## Network Analysis

## Wei Pan (\& Xiaotong Shen)

Division of Biostatistics and Health Data Science, School of Public Health, University of Minnesota, Minneapolis, MN 55455

Email: panxx014@umn.edu
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## Outline

- Network concepts/statistics
- Network community detection


## Basics

- Network/graph $\mathcal{G}=(V, E)$ :
- A set of nodes/vertices $V=\left\{v_{1}, \ldots, v_{p}\right\}$.
- A set of edges/links between nodes $E=\left\{e_{1}, \ldots, e_{m}\right\}$.
- $p \times p$ adjacency matrix $A: A_{i j}=0$ or 1 (or $w_{i}$ ) for a binary (or weighted network).
Undirected network: $A$ is symmetric
- Density: the proportion of edges present in a graph, i.e. (\# edges)/(the maximum possible number of edges).
- The number of edges observed is $|E|$.
- The number of possible edges is
- $p(p-1) / 2$ in an undirected graph
- $p(p-1)$ in a directed graph


## Nodal Degree

- Nodes vary in their involvement in the network. For binary relations, this heterogeneity can be summarized by the nodal degree.
- Undirected relation:
- The degree of a node is the node's number of edges.
- Directed relation:
- The outdegree of a node is the node's number of outgoing edges/links.
- The indegree of a node is the node's number of incoming edges.


## Nodal Degree

- The degrees are easy to calculate with adjacency matrix $A$ :

$$
\begin{aligned}
d_{i}^{o} & =\sum_{j: j \neq i} A_{i j} \\
d_{i}^{i} & =\sum_{j: j \neq i} A_{j i}
\end{aligned}
$$

- This calculation works for both directed and undirected relations. Specifically, for an undirected relation,

$$
d_{i}^{\circ}=d_{i}^{i}=d_{i}
$$

## Summary of Degrees

- Let $d=\left\{d_{1}, \ldots, d_{p}\right\}$ be a set of nodal degrees (either out-degrees, in-degrees, or undirected degrees).
- The entries of $d$ are often summarized further with
- Mean: $\bar{d}=\sum d_{i} / p=(p-1) \bar{U}$
- Variance: $s_{d}^{2}=\sum\left(d_{i}-\bar{d}\right)^{2} /(p-1)$
- Degree distribution is a set of counts $\left\{f_{0}, \ldots, f_{p-1}\right\}$ where
$f_{k}=\#\left\{d_{i}=k\right\}=$ number of nodes with degree equal to $k$


## Some concepts

- Node centrality:
- measures "importance" of a node in a network: e.g., deletion of which genes in a gene regulatory network is likely to be lethal to the corresponding organism; how critical is a given router in an Internet network to the flow of traffic...
- some common centrality measures:
- closeness: $1 / \sum_{u \in V} \operatorname{dist}(u, v)$; "central" means the node is "close" to many other nodes;
- betweenness: $\sum_{s, t \in V} \sigma(s, t \mid v) / \sigma(s, t)$, where $\sigma(s, t \mid v)$ is the total number of shortest paths between $s$ and $t$ that pass through $v$; measures the extent to which a vertex is located "between" other pairs of vertices;


## Some concepts

- Network cohesion:
- measures the extent to which subsets of nodes are cohesive / stuck together; e.g., do friends of a given actor in a social network tend to be friends of one another as well; what collections of proteins in a cell appear to work closely together...
- Some common cohesion measures:
- clique: A clique is a complete subgraph.
- maximal clique: is a clique but no other nodes can be added to make it a larger clique.
- density of a subgraph
- Connectivity
- "small worlds" property: the average distance between nodes is small


## Network community detection: Outline

- Introduction
- Spectral clustering
- Hierachical clustering
- Modularity-based methods
- Model-based methods
- Key refs:
1.Newman MEJ

2. Zhao Y, Levina E, Zhu J (2012, Ann Statist 40:2266-2292).
3. Fortunato $S$ (2010, Physics Reports 486:75-174).

- R package igraph: drawing networks, calculating some network statistics, some community detection algorithms, ...


## Introduction

- Given a binary (undirected) network/graph: $G=(V, E)$, $V=\{1,2, \ldots, n\}$, set of nodes; $E$, set of edges. Adjacency matrix $A=\left(A_{i j}\right): A_{i j}=1$ if there is an edge/link $\mathrm{b} / \mathrm{w}$ nodes $i$ and $j ; A_{i j}=0 \mathrm{o} / \mathrm{w} .\left(A_{i i}=0\right)$
- Goal: assign the nodes into $K$ "homogeneous" groups. often means dense connections within groups, but sparse b/w groups.
- Why? Figs 1-4 in Fortunato (2010).

Brain networks (Meunier et al, 2010).
Gene networks (Langfelder and Horvath, 2008).

## Spectral clustering

- Laplacian $L=D-A$, or $\ldots$
$D=\operatorname{Diag}\left(D_{11}, \ldots, D_{n n}\right), D_{i i}=\sum_{j} A_{i j}$.
- Intuition:

If a network separates perfectly into $K$ communities, then $L$ (or $A$ ) is block diagonal (after some re-ordering of the rows/columns).
If not perfectly but nearly, then the eigenvectors of $L$ are (nearly) linear combinations of the indicator vectors.

- Apply K-means (or ..) to a few (K) eigenvectors corresponding to the smallest eigenvalues of $L$. Note: the smallest eigen value is 0 , corresponding to eigenvector 1 .
- Two clusters $\Longrightarrow$ spectral bisection: use the eigenvector of the second smallest eigen value; partition by its positive/negative elements.
Generally, repeatedly apply the above to each cluster... vs apply SC once?
- Widely used; some theory (e.g consistency).


## Modified spectral clustering

- SC may not work well for sparse networks.
- Regularized SC (Qin and Rohe): replace $D$ with $D_{\tau}=D+\tau l$ for a small $\tau>0$.
- SC with perturbations (Amini, Chen, Bickel, Levina, 2013, Ann Statist 41: 2097-2122):
regularize $A$ by adding a small positive number on a random subset of off-diagonals of $A$.


## Hierarchical clustering

- Need to define some similarity or distance $\mathrm{b} / \mathrm{w}$ nodes.
- Euclidean distance: $A_{i .}=\left(A_{i 1}, A_{12}, \ldots, A_{i n}\right)^{\prime}$,

$$
x_{i j}=\left\|A_{i .}-A_{j .}\right\|_{2}
$$

- Or, Pearson's corr,

$$
x_{i j}=\operatorname{corr}\left(A_{i .}, A_{j .}\right)
$$

- Then apply a hierarchical clustering. can be used to re-arrange the rows/columns of $A$ to get a nearly block-diagonal $A$.
- Fig 3 in Neuman.
- Fig 2 in Meunier et al (2010).


## Algorithms based on edge removal

- Divisive: edges are progressively removed.
- Which edges? "bottleneck" ones.
- edge betweenness is defined to be the number of shortest paths between all pairs of all nodes that run through the two nodes.
- Algorithm (Girvam and Neuman 2002, PNAS):

1) calculate edge betweenness for each remaining edge in a network;
2) remove the edge with the higest edge betweenness;
3) repeat the above until ...

- A possible stopping critarion: modularity, to be discussed.
- Fig 4 in Neuman.
- Remarks: slow; some modifications, e.g. a Monte Carlo version in calculating edge betweenness using only a random subset of all pairs; or use a different criterion.
- R package igraph: cluster_edge_betweenness()


## Modularity-based methods

- Notation: degree of node $i: d_{i}=D_{i i}=\sum_{j=1}^{n} A_{i j}$, (twice) total number of edges: $m=\sum_{i=1}^{n} d_{i}$,
Community assignment: $C=\left(C_{1}, C_{2}, \ldots, C_{n}\right)$; unknown, $C_{i} \in\{1,2, \ldots, K\}$ : community containing node $i$.
- Modularity: given $C$,

$$
Q=Q(C)=\frac{1}{2 m} \sum_{i, j}\left(A_{i j}-\frac{d_{i} d_{j}}{m}\right) I\left(C_{i}=C_{j}\right)
$$

- Intuition: obs'ed - exp'ed
- Goal: $\hat{C}=\arg \max _{C} Q(C)$

Assumption: good to maximize $Q$, reasonable but ...

- Key: a combinatorial optimization problem! seeking exact solution will be too slow $\Longrightarrow$ many approximate algorithms, such as greedy searches (e.g. genetic algorithms, simulated annealing), relaxed algorithms, ...
Newman (2003): repeat: combining two nodes $i$ and $j$ with $A_{i j}=1$ and the largest increase (or smallest decrease) in $Q$; until all nodes in one community.
$\Longrightarrow$ hierarchical; choose one with the largest $Q$.
- Very nonparametric?!
- Problems: resolution limit; too many local solutions.
cannot detect relatively small communities; why? an implicit null model for the whole network (Fortunato 2010, p.40).
- R package igraph:
greedy search, approx./fast: cluster_fast();
combinatorial search, exact/slow: cluster_optimal(); heuristic, hierarchical communities for large networks (e.g. millions of nodes); see Blondel et al (2008) in the manual: cluster_louvain().


## Model-based methods

- Stochastic block model SBM (Holland et al 1983):

1) a $K \times K$ probability matrix $P$;
2) $A_{i j} \sim \operatorname{Bin}\left(1, P_{C_{i}, C_{j}}\right)$ independently.

- Simple; can model dense/weak within-/between-community edges.
But, treat all nodes/edges in a community equally; cannot model hub nodes!
Scale-free network: node degree distribution $\operatorname{Pr}(k)$ is heavy-tailed; a power law.
- SBM with $K=1$ : Erdos-Renyi Random Graph.
- Degree-corrected SBM (DCSBM) (Karrer and Newman 2011):

1) $P$; each node $i$ has a degree parameter $\theta_{i}$ (with some constraints for identifiability);
2) $A_{i j} \sim \operatorname{Bin}\left(1, \theta_{i} \theta_{j} P_{C_{i}, C_{j}}\right)$ independently

- More notations:
$n_{k}(C)=\sum_{i=1}^{n} I\left(C_{i}=k\right)$, number of nodes in community $k$;
$O_{k l}=\sum_{i, j=1}^{n} A_{i j} l\left(C_{i}=k, C_{j}=l\right)$, number of edges $\mathrm{b} / \mathrm{w}$
communities $k \neq 1$;
$O_{k k}=\sum_{i, j=1}^{n} A_{i j} I\left(C_{i}=k, C_{j}=k\right)$, (twice) number of edges within community $k$;
$O_{k}=\sum_{l=1}^{K} O_{k l}$, sum of node degrees in community $k$; $m=\sum_{i=1}^{n} d_{i}$, (twice) the number fo edges in the network.
- Objective function: A profile likelihood (profiling out nuisance parameters $P$ and $\theta$ 's based on a Poisson approximation to a binomial).
Given a likelihood $L(C, P)$,
a profile likelihood $L^{*}(C)=\max _{P} L(C, P)=L(C, \hat{P}(C))$.
- SBM:

$$
Q_{S B}(C)=\sum_{k, l=1}^{K}\left(O_{k l} \log \frac{O_{k l}}{n_{k} n_{l}}\right)
$$

- DCSBM:

$$
Q_{D C}(C)=\sum_{k, l=1}^{K}\left(O_{k l} \log \frac{O_{k l}}{O_{k} O_{l}}\right)
$$

- Neuman-Girvan modularity:

$$
Q_{N G}(C)=\frac{1}{2 m} \sum_{k}\left(O_{k k}-\frac{O_{k}^{2}}{m}\right)
$$

- Remarks: Still a combinatorial optimization problem; better theoretical properties.
- Numerical examples in Zhao et al (2012).


## Other topics

- Weighted networks; with or without negative weights (e.g. Pearson's correlations).
- Overlapping communities.
- Time-varying (dynamic) networks.
- With covariates. How to model covariates?
- Fast (approximate) algorithms; theory.
- WGCNA (Weighted Gene Co-expression Network Analysis): Langfelder and Horvath (2008, BI).

