{ij}\, c(j|i) + \sum_{j=1}^{n} p_{ij}\, o(k|j), \quad \text{for } i \neq k. \end{cases}$$



Random walk based similarities

The average commute time $n(i, j)$ is the average number of steps that a random walker, starting in state $i \neq j$, will take to enter state j for the first time and go back to i, i.e.,

$$n(i, j) = m(j|i) + m(i|j).$$



Paper review 4: "Random-Walk Computation of Similarities between Nodes of a Graph with Application to Collaborative Recommendation"
Submit by 10/1/2020

Homophily and Assortative Mixing

- the tendency of individuals to associate and bond with similar others.

Examples: social networks, citation networks, web pages languages, animals

Disassortative Mixing – opposite to assortative

Example: sexual contact networks

c_i - type of vertex i, $\delta(i,j)$ - Kronecker delta

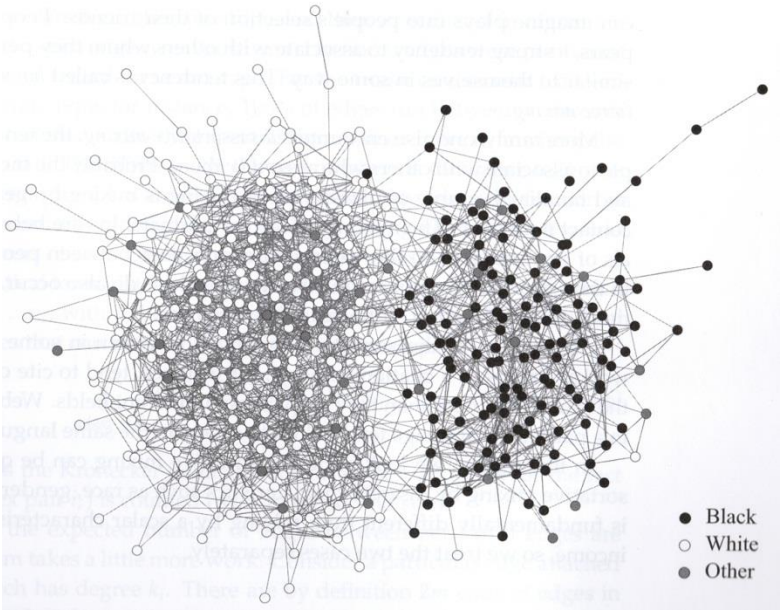
$$q = \frac{1}{2}\sum_{ij} A_{ij}\delta(c_i,c_j) - \frac{1}{2}\sum_{ij}\frac{d(i)d(j)}{2m}\delta(c_i,c_j)$$

total number of edges between similar vertices

expected number of edges between similar vertices in random model

$Q = q/m$ is called *modularity*.

Newman "Networks: An Introduction"



Friendship network at a US high school. 470 students, 14-18 yo

Q = 0.305

Modularity is a measure of the extent to which like is connected to like in a network.

Homophily and Assortative Mixing

c_i - type of vertex i, $\delta(i,j)$ - Kronecker delta

$$q = \frac{1}{2}\sum_{ij} A_{ij}\delta(c_i, c_j) - \frac{1}{2}\sum_{ij} \frac{d(i)d(j)}{2m}\delta(c_i, c_j)$$

total number of edges between similar vertices

expected number of edges between similar vertices in random model

or assortativity coefficient

$Q = q/m$ is called *modularity*.

$Q_{\max} = \frac{1}{2m}(2m - \sum_{ij} \frac{d(i)d(j)}{2m}\delta(c_i, c_j))$, normalized modularity is $Q/Q_{\max}$

LofEdges representation: $e_{rs} = \frac{1}{2m}\sum_{ij} \delta(c_i, r)\delta(c_j, s)$, $a_r = \frac{1}{2m}\sum_i d(i)\delta(c_i, r)$

$\Longrightarrow Q = \sum_r (e_{rr} - a_r^2)$.

LofEdges: nodes may have types but no info about degrees

fraction of edges between classes *r* and *s*

fraction of ends of edges attached to vertices of class *r*

Maximization of the modularity is a well-known clustering approach

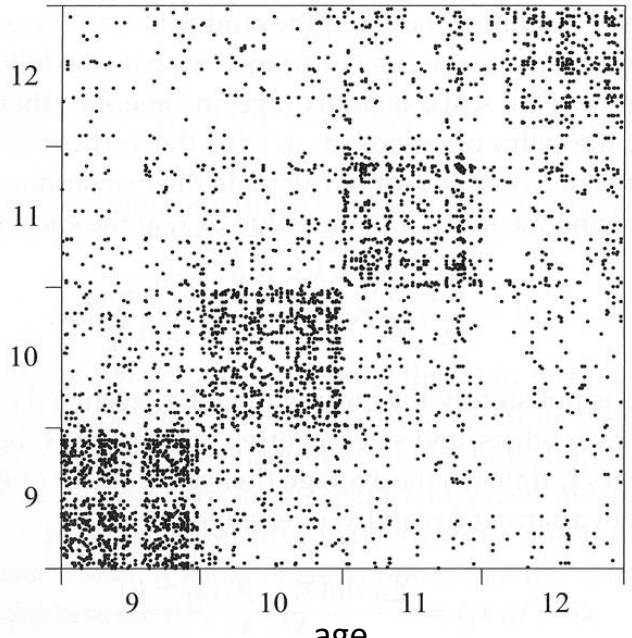
Assortative Mixing and Scalar Characteristics

values come in a particular order

In practice, the number of classes will be limited.
Reasons: complexity, bins, etc.
Example: school friends, age × age

Problem: vertices falling in different bins are different when in fact they may be similar (10.9yo≈11yo)

Newman "Networks: An Introduction"



r = 0.616

If x_i and x_j are scalars (instead of c_i and c_j then define

$$cov(x_i, x_j) = \frac{\sum_{ij} A_{ij}(x_i - \mu)(x_j - \mu)}{\sum_{ij} A_{ij}},$$

where mean $\mu = \frac{\sum_{ij} A_{ij} x_i}{\sum_{ij} A_{ij}} = 1/2m \cdot \sum_i d(i) x_i$

$$\Longrightarrow \ \ldots \ \Longrightarrow cov(x_i, x_j) = \frac{1}{2m} \sum_{ij} (A_{ij} - \frac{d(i)d(j)}{2m}) x_i x_j.$$

Assortative Coefficient

covariance

$$r = \frac{\sum_{ij}(A_{ij} - d(i)d(j)/2m)x_i x_j}{\sum_{ij}(d(i)\delta_{ij} - d(i)d(j)/2m)x_i x_j}$$

variance

1 – perfectly assortative network; **-1** - perfectly disassortative network

Example: Assortative Mixing by Degree

A special case of assortative mixing according to a scalar quantity, is that of mixing by degree. In a network that shows assortative mixing by degree the high-degree vertices will be preferentially connected to other high-degree vertices, and the low to low.

$$x_i = d(i)$$

$$cov(d(i), d(j)) = \frac{1}{2m} \sum_{ij} \left(A_{ij} - \frac{d(i)d(j)}{2m} \right) d(i)d(j)$$

$$r = \frac{\sum_{ij}(A_{ij} - d(i)d(j)/2m)d(i)d(j)}{\sum_{ij}(d(i)\delta_{ij} - d(i)d(j)/2m)d(i)d(j)}$$

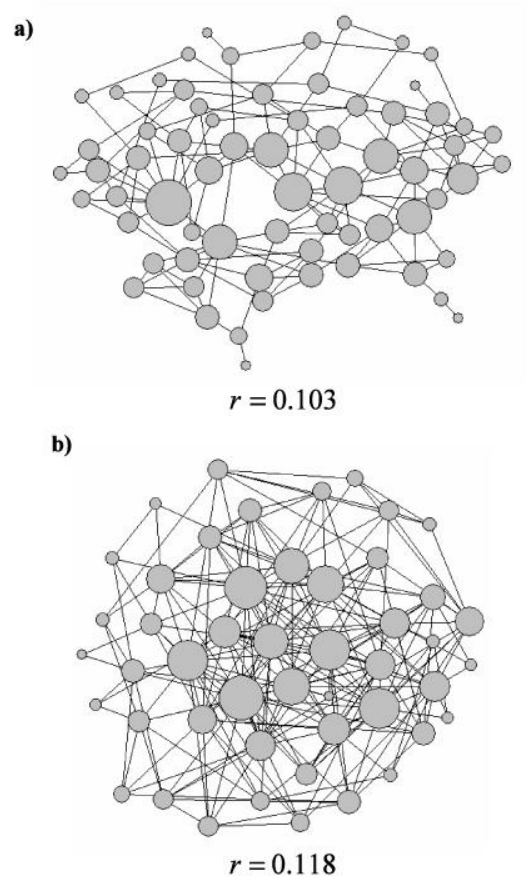
	network	n	r
real-world networks	physics coauthorship[a]	52 909	0.363
	biology coauthorship[a]	1 520 251	0.127
	mathematics coauthorship[b]	253 339	0.120
	film actor collaborations[c]	449 913	0.208
	company directors[d]	7 673	0.276
	Internet[e]	10 697	−0.189
	World-Wide Web[f]	269 504	−0.065
	protein interactions[g]	2 115	−0.156
	neural network[h]	307	−0.163
	food web[i]	92	−0.276
models	random graph[u]		0
	Callaway *et al.*[v]		$\delta/(1+2\delta)$
	Barabási and Albert[w]		0

TABLE I: Size n and assortativity coefficient r for a number of different networks: collaboration networks of (a) scientists in physics and biology [16], (b) mathematicians [17], (c) film actors [4], and (d) businesspeople [18]; (e) connections between autonomous systems on the Internet [19]; (f) undirected hyperlinks between Web pages in a single domain [6]; (g) protein-protein interaction network in yeast [20]; (h) undirected (and unweighted) synaptic connections in the neural network of the nematode *C. Elegans* [4]; (i) undirected trophic relations in the food web of Little Rock Lake, Wisconsin [21]. The last three lines give analytic results for model networks in the limit of large network size: (u) the random graph of Erdős and Rényi [22]; (v) the grown graph model of Callaway *et al.* [15]; (w) the preferential attachment model of Barabási and Albert [6].

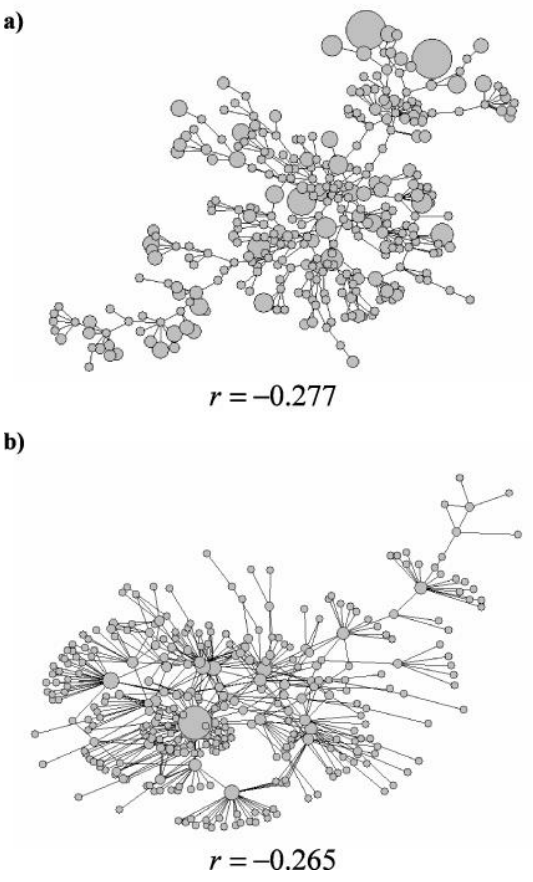
Newman "Assortative mixing in networks"

Example: Assortative Mixing by Degree

Estrada et al. "Clumpiness" mixing in complex networks



The network illustrated in Figure (a) corresponds to the inmates in a prison and that in Figure (b) to the food web. Both networks are almost of the same size, and both display uniform degree distributions and have almost identical assortativity coefficient, r = 0.103 and 0.118, respectively. However, while in the prison network the high-degree nodes are spread across the network, they are clumped together in the food web. This difference can have dramatic implications for the structure and functioning of these two systems.



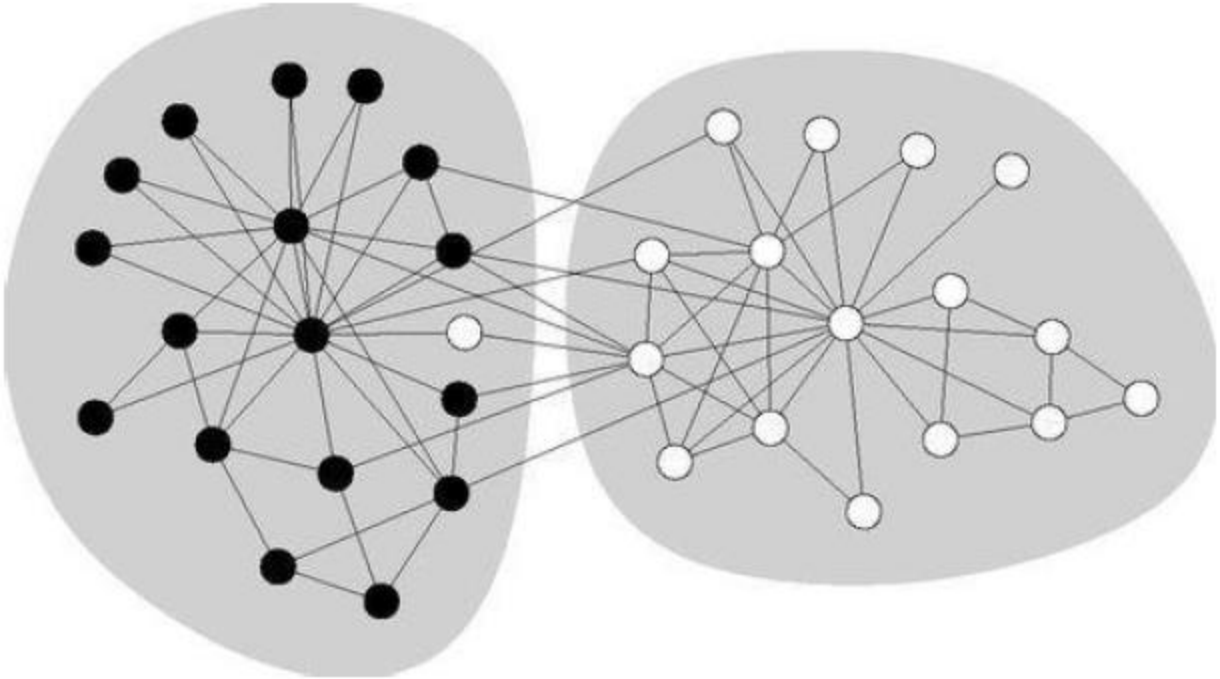
Disassortative networks. We can also find that the high-degree nodes can be separated by only two links with a low-degree node acting as a bridge or by very long paths. This situation is illustrated in sexual network in Colorado Springs (a) and the transcription interaction network of *E. coli* (b), which have almost equal negative assortative coefficients. In the former case the high-degree nodes are separated by very long chains while in the latter case most of the high-degree nodes are clumped together separated by only two or three links.

Simple Modularity Maximization

Iterative Algorithm (inspired by Kernighan-Lin algorithm for partitioning problem)

1. Choose initial division of a network into (equally sized) groups
2. Main sweep: repeatedly move the vertices that most increase or least decrease Q
3. Return to step 2 until Q no longer improves

Complexity of Step 2: $O(mn)$



Newman "Networks: An Introduction"

Spectral Modularity Maximization

$Q = \frac{1}{2m}\sum_{ij}\left(A_{ij} - \frac{d(i)d(j)}{2m}\right)\delta(c_i, c_j) = \frac{1}{2m}\sum_{ij} B_{ij}\delta(c_i, c_j)$
Note that B_{ij} has the property

$$\sum_j B_{ij} = \sum_j A_{ij} - \frac{d(i)}{2m}\sum_j d(j) = 0$$

Denote by s_i the indicator variable +1/-1 for cluster number, i.e., $\delta(c_i, c_j) = \frac{s_i s_j + 1}{2}$

modularity matrix

$$Q = \frac{1}{4m}\sum_{ij} B_{ij}s_i s_j = \frac{1}{4m}s^T B s$$

Method: relax integer constraint for s with reals and $s^T s = n$
Solve maximization problem by using Lagrange multiplier

eigenproblem

$$\frac{\partial}{\partial s_i}\left(\sum_{jk} B_{jk}s_j s_k + \beta(n - \sum_j s_j^2)\right) = 0 \Longrightarrow \sum_j B_{ij}s_j = \beta s_i \text{ or } Bs = \beta s$$

Note: In practice we cannot assign *s* with eigenvector corresponding to the largest eval (*s* is +1/-1 vector)
We choose s to be close to u_1 by maximizing $\sum_i s_i(u_1)_i$, i.e.,
$s_i = +1\ (-1)$ if $(u_1)_i\ >\ (<)\ 0$

Homework

Paper review 5 + computational problem (due 10/6/2020)

1. (50%) Paper review: Newman "Assortative mixing in networks"
2. (50%) Compute modularity

7.8 In a survey of couples in the US city of San Francisco, Catania *et al.* [65] recorded, among other things, the ethnicity of their interviewees and calculated the fraction of couples whose members were from each possible pairing of ethnic groups. The fractions were as follows:

		Women				
		Black	Hispanic	White	Other	Total
Men	Black	0.258	0.016	0.035	0.013	0.323
	Hispanic	0.012	0.157	0.058	0.019	0.247
	White	0.013	0.023	0.306	0.035	0.377
	Other	0.005	0.007	0.024	0.016	0.053
	Total	0.289	0.204	0.423	0.084	

Assuming the couples interviewed to be a representative sample of the edges in the undirected network of relationships for the community studied, and treating the vertices as being of four types—black, Hispanic, white, and other—calculate the numbers e_{rr} and a_r that appear in Eq. (7.76) for each type. Hence calculate the modularity of the network with respect to ethnicity.