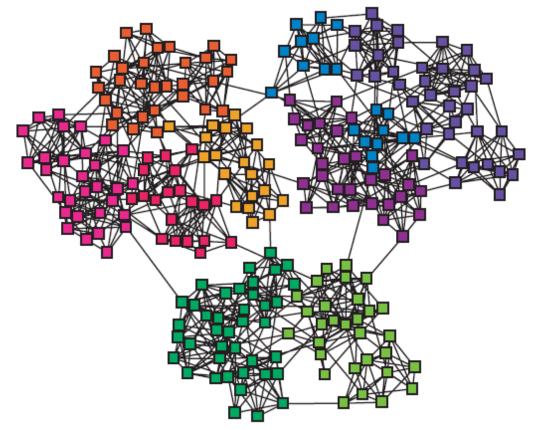
Online Social Networks and Media

Graph Partitioning (cuts, spectral clustering, density), Community evolution

Introduction

modules, cluster, communities, groups, *partitions* (*more on this today*)



Outline

Summary of Part I

PART II

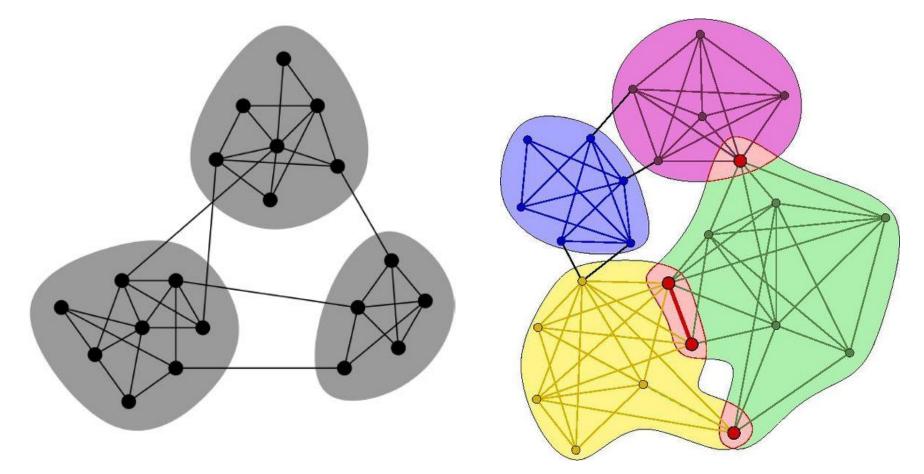
- 1. Cuts
- 2. Spectral Clustering
- 3. Dense Subgraphs

partitions

4. Community Evolution

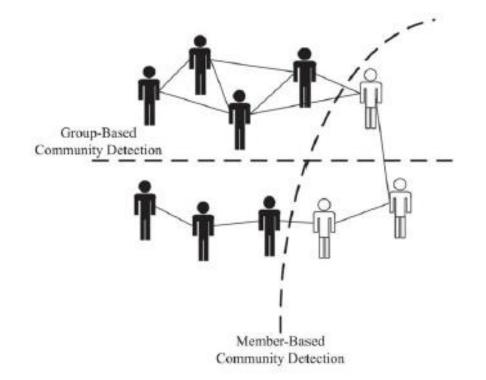
Community Types

Non-overlapping vs. overlapping communities



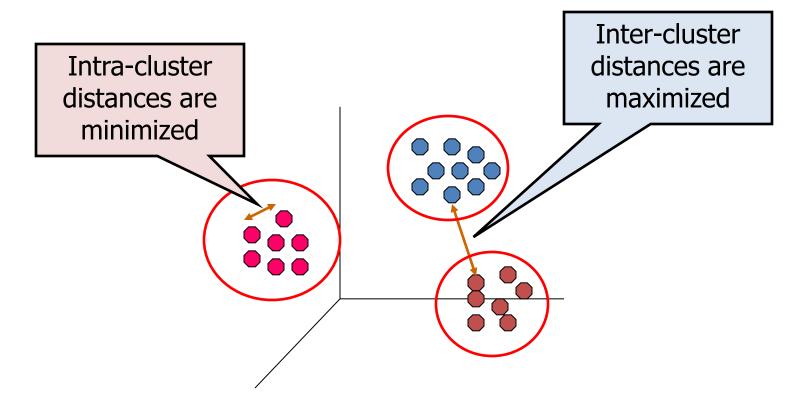
Community Types

Member-based (local) vs. group-based



What is Cluster Analysis?

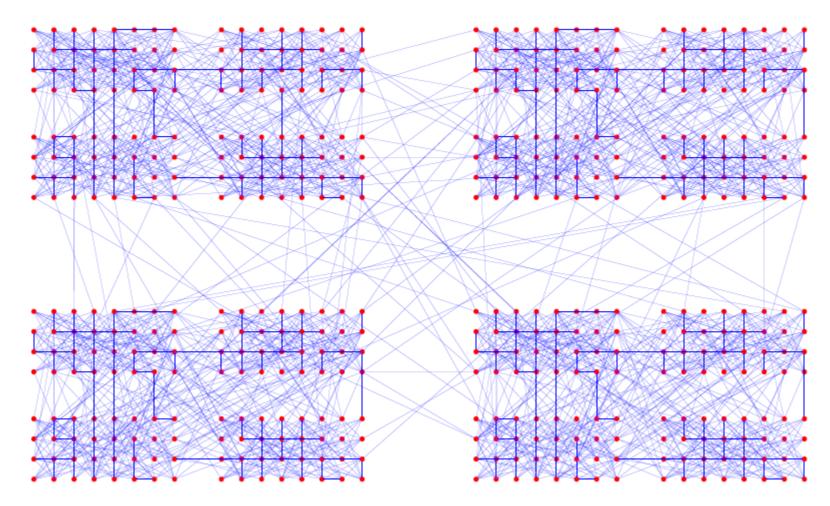
Finding groups of objects such that the objects in a group are similar (or related) to one another and different from (or unrelated to) the objects in other groups



Types of Clustering

- Important distinction between hierarchical and partitional sets of clusters
- Partitional Clustering
 - Division of data objects into subsets (clusters)
 - Assumes that the number of clusters is given
- Hierarchical clustering
 - A set of nested clusters organized as a hierarchical tree

Example of a Hierarchically Structured Graph



Example Partitioning: K-means Clustering

- 1: Select K points as the initial centroids.
- 2: repeat
- 3: Form K clusters by assigning all points to the closest centroid.
- 4: Recompute the centroid of each cluster.
- 5: **until** The centroids don't change

- Input: Number of clusters, K
- Each cluster is associated with a *centroid* (center point)
- Each point is assigned to the cluster with the closest centroid

Sum of Squared Error (SSE)

- Most common measure is Sum of Squared Error (SSE)
 - For each point, the error is the distance to the nearest cluster
 - To get SSE, we square these errors and sum them.

$$SSE = \sum_{i=1}^{K} \sum_{x \in C_i} dist^2(m_i, x)$$

- x is a data point in cluster C_i and m_i is the representative point for cluster C_i
 - can show that m_i corresponds to the center (mean) of the cluster

Hierarchical Clustering

- Two main types of hierarchical clustering
 - Agglomerative:
 - Start with the points (vertices) as individual clusters
 - At each step, merge the closest pair of clusters until only one cluster (or k clusters) left
 - Divisive:
 - Start with one, all-inclusive cluster (the whole graph)
 - At each step, split a cluster until each cluster contains a point (vertex) (or there are k clusters)
- Traditional hierarchical algorithms use a similarity or distance matrix
 - Merge or split one cluster at a time

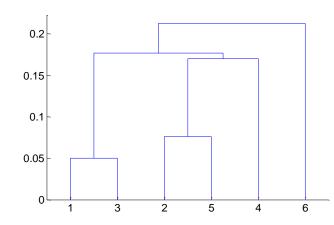
Agglomerative Clustering Algorithm

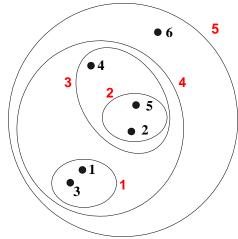
Popular hierarchical clustering technique

- Basic algorithm is straightforward
 - 1. [Compute the proximity matrix]
 - 2. Let each data point be a cluster
 - 3. Repeat
 - 4. Merge the *two closest clusters*
 - 5. [Update the proximity matrix]
 - 6. Until only a single cluster remains
- Key operation is the *computation of the proximity of two clusters*
 - Different approaches to defining the distance between clusters distinguish the different algorithms

Hierarchical Clustering

- Produces a set of nested clusters organized as a hierarchical tree
- Can be visualized as a dendrogram
 - A tree like diagram that records the sequences of merges or splits





Pre-processing and Post-processing

- Pre-processing
 - Normalize the data
 - Eliminate outliers
 - Find connected components
- Post-processing
 - Eliminate small clusters that may represent outliers
 - Split 'loose' clusters, i.e., clusters with relatively high SSE
 - Merge clusters that are 'close' and that have relatively low SSE
 - Can use these steps during the clustering process

Communities

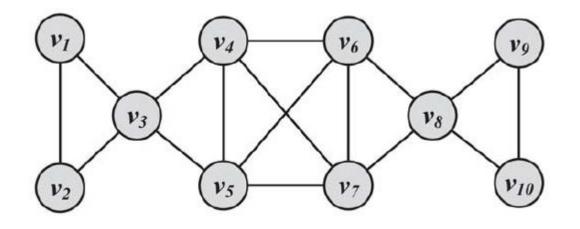
Algorithms

- 1. Cliques (PCM)
- 2. Vertex similarity
- 3. Divisive hierarchical clustering using betweenness
- 4. Modularity
- 5. Label Propagation

Evaluation

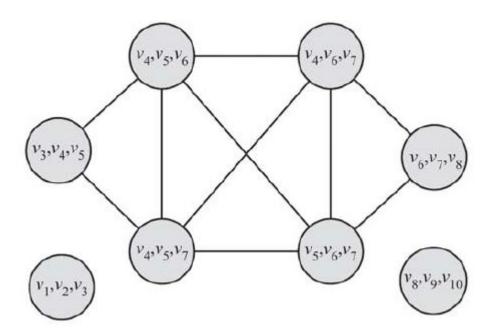
Clique Percolation Method (CPM): Using cliques as seeds

Input graph, let k = 3



Clique Percolation Method (CPM): Using cliques as seeds

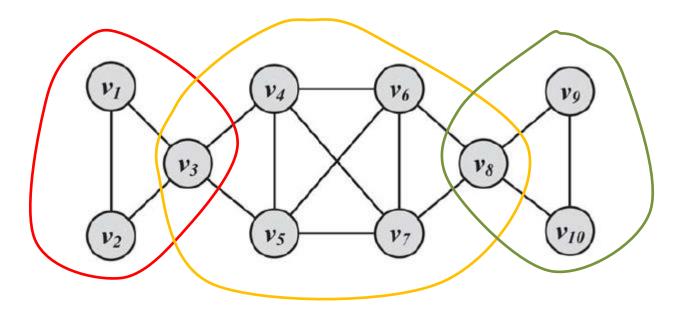
Clique graph for k = 3



(v1, v2, ,v3), (v8, v9, v10), and (v3, v4, v5, v6, v7, v8)

Clique Percolation Method (CPM): Using cliques as seeds

Result



(v1, v2, ,v3), (v8, v9, v10), and (v3, v4, v5, v6, v7, v8)

Vertex similarity

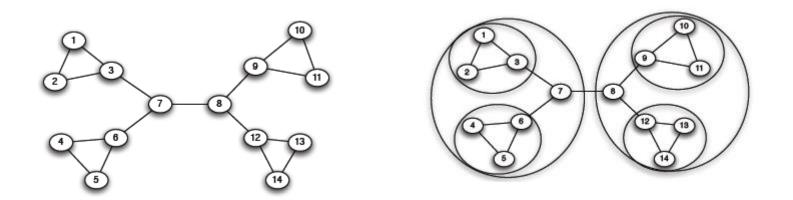
- Define similarity between two vertices
- Place similar vertices in the same cluster

Use traditional *cluster analysis*

Graph Partitioning

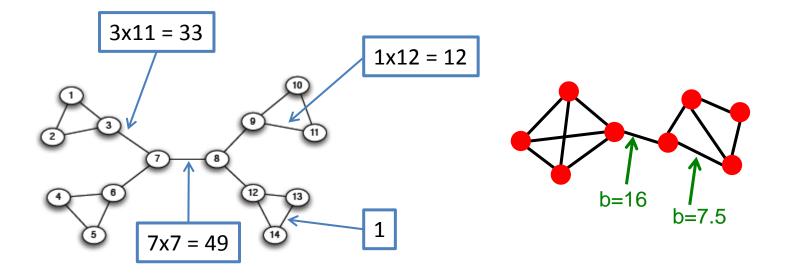
Divisive methods: try to identify and remove the "spanning links" between densely-connected regions

 Agglomerative methods: Find nodes that are likely to belong to the same region and merge them together (bottom-up)



Edge Betweenness

$$bt(a,b) = \sum_{x,y} \frac{\#shortest_paths(x, y)through(a,b)}{\#shortest_paths(x, y)}$$



The Girvan Newman method

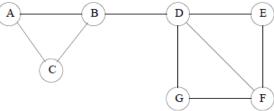
» Undirected unweighted networks

- Repeat until no edges are left:
 - Calculate betweenness of edges
 - Remove edges with highest betweenness
- Connected components are communities
- Gives a hierarchical decomposition of the network

Computing Betweenness

- 1. Perform a BFS starting from A
- 2. Determine the number of shortest path from A to each other node
- 3. Based on these numbers, determine the amount of flow from A to all other nodes that uses each edge

Repeat the process for all nodes Sum over all BFSs



Modularity

- Modularity of partitioning S of graph G:
 - $-Q \propto \sum_{s \in S} [(\# \text{ edges within group } s) (\text{expected } \# \text{ edges within group } s)]$

$$-Q(G,S) = \frac{1}{2m} \sum_{s \in S} \sum_{i \in S} \sum_{j \in S} \left(A_{ij} - \frac{d_i d_j}{2m} \right)$$

Normalizing cost.: -1<Q<1

- Modularity values take range [-1, 1]
 - It is positive if the number of edges within groups exceeds the expected number
 - 0.3-0.7 < Q means significant community structure</p>

Modularity

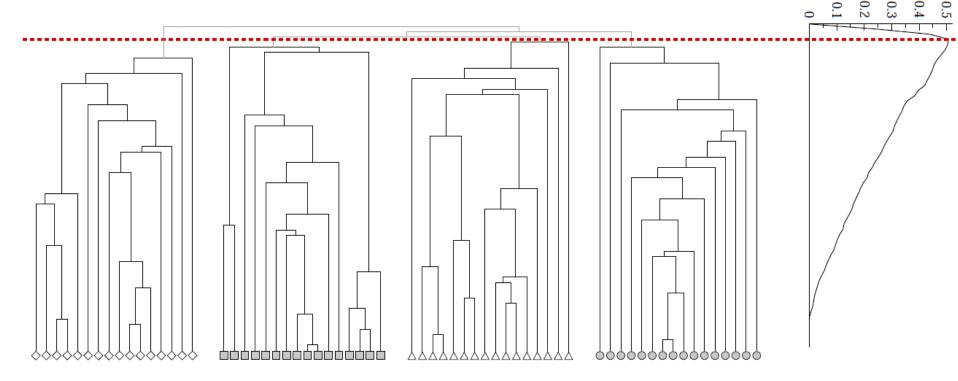
Greedy method of Newman (one of the many ways to use modularity)

Agglomerative hierarchical clustering method

- 1. Start with a state in which each vertex is the sole member of one of *n* communities
- 2. Repeatedly join communities together in pairs, choosing at each step the join that results in the greatest increase (or smallest decrease) in Q.

Modularity: Number of clusters

• Modularity is useful for selecting the number of clusters:



modularity

Label propagation

Vertices are initially given unique labels (e.g. their vertex labels). At each iteration,

sweep over all vertices, in random sequential order:

each vertex takes the label shared by the majority of its neighbors.

If no unique majority, one of the majority labels is picked at random. Stop (convergence) when each vertex has the majority label of its neighbors

Communities: groups of vertices having identical labels at convergence

Label propagation

- Labels propagate across the graph: most labels will disappear, others will dominate.
- By construction, each vertex has more neighbors in its community than in any other community.
- Due to many possible ties, different partitions starting from the same initial condition, with different random seeds
 - Aggregate partition label each vertex with the
 - set of all labels it has in different partitions → overlapping communities

Cluster quality

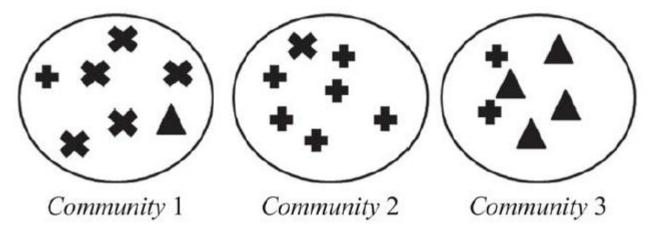
When a given clustering is "good"?

- With ground truth
- Without ground truth

Metrics: purity

the fraction of instances that have labels equal to the label of the community's majority

$$Purity = \frac{1}{N} \sum_{i=1}^{k} \max_{j} |C_i \cap L_j|$$



(5+6+4)/20 = 0.75

Metrics: pairs

Precision (P): the fraction of pairs that have been correctly assigned to the same community.

TP/(TP+FP)

Recall (R): the fraction of pairs assigned to the same community of all the pairs that should have been in the same community.

TP/(TP+FN)

F-measure

2PR/(P+R)

Metrics

Based on pair counting: the number of pairs of vertices which are classified in the same (different) clusters in the two partitions.

- True Positive (TP) Assignment: when similar members are assigned to the same community. This is a correct decision.
- True Negative (TN) Assignment: when dissimilar members are assigned to different communities. This is a correct decision.
- False Negative (FN) Assignment: when similar members are assigned to different communities. This is an incorrect decision.
- False Positive (FP) Assignment: when dissimilar members are assigned to the same community. This is an incorrect decision.

Evaluation without ground truth

$$\delta_{int}(\mathcal{C}) = \frac{\# \text{ internal edges of } \mathcal{C}}{n_c(n_c - 1)/2}.$$

$$\delta_{ext}(\mathcal{C}) = \frac{\# \text{ inter-cluster edges of } \mathcal{C}}{n_c(n - n_c)}$$

Modularity

Evaluation without ground truth

With semantics:

- (ad hoc) analyze other attributes (e.g., profile, content generated) for coherence
- human subjects (user study) Mechanical Turk
 Visual representation (similarity/adjacency matric, word clouds, etc)



(a) U.S. Constitution

(b) Sports

Outline

PART II

- 1. Cuts
- 2. Spectral Clustering
- 3. Dense Subgraphs



4. Community Evolution

Graph partitioning

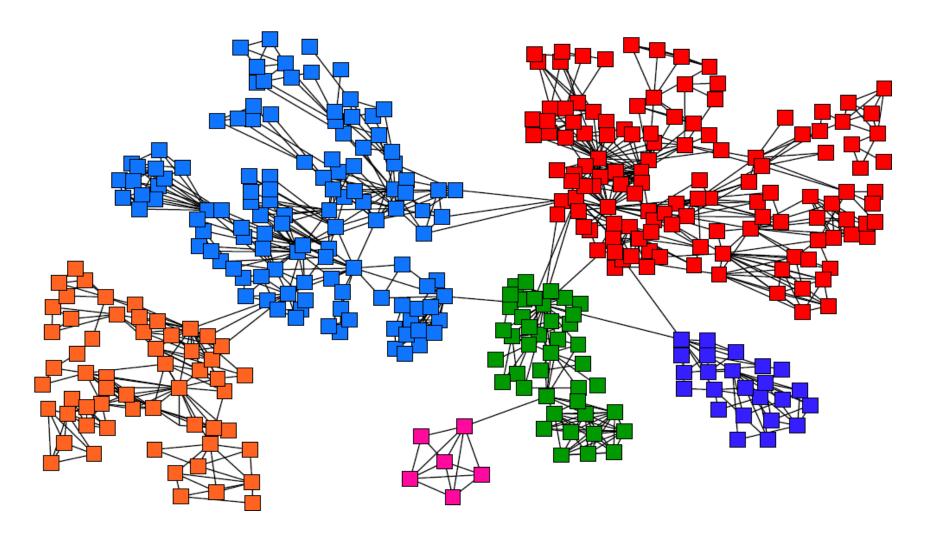
The general problem

- Input: a graph G = (V, E)
 - edge (u, v) denotes similarity between u and v
 - weighted graphs: weight of edge captures the degree of similarity

Partitioning as an optimization problem:

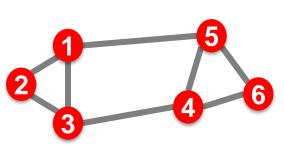
- Partition the nodes in the graph such that nodes *within clusters* are *well interconnected* (high edge weights), and nodes *across clusters* are *sparsely interconnected* (low edge weights)
- most graph partitioning problems are NP hard

Graph Partitioning



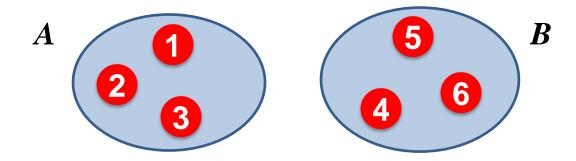
Graph Partitioning

Undirected graph G(V, E):



Bi-partitioning task:

Divide vertices into two disjoint groups A, B

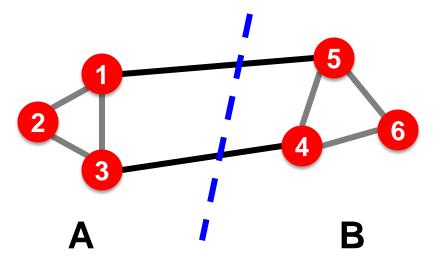


How can we define a "good" partition of **G**? How can we efficiently identify such a partition?

Graph Partitioning

What makes a good partition?

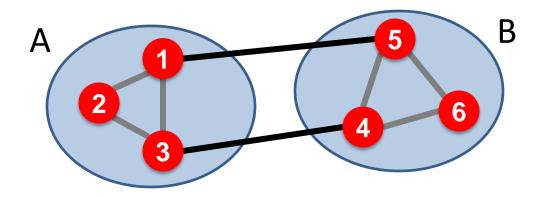
- Maximize the number of within-group connections
- Minimize the number of between-group connections



Graph Cuts

Express *partitioning objectives* as a function of the "edge cut" of the partition

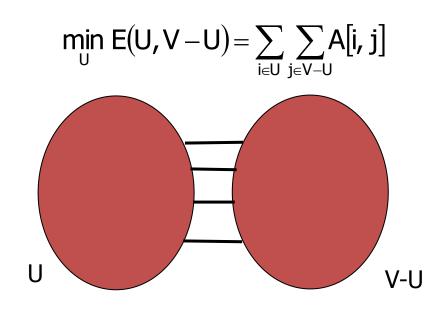
Cut: Set of edges with only one vertex in a group: $cut(A,B) = \sum_{i \in A, j \in B} w_{ij}$



$$cut(A,B) = 2$$

Min Cut

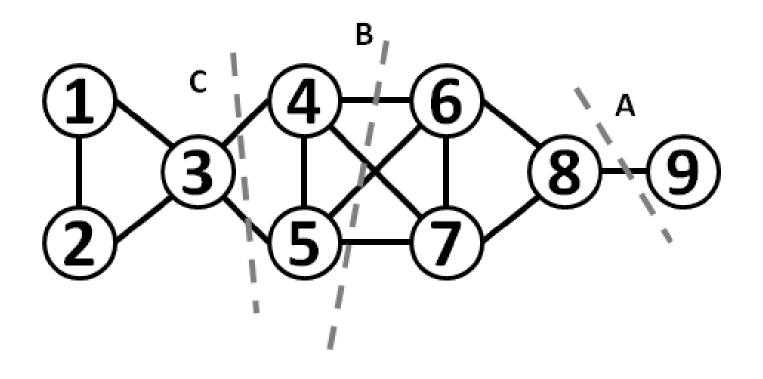
 $\begin{array}{l} \mbox{min-cut: the min number of edges such that when} \\ \mbox{removed cause the graph to become disconnected} \\ \mbox{Minimizes the number of connections between partition} \\ \mbox{arg min}_{A,B}\ cut(A,B) \end{array}$



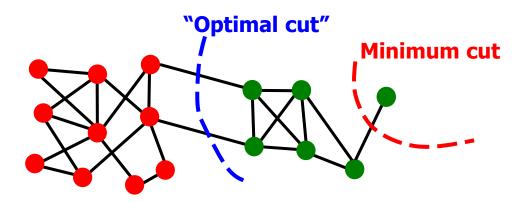
This problem can be solved in polynomial time

Min-cut/Max-flow algorithm

An example



Min Cut



Problem:

- Only considers external cluster connections
- Does not consider internal cluster connectivity

Graph Bisection

- Since the minimum cut does not always yield good results we need extra constraints to make the problem meaningful.
- Graph Bisection refers to the problem of partitioning the nodes of the graph into two equal sets.
- Kernighan-Lin algorithm: Start with random equal partitions and then swap nodes to improve some quality metric (e.g., cut, modularity, etc).

Cut Ratio

Ratio Cut Normalize cut by the *size* of the groups

Ratio-cut=
$$\frac{Cut(U,V-U)}{|U|} + \frac{Cut(U,V-U)}{|V-U|}$$

Normalized Cut

Normalized-cut

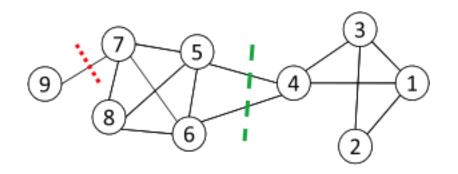
Connectivity between groups relative to the *density* of each group Normalized-cut= $\frac{Cut(U,V-U)}{Vol(U)} + \frac{Cut(U,V-U)}{Vol(V-U)}$

> vol(U): total weight of the edges with at least one endpoint in U: $vol(U) = \sum_{i \in U} d_i$

Why use these criteria?

Produce more balanced partitions

An example



Red is Min-Cut

Ratio-Cut(Red) =
$$\frac{1}{1} + \frac{1}{8} = \frac{9}{8}$$

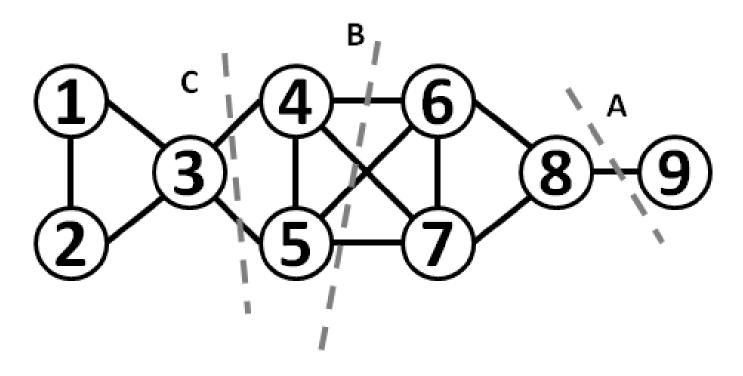
Ratio-Cut(Green) = $\frac{2}{5} + \frac{2}{4} = \frac{18}{20}$

Normalized-Cut(Red) = $\frac{1}{1} + \frac{1}{27} = \frac{28}{27}$

Normalized-Cut(Green) =
$$\frac{2}{12} + \frac{2}{16} = \frac{14}{48}$$

Normalized is even better for Green due to density

An example



Which of the three cuts has the best (min, normalized, ratio) cut?

Graph expansion

Graph expansion:

$$\alpha = \min_{\mathbf{U}} \frac{\operatorname{cut}(\mathbf{U}, \mathbf{V} - \mathbf{U})}{\min\{|\mathbf{U}|, |\mathbf{V} - \mathbf{U}|\}}$$

Graph conductance (similar for volume)

Graph Cuts

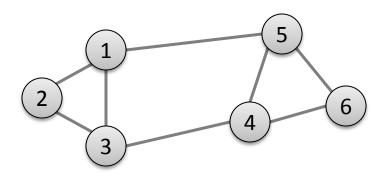
Ratio and normalized cuts can be reformulated in matrix format and solved using spectral clustering

SPECTRAL CLUSTERING

Matrix Representation

Adjacency matrix (A):

- $-n \times n$ matrix
- $-A = [a_{ij}], a_{ij} = 1$ if edge between node *i* and *j*



Important properties:

- Symmetric matrix
- Eigenvectors are real and orthogonal

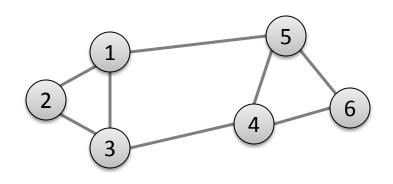
If the graph is weighted, $a_{ij} = w_{ij}$

	1	2	3	4	5	6
1	0	1	1	0	1	0
2	1	0	1	0	0	0
3	1	1	0	1	0	0
4	0	0	1	0	1	1
5	1	0	0	1	0	1
6	0	0	0	1	1	0

Matrix Representation

Degree matrix (D):

- $-n \times n$ diagonal matrix
- $-D = [d_{ii}], d_{ii} = \text{degree of node } i$



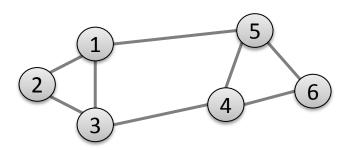
	1	2	3	4	5	6
1	3	0	0	0	0	0
2	0	2	0	0	0	0
3	0	0	3	0	0	0
4	0	0	0	3	0	0
5	0	0	0	0	3	0
6	0	0	0	0	0	2

Matrix Representation

Laplacian matrix (L):

 $-n \times n$ symmetric matrix

L = D - A



	1	2	3	4	5	6
1	3	-1	-1	0	-1	0
2	-1	2	-1	0	0	0
3	-1	-1	3	-1	0	0
4	0	0	-1	3	-1	-1
5	-1	0	0	-1	3	-1
6	0	0	0	-1	-1	2

Spectral Graph Partitioning

x is a vector in \Re^n with components (x_1, \dots, x_n) — Think of it as a label/value of each node of G

• What is the meaning of $A \cdot x$? $\begin{bmatrix} a_{11} & \dots & a_{1n} \\ \vdots & & \vdots \\ a_{n1} & \dots & a_{nn} \end{bmatrix} \begin{bmatrix} x_1 \\ \vdots \\ x_n \end{bmatrix} = \begin{bmatrix} y_1 \\ \vdots \\ y_n \end{bmatrix} \qquad y_i = \sum_{j=1}^n A_{ij} x_j = \sum_{(i,j) \in E} x_j$

Entry y_i is a sum of labels x_i of neighbors of i

Spectral Analysis

i^{th} coordinate of $A \cdot x$:

 Sum of the x-values of neighbors of *i*

 $\begin{bmatrix} a_{11} & \dots & a_{1n} \\ \vdots & & \vdots \\ a_{n1} & \dots & a_{nn} \end{bmatrix} \begin{bmatrix} x_1 \\ \vdots \\ x_n \end{bmatrix} = \lambda \begin{bmatrix} x_1 \\ \vdots \\ x_n \end{bmatrix}$ – Make this a new value at node *i* $A \cdot x = \lambda \cdot x$

Spectral Graph Theory:

- Spectrum: Eigenvectors x_i of a graph, ordered by the magnitude (strength) of their corresponding eigenvalues λ_i : $\Lambda = \{\lambda_1, \lambda_2, ..., \lambda_n\}$ $\lambda_1 \leq \lambda_2 \leq ... \leq \lambda_n$

Spectral clustering: use the eigenvectors of A or graphs derived by it

Most based on the graph Laplacian

Laplacian Matrix properties

• The matrix L is symmetric and positive semidefinite

– all eigenvalues of ${\bf L}$ are positive

positive definite: if z^TMz is non-negative, for every non-zero column vector z

The matrix L has 0 as an eigenvalue, and corresponding eigenvector w₁ = (1,1,...,1)
 - λ₁ = 0 is the smallest eigenvalue

Proof: Let w_1 be the column vector with all $1s - show Lw_1 = 0w_1$

The second smallest eigenvalue

The second smallest eigenvalue (also known as Fielder value) λ_2 satisfies

$$\lambda_2 = \min_{x \perp w_1, \|x\| = 1} x^\mathsf{T} L x$$

The second smallest eigenvalue

• For the Laplacian

$$\mathbf{x} \perp \mathbf{w}_1 \implies \sum_i \mathbf{x}_i = \mathbf{0}$$

• The expression:

is

$$\sum_{(i,j)\in E} (x_i - x_j)^2$$

The second smallest eigenvalue

Thus, the eigenvector for eigenvalue λ_2 (called the Fielder vector) minimizes

$$\min_{x \neq 0} \sum_{(i,j) \in E} (x_i - x_j)^2 \quad \text{where} \quad \sum_i x_i = 0$$

Intuitively, minimum when x_i and x_j close whenever there is an edge between nodes i and j in the graph.

x must have some positive and some negative components

Cuts + eigenvalues: intuition

• A *partition* of the graph by taking:

- one set to be the nodes i whose corresponding vector component x_i is *positive* and
- the other set to be the nodes whose corresponding vector component is *negative*.
- The *cut* between the two sets will have a small number of edges because (x_i-x_j)² is likely to be smaller if both x_i and x_j have the same sign than if they have different signs.
- Thus, minimizing x^TLx under the required constraints will end giving x_i and x_i the same sign if there is an edge (i, j).

Cuts + eigenvalues: summary

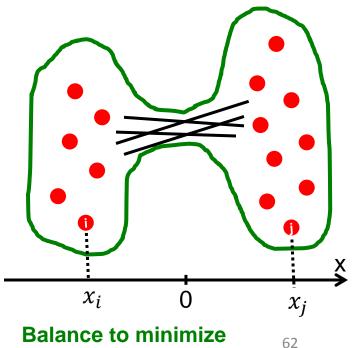
• What we know about *x*?

– x is unit vector:
$$\sum_i x_i^2 = 1$$

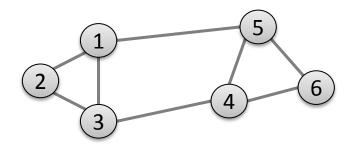
- x is orthogonal to 1st eigenvector (1, ..., 1) thus: $\sum_{i} x_{i} \cdot 1 = \sum_{i} x_{i} = 0$

$$\lambda_{2} = \min \frac{\sum_{\substack{(i,j) \in E}} (x_{i} - x_{j})^{2}}{\sum_{\substack{\text{of nodes } i \text{ so} \\ \text{that } \sum x_{i} = 0}} \sum_{i} x_{i}^{2}$$

We want to assign values x_i to nodes *i* such that few edges cross 0. (we want x_i and x_j to subtract each other)



Example



Eigenvalue	0	1	3	3	4	5
Eigenvector	1	1	-5	-1	-1	-1
	1	2	4	-2	1	0
	1	1	1	3	-1	1
	1	-1	-5	-1	1	1
	1	-2	4	-2	-1	0
	1	-1	1	3	1	-1

Spectral Partitioning Algorithm

Three basic stages:

Pre-processing

• Construct a matrix representation of the graph

Decomposition

• Compute eigenvalues and eigenvectors of the matrix

Grouping

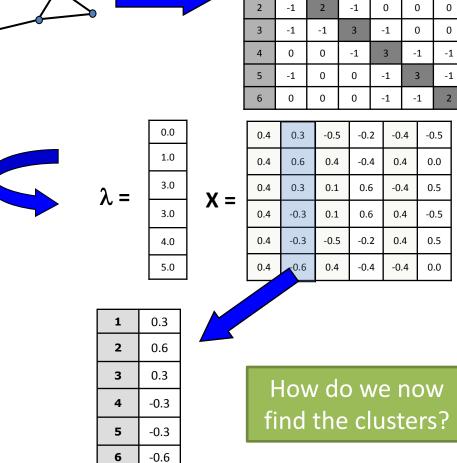
 Assign points to two or more clusters, based on the new representation

Spectral Partitioning Algorithm

Pre-processing: Build Laplacian matrix *L* of the graph

Decomposition:

- Find eigenvalues λ and eigenvectors xof the matrix L
- Map vertices to corresponding components of λ_2



2

-1

1

3

1

3

-1

4

0

5

-1

6

0

Spectral Partitioning Algorithm

Grouping:

- Sort components of reduced 1-dimensional vector
- Identify clusters by splitting the sorted vector in two
- How to choose a splitting point?
 - Naïve approaches:
 - Split at 0 or median value
 - More expensive approaches:
 - Attempt to minimize normalized cut in 1-dimension (sweep over ordering of nodes induced by the eigenvector)

4

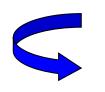
5

6

-0.3

-0.3

-0.6



2	0.6	
3	0.3	
4	-0.3	
5	-0.3	
6	-0.6	

0.3

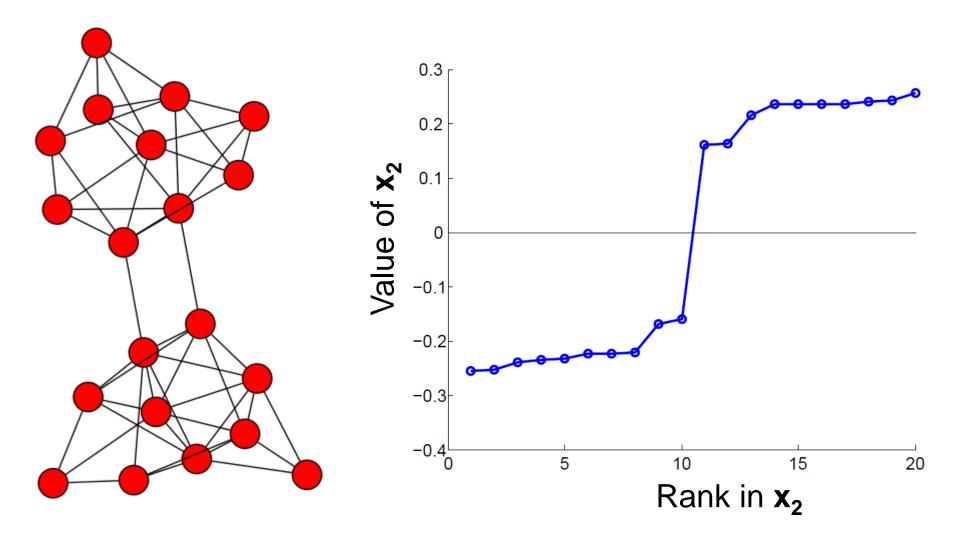
Split at 0:

Cluster A: Positive points

Cluster B: Negative points

1	0.3	
2	0.6	
3	0.3	

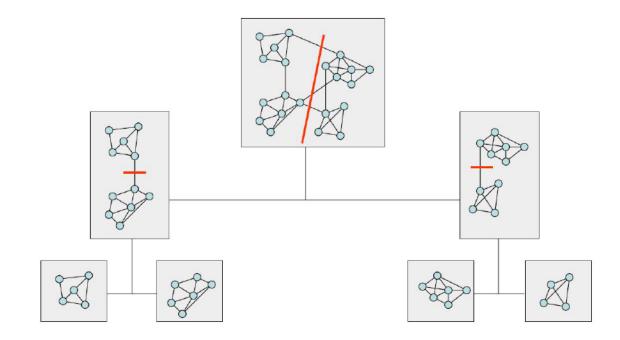
Example: Spectral Partitioning



k-Way Spectral Clustering

How do we partition a graph into k clusters?

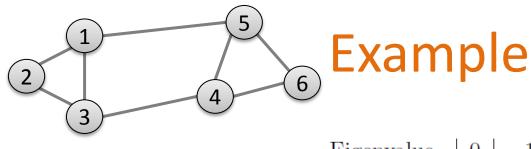
- Recursively apply a bi-partitioning algorithm in a hierarchical divisive manner
 - Disadvantages: Inefficient, unstable



k-Way Spectral Clustering

Use *several of the eigenvectors* to partition the graph.

- Use m eigenvectors, and set a threshold for each,
- Get a partition into 2^m groups, each group consisting of the nodes that are above or below threshold for each of the eigenvectors, in a particular pattern.



 Eigenvalue
 0
 1
 3
 3
 4
 5

 Eigenvector
 1
 1
 -5 -1 -1 -1

 1
 2
 4
 -2 1
 0

 1
 1
 1
 3
 -1 1

 1
 1
 1
 3
 -1 1

 1
 -1 -5 -1 1 1

 1
 -1 -5 -1 1 1

 1
 -2 4 -2 -1 0

 genvectors,
 1 -1 1 3 1 -1

If we use both the 2nd and 3rd eigenvectors, nodes 2 and 3 (negative in both) 5 and 6 (negative in 2nd, positive in 3rd) 1 and 4 alone

- Note that each eigenvector except the first is the vector x that minimizes x^TLx, subject to the constraint that it is orthogonal to all previous eigenvectors.
- Thus, while each eigenvector tries to produce a minimum-sized cut, successive eigenvectors have to satisfy more and more constraints => the cuts progressively worse.

Other properties of L

Let G be an undirected graph with non-negative weights. Then

- the multiplicity k of the eigenvalue 0 of L equals the number of connected components A₁, . . . , A_k in the graph
- the eigenspace of eigenvalue 0 is spanned by the indicator vectors $1A_1$, . . , $1A_k$ of those components

Proof (sketch)

If connected (k = 1)

$$0 = x^{\tau} L x = \sum_{(i,j)\in E} (x_i - x_j)^2$$

Assume k connected components, both A and L block diagonal, if we order vertices based on the connected component they belong to (recall the "tile" matrix)

$$L = \begin{pmatrix} L_1 & & \\ & L_2 & \\ & & \ddots & \\ & & & L_k \end{pmatrix}$$

L_i Laplacian of the i-th component

For all block diagonal matrices, the spectrum is given by the union of the spectra of each block, and the corresponding eigenvectors are the eigenvectors of the block, filled with 0 at the positions of the other blocks.

Normalized Graph Laplacians

$$L_{sym} = D^{-1/2} L D^{-1/2} = I - D^{-1/2} W D^{-1/2}$$

$$L_{rw} = D^{-1}L = I - D^{-1}W$$

L_{rw} closely connected to random walks (to be discussed in future lectures)

$$x^{\tau}L_{sym}x = \sum_{(i,j)\in E} \left(\frac{X_i}{\sqrt{d_i}} - \frac{X_j}{\sqrt{d_j}}\right)^2$$

Cuts and spectral clustering

$$\operatorname{cut}(A_1,\ldots,A_k) := \sum_{i=1}^k \operatorname{cut}(A_i,\overline{A}_i)$$

RatioCut
$$(A_1, \dots, A_k) = \sum_{i=1}^k \frac{\operatorname{cut}(A_i, \overline{A}_i)}{|A_i|}$$

$$\operatorname{Ncut}(A_1,\ldots,A_k) = \sum_{i=1}^k \frac{\operatorname{cut}(A_i,\overline{A}_i)}{\operatorname{vol}(A_i)}.$$

Relaxing Ncut leads to normalized spectral clustering, while relaxing RatioCut leads to unnormalized spectral clustering

Spectral Clustering

- Use the lowest k eigenvalues of L to construct the nxk graph G' that has these eigenvectors as columns
- The n-rows represent the graph vertices in a k-dimensional Euclidean space
- Group these vertices in k clusters using kmeans clustering or similar techniques

Spectral clustering (besides graphs)

Can be used to cluster any points (not just vertices), as long as an appropriate similarity matrix

Needs to be *symmetric* and *non-negative*

How to construct a graph:

- ε-neighborhood graph: connect all points whose pairwise distances are smaller than ε
- k-nearest neighbor graph: connect each point with each k nearest neighbor
- full graph: connect all points with weight in the edge (i, j) equal to the similarity of i and j

Summary

• The values of x minimize

$$\min_{\mathbf{x}\neq\mathbf{0}}\sum_{(i,j)\in E} (x_i - x_j)^2 \qquad \sum_{i} \mathbf{x}_i = \mathbf{0}$$

• For weighted matrices

$$\min_{x \neq 0} \sum_{(i,j)} A[i,j] (x_i - x_j)^2 \sum_{i} x_i = 0$$

- The ordering according to the x_i values will group similar (connected) nodes together
- Physical interpretation: The stable state of springs placed on the edges of the graph

Parallel computation

Edge cuts -> Vertex partition Vertex cuts -> Edge partition

Thanks to Aris Gionis

MAXIMUM DENSEST SUBGRAPH

Finding dense subgraphs

- Dense subgraph: A collection of vertices such that there are a lot of edges between them
 - E.g., find the subset of email users that talk the most between them
 - Or, find the subset of genes that are most commonly expressed together
- Similar to community identification but we do not require that the dense subgraph is sparsely connected with the rest of the graph.

Definitions

- Input: undirected graph G = (V, E).
- Degree of node u: deg(u)
- For two sets $S \subseteq V$ and $T \subseteq V$: $E(S,T) = \{(u,v) \in E : u \in S, v \in T\}$
- E(S) = E(S, S): edges within nodes in S
- Graph Cut defined by nodes in $S \subseteq V$: $E(S, \overline{S})$: edges between S and the rest of the graph
- Induced Subgraph by set $S: G_S = (S, E(S))$

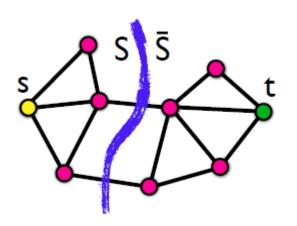
Definitions

- How do we define the density of a subgraph?
- Average Degree:

$$d(S) = \frac{2|E(S)|}{|S|}$$

- Problem: Given graph G, find subset S, that maximizes density d(S)
 - Surprisingly there is a polynomial-time algorithm for this problem.

Min-Cut Problem



Given a graph* G = (V, E), A source vertex $s \in V$, A destination vertex $t \in V$

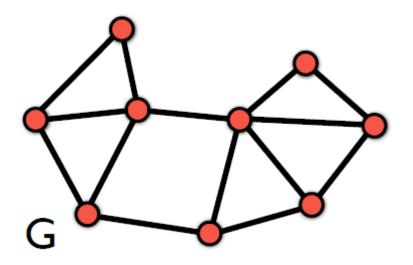
Find a set $S \subseteq V$ Such that $s \in S$ and $t \in \overline{S}$ That minimizes $E(S, \overline{S})$

* The graph may be weighted

Min-Cut = Max-Flow: the minimum cut maximizes the flow that can be sent from s to t. There is a polynomial time solution.

Decision problem

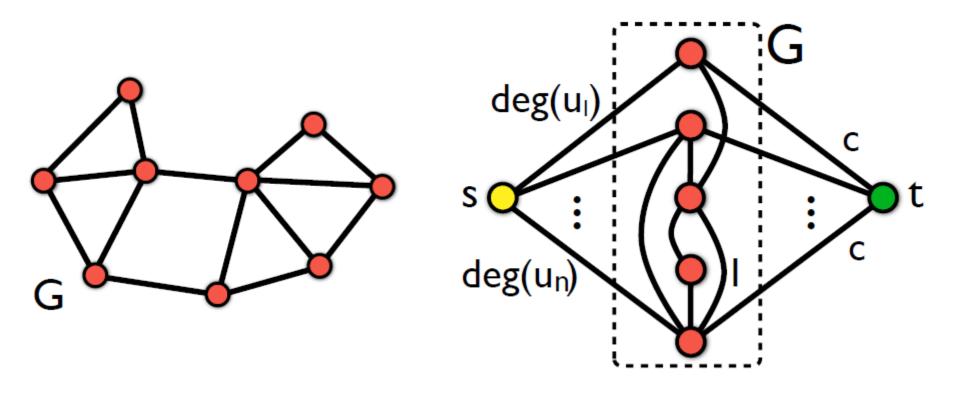
- Consider the decision problem – Is there a set *S* with $d(S) \ge c$?
- $d(S) \ge c$
- $2|E(S)| \ge c|S|$



- $\sum_{v \in S} \deg(v) E(S, \overline{S}) \ge c|S|$
- $2|E| \sum_{v \in \overline{S}} \deg(v) E(S, \overline{S}) \ge c|S|$
- $\sum_{v \in \overline{S}} \deg(v) + E(S, \overline{S}) + c|S| \le 2|E|$

Transform to min-cut

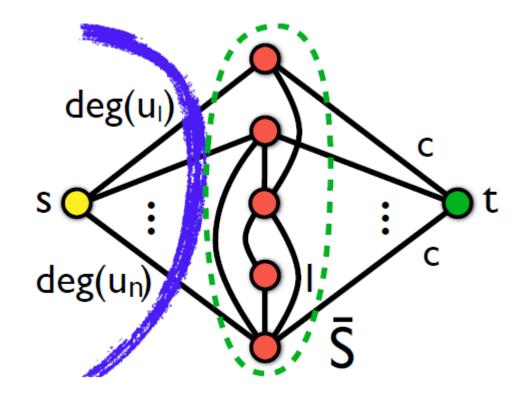
• For a value *c* we do the following transformation



We ask for a min s-t cut in the new graph

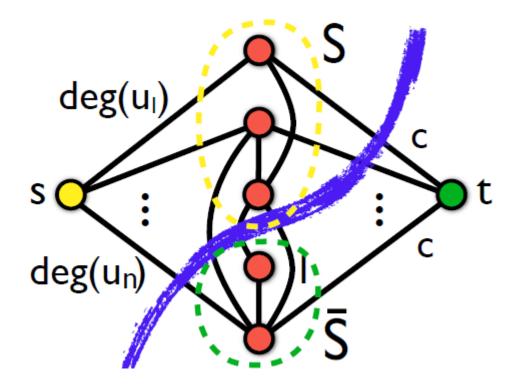
Transformation to min-cut

• There is a cut that has value 2|E|



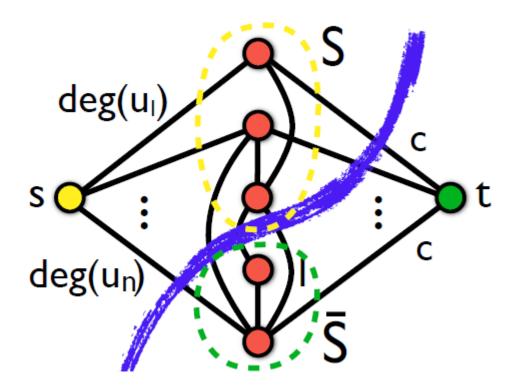
Transformation to min-cut

- Every other cut has value:
- $\sum_{v \in \overline{S}} \deg(v) + E(S, \overline{S}) + c|S|$



Transformation to min-cut

• If $\sum_{v \in \overline{S}} \deg(v) + E(S, \overline{S}) + c|S| \le 2|E|$ then $S \ne \emptyset$ and $d(S) \ge c$



Algorithm (Goldberg)

Given the input graph G, and value c

- 1. Create the min-cut instance graph
- 2. Compute the min-cut
- 3. If the set S is not empty, return YES
- 4. Else return NO

How do we find the set with maximum density?

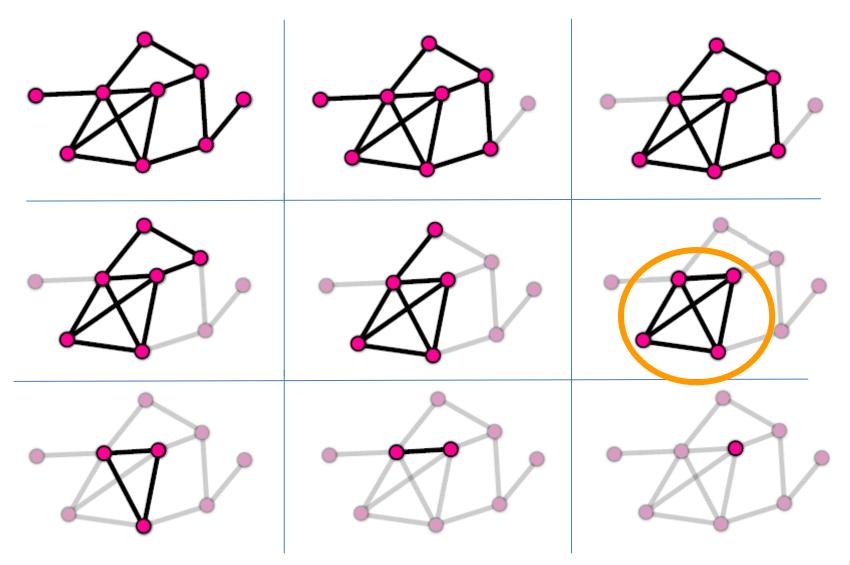
Min-cut algorithm

- The min-cut algorithm finds the optimal solution in polynomial time O(nm), but this is too expensive for real networks.
- We will now describe a simpler approximation algorithm that is very fast
 - Approximation algorithm: the ratio of the density of the set produced by our algorithm and that of the optimal is bounded.
 - We will show that the ratio is at most $\frac{1}{2}$
 - The optimal set is at most twice as dense as that of the approximation algorithm.
- Any ideas for the algorithm?

Greedy Algorithm

- Given the graph G = (V, E)
- 1. $S_0 = V$
- 2. For $i = 1 \dots |V|$
 - a. Find node $v \in S$ with the minimum degree
 - b. $S_i = S_{i-1} \setminus \{v\}$
- 3. Output the densest set S_i

Example



Analysis

- We will prove that the optimal set has density at most 2 times that of the set produced by the Greedy algorithm.
- Density of optimal set: $d_{opt} = \max_{S \subseteq V} d(S)$
- Density of greedy algorithm d_g
- We want to show that $d_{opt} \leq 2 \cdot d_g$

Upper bound

- We will first upper-bound the solution of optimal
- Assume an arbitrary assignment of an edge

 (u, v) to either u or v



- Define:
 - -IN(u) = # edges assigned to u
 - $-\Delta = \max_{u \in V} IN(u)$
- We can prove that

 $-d_{opt} \leq 2 \cdot \Delta$

This is true for any assignment of the edges!

Lower bound

- We will now prove a lower bound for the density of the set produced by the greedy algorithm.
- For the lower bound we consider a specific assignment of the edges that we create as the greedy algorithm progresses:
 - When removing node u from S, assign all the edges to u
- So: $IN(u) = \text{degree of } u \text{ in } S \le d(S) \le d_g$
- This is true for all u so $\Delta \leq d_g$
- It follows that $d_{opt} \leq 2 \cdot d_g$

The k-densest subgraph

- The k-densest subgraph problem: Find the set of k nodes S, such that the density d(S) is maximized.
 - The k-densest subgraph problem is NP-hard!

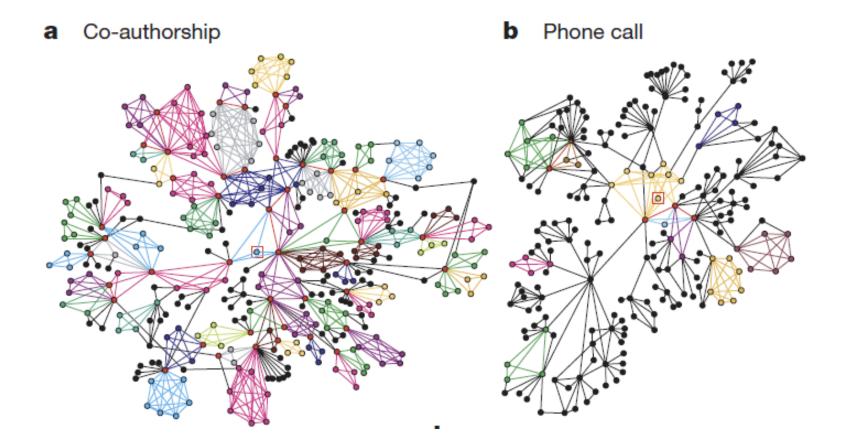
QUANTIFYING SOCIAL GROUP EVOLUTION

G Palla, AL Barabási, T Vicsek, Nature 446 (7136), 664-667

Datasets

- monthly list of articles in the Cornell University Library e-print condensed matter (cond-mat) archive spanning 142 months, with over 30,000 authors,
- phone calls between the customers of a mobile phone company spanning 52 weeks (accumulated over two-week-long periods) containing the communication patterns of over 4 million users.

Datasets



black nodes/edges do not belong to any community, red nodes belong to two or more communities

Datasets

Different local structure:

- Co-authorship: dense network with significant overlap among communities (co-authors of an article form cliques) -- Phone-call: communities less interconnected, often separated by one or more inter-community node/edge
- Co-authorship long-term collaborations -- Phone-call: the links correspond to instant communication events

Fundamental differences suggest that any common features represent potentially generic characteristics

Approach

 Communities at each time step extracted using the clique percolation method (CPM)

Why CPM?

their members can be reached through well connected subsets of nodes, and communities may overlap

Parameters

k = 4

Weighted graph – use a weight threshold w* (links weaker than w* are ignored)

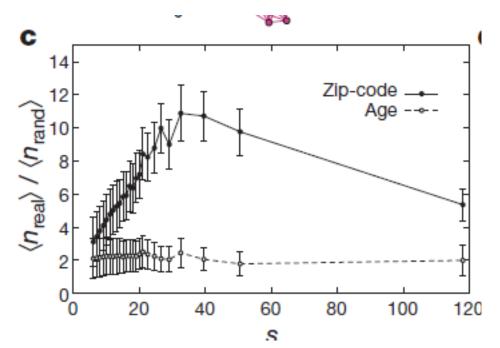
Evaluation

1. compare the average weight of the links inside communities, to the average weight of the inter-community links (2.9 authors – 5.9 phone)

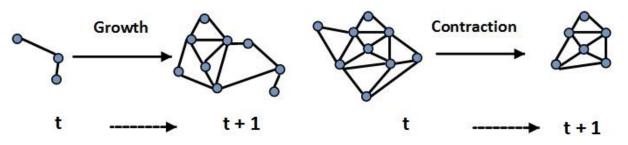
2. (homogeneity)

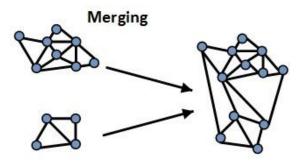
n_{real}: the size of the largest subset of people having the same zipcode averaged over time steps and the set of available communities,

n_{rand} represents the same average but with randomly selected users s: size

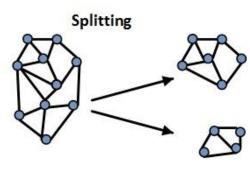


Basic Events

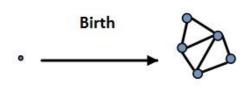




t ----→ t+1







t ----→ t+1



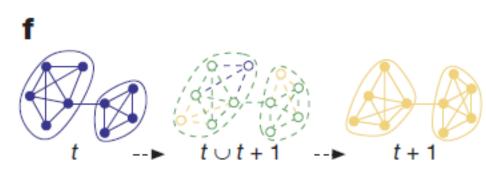
t ----- t+1

Identifying Events

Run CPM on snapshot t

Run CPM on snapshot t+1

For each pair of consecutive time steps *t* and *t+1*, construct a joint graph consisting of the union of links from the corresponding two networks, and extract the CPM community structure of this joint network

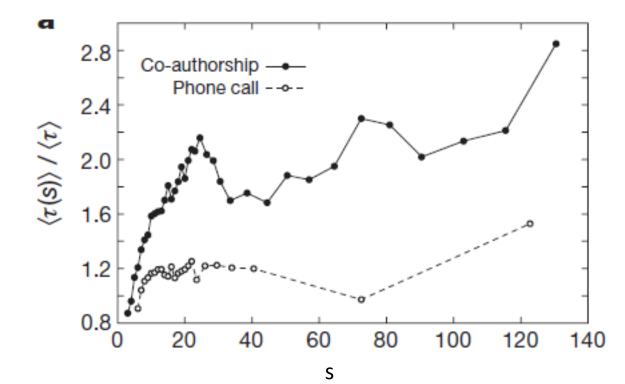


- Any community from either the t or the t+1 snapshot is contained in exactly one community in the joint graph (since we only add edges, communities can only grow larger)
- I. If a community in the joint graph contains *a single community* from *t* and a single community from *t*+1, then they are matched.
- II. If the joint group contains more than one community from either time steps, the communities are matched in descending order of their *relative node overlap*

s: size

t: age

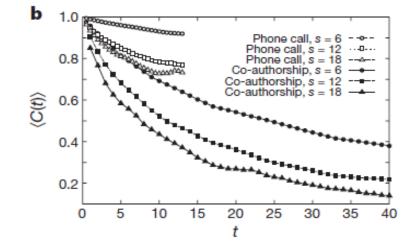
s and t are positively correlated: larger communities are on average older



Auto-correlation function

$$C(t) \equiv \frac{|A(t_0) \cap A(t_0 + t)|}{|A(t_0) \cup A(t_0 + t)|}$$

where A(t) members of community A at t



- the collaboration network is more "dynamic" (decays faster)
- in both networks, the auto-correlation function decays faster for the larger communities, showing that the membership of the larger communities is changing at a higher rate.

$$\zeta \equiv \frac{\sum_{t=t_0}^{t_{\max}-1} C(t,t+1)}{t_{\max}-t_0-1}$$

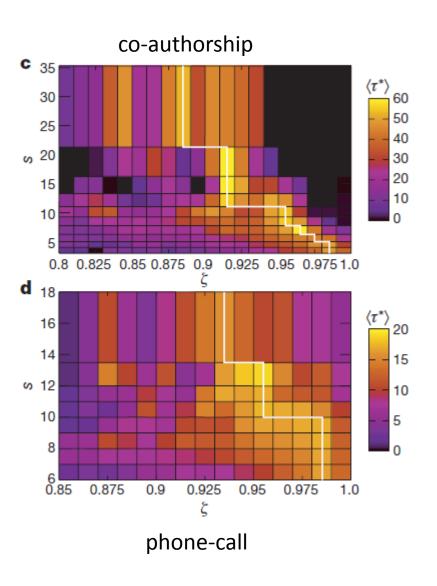
ζ stationarity: average correlation between two states

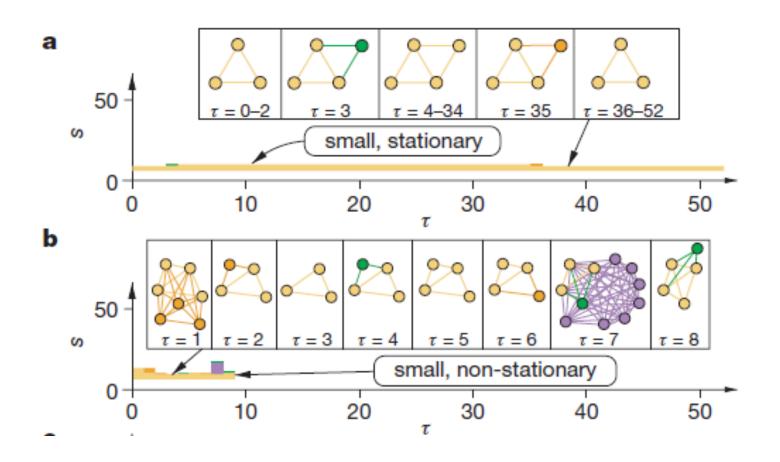
1- ζ : the average ratio of members changed in one step

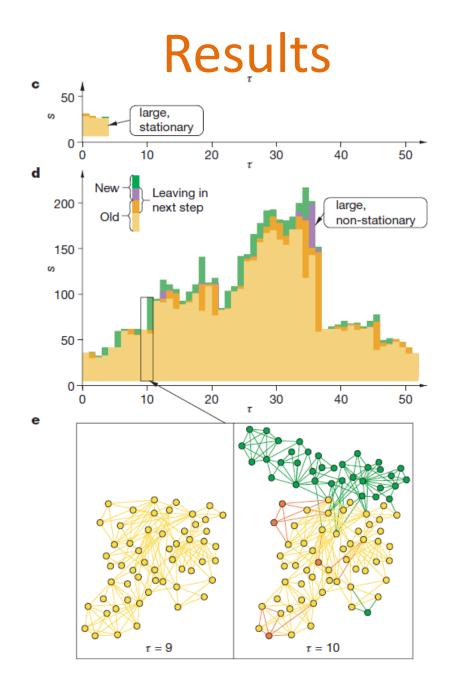
τ^* : life-span

the average life-span $<t^*>$ (color coded) as a function of ζ and s

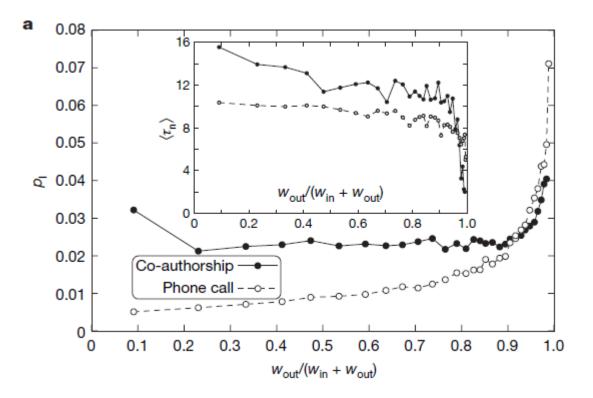
- for *small communities* optimal ζ near 1, better to have static, timeindependent
- For *large communities*, the peak is shifted towards low ζ values, better to have continually changing membership





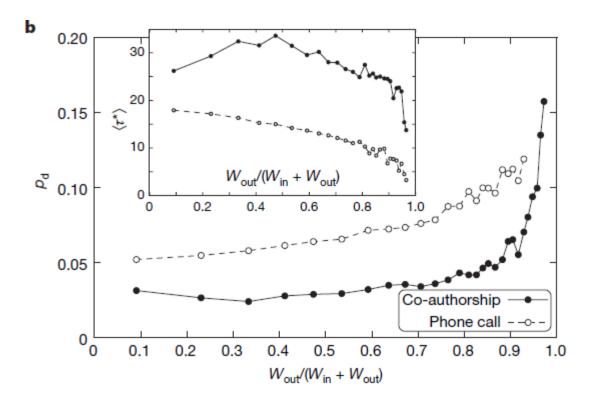


Can we predict the evolution?



w_{out}: individual commitment to outside the community
w_{in}: individual commitment inside the community
p: probability to abandon the community

Can we predict the evolution?



W_{out}: total weight of links to nodes outside the community
W_{in}: total weight of links inside the community
p: probability of a community to disintegrate in the next step
for co-authorship max lifetime at intermediate values

Conclusions

Significant difference between smaller collaborative or friendship circles and institutions.

- At the heart of small communities are a few strong relationships, and as long as these persist, the community around them is stable.
- The condition for stability of large communities is continuous change, so that after some time practically all members are exchanged.
- Loose, rapidly changing communities reminiscent of institutions, which can continue to exist even after all members have been replaced by new members (e.g., members of a school).

Basic References

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- Ulrike von Luxburg: A Tutorial on Spectral Clustering. <u>CoRR abs/0711.0189</u> (2007)
- G Palla, A. L. Barabási, T Vicsek, Quantyfying Social Group Evolution. Nature 446 (7136), 664-667

Questions?