Class 14: Degree Correlations I
(Chapter 7 in Textbook)

Boleslaw Szymanski

based on slides by Albert-László Barabási and Roberta Sinatra

www.BarabasiLab.com
\[ P(k) \sim (k + \kappa(p,q,m))^{-\gamma(p,q,m)} \quad \gamma \in [1, \infty) \]

-> Predicts a small-k cutoff
-> A correct model should predict all aspects of the degree distribution, not only the degree exponent.
-> Degree exponent is a continuous function of \( p, q, m \)

\[ p = 0.937 \]
\[ m = 1 \]
\[ \kappa = 31.68 \]
\[ \gamma = 3.07 \]
• Non-linear preferential attachment:

\[ \Pi(k) = \frac{k^\alpha}{\sum_i k_i^\alpha} \]

→ \( P(k) \) does not follow a power law for \( \alpha \neq 1 \)

\[ \Rightarrow \alpha < 1 : \text{stretch-exponential} \quad P(k) \approx \exp\left(-\left(k/k_0\right)^\beta\right) \]

\[ \Rightarrow \alpha > 1 : \text{no-scaling} \quad (\alpha > 2 : \text{“gelation”}) \]

BA model: $k=0$ nodes cannot acquire links, as $\Pi(k=0)=0$ (the probability that a new node will attach to it is zero)

$$\Pi(k) \approx A + k^\alpha, \alpha \leq 1$$

$A$ - initial attractiveness

Initial attractiveness shifts the degree exponent:

$$\gamma_{in} = 2 + \frac{A}{m}$$

Note: the parameter $A$ can be measured from real data, being the rate at which $k=0$ nodes acquire links, i.e. $\Pi(k=0)=A$

GROWTH CONSTRAINTS AND AGING CAUSE CUTOFFS

- Finite lifetime to acquire new edges

L. A. N. Amaral et al., PNAS 97, 11149 (2000)

- Gradual aging:
  \[ \Pi(k_i) \propto k_i(t - t_i)^{-\nu} \]
  \( \gamma \) increases with \( \nu \)

THE LAST PROBLEM: HIGH, SYSTEM-SIZE INDEPENDENT $C(N)$

Pathlength Clustering Degree Distr.

$P(k) \sim k^{-\gamma}$

Regular network

$I_{rand} = \frac{\log N}{\log \langle k \rangle}$

$C_{rand} = p = \frac{k}{N}$

$P(k) = e^{-k} \frac{\leq k \leq k}{k!}$

Erdos-Renyi

Watts-Strogatz

Barabasi-Albert

$C \sim \text{const}$

$C \sim (\ln N)^2 \frac{N}{N}$

Network Science: Evolving Network Models
Each node of the network can be either active or inactive. There are $m$ active nodes in the network in any moment.

1. Start with $m$ active, completely connected nodes.
2. Each timestep add a new node (active) that connects to $m$ active nodes.
3. Deactivate one active node with probability: $P_d(k_i) \propto (a + k_j)^{−1}$

**A MODEL WITH HIGH CLUSTERING COEFFICIENT**

\[ \Pi(k) \approx a + k \]

\[ P(k) \approx k^{−2−a/m} \]

$m = a = 2$

$m = a = 10$

$C \rightarrow C^*$ when $N \rightarrow \infty$

<table>
<thead>
<tr>
<th>Attachment Type</th>
<th>Model</th>
</tr>
</thead>
<tbody>
<tr>
<td>Linear growth, linear pref. attachment</td>
<td>$\gamma = 3$</td>
</tr>
<tr>
<td>Nonlinear preferential attachment</td>
<td>$\Pi(k_i) \sim k_i^\alpha$ no scaling for $\alpha \neq 1$</td>
</tr>
<tr>
<td>Asymptotically linear pref. attachment</td>
<td>$\gamma \rightarrow 2$ if $a_m \rightarrow \infty$</td>
</tr>
<tr>
<td></td>
<td>$\gamma \rightarrow 0$ if $a_m \rightarrow 0$</td>
</tr>
<tr>
<td>Initial attractiveness</td>
<td>$\gamma = 2$ if $A = 0$</td>
</tr>
<tr>
<td></td>
<td>$\gamma \rightarrow \infty$ if $A \rightarrow \infty$</td>
</tr>
<tr>
<td>Accelerating growth $\langle k \rangle \sim t^\theta$</td>
<td>$\gamma = 1.5$ if $\theta \rightarrow 1$</td>
</tr>
<tr>
<td>constant initial attractiveness</td>
<td>$\gamma \rightarrow 2$ if $\theta \rightarrow 0$</td>
</tr>
<tr>
<td>Internal edges with probab. $p$</td>
<td>$\gamma = 2$ if $\frac{1-p+m}{1+2m}$</td>
</tr>
<tr>
<td>Rewiring of edges with probab. $q$</td>
<td>$\gamma \rightarrow \infty$ if $p, q, m \rightarrow 0$</td>
</tr>
<tr>
<td>$c$ internal edges or removal of $c$ edges</td>
<td>$\gamma = 2$ if $c \rightarrow \infty$</td>
</tr>
<tr>
<td>Gradual aging $\Pi(k_i) \sim k_i(t-t_i)^{-\nu}$</td>
<td>$\gamma = 2$ if $\nu \rightarrow -\infty$</td>
</tr>
<tr>
<td></td>
<td>$\gamma \rightarrow \infty$ if $\nu \rightarrow 1$</td>
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<tr>
<td>Multiplicative node fitness</td>
<td>$P(k) \sim \frac{k^{-1-c}}{\ln(k)}$</td>
</tr>
<tr>
<td>Edge inheritance</td>
<td>$P(k_{in}) = \frac{d}{k_{in}^2} \ln(ak_{in})$</td>
</tr>
<tr>
<td>Copying with probab. $p$</td>
<td>$\gamma = (2-p)/(1-p)$</td>
</tr>
<tr>
<td>Redirection with probab. $r$</td>
<td>$\gamma = 1 + 1/r$</td>
</tr>
<tr>
<td>Walking with probab. $p$</td>
<td>$\gamma = 2$ for $p &gt; p_c$</td>
</tr>
<tr>
<td>Attaching to edges</td>
<td>$\gamma = 3$</td>
</tr>
<tr>
<td>$p$ directed internal edges</td>
<td>$\gamma_{in} = 2 + p\lambda$</td>
</tr>
<tr>
<td>$\Pi(k_i,k_j) \sim (k_{i,n}^{in} + \lambda)(k_{j,n}^{out} + \mu)$</td>
<td>$\gamma_{out} = 1 + (1-p)^{-1} + \mu p / (1-p)$</td>
</tr>
<tr>
<td>Barabási and Albert, 1999</td>
<td>Krapivsky, Redner, and Leyvraz, 2000</td>
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<tr>
<td>Krapivsky, Redner, and Leyvraz, 2000</td>
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<td>Dorogovtsev, Mendes, and Samukhin, 2000a, 2000b</td>
<td>Dorogovtsev and Mendes, 2001a</td>
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<td>Dorogovtsev and Mendes, 2000c</td>
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<td>Bianconi and Barabási, 2001a</td>
<td>Albert and Barabási, 2000</td>
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<td>Kumar et al., 2000a, 2000b</td>
<td>Krapivsky et al., 2000b</td>
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<td>Krapivsky and Redner, 2001</td>
<td>Vázquez, 2000</td>
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<tr>
<td>Vázquez, 2000</td>
<td>Dorogovtsev, Mendes, and Samukhin, 2001a</td>
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</tbody>
</table>
The network grows, but the degree distribution is stationary.
Consequently, the modeling philosophy behind the model is simple: to understand the topology of a complex system, we need to describe how it came into being.

The network grows, but the degree distribution is stationary.
Section 11: Summary

- The model predicts $\gamma=3$ while the degree exponent of real networks varies between 2 and 5 (Table 4.2).

- Many networks, like the WWW or citation networks, are directed, while the model generates undirected networks.

- Many processes observed in networks, from linking to already existing nodes to the disappearance of links and nodes, are absent from the model.

- The model does not allow us to distinguish between nodes based on some intrinsic characteristics, like the novelty of a research paper or the utility of a webpage.

- While the Barabási-Albert model is occasionally used as a model of the Internet or the cell, in reality it is not designed to capture the details of any particular real network. It is a minimal, proof of principle model whose main purpose is to capture the basic mechanisms responsible for the emergence of the scale-free property. Therefore, if we want to understand the evolution of systems like the Internet, the cell or the WWW, we need to incorporate the important details that contribute to the time evolution of these systems, like the directed nature of the WWW, the possibility of internal links and node and link removal.
1. There is no universal exponent characterizing all networks.

2. Growth and preferential attachment are responsible for the emergence of the scale-free property.

3. The origins of the preferential attachment is system-dependent.

4. Modeling real networks:
   - identify the microscopic processes that take place in the system
   - measure their frequency from real data
   - develop dynamical models that capture these processes.

5. If the model is correct, it should correctly predict not only the degree exponent, but both small and large k-cutoffs.
Philosophical change in network modeling:

ER, WS models are static models – the role of the network modeler is to cleverly place the links between a fixed number of nodes to that the network topology mimic the networks seen in real systems.

BA and evolving network models are dynamical models: they aim to reproduce how the network was built and evolved. Thus their goal is to capture the network dynamics, not the structure. → as a byproduct, you get the topology correctly.
TOPOLOGY OF THE PROTEIN NETWORK

Nodes: proteins
Links: physical interactions (binding)

Puzzling pattern:
Hubs tend to link to small degree nodes.
Why is this puzzling?

In a random network, the probability that a node with degree $k$ links to a node with degree $k'$ is:

$$p_{kk'} = \frac{kk'}{2L}$$

$k=50$, $k'=13$, $N=1,458$, $L=1,746$

$$p_{50,13} = 0.15$$
$$p_{2,1} = 0.0004$$

Yet, we see many links between degree 2 and 1 links, and no links between the hubs.

DEGREE CORRELATIONS IN NETWORKS

Assortative:
hubs show a tendency to link to each other.

Neutral:
nodes connect to each other with the expected random probabilities.

Disassortative:
Hubs tend to avoid linking to each other.

Quantifying degree correlations (three approaches):
- full statistical description (Maslov and Sneppen, Science 2001)
- degree correlation function (Pastor Satorras and Vespignani, PRL 2001)
- correlation coefficient (Newman, PRL 2002)
$e_{jk}$: probability to find a node with degree $j$ and degree $k$ at the two ends of a randomly selected edge

$$\sum_{j,k} e_{jk} = 1 \quad \sum_j e_{jk} = q_k$$

$q_k$: the probability to have a degree $k$ node at the end of a link.

Where:

$$q_k = \frac{kp_k}{\langle k \rangle}$$

Probability to find a node at the end of a link is biased towards the more connected nodes, i.e. $q_k = Ck^p_k$, where $C$ is a normalization constant. After normalization we find $C=1/\langle k \rangle$, or $q_k = kp_k/\langle k \rangle$

If the network has no degree correlations:

$$e_{jk} = q_j q_k$$

Deviations from this prediction are a signature of degree correlation.

Neutral

**Disassortative:**
Hubs tend to connect to small nodes.

**Assortative:**
More strength in the diagonal, hubs tend to link to each other.

Each matrix is the average of a 100 independent scale-free networks, generated using the static model with $N=10^4$, $\gamma=2.5$ and $<k>=3$. 
Perfectly assortative network:

\[ e_{jk} = q_k \delta_{jk} \]

Assortative:
More strength in the diagonal, hubs tend to link to each other.

Perfectly disassortative network:

Disassortative:
Hubs tend to connect to small nodes.

Each matrix is the average of a 100 independent scale-free networks, generated using the static model with \( N = 10^4 \), \( \gamma = 2.5 \) and \( \langle k \rangle = 3 \).
REAL-WORLD EXAMPLES

Astrophysics co-authorship network

Disassortative:
Hubs tend to connect to small nodes.

Yeast PPI

Assortative:
More strength in the diagonal, hubs tend to link to each other.
(1) Difficult to extract information from a visual inspection of a matrix.

(2) Based on $e_{jk}$ and hence requires a large number of elements to inspect:

$$\frac{k_{\text{max}} (k_{\text{max}} - 1)}{2} - 1 - k_{\text{max}}$$

Undirected network: $k_{\text{max}} \times k_{\text{max}}$ matrix

Constraints

$$\sum_{j,k} e_{jk} = 1$$

$$\sum_{j=1,k_{\text{max}}} e_{jk} = q_k$$

Nr. of independent elements

We need to find a way to reduce the information contained in $e_{jk}$

Average next neighbor degree

\( k_{\text{annn}}(k) \): average degree of the first neighbors of nodes with degree \( k \).

\[
    k_{\text{annn}}(k) = \sum_{k'} k' P(k' | k) = \frac{\sum k' e_{kk'}}{\sum e_{kk'}}
\]

No degree correlations:

\[
    k_{\text{annn}}(k) = \frac{\sum k' e_{kk'}}{\sum e_{kk'}} = \frac{\sum k' q_k q_{k'}}{q_k} = \sum k' q_{k'} = \sum k' p(k') < k > = \left\langle \frac{k^2}{k} \right\rangle
\]

If there are no degree correlations, \( k_{\text{annn}}(k) \) is independent of \( k \).

$k_{\text{anno}}(k)$ FOR REAL NETWORKS

Astrophysics co-authorship network: Assortative

Yeast PPI: Disassortative

exponent: 0.37$\pm$0.11

exponent: -0.27$\pm$0.03
**Average next neighbor degree**

$k_{\text{annnd}}(k)$: average degree of the first neighbors of nodes with degree $k$.

\[ \sum_k k_{\text{annnd}}(k) \cdot k N p_k = \sum_k k^2 \cdot N p_k \]

Constraint:

\[ \langle k_{\text{annnd}}(k) k \rangle = \langle k^2 \rangle \]

$k_{\text{annnd}}(k)$ is a $k$-dependent function, hence it has much fewer parameters, and it is easier to interpret/read.

If there are degree correlations, $e_{jk}$ will differ from $q_j q_k$. The magnitude of the correlation is captured by $\langle jk \rangle - \langle j \rangle \langle k \rangle$ difference, which is:

$$\sum_{jk} jk(e_{jk} - q_j q_k)$$

$\langle jk \rangle - \langle j \rangle \langle k \rangle$ is expected to be:
- positive for assortative networks,
- zero for neutral networks,
- negative for disassortative networks

To compare different networks, we should normalize it with its maximum value; the maximum is reached for a perfectly assortative network, i.e. $e_{jk} = q_k \delta_{jk}$

normalization: $\sigma_r^2 = \max \sum_{jk} jk(e_{jk} - q_j q_k) = \sum_{jk} jk(q_k \delta_{jk} - q_j q_k)$

$$r = \frac{\sum_{jk} jk(e_{jk} - q_j q_k)}{\sigma_r^2} \quad -1 \leq r \leq 1$$

- $r \leq 0$ disassortative
- $r = 0$ neutral
- $r \geq 0$ assortative

Social networks are **assortative**

<table>
<thead>
<tr>
<th>Network</th>
<th>( n )</th>
<th>( r )</th>
</tr>
</thead>
<tbody>
<tr>
<td>Physics coauthorship (a)</td>
<td>52,909</td>
<td>0.363</td>
</tr>
<tr>
<td>Biology coauthorship (a)</td>
<td>1,520,251</td>
<td>0.127</td>
</tr>
<tr>
<td>Mathematics coauthorship (b)</td>
<td>253,339</td>
<td>0.120</td>
</tr>
<tr>
<td>Film actor collaborations (c)</td>
<td>449,913</td>
<td>0.208</td>
</tr>
<tr>
<td>Company directors (d)</td>
<td>7,673</td>
<td>0.276</td>
</tr>
<tr>
<td>Internet (e)</td>
<td>10,697</td>
<td>−0.189</td>
</tr>
<tr>
<td>World-Wide Web (f)</td>
<td>269,504</td>
<td>−0.065</td>
</tr>
<tr>
<td>Protein interactions (g)</td>
<td>2,115</td>
<td>−0.156</td>
</tr>
<tr>
<td>Neural network (h)</td>
<td>307</td>
<td>−0.163</td>
</tr>
<tr>
<td>Marine food web (i)</td>
<td>134</td>
<td>−0.247</td>
</tr>
<tr>
<td>Freshwater food web (j)</td>
<td>92</td>
<td>−0.276</td>
</tr>
<tr>
<td>Random graph (u)</td>
<td></td>
<td>0</td>
</tr>
<tr>
<td>Callaway et al. (v)</td>
<td></td>
<td>( \delta/(1 + 2\delta) )</td>
</tr>
<tr>
<td>Barabási and Albert (w)</td>
<td></td>
<td>0</td>
</tr>
</tbody>
</table>

**r > 0: assortative network:**
Hubs tend to connect to other hubs.

**r < 0: disassortative network:**
Hubs tend to connect to small nodes.

Biological, technological networks are **disassortative**
RELATIONSHIP BETWEEN $r$ AND $k_{annd}$

\[
\frac{\sum_{k,j}(e_{kj} - \bar{e}_{k})q_{j}}{\sigma_r^2} = \frac{\sum_{k}q_{k}\sum_{j}e_{kj}\left(\sum_{k}q_{k}\right)^2}{\sigma_r^2} = \frac{\sum_{k}kk_{annd}(k)q_{k}}{\sigma_r^2} - \frac{\langle k^2 \rangle^2}{\langle k \rangle^2} = k_{annd}(k) = \sum_{k'}k'P(k' | k) = \frac{\sum_{k'}k'e_{kk'}}{\sum_{k'}e_{kk'}} = \frac{\sum_{k'}k'e_{kk'}}{q_{k}}
\]

In general case we need to know $q_k$ and $k_{annd}(k)$ to calculate $r$.

Assuming: $k_{annd}(k) = a \cdot k + b$

Using the constraint for ANND:

\[
\langle k^2 \rangle = \langle k_{annd}(k) \rangle = \sum_{k'}a \cdot k^2 p_{k} + b \cdot kp_{k} = a\langle k^2 \rangle + b\langle k \rangle \quad \Rightarrow \quad b = \frac{(1-a)\langle k^2 \rangle}{\langle k \rangle}
\]

\[
r = \frac{\sum_{k}k \cdot (a \cdot k + b)q_{k}}{\sigma_r^2} = \frac{\sum_{k}k \left( a \cdot k + \frac{(1-a)\langle k^2 \rangle}{\langle k \rangle} \right) p_{k} - \langle k^2 \rangle^2}{\sigma_r^2} = a \left( \frac{\sum_{k}k^3 p_{k} - \langle k^2 \rangle^2}{\langle k \rangle^2} \right) + \frac{\langle k^2 \rangle}{\langle k \rangle} - \frac{\langle k^2 \rangle}{\langle k \rangle} = a \left( \frac{\sum_{k}k^2 p_{k} - \langle k^2 \rangle^2}{\langle k \rangle^2} \right) \frac{\langle k \rangle^2}{\langle k \rangle} - \frac{\langle k^2 \rangle}{\langle k \rangle} = a
\]

Network Science: Degree Correlations
PROBLEM WITH THE PREVIOUS DEVIATION: $k_{\text{ann}}(k) \sim k^\beta$

Astrophysics co-authorship network

**Assortative**

Yeast PPI

**Disassortative**

- exponent: $0.37 \pm 0.11$
- exponent: $-0.27 \pm 0.03$
CONNECTION WITH ANND

Assuming: \( k_{ann}(k) = a \cdot k^\beta \)

Using the constraint for ANND: \( \langle k^2 \rangle = \langle k_{ann}(k)k \rangle = \sum_{k'} a \cdot k^{\beta+1} p_{k'} = a \langle k^{\beta+1} \rangle \rightarrow a = \frac{\langle k^2 \rangle}{\langle k^{\beta+1} \rangle} \)

\[
\begin{align*}
\sum_k k \cdot ak^\beta \cdot q_k - \langle k^2 \rangle^2 \quad &\Rightarrow \quad \sum_k a \cdot k^{\beta+2} \frac{p_k}{\langle k \rangle^2} - \langle k^2 \rangle^2 \\
\Rightarrow \quad r &\equiv \frac{\sigma_r^2}{\langle k \rangle^2} = \frac{\langle k^2 \rangle \langle k^{\beta+2} \rangle - \langle k^2 \rangle^2}{\langle k^{\beta+1} \rangle \langle k \rangle - \langle k^2 \rangle^2} \\
\Rightarrow \quad \frac{\sigma_r^2}{\langle k \rangle^2} &\equiv \frac{1}{\langle k \rangle} \left( \frac{\langle k^{\beta+2} \rangle}{\langle k^{\beta+1} \rangle} - \frac{\langle k^2 \rangle}{\langle k \rangle} \right) \\
\Rightarrow \quad \sigma_r^2 &\equiv \sum_{jk} jk(q_j \delta_{jk} - q_j q_k) = \frac{\langle k^3 \rangle}{\langle k \rangle} - \frac{\langle k^2 \rangle^2}{\langle k \rangle^2}
\end{align*}
\]

\[ \beta < 0 \quad \rightarrow \quad r < 0 \]
\[ \beta = 0 \quad \rightarrow \quad r = 0 \]
\[ \beta > 0 \quad \rightarrow \quad r > 0 \]
CONNECTION BETWEEN R AND $k_{\text{ANND}}$

\[ \beta = 0 : \quad \frac{\langle k^{\beta+2} \rangle}{\langle k^{\beta+1} \rangle} - \frac{\langle k^2 \rangle}{\langle k \rangle} = \frac{\langle k^2 \rangle}{\langle k \rangle} - \frac{\langle k^2 \rangle}{\langle k \rangle} = 0 \quad \Rightarrow \quad r = 0 \]

\[ \langle k^{\alpha+\beta} \rangle = \sum_{k_{\min}}^{k_{\max}} k^{\alpha+\beta} p_k = k_{\max}^{\beta} \sum_{k_{\min}}^{k_{\max}} k^{\alpha} p_k = k_{\min}^{\beta} \langle k^\alpha \rangle \]

\[ 0 > \beta > -1 : \quad \frac{\langle k^2 \rangle}{\langle k \rangle} > \left( \frac{k_{\min}}{k_{\max}} \right)^\beta \frac{\langle k^{\beta+2} \rangle}{\langle k^{\beta+1} \rangle} > \frac{\langle k^{\beta+2} \rangle}{\langle k^{\beta+1} \rangle} \quad \Rightarrow \quad r < 0 \]

\[ +1 > \beta > 0 : \quad \frac{\langle k^{\beta+2} \rangle}{\langle k^{\beta+1} \rangle} > \left( \frac{k_{\min}}{k_{\max}} \right)^\beta \frac{\langle k^2 \rangle}{\langle k \rangle} > \frac{\langle k^2 \rangle}{\langle k \rangle} \quad \Rightarrow \quad r > 0 \]
DEGREE CORRELATION IN NETWORKS

\[ e_{jk} \]

\[ k_{\text{ann}}(k) \]

\[ r = 0.31 \]

\[ -0.16 \]

\[ \frac{k_{\text{max}}(k_{\text{max}} - 1)}{2} - k_{\text{max}} - 1 \]
We have a desired $e_{jk}$ distribution, which also specifies $p_k$.

1. Generate a network with the desired degree distribution using the configuration model.
2. Choose two links at random from the network: $(v_1, w_1)$ and $(v_2, w_2)$.
3. Measure the degrees $j_1, k_1, j_2, k_2$ of nodes $v_1, w_1, v_2, w_2$. Replace the two selected links with two new ones $(v_1, v_2)$ and $(w_1, w_2)$ with probability

$$P = \begin{cases} 
\frac{e_{j_1 j_2} e_{k_1 k_2}}{e_{j_1 k_1} e_{k_2 j_2}} & \text{if } e_{j_1 j_2} e_{k_1 k_2} < e_{j_1 k_1} e_{k_2 j_2} \\
1 & \text{otherwise}
\end{cases}$$

1. Repeat from step 2.

The algorithm is ergodic and satisfies detailed balance, therefore in the long time limit it samples the desired network ensemble correctly.

2. Choose two edges random from the network: \((v_1, w_1)\) and \((v_2, w_2)\).
3. Measure the degrees \(j_1, k_1, j_2, k_2\) of vertices \(v_1, w_1, v_2, w_2\). Replace the two selected edges with two new ones \((v_1, v_2)\) and \((w_1, w_2)\) with probability

\[
P = \begin{cases} 
\frac{e_{j_1j_2} e_{k_1k_2}}{e_{j_1k_1} e_{k_2j_2}} & \text{if } e_{j_1j_2} e_{k_1k_2} < e_{j_1k_1} e_{k_2j_2} \\
1 & \text{otherwise}
\end{cases}
\]
If we only specify $r$ we have great degree of freedom in choosing $e_{jk}$.

Possible choice for disassortative case:

$$e^{(d)}_{jk} = q_j x_k + x_j q_k - x_j x_k$$

Where $x_k$ is any normalized distribution.

This form satisfies the constraints on $e_{jk}$:

$$\sum_{jk} e_{jk} = \sum_{jk} q_j x_j + x_j q_k - x_j x_k = 1 + 1 - 1 = 1$$

$$\sum_{j} e_{jk} = \sum_{j} q_j x_j + x_j q_k - x_j x_k = q_k + x_k - x_k = q_k$$

The $r$ value can be easily calculated:

$$r_d = \frac{\sum_{jk} (q_k x_j + x_k q_j - x_k x_j - q_k q_j)}{\sigma_r^2} = \frac{2 \langle k \rangle_q \langle k \rangle_x - \langle k \rangle_x^2 - \langle k \rangle_q^2}{\sigma_r^2} = -\frac{\langle k \rangle_x - \langle k \rangle_q^2}{\sigma_r^2}$$

Assortative case:

$$e^{(a)}_{jk} = q_j q_k - e^{(d)}_{jk} \quad \rightarrow \quad r_a = -r_d$$

EXAMPLE: Erdős-Rényi
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Network Science: Degree Correlations
Structural cut-off

High assortativity $\rightarrow$ high number of links between the hubs.

If we allow only one link between two nodes, we can simply run out of hubs to connect to each other to satisfy the assortativity criteria.

Number of edges between the set of nodes with degree $k$ and degree $k'$:

$$E_{kk'} = e_{kk'} \langle k \rangle N$$

Maximum number of edges between the two groups:

$$m_{kk'} = \min \{ kN_k, k'N_{k'}, N_kN_{k'} \}$$

If we only have simple edges, we cannot have more links between the two groups, than if we connect every node with degree $k$ to every node with degree $k'$ once.

This is true even if we allow multiple edges.