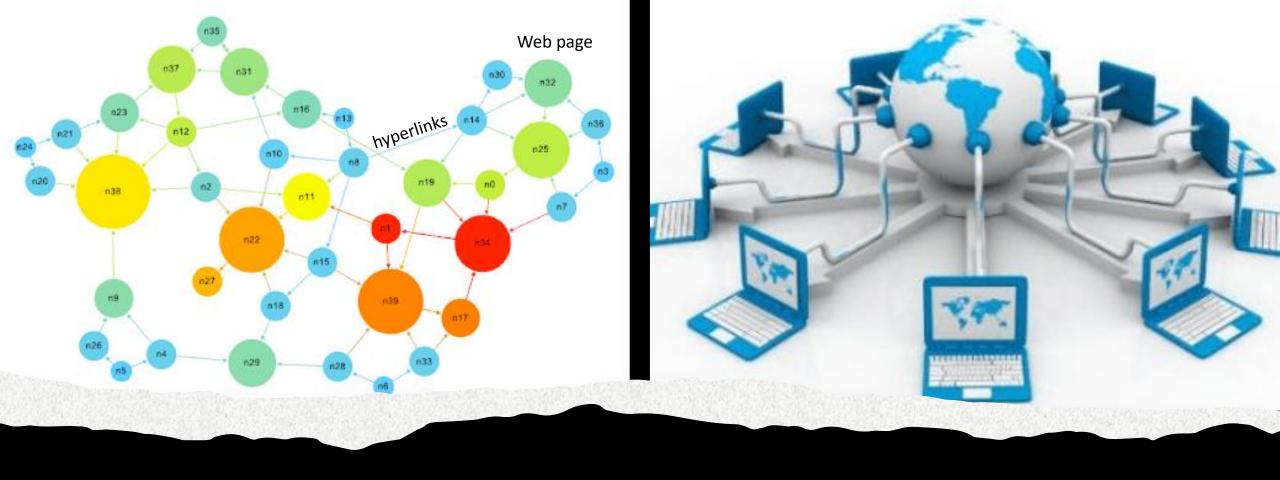


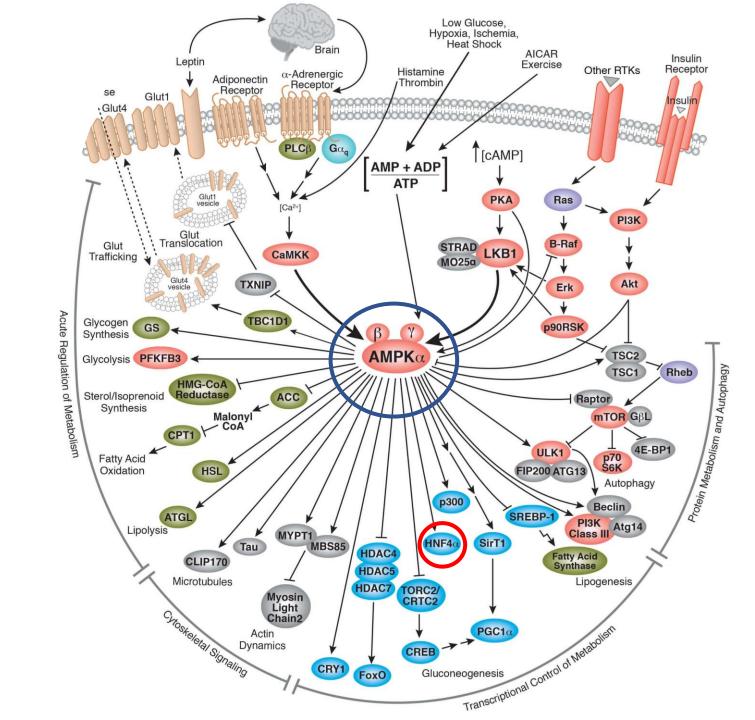
- Creation of directed and undirected networks
- Sociometric factors
- Random networks and their properties
- Small world phenomenon



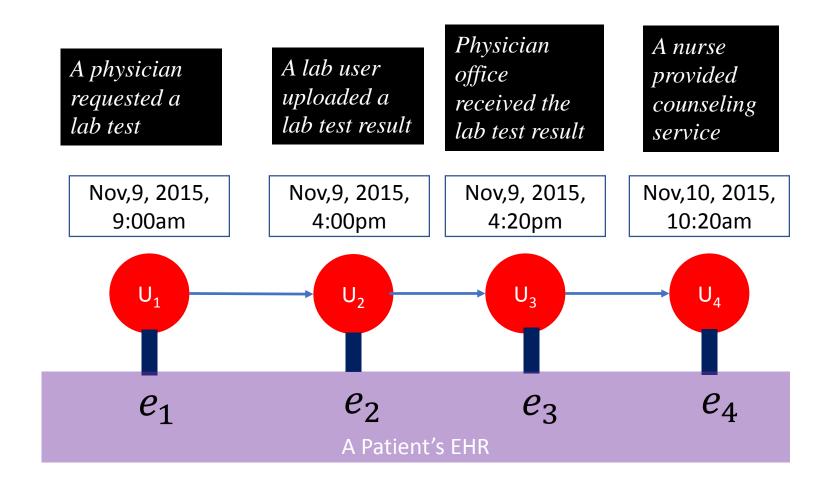
Directed networks – world wide web (hyperlinks between edges)

Metabolic networks (biochemical reactions between molecules)

- The links are the biochemical reactions that take place between these molecules
- AMP-activated protein kinase (AMPK)
 - It is an enzyme that plays a role in cellular energy homeostasis, largely to activate glucose and fatty acid uptake and oxidation when cellular energy is low
 - AMPK directly impacts HNF4alpha and represses its transcriptional activity

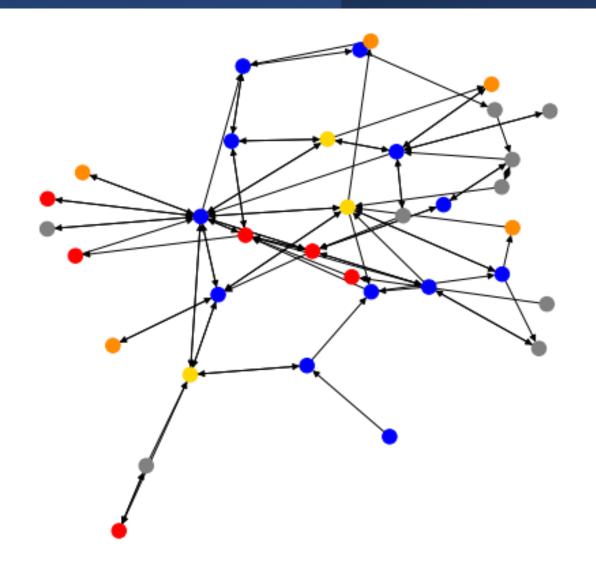


EHR audit log data: User-EHR interactions User: healthcare worker EHR: electronic health record



Networks of healthcare workers



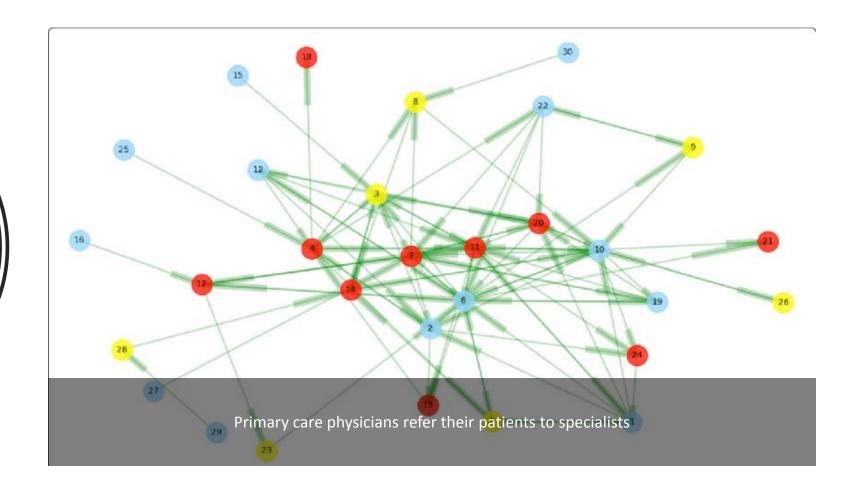


Health insurance claims



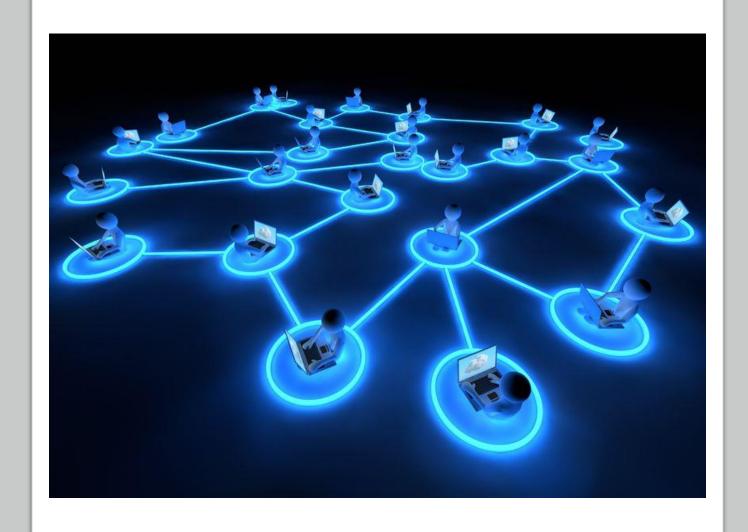
- A request for payment that you or your health care provider submits to your health insurer when you get items or services you think are covered
- A claim contain patient, physician, healthcare service, and referral information

Patient referral network

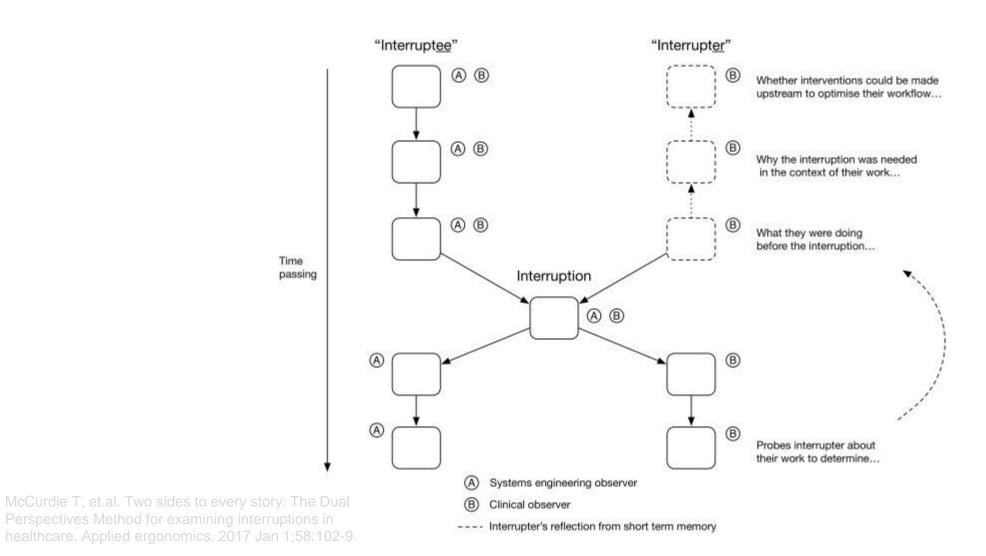


Undirected networks

- The topology of connections in a computer network or a digital social network
- The graph is undirected because we can assume that if one device is connected to another, then the second one is also connected to the first
- The topology of digital social networks, where each friend of someone is that someone's friend

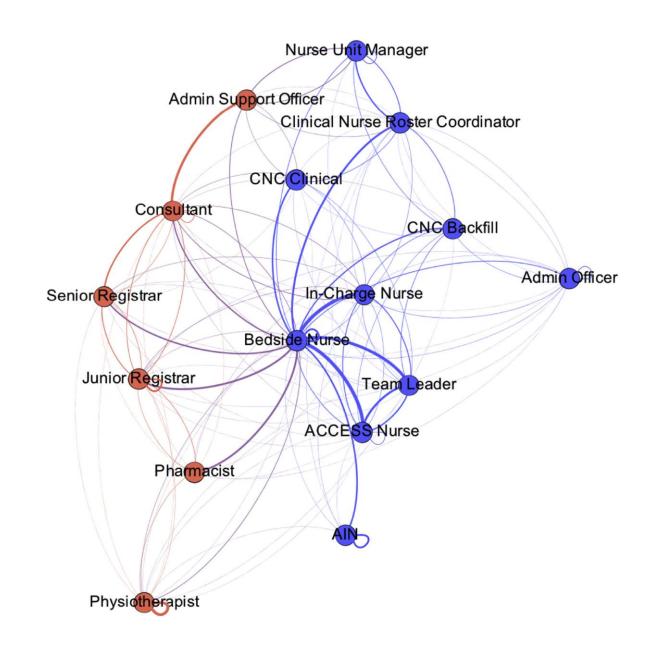


Dual Perspectives Method - Observing clinical interruptions



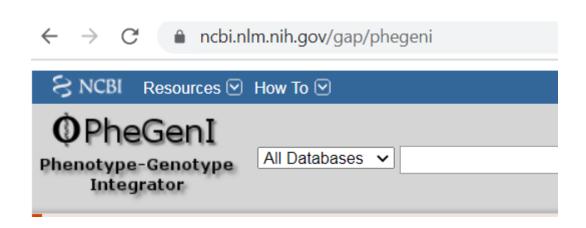
Inter-disciplinary interruption network observed in the ICU

- The relationships are based on interruptions, upon which care work can continue
- Dependency between the Bedside Nurse, Team Leader, ACCESS (Assistance, Coordination, Contingency, Education, Supervision, Support) Nurse, and In-Charge Nurse roles
- These dependencies are potential focal points for intervention



Data resources to create human disease network



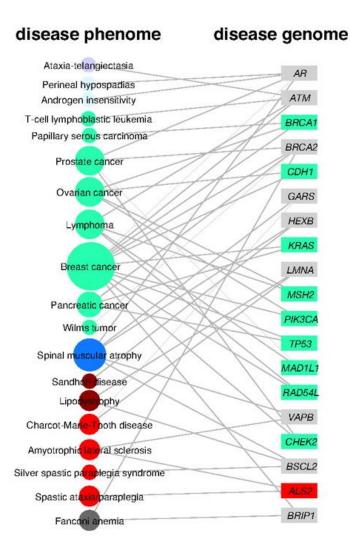




Neanderthal PheWAS: Discovery & Replication Results



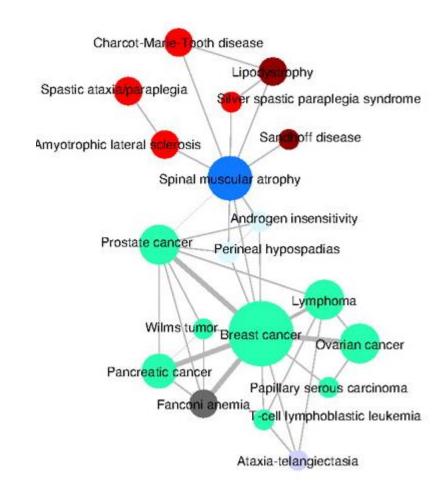
GWAS and PheWAS study findings



- Circles: disease phenome (disorder)
- **Rectangles:** disease genes
- **Links:** a link is placed between a disorder and a disease gene if mutations in that gene lead to the specific disorder
- The size of a circle is proportional to the number of genes participating in the corresponding disorder
- The color corresponds to the disorder class to which the disease belongs

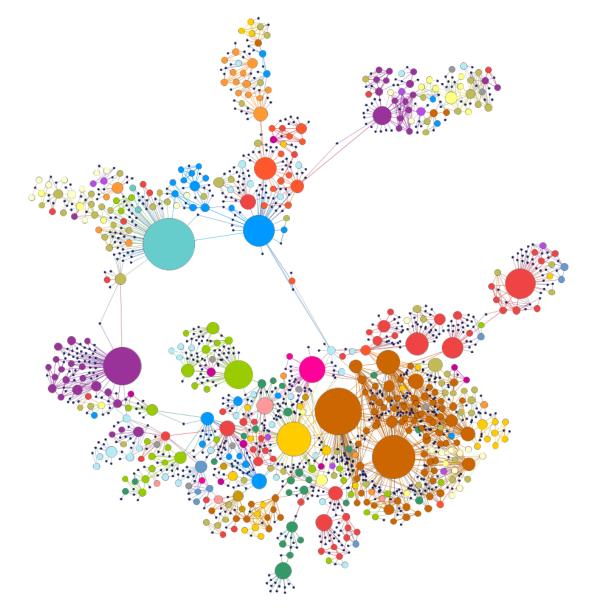
Projection of the bipartite graph of diseases and genes

- If there is a gene that is implicated in two disorders, then the two are connected.
- The width of a link is proportional to the number of genes that are implicated in both diseases.
- Three genes are implicated in both breast cancer and prostate cancer, resulting in a link of weight three between them



Human disease network

- Nodes represent diseases and two diseases are connected to each other if they share at least one gene in which mutations are associated with both diseases
- Each disease class is represented by a different color; the diseases include Bone, cancer, cardiovascular, skeletal, or metabolic diseases
- The size of a node is proportional to the number of genes participating in the corresponding disease



Goh KI, et.al. The human disease network. Proceedings of the National Academy of Sciences. 2007 May 22;104(21):8685-90.

PageRank method - a major ingredient of Google search engine

$$PR(A) = (1-d) + d (PR(T1)/C(T1) + ... + PR(Tn)/C(Tn))$$

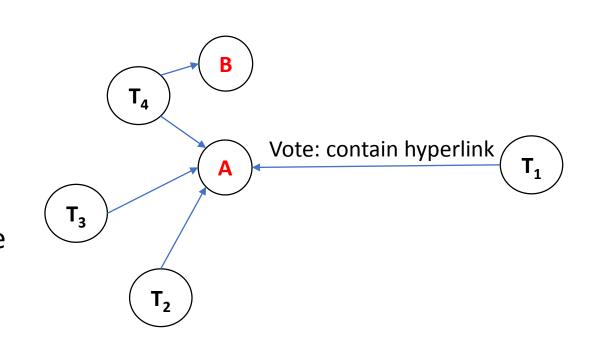
d: a damping factor – 0.85

PR(Ti): PageRank score of Ti

C(Ti): The number of edges

going out of Ti

PR(Ti)/C(Ti): the share of the vote



If there's no link pointing to a page (no vote), then the default PageRank score would be 0.15

An example to illustrate the process of PageRank calculation

$$PR(A) = (1-d) + d (PR(T1)/C(T1) + ... + PR(Tn)/C(Tn))$$

Guess:
$$PR(A) = 40$$
; $PR(B) = 40$

First calculation

$$PR(A) = 0.15 + 0.85 * 40 = 34.15$$

$$PR(B) = 0.15 + 0.85 * 34.15 = 29.1775$$



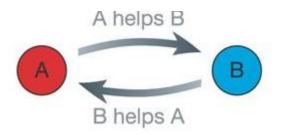
And again

repeat the calculations lots of times until the numbers stop changing much

$$PR(A) = 1.0$$

$$PR(B) = 1.0$$

Reciprocity



- In network science, reciprocity is a measure of the likelihood of vertices in a directed network to be mutually linked
- A common interest in looking at directed dyadic relationships is the extent to which ties are reciprocated
- There is an equilibrium tendency toward dyadic relationships to be either null or reciprocated (stable)
- The useful information from reciprocity is not the value itself, but whether mutual links occur more or less often than expected by chance

Reciprocity in healthcare

- The **what** of reciprocity refers to equivalence reciprocity, which is defined as the extent to which what is exchanged is directly comparable to what was received.
- The when of reciprocity refers to immediacy reciprocity, which is defined as the length of time between an initial action and its response
- Assigning and completing a clinical task
- Patient safety- be awareness of adverse events and report to teammates

Calculation – network level

$$ho \equiv rac{\sum_{i
eq j} (a_{ij} - ar{a})(a_{ji} - ar{a})}{\sum_{i
eq j} (a_{ij} - ar{a})^2}$$

For the Web, the reciprocity is about 57%, meaning that more than half of the links link back. For the network of who has whom in the email address book the reciprocity was found about 23%.

$$ar{a} \equiv rac{\sum_{i
eq j} a_{ij}}{N(N-1)} = rac{L}{N(N-1)}$$

measures the ratio of observed to possible directed links (N(N-1)) (link density), and self-linking loops are now excluded from L because of i not equal to j

$$r=\frac{L^{<->}}{L}$$

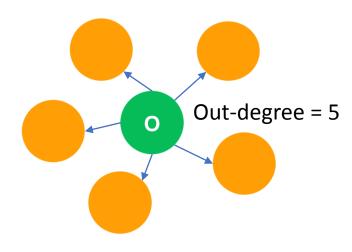
the ratio of the number of links pointing in both directions to the total number of links

$$\rho = \frac{r - \bar{a}}{1 - \bar{a}}$$

If r=0, then $\rho = \rho_{min}$

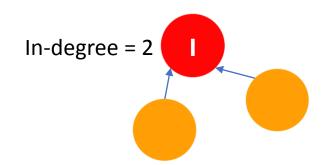
If all links occur in reciprocal pairs, r=1

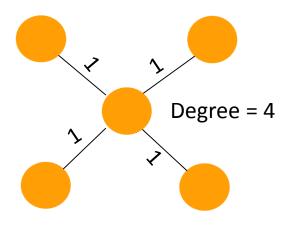
Degree

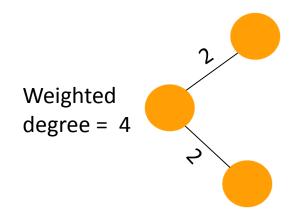




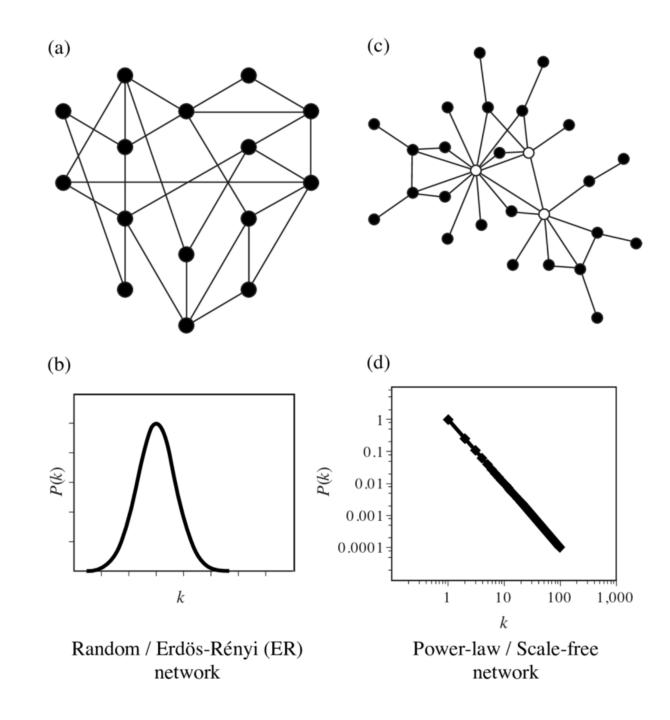
Isolate

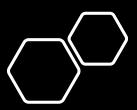






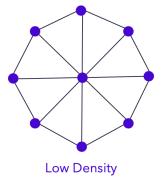
Degree distribution





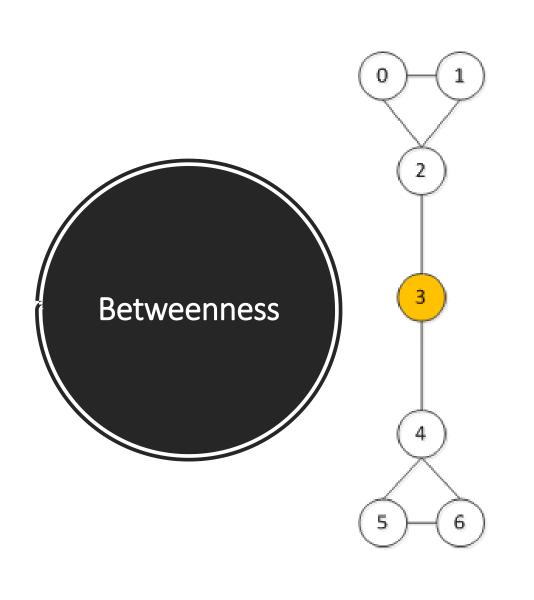
Density

- Number of ties expressed as percentage of number of expected pairs
- Actual connections/maximum possible connections





$$D = \frac{2|E|}{|V|\left(|V|-1\right)}$$



Betweenness of node 2:

Node $3 \rightarrow 0$: 1 Node $3 \rightarrow 1$: 1 Node $4 \rightarrow 0$:1 Node $4 \rightarrow 1$:1 Node $5 \rightarrow 0$:1

Node 5→1:1

Node $6 \rightarrow 0:1$ Node $6 \rightarrow 1:1$

Betweenness Centrality of node 2:8

Betweenness of node 3:

Node $4 \rightarrow 0$: 1 Node $4 \rightarrow 1$: 1 Node $4 \rightarrow 2$:1 Node $5 \rightarrow 0$:1 Node $5 \rightarrow 1$:1 Node $5 \rightarrow 2$:1 Node $6 \rightarrow 0$:1

Node 6→1:1 Node 6→2:1

Betweenness Centrality of node 3:9

Betweenness of node 4:

Node $5 \rightarrow 0:1$ Node $5 \rightarrow 1:1$ Node $5 \rightarrow 2:1$ Node $5 \rightarrow 3:1$

Node 6→0:1

Node 6→1:1

Node 6→2:1

Node 6→3:1

Betweenness Centrality of node 4:8

Betweenness Centrality of node 0: 0

Betweenness Centrality of node 1: 0

Betweenness Centrality of node 5: 0

Betweenness Centrality of node 6: 0

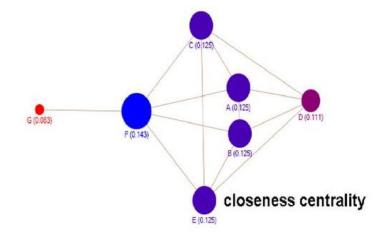
Closeness

$$C_{i} = 1 / \sum_{j=1}^{n} d(i,j)$$

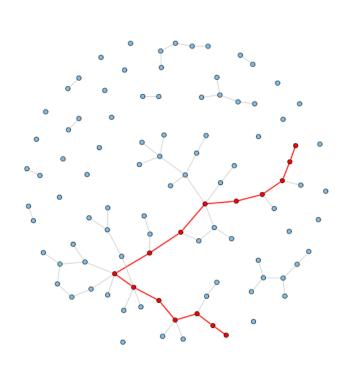
$$C_{A} = \frac{1}{d(AB) + d(AC) + d(AD) + d(AE) + d(AF) + d(AG)}$$

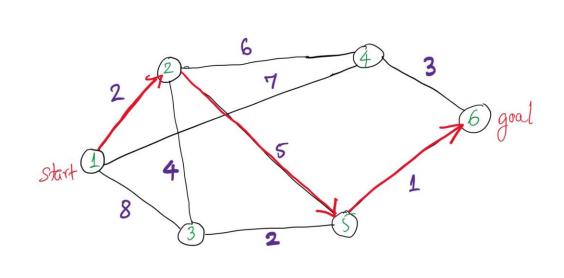
$$C_A = \frac{1}{1+1+1+2+1+2}$$

$$C_A = \frac{1}{8} = 0.125$$



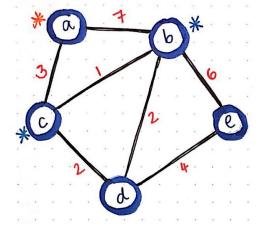
Shortest path - Dijkstra's shortest path algorithm





Dijkstra's shortest path algorithm rules

- There is no negative edges
- Set distance to source vertex as 0, and set all other distances to infinity



VERTEX	SHIRTEST DIST. FROM @					PREVIOUS VERTEX	
a			0				
· р .	00		×		i		
С	00						
d	00				ı		
e	00		٠				

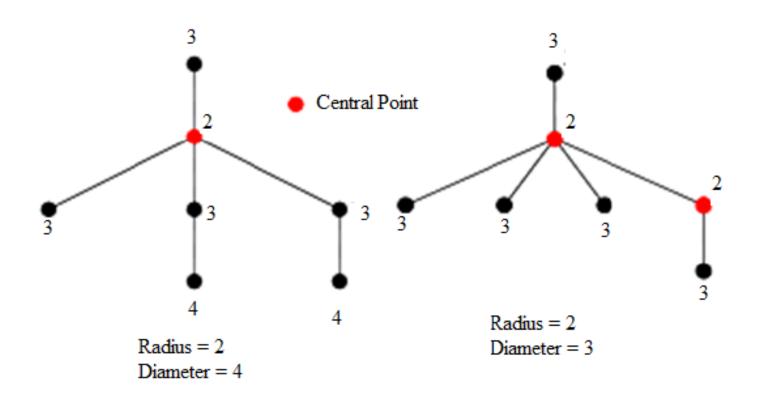
Visited =

* Examine its neighboring nodes, and calculate the distance to them from the vertex we are visiting.

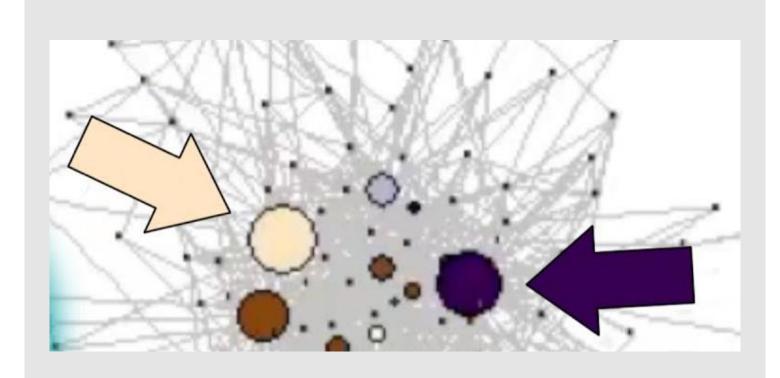
* If the calculated distance is less than our currently-known shortest distance, update the shortest distance for these vertices.

• for node (6): 7 < 00 } We will update table's values for node (6): 3 < 00 } node's shortest distance for node (6): 3 < 00 } node's shortest distance is less add to

Diameter and radius



Eigenvector centrality



 Eigenvector centrality is extensively used in complex network theory to assess the significance of nodes in a network based on the eigenvector of the network adjacency matrix

Eigenvalue and Eigenvector

- A is a square matrix
- A scalar λ is called an Eigenvalue of A
 if there is a nonzero vector X such that
 AX = λX. Such a vector X is called an
 Eigenvector of A corresponding to λ.

Finding eigenvalues and eigenvectors

(4) Solving for
$$\lambda$$
:
 $(\lambda - 8) (\lambda + 2) = 0$
 $\lambda = 8$ and $\lambda = -2$ are the Eigen values

(5) Consider A – λ I

$$\begin{bmatrix}
3 & -1-\lambda \\
3 & -1-\lambda
\end{bmatrix}$$

$$\begin{bmatrix}
7-8 & 3 \\
3 & -1-\delta
\end{bmatrix} = \begin{bmatrix}
-1 & 3 \\
3 & -9
\end{bmatrix} = B$$

Solve B X = 0
$$\begin{bmatrix}
-1 & 3 \\
3 & -9
\end{bmatrix}
\begin{bmatrix}
X1 \\
X2
\end{bmatrix} = \begin{bmatrix}
0 \\
0
\end{bmatrix}$$

$$-X1 + 3X2 = 0 \longrightarrow X1 = 3X2$$

$$3X1 - 9X2 = 0 \longrightarrow 3X1 = 9X2 \longrightarrow X1 = 3X2$$
If X2 = 1;
$$\begin{bmatrix}
3
\end{bmatrix}$$
 is an eigenvector

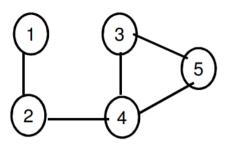
If
$$X2 = 1$$
;
 $X1 = 3$ is an eigenvector for $\lambda = 8$

Matrix determinant

$$\det(A) = \det\begin{bmatrix} a & b & C \\ d & e & f \\ g & h & i \end{bmatrix} = a \cdot \det\begin{bmatrix} e & f \\ h & i \end{bmatrix} - b \cdot \det\begin{bmatrix} d & f \\ g & i \end{bmatrix} + c \cdot \det\begin{bmatrix} d & e \\ g & h \end{bmatrix}$$

$$\det \begin{bmatrix} 2 & -3 & 1 \\ 2 & 0 & -1 \\ 1 & 4 & 5 \end{bmatrix} = 2 \cdot \det \begin{bmatrix} 0 & -1 \\ 4 & 5 \end{bmatrix} - (-3) \cdot \det \begin{bmatrix} 2 & -1 \\ 1 & 5 \end{bmatrix} + 1 \cdot \det \begin{bmatrix} 2 & 0 \\ 1 & 4 \end{bmatrix}$$

Eigenvector centrality



Iteration 1

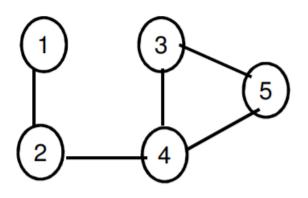
$$\begin{bmatrix} 0 & 1 & 0 & 0 & 0 \\ 1 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 & 1 \\ 0 & 1 & 1 & 0 & 1 \\ 0 & 0 & 1 & 1 & 0 \end{bmatrix} \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \\ 1 \end{bmatrix} = \begin{bmatrix} 1 \\ 2 \\ 2 \\ 3 \\ 2 \end{bmatrix} \equiv \begin{bmatrix} 0.213 \\ 0.426 \\ 0.426 \\ 0.639 \\ 0.426 \end{bmatrix}$$

Normalized Value = 4.69

Iteration 2

$$\begin{bmatrix} 0 & 1 & 0 & 0 & 0 \\ 1 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 & 1 \\ 0 & 1 & 1 & 0 & 1 \\ 0 & 0 & 1 & 1 & 0 \end{bmatrix} \begin{bmatrix} 0.213 \\ 0.426 \\ 0.426 \\ 0.639 \\ 0.426 \end{bmatrix} = \begin{bmatrix} 0.426 \\ 0.852 \\ 1.065 \\ 1.278 \\ 1.065 \end{bmatrix} \equiv \begin{bmatrix} 0.195 \\ 0.389 \\ 0.486 \\ 0.584 \\ 0.486 \end{bmatrix}$$

Normalized Value = 2.19



Iteration 3

Normalized Value = 2.21

0 1 0 0 0 1 0 0 1 0 0 0 0 1 1 0 1 1 0 1 0 0 1 1 0

Let X0 =

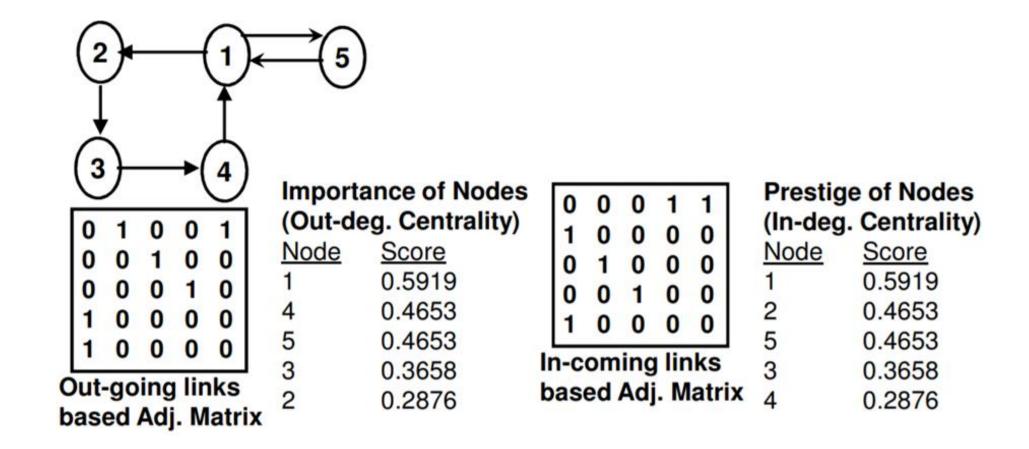
Eigen Vector Centrality

1 0.176
2 0.352
3 0.484
4 0.616
5 0.484

Normalized Value = 2.21 converges

Eigenvector centrality in directed graph

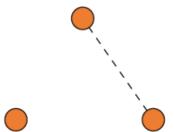
- Importance (out-going links)— out-degree eigenvector
- Prestige (in-coming links) in-degree eigenvector



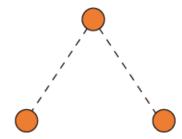
Embeddedness

Type 1: completely unembedded

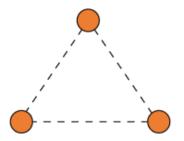
Type 2: One edge embedded



Type 3: Two edges embedded

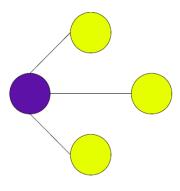


Type 4: Fully embedded

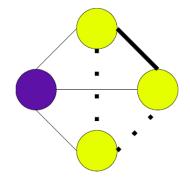


4 clique

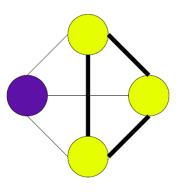
Cluster coefficient and clique



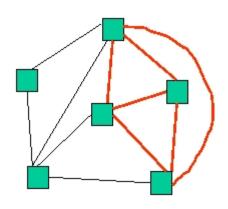
(a) No pairs formed among neighbors: $C = \theta$



(b) One pair formed among neighbors: C = 1/3



(c) Three pairs formed among neighbors: C = 3/3

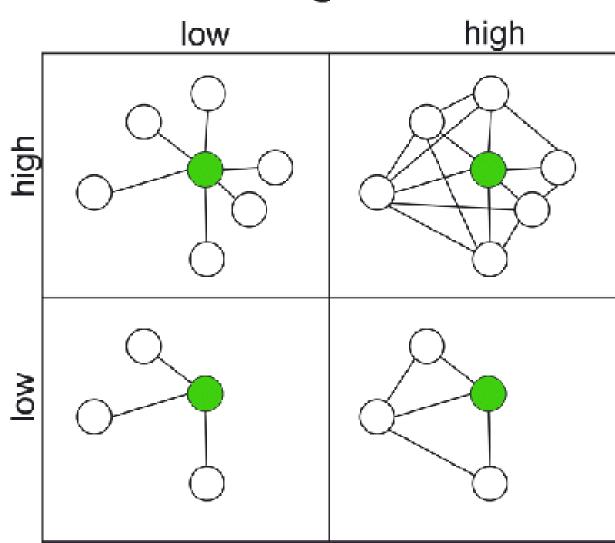


4-clique

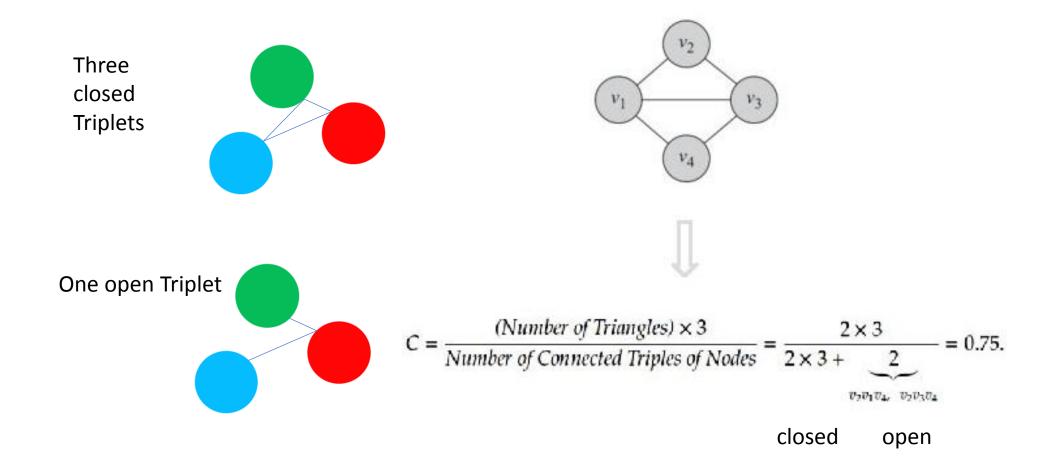
Clustering Coefficient

Degree and clustering coefficient

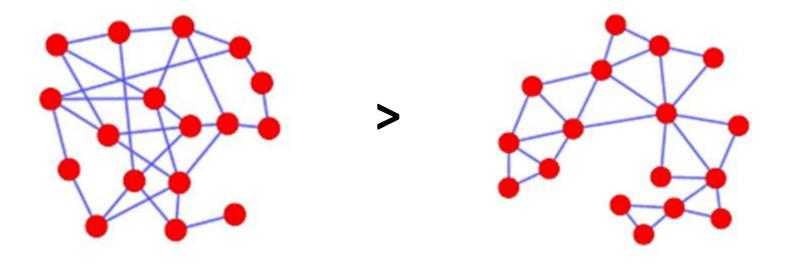
Degree



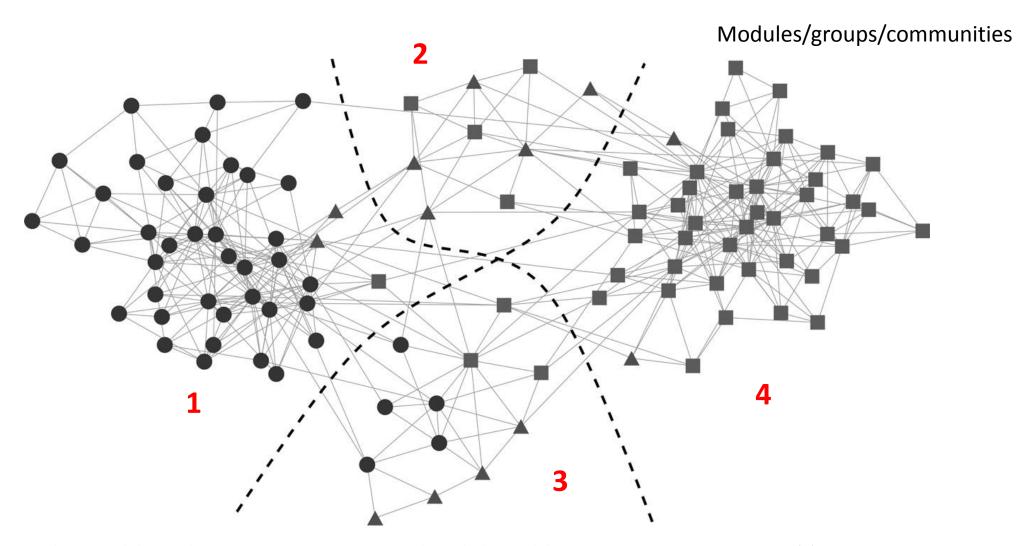
Cluster coefficient - network level



Clustering



Modularity – NP hard to optimize

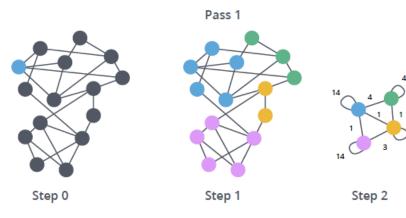


Brandes U, et.al. On modularity clustering. IEEE transactions on knowledge and data engineering. 2007 Dec 26;20(2):172-88.

Newman ME. Modularity and community structure in networks. Proceedings of the national academy of sciences. 2006 Jun 6;103(23):8577-82.

Greedy Heuristic

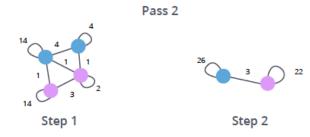
- Measures the relative density of edges inside communities with respect to edges outside communities
- Optimizing this value theoretically results in the best possible grouping of the nodes of a given network.
- Going through all possible iterations of the nodes into groups is impractical, heuristic algorithms are used



Choose a start node and calculate the change in modularity that would occur if that node joins and forms a community with each of its immediate neighbors.

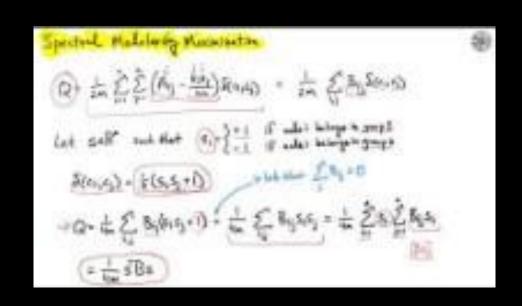
The start node joins the node with the highest modularity change. The process is repeated for each node with the above communities formed.

Communities are aggregated to create super communities and the relationships between these super nodes are weighted as a sum of previous links. (Self-loops represent the previous relationships now hidden in the super node.)



Steps 1 and 2 repeat in passes until there is no further increase in modularity or a set number of iterations have occurred.

Louvain Modularity Algorithm



Spectral Method for Modularity Maximization

-eigenvector indicating which groups a node belonging

https://www.youtube.com/watch?v=LnJk3LRx82U

Modularity based overlapping community detection algorithms

