# MITx: Statistics, Computation & Applications

Criminal Networks Module

Lecture 4: Applications Beyond Criminal Networks

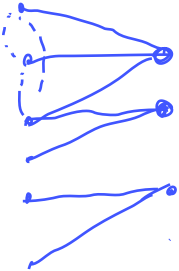
# Co-offender network

- All arrests in Quebec between 2003 and 2010
- Information on criminals and crime events they were arrested for
- Co-offender network: nodes are the offenders, and two offenders share a (possibly weighted) edge whenever they are arrested for the same crime event
- Summarizing the data of all arrests in Quebec as a network of co-offenders only portrays one side of the story

What information is lost in this representation of the data? What other representations are possible and what questions can be analyzed?

criminals

crimes



$A$

$AA^T$

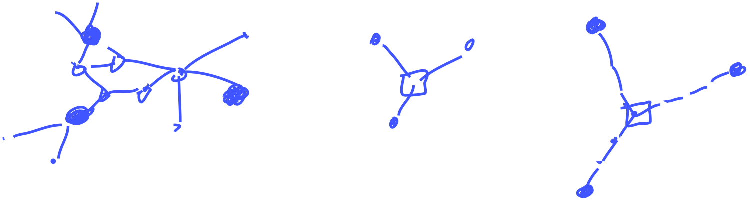
$A^TA$

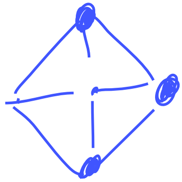
# Caviar network

- Investigation by Montréal police between 1994 and 1996
- Drug trafficking network investigated over time
- New criminals were added to the network by wire-tapping phones
- 11 seizures (money or drugs) throughout the investigation, but criminals were arrested only at the end
- Unique opportunity to analyze how a network reorganizes itself when subjected to stress

# Related scenario

- Given a social network and $k$ criminal suspects, how to determine other suspects?
- Same question is extremely important in biology: given certain genes that are known to cause a certain disease, determine other candidate genes (e.g. based on protein-protein interaction network for determining autism genes: http://dx.doi.org/10.1101/057828)





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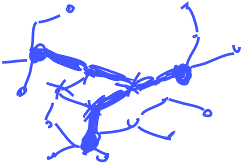
- How do we identify nodes that are "between" a given set of seed nodes?



# Steiner trees

Determine a small subnetwork that contains the given suspects / genes and connects these nodes

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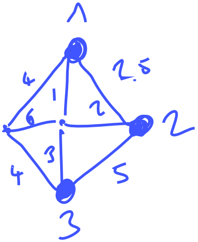
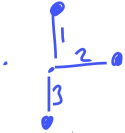
- shortest subnetwork that contains a given set of nodes
- NP-complete problem
- polynomial time approximations:

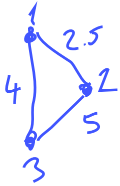


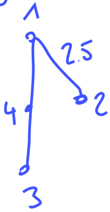

Steiner tree




weight 6

$$\begin{array}{c|c} & 1 \quad 2 \quad 3 \\ \hline \begin{array}{c}1\\2\\3\end{array} & \begin{bmatrix} & 2.5 & 4 \\ & & 5 \\ & & \end{bmatrix} \end{array}$$



# Steiner trees

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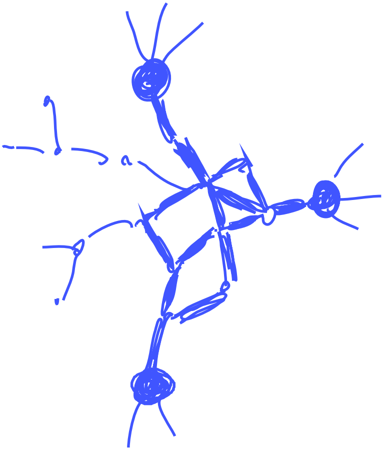
**Steiner tree:**

- shortest subnetwork that contains a given set of nodes
- NP-complete problem
- polynomial time approximations:
  - compute minimum distance between the given set of nodes and determine minimum spanning tree in this new network $\rightarrow$ weight of resulting tree is within 2 times weight of optimal Steiner tree
  - best known approximation is of a factor of $\ln 4 + \epsilon < 1.39$ given by linear programming relaxation combined with iterative, randomized rounding (Byrka et al., 2013)

$\Rightarrow$ use collection of approximate Steiner trees for further analysis: autism interactome / criminal interactome

Genomics application: http://fraenkel-nsf.csbi.mit.edu/steinernet/tutorial.html



Interactome

# Analysis of autism interactome / criminal interactome

Is interactome indeed more tightly connected than at random?

- assume interactome was built with $k$ seed nodes
- choose $k$ nodes at random and compute resulting interactome
- perform hypothesis test based on diameter / average geodesic

$\Rightarrow$ compute nodes with high betweenness centrality in interactome to obtain candidate genes / suspects

# Co-offending network

- summarizing the data of all arrests in Quebec as a network of co-offenders only portrays one side of the story
- data can be represented by a binary matrix $A$ where the rows correspond to persons and the columns to crimes
- the co-offending network has (weighted) adjacency matrix $AA^T$
- similarly, we can build a network of crimes based on the (weighted) adjacency matrix $A^T A$
- or we could analyze the bipartite network given by the adjacency matrix

$$\begin{bmatrix} 0 & A \\ A^T & 0 \end{bmatrix}$$

**How do we go about detecting communities in these networks?**

# Community detection

## Community detection:

- detect subsets of nodes that are more densely connected between each other in the network than outside the community

## Clustering

- determine subsets of points that are 'close' to each other given a pairwise distance or similarity measure
- can be used also for community detection by defining a vertex similarity measure (e.g., geodesic distance, number of different neighbors, correlation between adjacency matrix columns, etc.)
- we already discussed some clustering methods in Module 1 (e.g. hierarchical clustering, k-means)

# Other methods: Divisive algorithm using betweenness

- Intuition: intercommunity edges have a large value of edge betweenness, because many shortest paths connecting vertices of different communities will pass through them
- Algorithm of Girvan and Newman (2002): iteratively remove edges with highest betweenness centrality
- can define betweenness using geodesic, flow or random walk

# Other methods: Modularity maximization

- quality function: function that assigns a number (quality measure) to each partition of a graph

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- most popular quality function: modularity

$$Q = \frac{1}{2m} \sum_{i,j} (A_{ij} - P_{ij})\, \delta(C_i, C_j),$$

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  - compares actual edge density to expected edge density in null model
  - for Erdös-Renyi model $P_{ij} = \frac{2m}{n(n-1)}$
  - for configuration model $P_{ij} = \frac{k_i k_j}{2m-1}$
  - for bipartite graphs: $Q = \frac{1}{2m} \sum_i \sum_j (A_{ij} - \frac{k_i^{(1)} k_j^{(2)}}{2m})\, \delta(C_i, C_j)$,

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  - iterate process until $Q$ cannot be improved
- provides decomposition of network into communities for different levels of organization
- extremely fast: runs in $\mathcal{O}(m)$
- can be applied to find communities in bipartite networks either using $AA^T$, $A^TA$ or $\begin{bmatrix} 0 & A \\ A^T & 0 \end{bmatrix}$

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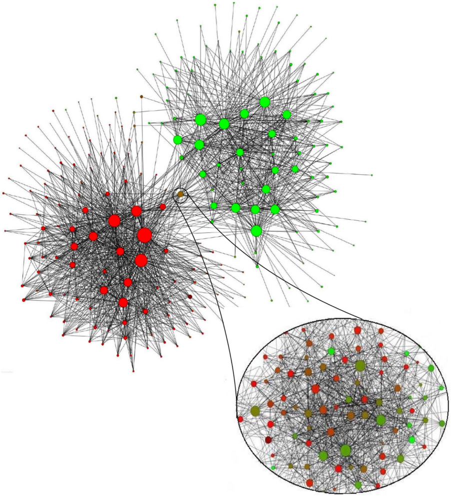

Belgian mobile phone network with 2M customers (red: French-speaking, green: Dutch-speaking).

# References


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