Looking for clusters in your data ... (in theory and in practice)

Michael W. Mahoney

Stanford University

4/7/11

(For more info, see:
http:// cs.stanford.edu/people/mmahoney/
or Google on "Michael Mahoney")

Outline (and lessons)

1. Matrices and graphs are basic structures for modeling data, and many algorithms boil down to matrix/graph algorithms.
2. Often, algorithms work when they "shouldn't," don't work when they "should," and interpretation is tricky but often of interest downstream.
3. Analysts tell stories since they often have no idea of what the data "look like," but algorithms can be used to "explore" or "probe" the data.
4. Large networks (and large data) are typically very different than small networks (and small data), but people typically implicitly assume they are the same.

Outline (and lessons)

1. Matrices and graphs are basic structures for modeling data, and many algorithms boil down to matrix/graph algorithms.
2. Often, algorithms work when they "shouldn't," don't work when they "should," and interpretation is tricky but often of interest downstream.
3. Analysts tell stories since they often have no idea of what the data "look like," but algorithms can be used to "explore" or "probe" the data.
4. Large networks (and large data) are typically very different than small networks (and small data), but people typically implicitly assume they are the same.

Machine learning and data analysis, versus "the database" perspective

Many data sets are better-described by graphs or matrices than as dense flat tables

- Obvious to some, but a *big challenge* given the way that databases are constructed and supercomputers are designed
- *Sweet spot* between descriptive flexibility and algorithmic tractability
- Very different questions than traditional NLA and graph theory/practice as well as traditional database theory/practice

Often, the first step is to partition/cluster the data

- Often, this can be done with natural matrix and graph algorithms
- Those *algorithms always return answers* whether or not the data cluster well
- Often, there is a *"positive-results" bias* to find things like clusters

Modeling the data as a matrix

We are given *m* objects and *n* features describing the objects.

(Each object has *n* numeric values describing it.)

Dataset

An *m-by-n* matrix *A*, A_{ij} shows the "importance" of feature *j* for object *i*.

Every row of *A* represents an object.

Goal

We seek to understand the structure of the data, e.g., the underlying process generating the data.

Market basket matrices

Common representation for association rule mining in databases.

(Sometimes called a "flat table" if matrix operations are not performed.)

n products

(e.g., milk, bread, wine, etc.)

m customers

$$\begin{pmatrix} \\ A \\ \\ \end{pmatrix}$$

A_{ij} = quantity of j-th product purchased by the i-th customer

<u>Data mining tasks</u>

- Find association rules, E.g., customers who buy product x buy product y with probability 89%.

- Such rules are used to make item display decisions, advertising decisions, etc.

Term-document matrices

A collection of documents is represented by an *m-by-n* matrix (bag-of-words model).

n terms (words)

m documents

$$A$$

A_{ij} = frequency of j-th term in i-th document

Data mining tasks

- Cluster or classify documents
- Find "nearest neighbors"
- Feature selection: find a subset of terms that (accurately) clusters or classifies documents.

Recommendation system matrices

The *m-by-n* matrix A represents *m* customers and *n* products.

$$
\begin{array}{cc}
 & n \text{ products} \\
\begin{array}{c} m \\ \text{customers} \end{array} & \left(\begin{array}{c} \\ \\ A \\ \\ A_{ij} = \text{utility of j-th} \\ \text{product to i-th customer} \\ \\ \end{array} \right)
\end{array}
$$

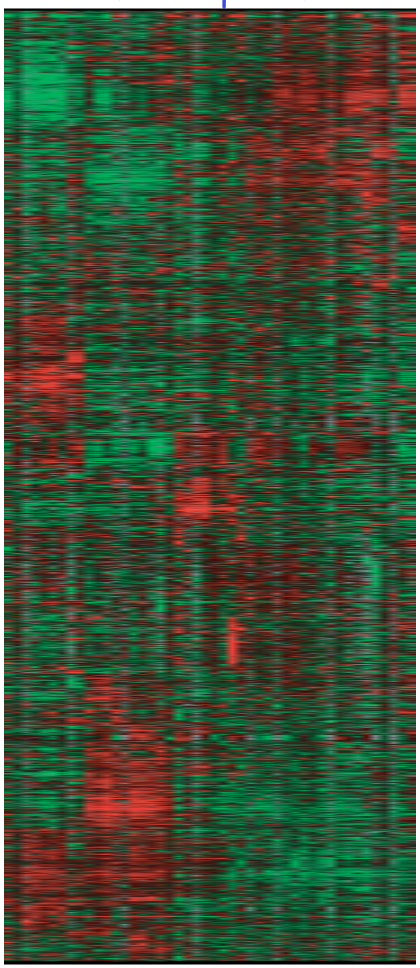
Data mining task

- Given a few samples from A, recommend high utility products to customers.
- Recommend queries in advanced match in sponsored search

DNA microarray data matrices

tumour specimens

genes



Microarray Data

Rows: genes (ca. 5,500)

Columns: e.g., 46 soft-issue tumor specimens

Tasks:

Pick a subset of genes (if it exists) that suffices in order to identify the “cancer type” of a patient

Nielsen et al., Lancet, 2002

DNA SNP data matrices

Single Nucleotide Polymorphisms: the most common type of genetic variation in the genome across different individuals.

They are known locations at the human genome where two alternate nucleotide bases (alleles) are observed (out of A, C, G, T).

SNPs

individuals

… AG CT GT GG CT CC CC CC CC AG AG AG AG AG AA CT AA GG GG CC GG AG CG AC CC AA CC AA GG TT AG CT CG CG CG AT CT CT AG CT AG GG GT GA AG …
… GG TT TT GG TT CC CC CC CC GG AA AG AG AG AA CT AA GG GG CC GG AA GG AA CC AA CC AA GG TT AA TT GG GG GG TT TT CC GG TT GG GG TT GG AA …
… GG TT TT GG TT CC CC CC CC GG AA AG AG AA AG CT AA GG GG CC AG AG CG AC CC AA CC AA GG TT AG CT CG CG CG AT CT CT AG CT AG GG GT GA AG …
… GG TT TT GG TT CC CC CC CC GG AA AG AG AG AA CC GG AA CC CC AG GG CC AC CC AA CG AA GG TT AG CT CG CG CG AT CT CT AG CT AG GT GT GA AG …
… GG TT TT GG TT CC CC CC CC GG AA GG GG GG AA CT AA GG GG CT GG AA CC AC CG AA CC AA GG TT GG CC CG CG CG AT CT CT AG CT AG GG TT GG AA …
… GG TT TT GG TT CC CC CG CC AG AG AG AG AG AA CT AA GG GG CT GG AG CC CC CG AA CC AA GT TT AG CT CG CG CG AT CT CT AG CT AG GG TT GG AA …
… GG TT TT GG TT CC CC CC CC GG AA AG AG AG AA TT AA GG GG CC AG AG CG AA CC AA CG AA GG TT AA TT GG GG GG TT TT CC GG TT GG GT TT GG AA …

Matrices including 100s of individuals and more than 300K SNPs are publicly available.

Task: split the individuals in different clusters depending on their ancestry, and

find a small subset of genetic markers that are "ancestry informative".

Social networks (e.g., an e-mail network)

Represents, e.g., the email communications between groups of users.

$$\begin{array}{cc} & n \text{ users} \\ n \text{ users} & \left(\begin{array}{c} \\ \\ \mathcal{A} \\ \\ \end{array} \right) \end{array}$$

A_{ij} = number of emails exchanged between users i and j during a certain time period

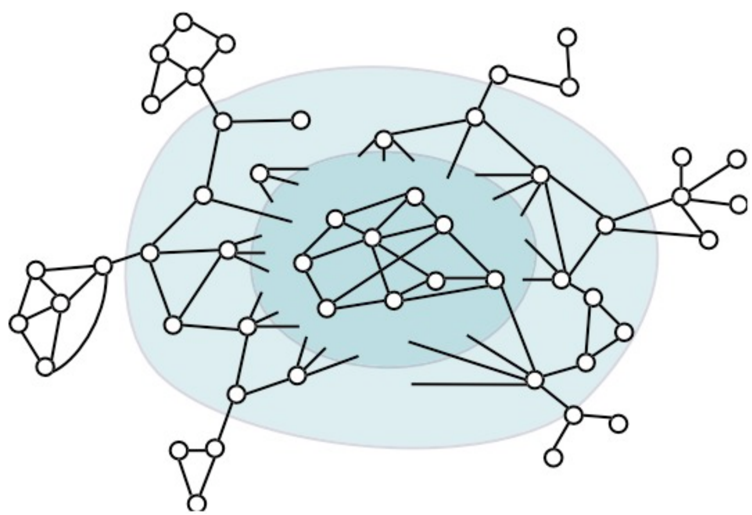
<u>Data mining tasks</u>

- cluster the users
- identify "dense" networks of users (dense subgraphs)
- recommend friends
- clusters for bucket testing
- etc.

How people think about networks

"Interaction graph" ***model*** of networks:

- Nodes represent "entities"
- Edges represent "interaction" between pairs of entities



Graphs are combinatorial, not obviously-geometric

- Strength: powerful framework for analyzing *algorithmic complexity*
- Drawback: geometry used for learning and *statistical inference*

Matrices and graphs

Networks are often represented by a graph $G=(V,E)$

- V = vertices/things
- E = edges = interactions between pairs of things

Close connections between matrices and graphs; given a graph, one can study:

- Adjacency matrix: $A_{ij} = 1$ if an edge between nodes i and j
- Combinatorial Laplacian: $D-A$, where D is diagonal degree matrix
- Normalized Laplacian: $I-D^{-1/2}AD^{-1/2}$, related to random walks

The Singular Value Decomposition (SVD)

The formal definition:

Given any m x n matrix A, one can decompose it as:

$$\begin{pmatrix} & & \\ & A & \\ & & \end{pmatrix} = \underbrace{\begin{pmatrix} & & \\ & U & \\ & & \end{pmatrix}}_{m \times \rho} \cdot \underbrace{\begin{pmatrix} & \Sigma & \end{pmatrix}}_{\rho \times \rho} \cdot \underbrace{\begin{pmatrix} & V & \end{pmatrix}^T}_{\rho \times n}$$

ρ: rank of A

U (V): orthogonal matrix containing the left (right) singular vectors of A.

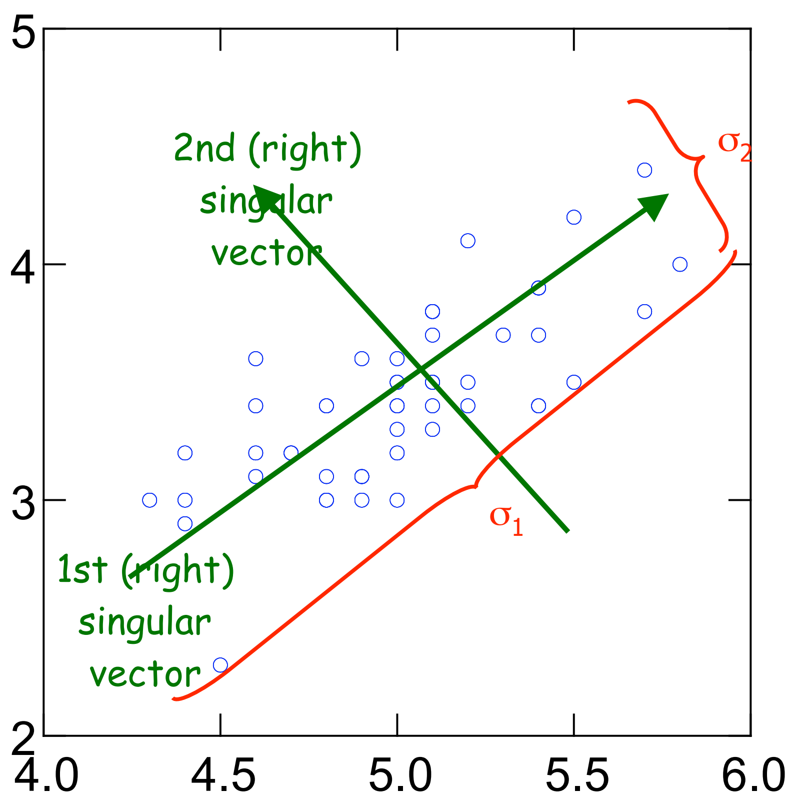
Σ: diagonal matrix containing $\sigma_1 \geq \sigma_2 \geq \ldots \geq \sigma_\rho$, the singular values of A.

Often people use this via PCA or MDS or other related methods.

Singular values and vectors, intuition

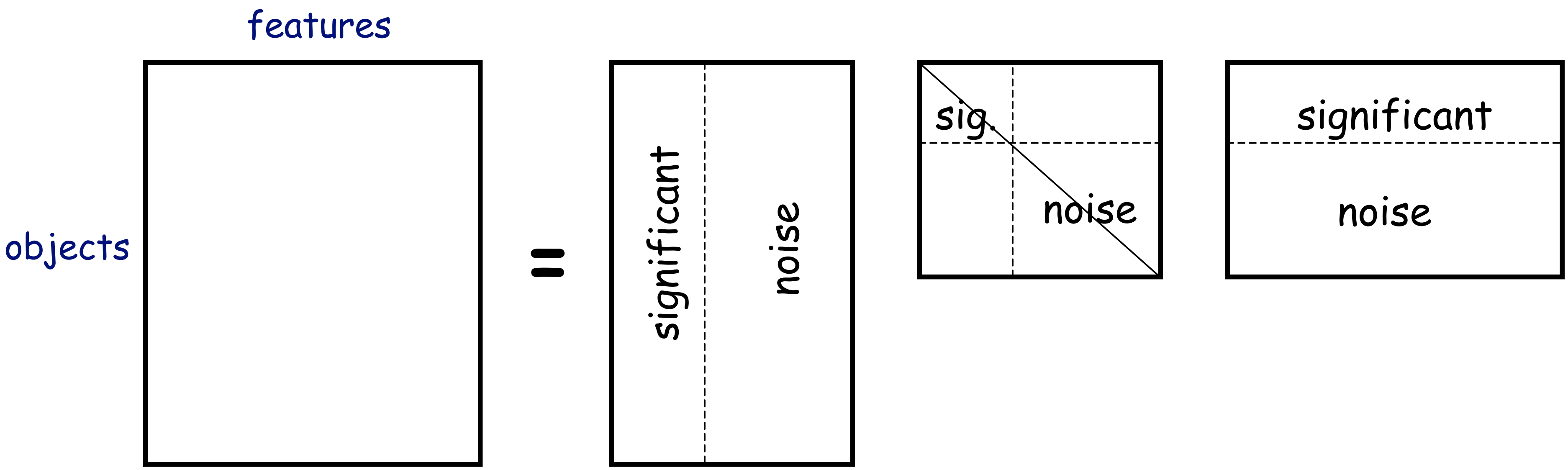
The SVD of the *m-by-2* data matrix (*m* data points in a 2-D space) returns:

- $V^{(i)}$: Captures (successively orthogonalized) directions of variance.
- σ_i: Captures how much variance is explained by (each successive) direction.



Rank-k approximations via the SVD

$$A = U \Sigma V^T$$



Very important: Keeping top k singular vectors provides "best" rank-k approximation to A!

Computing the SVD

Many ways; e.g.,

- LAPACK - high-quality software library in Fortran for NLA
- MATLAB - call "svd," "svds," "eig," "eigs," etc.
- R - call "svd" or "eigen"
- NumPy - call "svd" in LinAlgError class

In the past:

- you *never* computed the full SVD.
- Compute just what you need.

Ques: How true will that be true in the future?

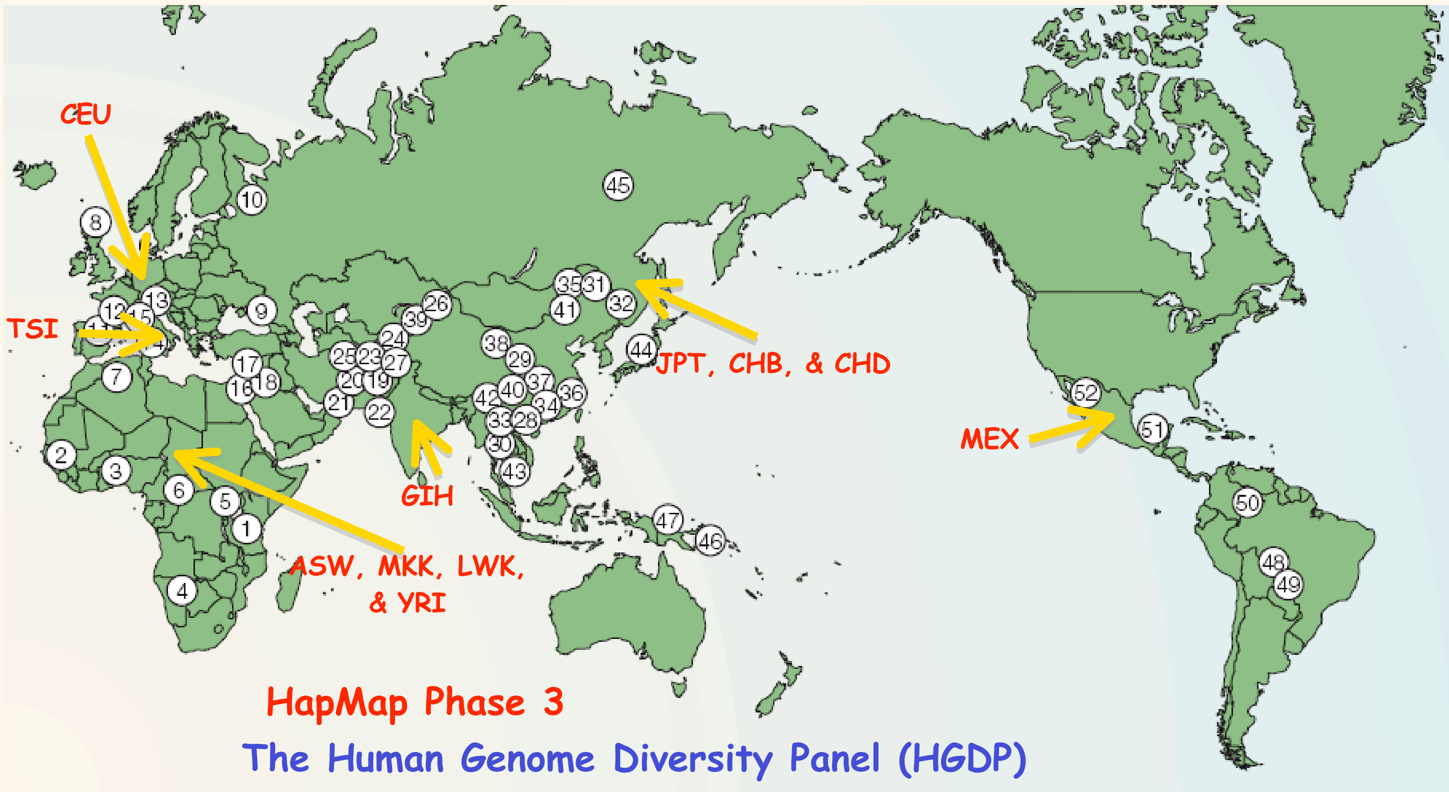
Eigen-methods in ML and data analysis

Eigen-tools appear (*explicitly* or *implicitly*) in many data analysis and machine learning tools:

- Latent semantic indexing
- PCA and MDS
- Manifold-based ML methods
- Diffusion-based methods
- k-means clustering
- Spectral partitioning and spectral ranking

Outline (and lessons)

1. Matrices and graphs are basic structures for modeling data, and many algorithms boil down to matrix/graph algorithms.
2. Often, algorithms work when they "shouldn't," don't work when they "should," and interpretation is tricky but often of interest downstream.
3. Analysts tell stories since they often have no idea of what the data "look like," but algorithms can be used to "explore" or "probe" the data.
4. Large networks (and large data) are typically very different than small networks (and small data), but people typically implicitly assume they are the same.



Africans
1 Bantu
2 Mandenka
3 Yoruba
4 San
5 Mbuti pygmy
6 Biaka
7 Mozabite

Europeans
8 Orcadian
9 Adygei
10 Russian
11 Basque
12 French
13 North Italian
14 Sardinian
15 Tuscan

Western Asians
16 Bedouin
17 Druze
18 Palestinian

Central and Southern Asians
19 Balochi
20 Brahui
21 Makrani
22 Sindhi
23 Pathan
24 Burusho
25 Hazara
26 Uygur
27 Kalash

Eastern Asians
28 Han (S. China)
29 Han (N. China)
30 Dai
31 Daur
32 Hezhen
33 Lahu
34 Miao
35 Oroqen
36 She
37 Tujia
38 Tu
39 Xibo
40 Yi
41 Mongola
42 Naxi
43 Cambodian
44 Japanese
45 Yakut

Oceanians
46 Melanesian
47 Papuan

Native Americans
48 Karitiana
49 Surui
50 Colombian
51 Maya
52 Pima

Cavalli-Sforza (2005) *Nat Genet Rev*

Rosenberg et al. (2002) *Science*

Li et al. (2008) *Science*

The International HapMap Consortium (2003, 2005, 2007), *Nature*

HGDP data

- 1,033 samples
- 7 geographic regions
- 52 populations

HapMap Phase 3 data

- 1,207 samples
- 11 populations

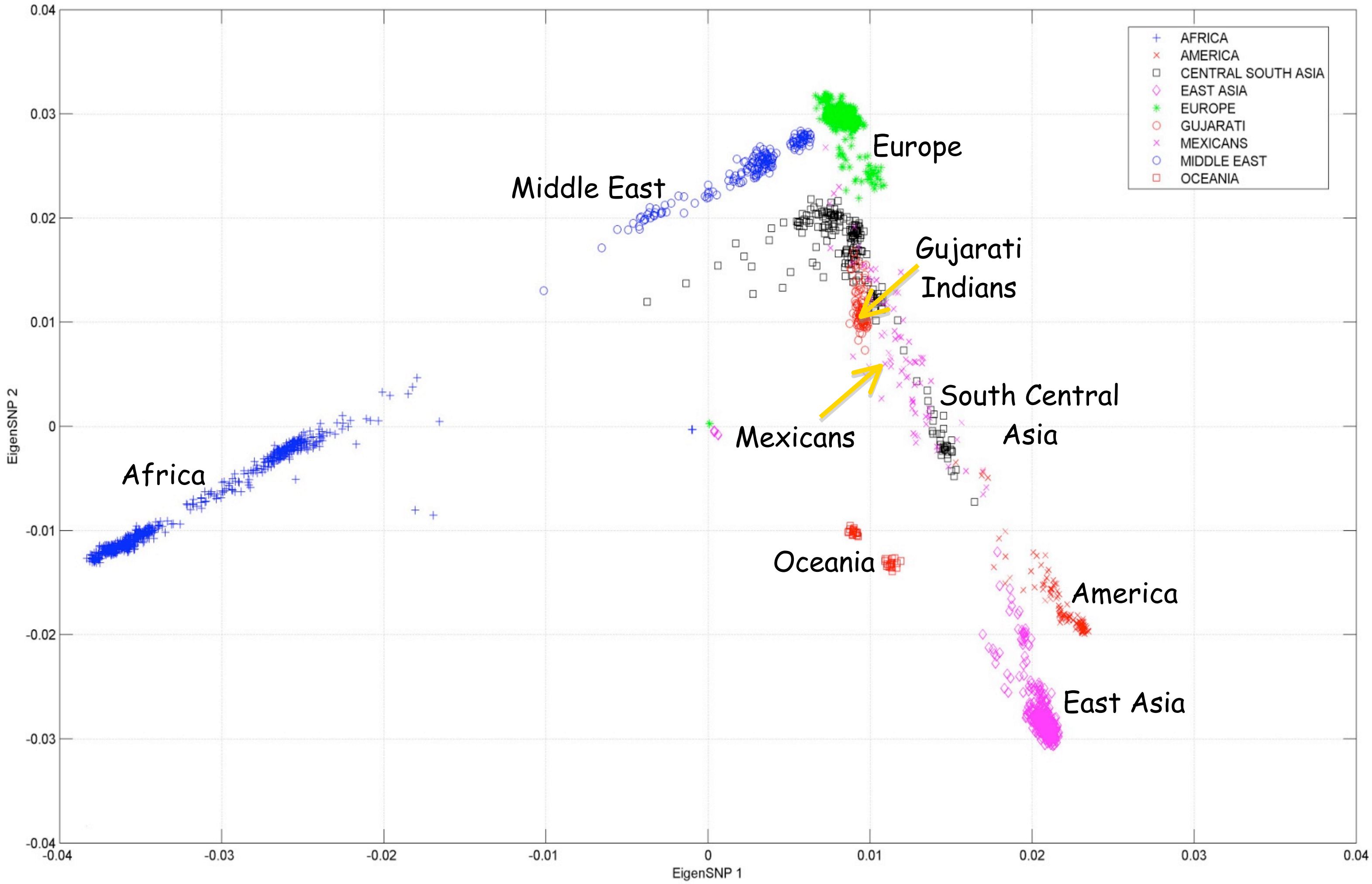
Matrix dimensions:

2,240 subjects (rows)

447,143 SNPs (columns)

SVD/PCA returns…

Paschou, Lewis, Javed, & Drineas (2010) J Med Genet



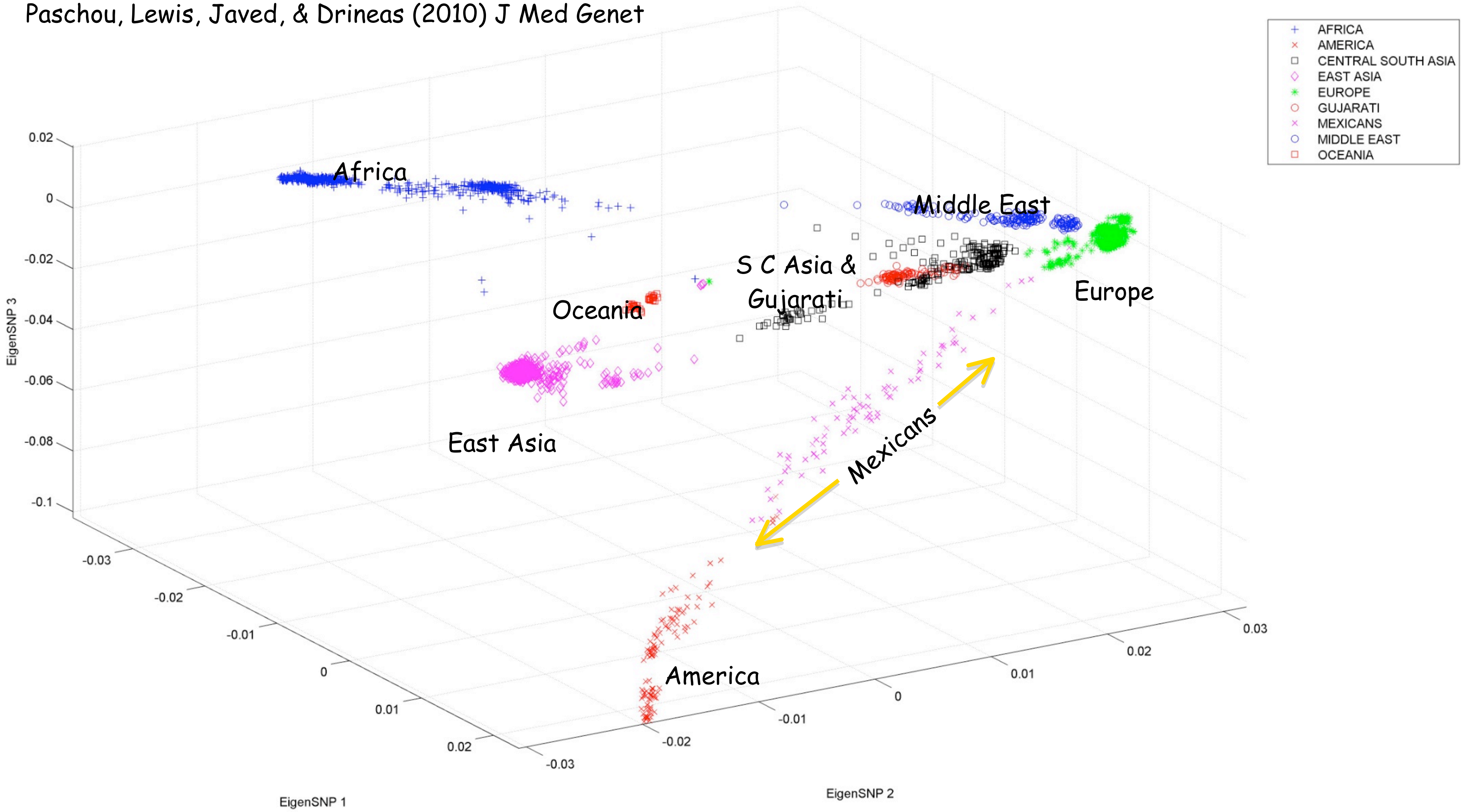
• <u>Top two Principal Components</u> (PCs or eigenSNPs)

(Lin and Altman (2005) *Am J Hum Genet*)

• The figure renders visual support to the “out-of-Africa” hypothesis.

• Mexican population seems out of place: we move to the top three PCs.

Paschou, Lewis, Javed, & Drineas (2010) J Med Genet



Not altogether satisfactory: the principal components are linear combinations of all SNPs, and – of course – can not be assayed!

Can we find **actual SNPs** that capture the information in the singular vectors?

Some thoughts ...

When is SVD/PCA "the right" tool to use?

- When most of the "information" is in a low-dimensional, k << m,n, space.
- No small number of high-dimensional components contain most of the "information."

Can I get a small number of actual columns that are (1+ε)-as the best rank-k eigencolumns?

- Yes! (And CUR decompositions cost no more time!)
- Good, since biologists don't study eigengenes in the lab

Problem 1: SVD & "heavy-tailed" data

Theorem: (Mihail and Papadimitriou, 2002)

The largest eigenvalues of the adjacency matrix of a graph with power-law distributed degrees are also power-law distributed.

What this means:

- I.e., heterogeneity (e.g., heavy-tails over degrees) plus noise (e.g., random graph) implies heavy tail over eigenvalues.
- Idea: 10 components may give 10% of mass/information, but to get 20%, you need 100, and to get 30% you need 1000, etc; i.e., no scale at which you get most of the information
- No "latent" semantics without preprocessing.

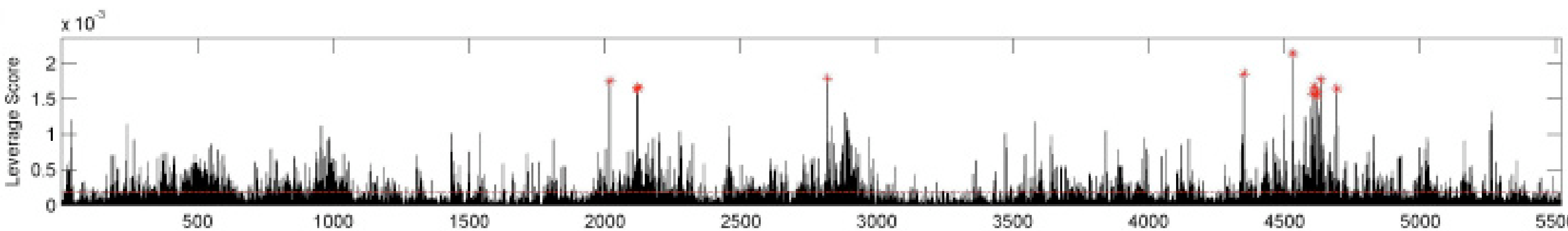
Problem 2: SVD & "high-leverage" data

Given an m x n matrix A and rank parameter k:

- How localized, or coherent, are the (left) singular vectors?
- Let $\rho_i = (P_{Uk})_{ii} = ||U_k^{(i)}||\_2$ (where U_k is any o.n. basis spanning that space)

These "statistical leverage scores" quantify which rows have the most influence/leverage on low-rank fit

- Often *very* non-uniform (in interesting ways!) in practice



Q: Why do SVD-based methods work at all?

Given that "assumptions" underlying its use (approximately low-rank and no high-leverage data points) are so manifestly violated.

A1: Low-rank spaces are *very* structured places.

• If "all models are wrong, but some are useful," those that are useful have "capacity control"

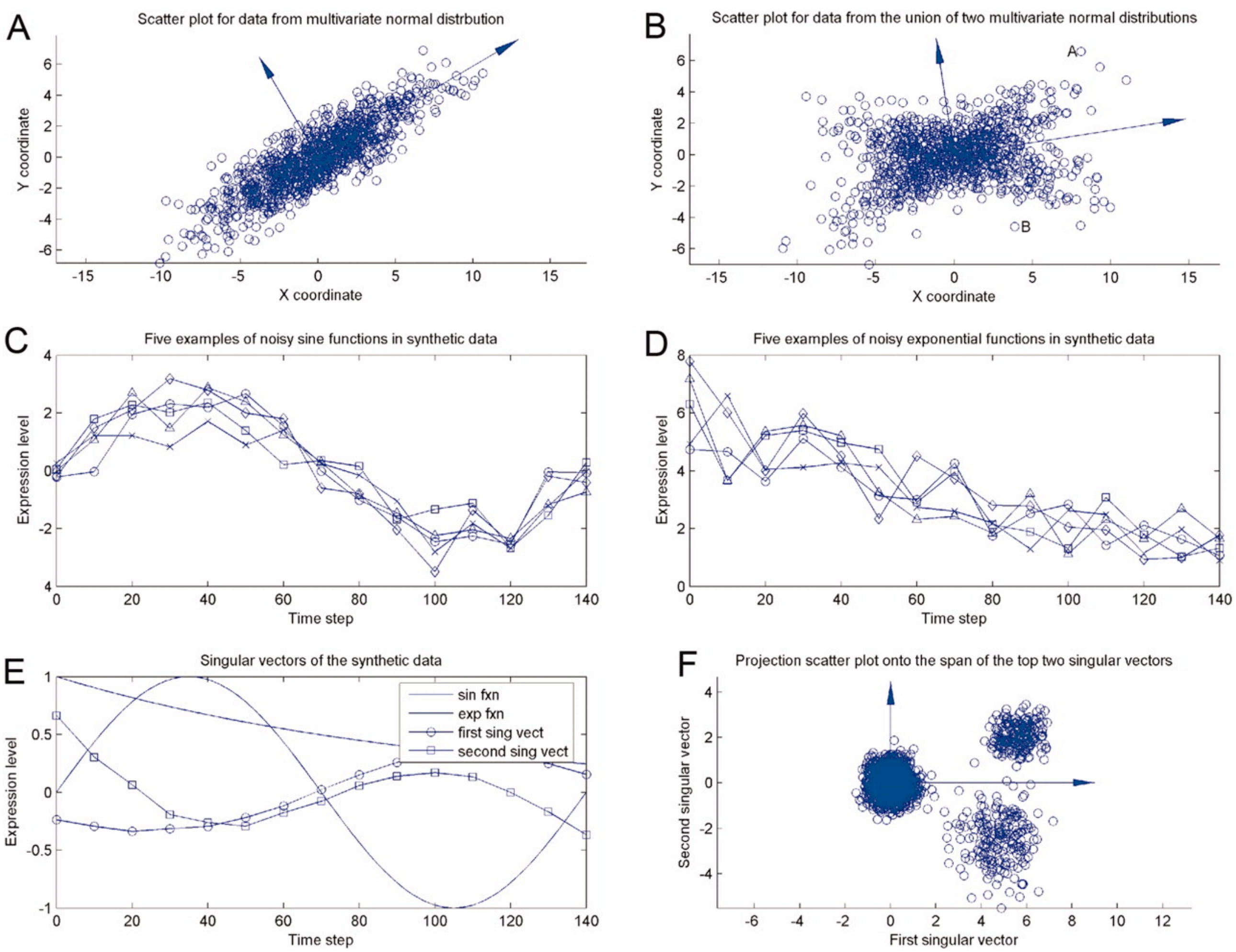
• I.e., that don't *give* you too many places to hide your sins, which is similar to bias-variance tradeoff in machine learning.

A2: They don't work all *that* well.

• They are *much* worst than current "engineered" models---although *much* better than very combinatorial methods that predated LSI.

Interpreting the SVD - be *very* careful

Mahoney and Drineas (PNAS, 2009)



Reification

- assigning a "physical reality" to large singular directions
- invalid in general

Just because "If the data are 'nice' then SVD is appropriate" does NOT imply converse.

Some more thoughts …

BIG tradeoff between insight/interpretability and marginally-better prediction in "next user interaction"

- Think the Netflix prize---a half dozen models capture the basic ideas but > 700 needed to win.
- Clustering often used to gain insight---then pass to downstream analyst who used domain-specific insight.

Publication/production/funding/etc pressures provide a BIG bias toward finding false positives

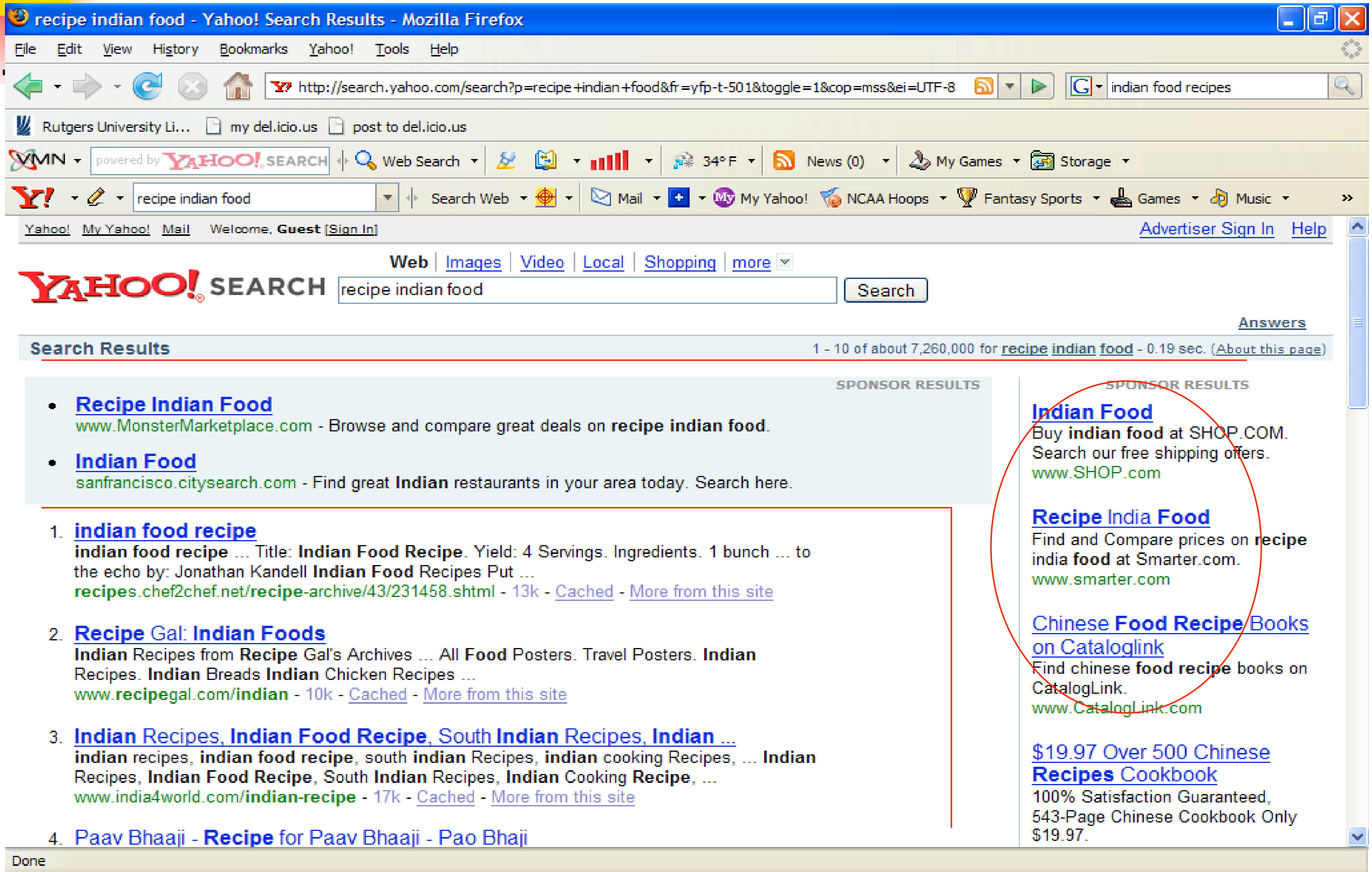
- BIG problem if data are so big you can't even examine them.

Outline (and lessons)

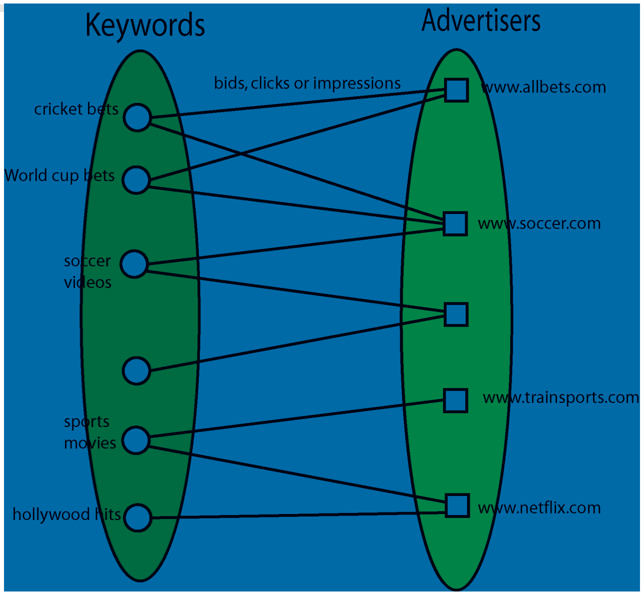
1. Matrices and graphs are basic structures for modeling data, and many algorithms boil down to matrix/graph algorithms.
2. Often, algorithms work when they "shouldn't," don't work when they "should," and interpretation is tricky but often of interest downstream.
3. Analysts tell stories since they often have no idea of what the data "look like," but algorithms can be used to "explore" or "probe" the data.
4. Large networks (and large data) are typically very different than small networks (and small data), but people typically implicitly assume they are the same.

Sponsored ("paid") Search

Text-based ads driven by user query



Sponsored Search Problems



Keyword-advertiser graph:

- provide new ads
- maximize CTR, RPS, advertiser ROI

Motivating cluster-related problems:

- Marketplace depth broadening:

  find new advertisers for a particular query/submarket

- Query recommender system:

  suggest to advertisers new queries that have high probability of clicks

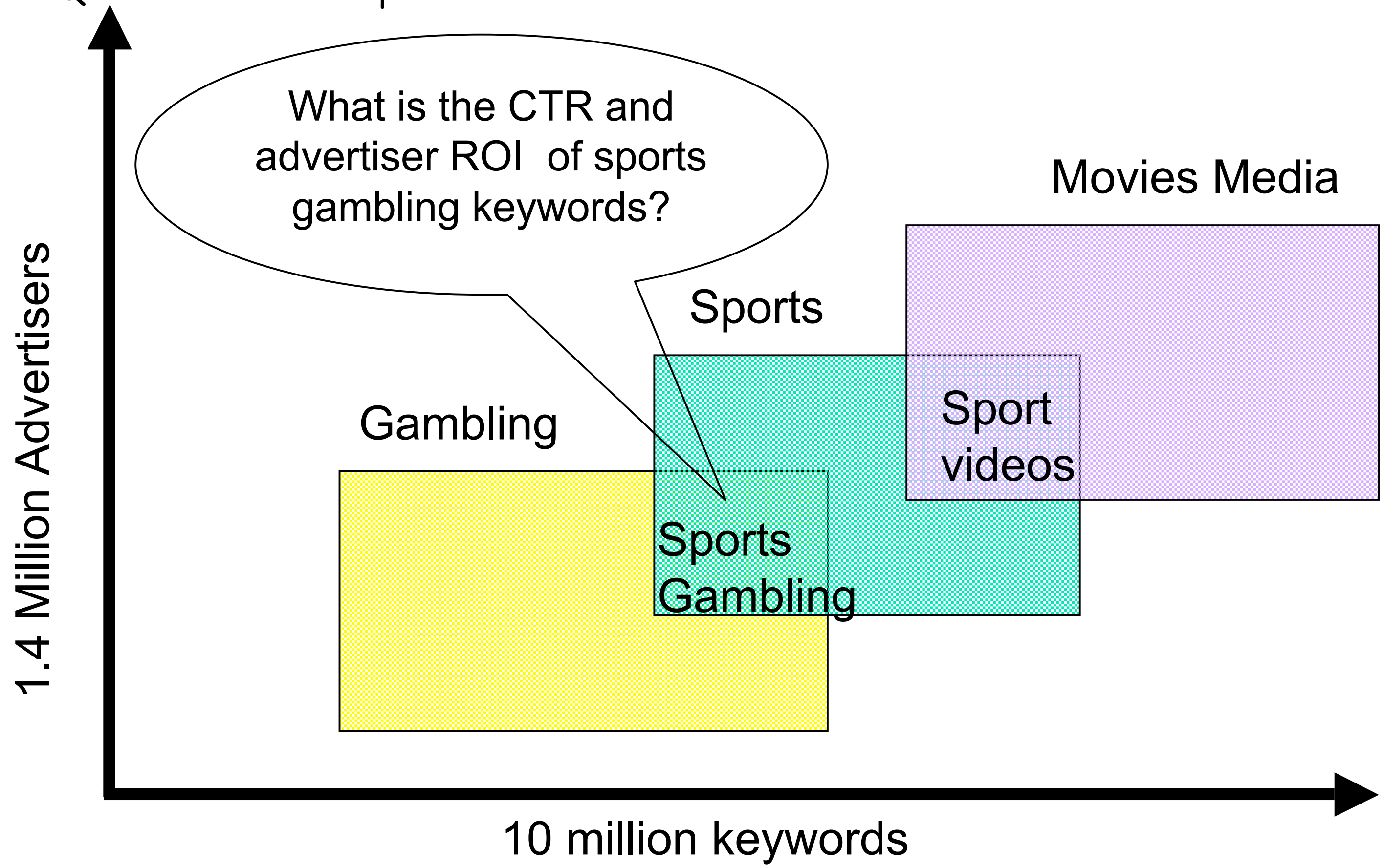
- Contextual query broadening:

  broaden the user's query using other context information

Micro-markets in sponsored search

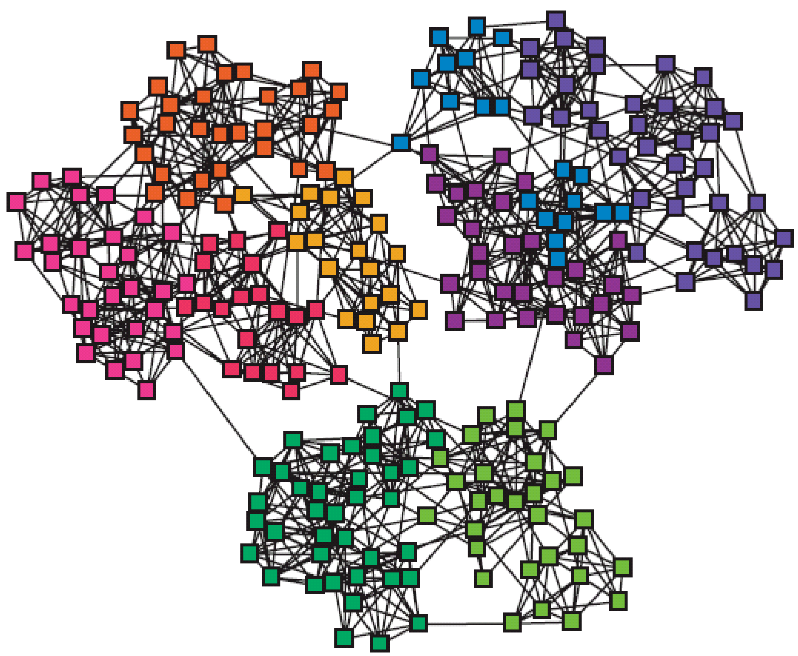
Goal: Find *isolated* markets/clusters (in an advertiser-bidded phrase bipartite graph) with *sufficient money/clicks* with *sufficient coherence.*

Ques: Is this even possible?



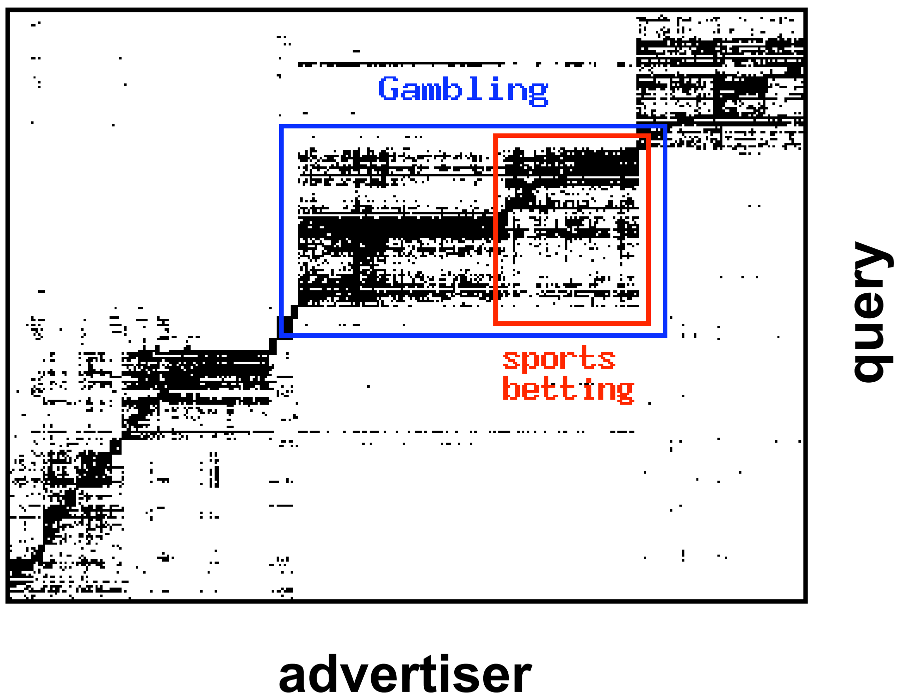
How people think about networks

A schematic illustration …



… of hierarchical clusters?

Some evidence for micro-markets in sponsored search?



Questions of interest ...

What are degree distributions, clustering coefficients, diameters, etc.?

Heavy-tailed, small-world, expander, geometry+rewiring, local-global decompositions, ...

Are there natural clusters, communities, partitions, etc.?

Concept-based clusters, link-based clusters, density-based clusters, ...

(e.g., *isolated* micro-markets with *sufficient money/clicks* with *sufficient coherence*)

How do networks grow, evolve, respond to perturbations, etc.?

Preferential attachment, copying, HOT, shrinking diameters, ...

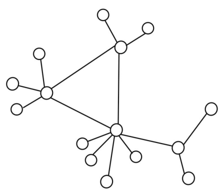
How do dynamic processes - search, diffusion, etc. - behave on networks?

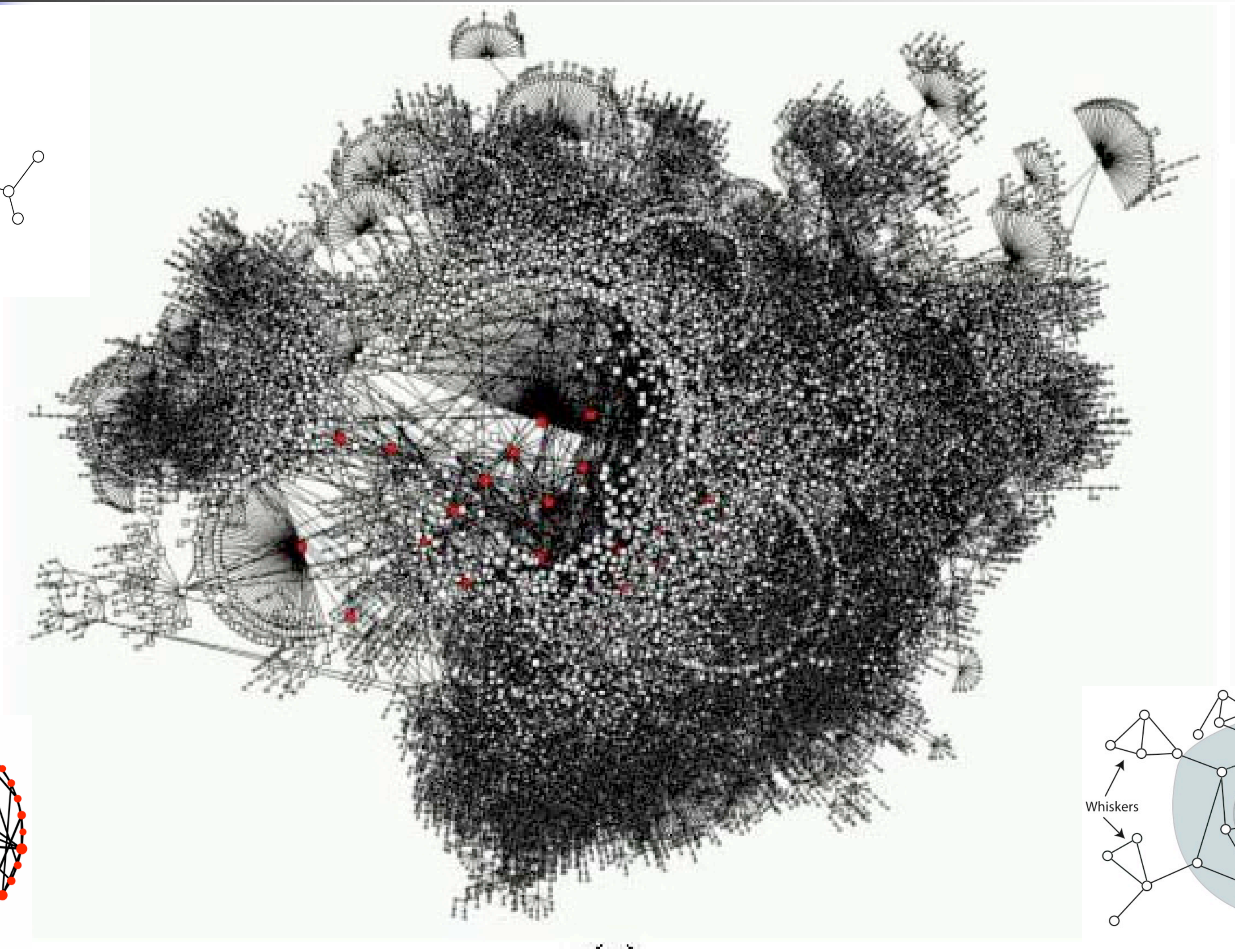
Decentralized search, undirected diffusion, cascading epidemics, ...

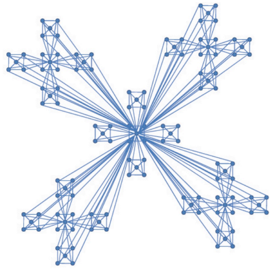
How best to do learning, e.g., classification, regression, ranking, etc.?

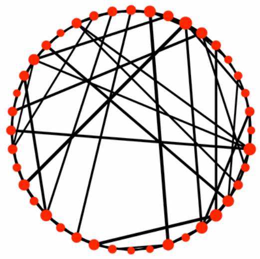
Information retrieval, machine learning, ...

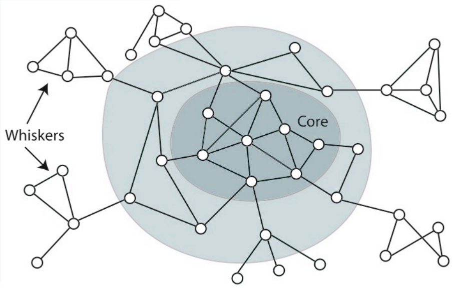
What do these networks "look" like?





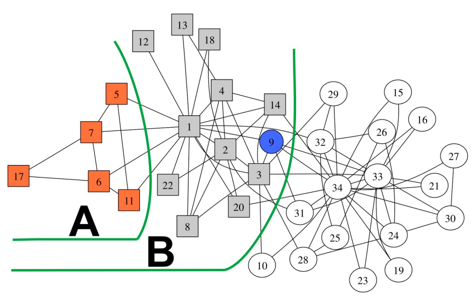


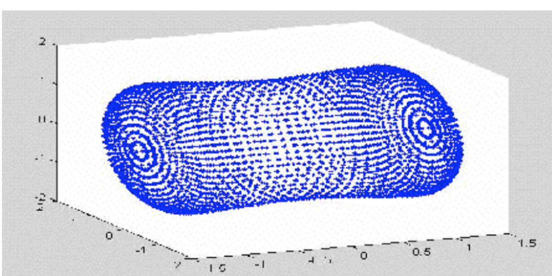




What do the data "look like" (if you *squint* at them)?

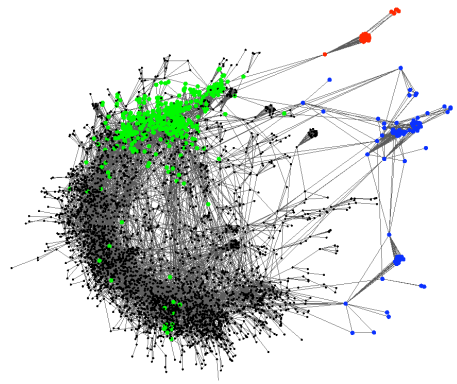
A "hot dog"?

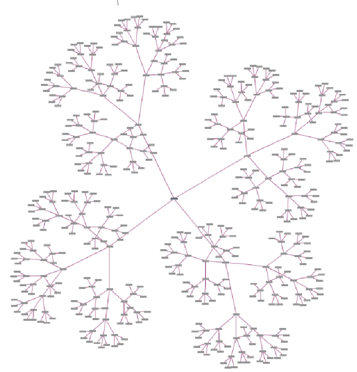




(or pancake that embeds well in low dimensions)

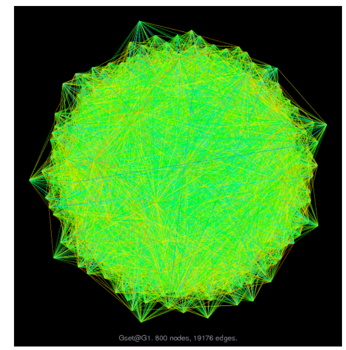
A "tree"?

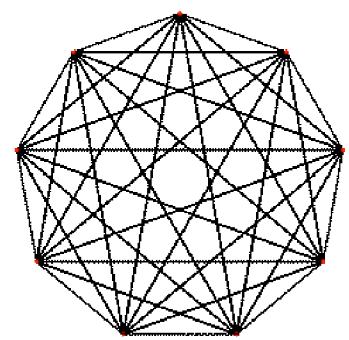




(or tree-like hyperbolic structure)

A "point"?





(or clique-like or expander-like structure)

Squint at the data graph …

Say we want to find a "best fit" of the adjacency matrix to:

α	β
β	γ

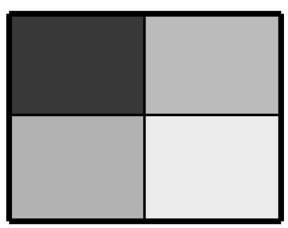
What does the data "look like"? How big are α, β, γ?

$\alpha \approx \gamma \gg \beta$

low-dimensional

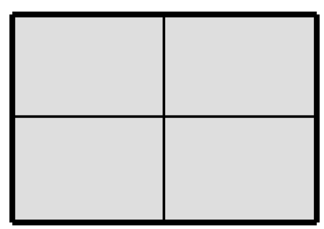
$\alpha \gg \beta \gg \gamma$

core-periphery



$\alpha \approx \beta \approx \gamma$

expander or K_n



$\beta \gg \alpha \approx \gamma$

bipartite graph

Exptl Tools: Probing Large Networks with Approximation Algorithms

Idea: Use approximation algorithms for NP-hard graph partitioning problems as experimental probes of network structure.

Spectral - (quadratic approx) - confuses "long paths" with "deep cuts"

Multi-commodity flow - (log(n) approx) - difficulty with expanders

SDP - (sqrt(log(n)) approx) - best in theory

Metis - (multi-resolution for mesh-like graphs) - common in practice

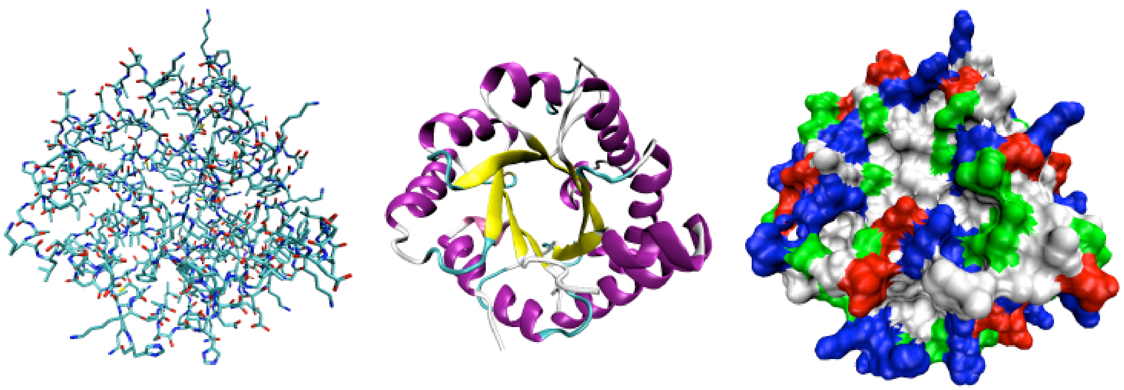
X+MQI - post-processing step on, e.g., Spectral of Metis

Metis+MQI - best conductance (empirically)

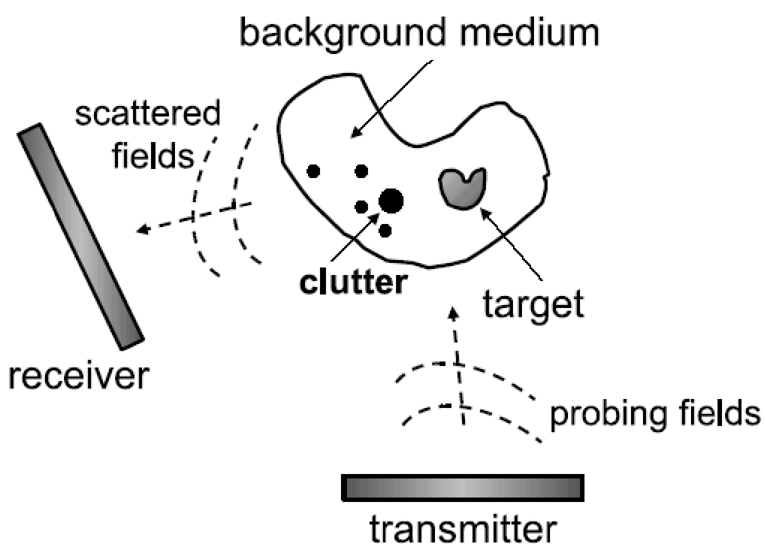
Local Spectral - connected and tighter sets (empirically, regularized communities!)

We are not interested in partitions per se, but in probing network structure.

Analogy: What does a protein look like?



Three possible representations (all-atom; backbone; and solvent-accessible surface) of the three-dimensional structure of the protein triose phosphate isomerase.



Experimental Procedure:

- Generate a bunch of output data by using the unseen object to filter a known input signal.
- Reconstruct the unseen object given the output signal and what we know about the artifactual properties of the input signal.

Outline (and lessons)

1. Matrices and graphs are basic structures for modeling data, and many algorithms boil down to matrix/graph algorithms.

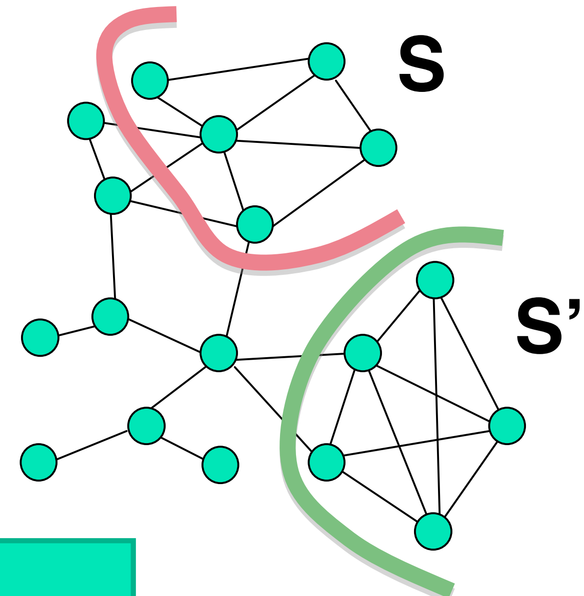
2. Often, algorithms work when they "shouldn't," don't work when they "should," and interpretation is tricky but often of interest downstream.

3. Analysts tell stories since they often have no idea of what the data "look like," but algorithms can be used to "explore" or "probe" the data.

4. Large networks (and large data) are typically very different than small networks (and small data), but people typically implicitly assume they are the same.

Community Score: Conductance

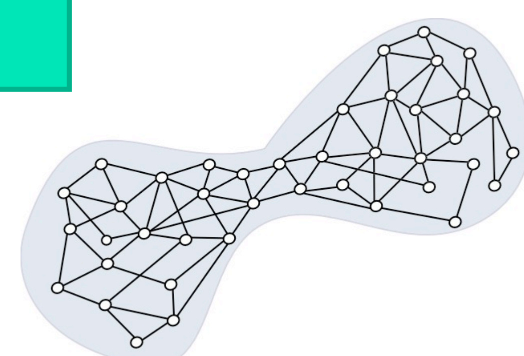
- How community like is a set of nodes?
- Need a natural intuitive measure:



- **Conductance** (normalized cut)

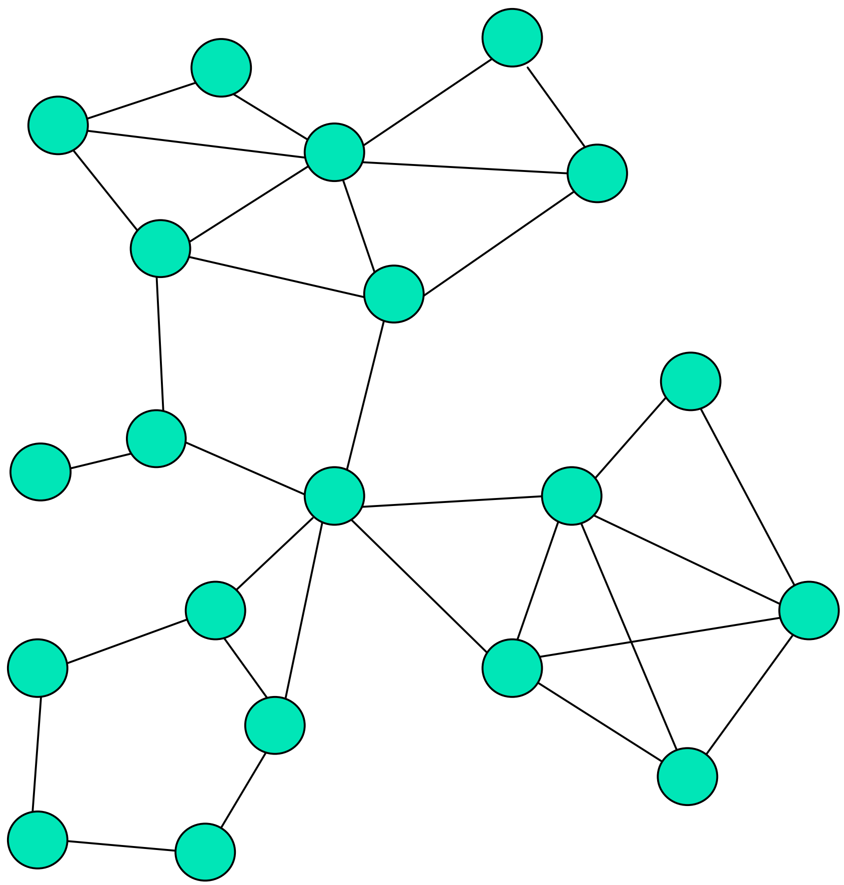
ϕ(S) ≈ # edges cut / # edges inside

- Small ϕ(S) corresponds to more community-like sets of nodes



Community Score: Conductance

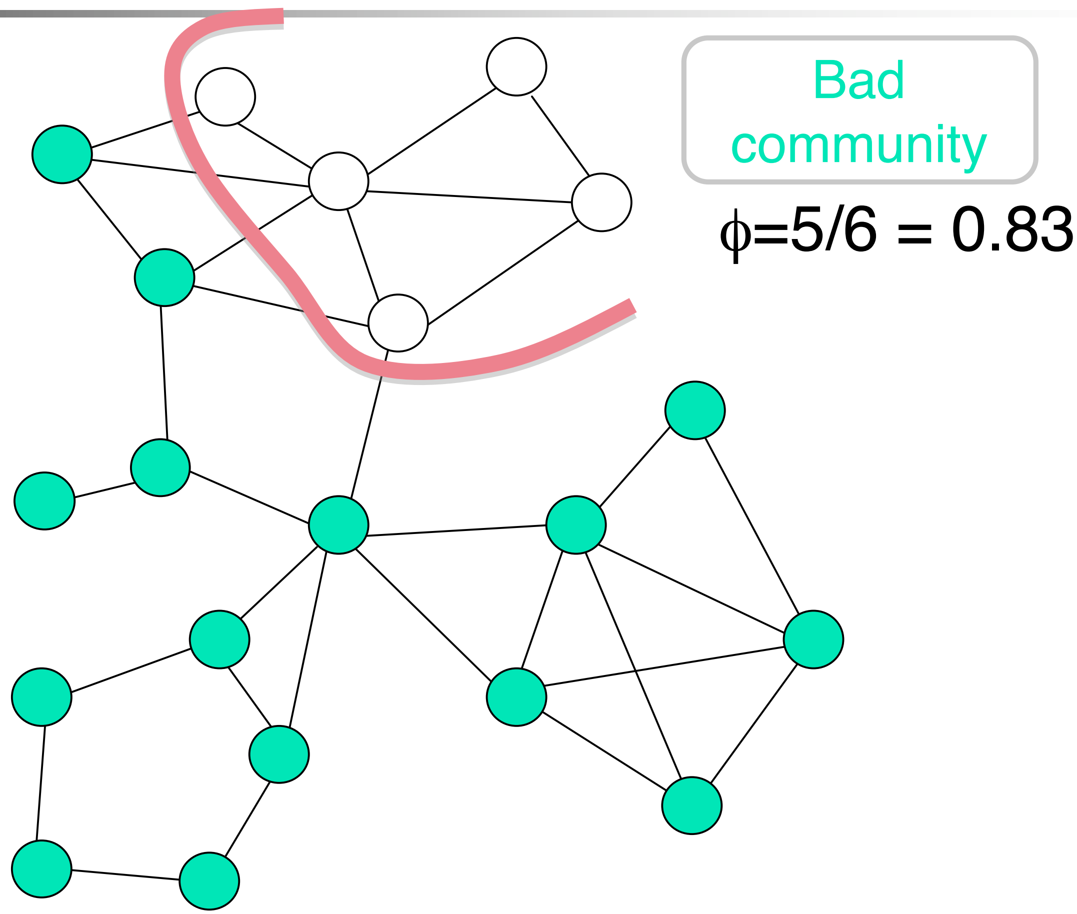
What is “best” community of 5 nodes?



Score: $\phi(S)$ **= # edges cut / # edges inside**

Community Score: Conductance

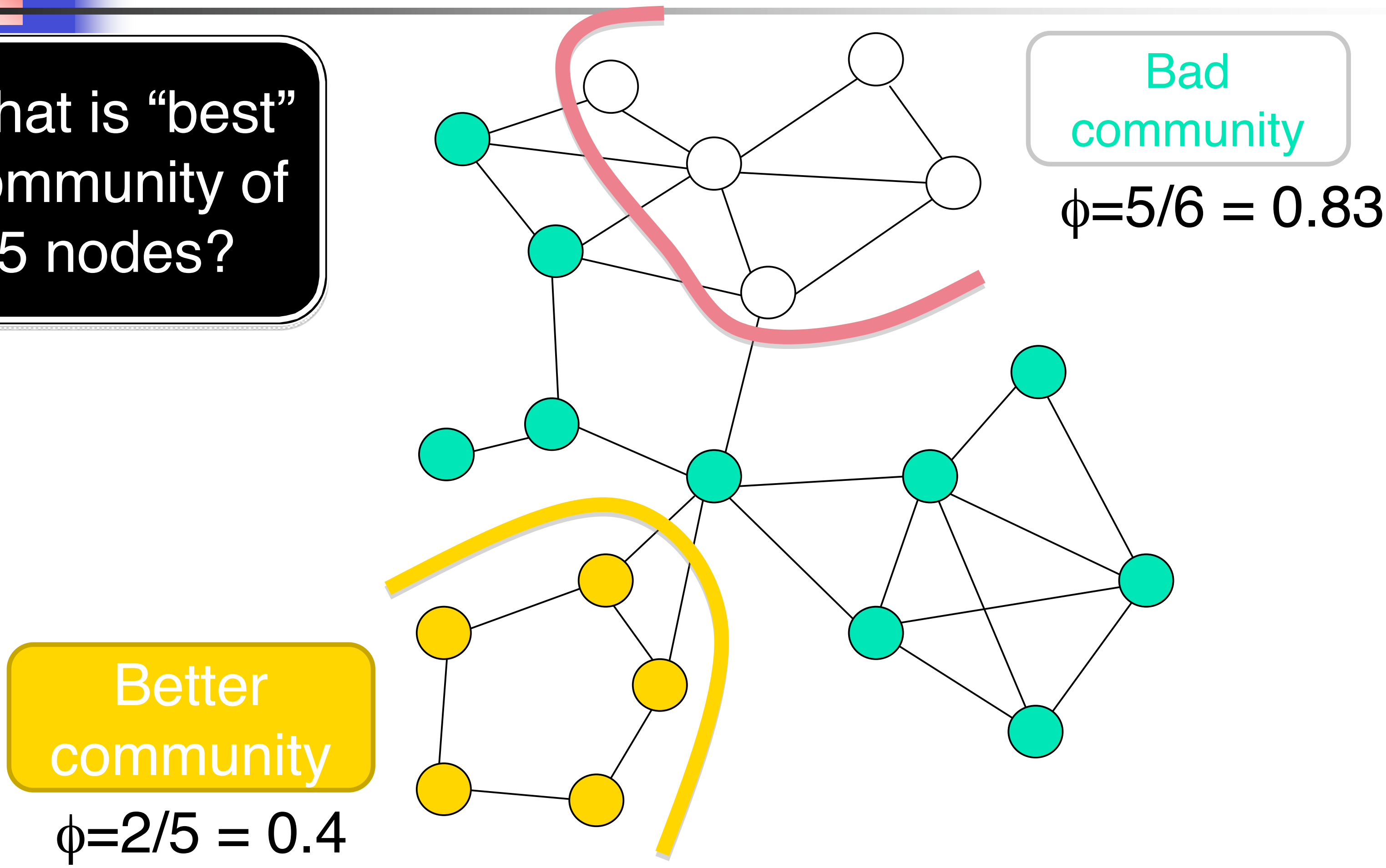
What is "best" community of 5 nodes?



Score: $\phi(S)$ **= # edges cut / # edges inside**

Community Score: Conductance

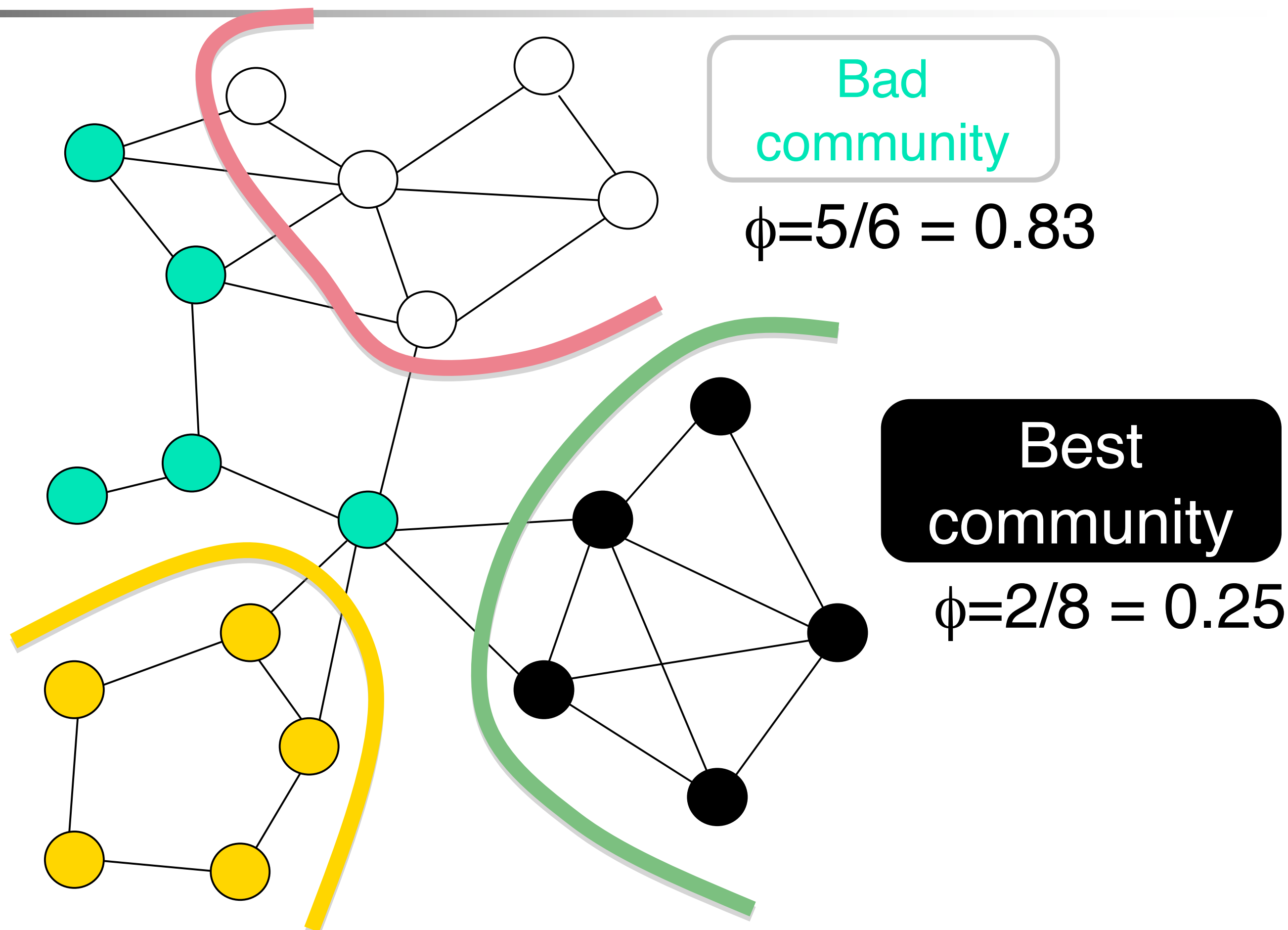
What is “best” community of 5 nodes?



Score: $\phi(S)$ = # edges cut / # edges inside

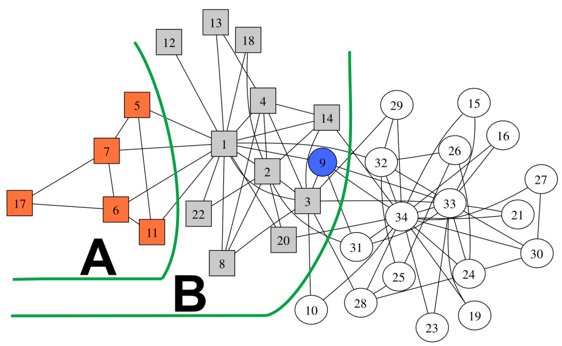
Community Score: Conductance

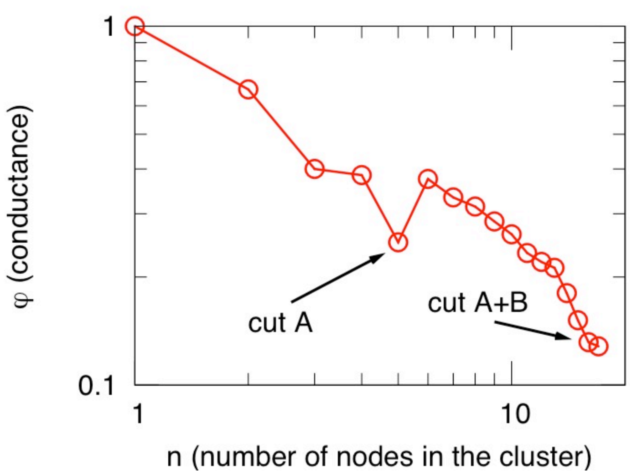
What is "best" community of 5 nodes?



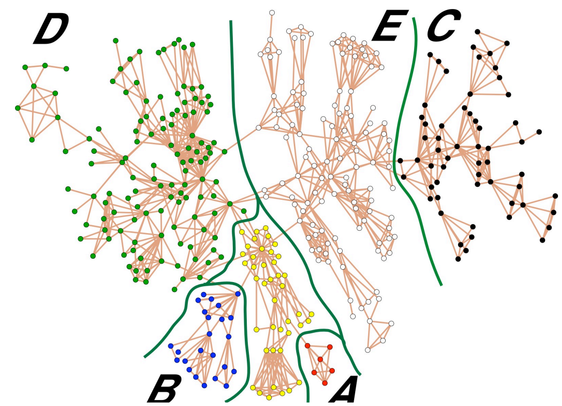
Score: $\phi(S)$ **= # edges cut / # edges inside**

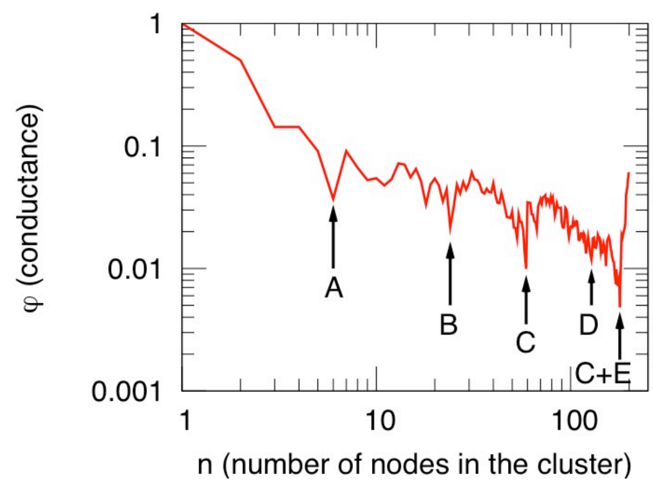
Widely-studied small social networks





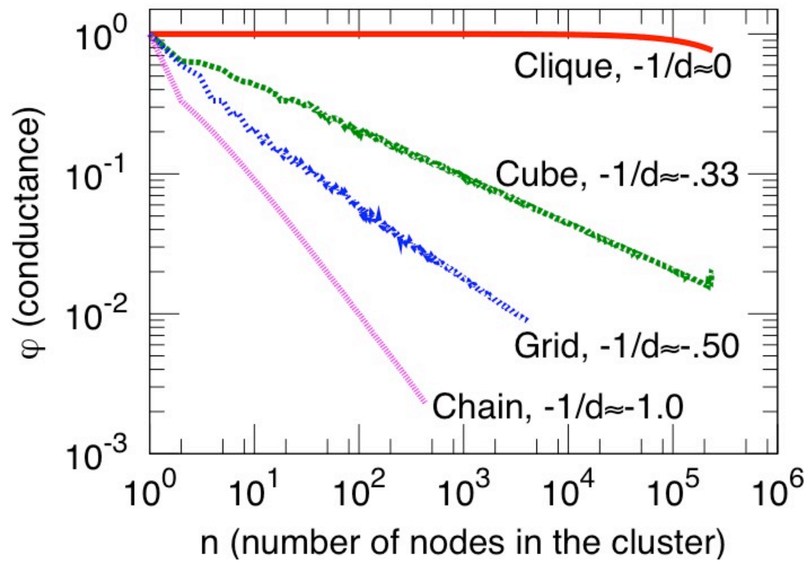
Zachary's karate club



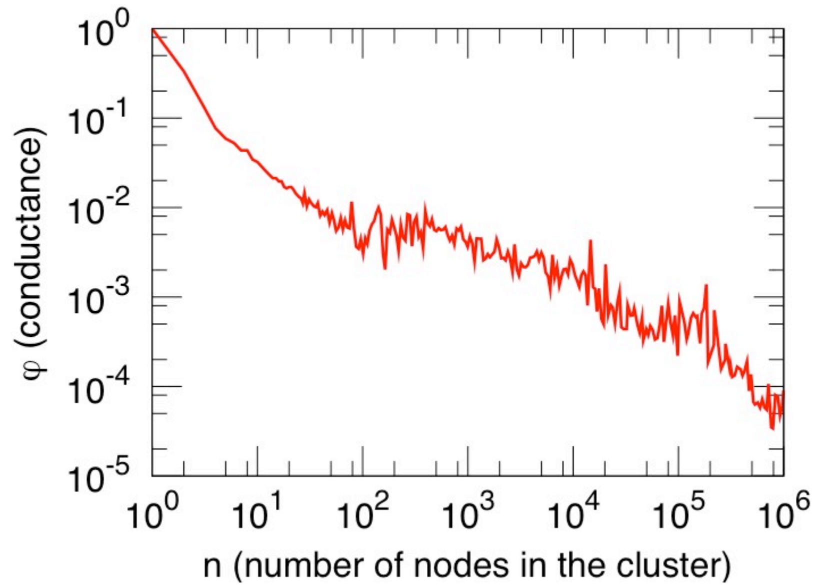


Newman's Network Science

“Low-dimensional” graphs (and expanders)

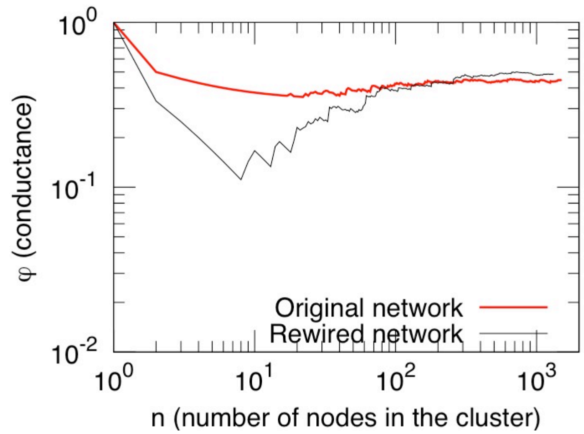


d-dimensional meshes

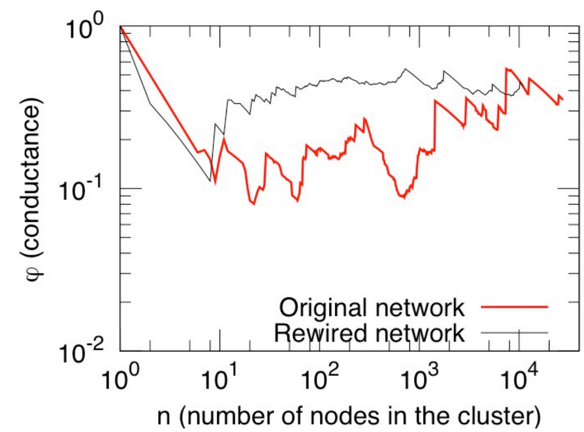


RoadNet-CA

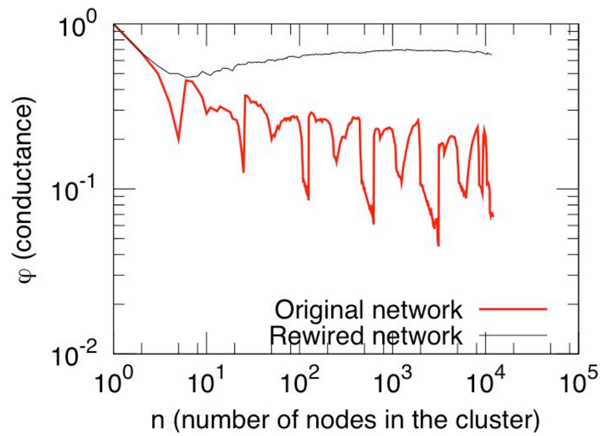
NCPP for common generative models



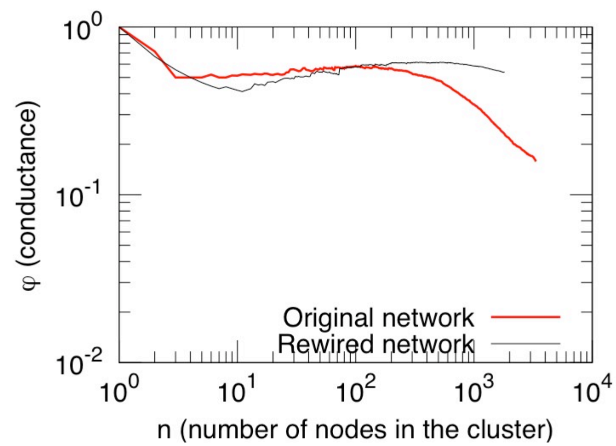
Preferential Attachment



Copying Model

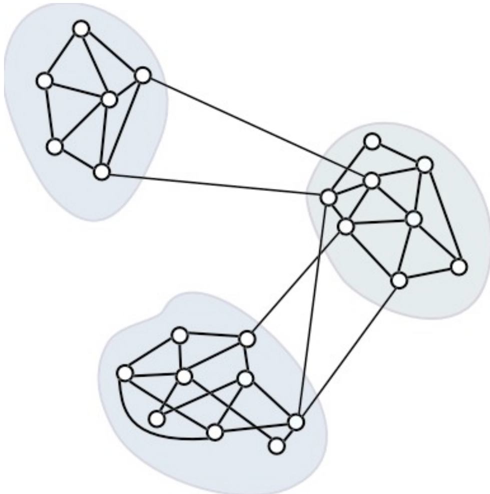


RB Hierarchical



Geometric PA

What do large networks look like?



Downward sloping NCPP

- small social networks (validation)
- "low-dimensional" networks (intuition)
- hierarchical networks (model building)
- existing generative models (incl. community models)

Natural interpretation in terms of isoperimetry

- implicit in modeling with low-dimensional spaces, manifolds, k-means, etc.

Large social/information networks are very *very* different

- We examined more than 70 large social and information networks
- We developed principled methods to interrogate large networks
- Previous community work: on small social networks (hundreds, thousands)

Large Social and Information Networks

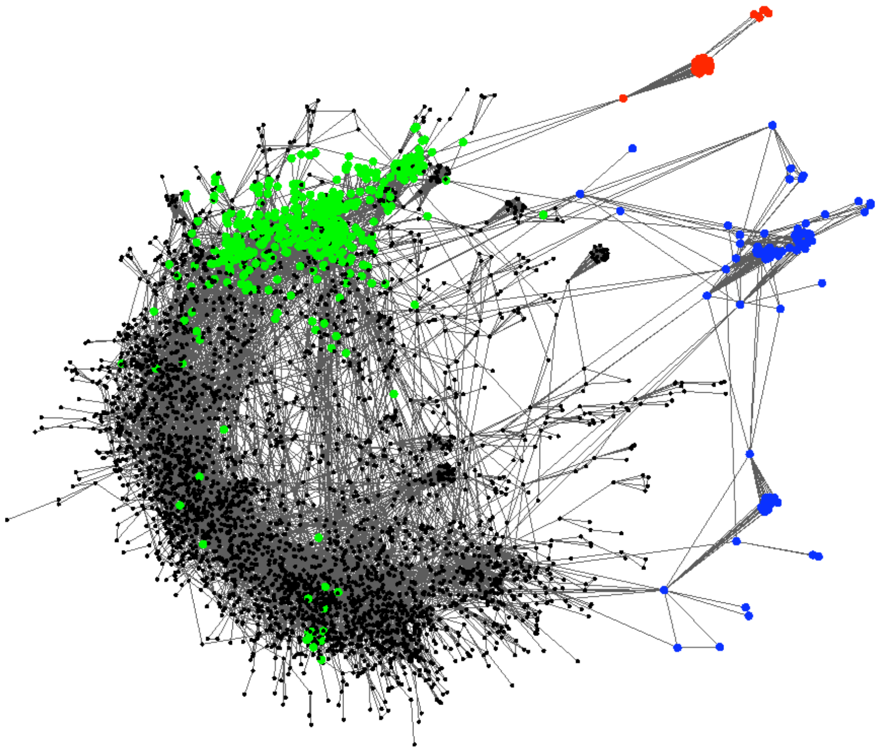
• Social nets	Nodes	Edges	Description
LiveJournal	4,843,953	42,845,684	Blog friendships [4]
Epinions	75,877	405,739	Who-trusts-whom [35]
Flickr	404,733	2,110,078	Photo sharing [21]
Delicious	147,567	301,921	Collaborative tagging
CA-DBLP	317,080	1,049,866	Co-authorship (CA) [4]
CA-cond-mat	21,363	91,286	CA cond-mat [25]
• Information networks			
Cit-hep-th	27,400	352,021	hep-th citations [13]
Blog-Posts	437,305	565,072	Blog post links [28]
• Web graphs			
Web-google	855,802	4,291,352	Web graph Google
Web-wt10g	1,458,316	6,225,033	TREC WT10G web
• Bipartite affiliation (authors-to-papers) networks			
Atp-DBLP	615,678	944,456	DBLP [25]
AtP-astro-ph	54,498	131,123	Arxiv `astro-ph` [25]
• Internet networks			
AS	6,474	12,572	Autonomous systems
Gnutella	62,561	147,878	P2P network [36]

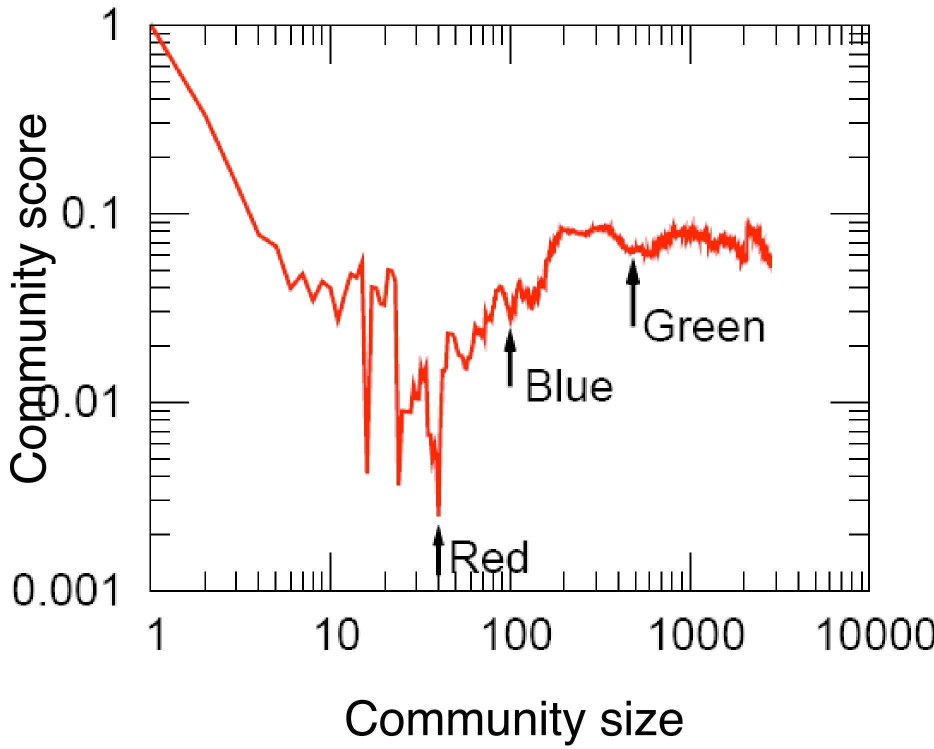
Table 1: Some of the network datasets we studied.

Typical example of our findings

Leskovec, Lang, Dasgupta, and Mahoney (WWW 2008 & arXiv 2008)

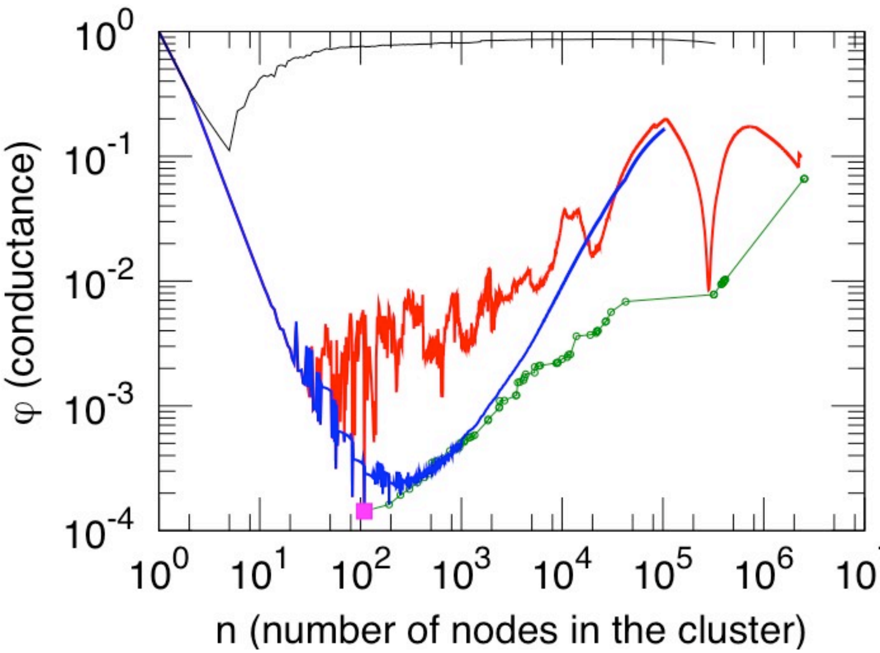
General relativity collaboration network
(4,158 nodes, 13,422 edges)



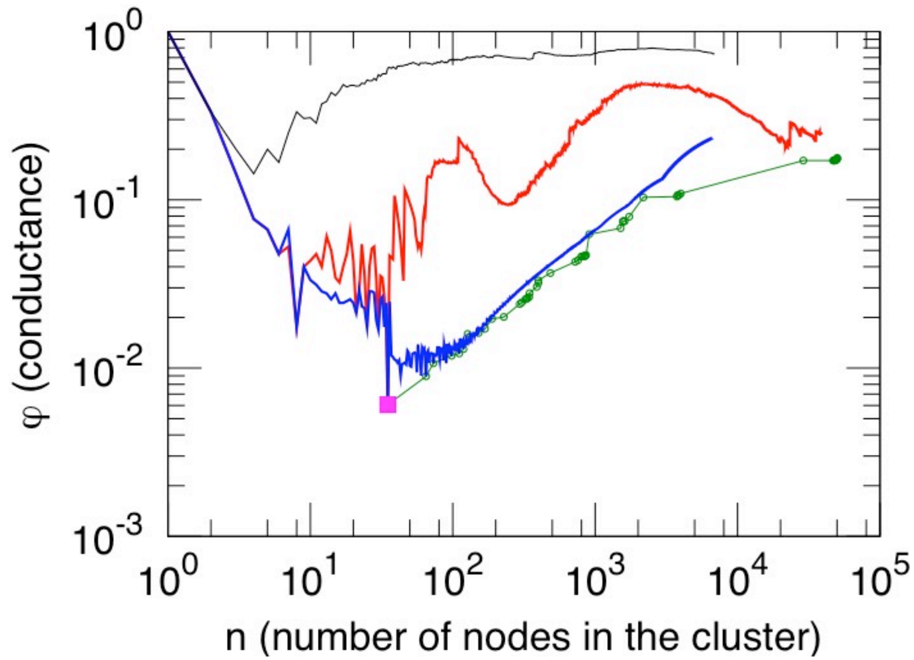


Large Social and Information Networks

Leskovec, Lang, Dasgupta, and Mahoney (WWW 2008 & arXiv 2008)



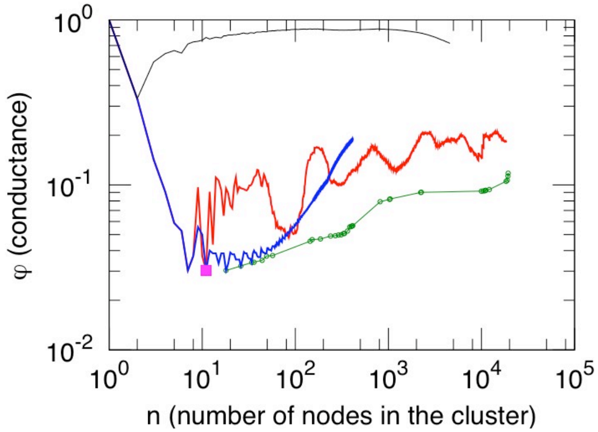
LiveJournal



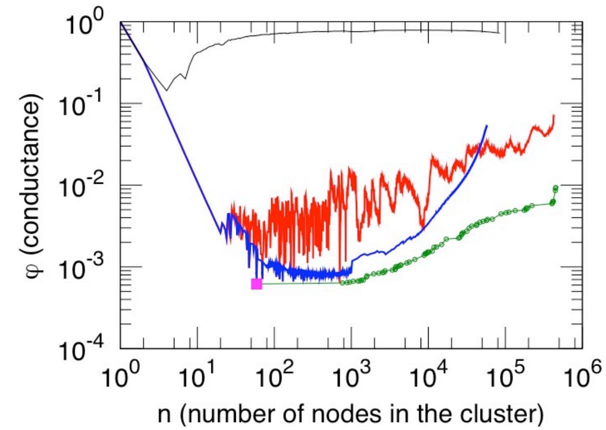
Epinions

Focus on the red curves (local spectral algorithm) - blue (Metis+Flow), green (Bag of whiskers), and black (randomly rewired network) for consistency and cross-validation.

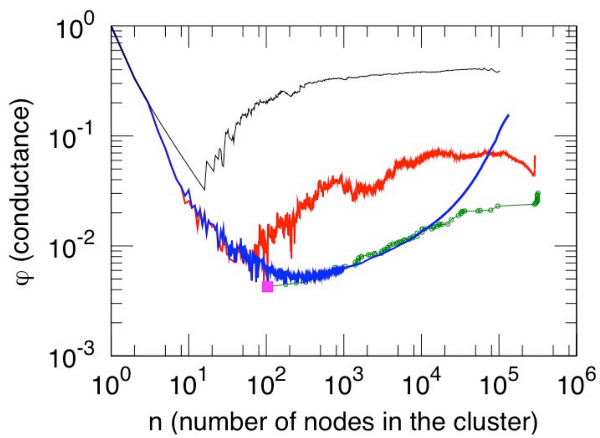
More large networks



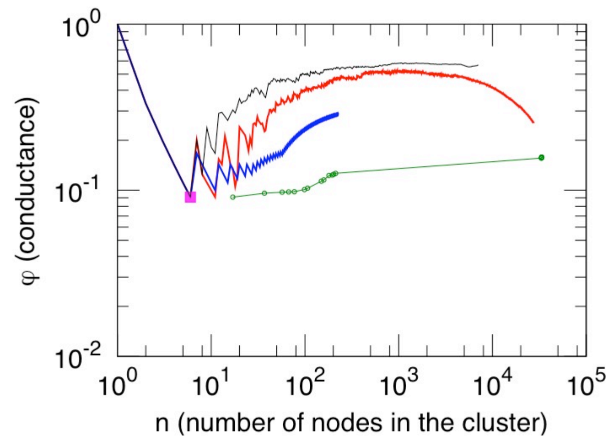
Cit-Hep-Th



Web-Google

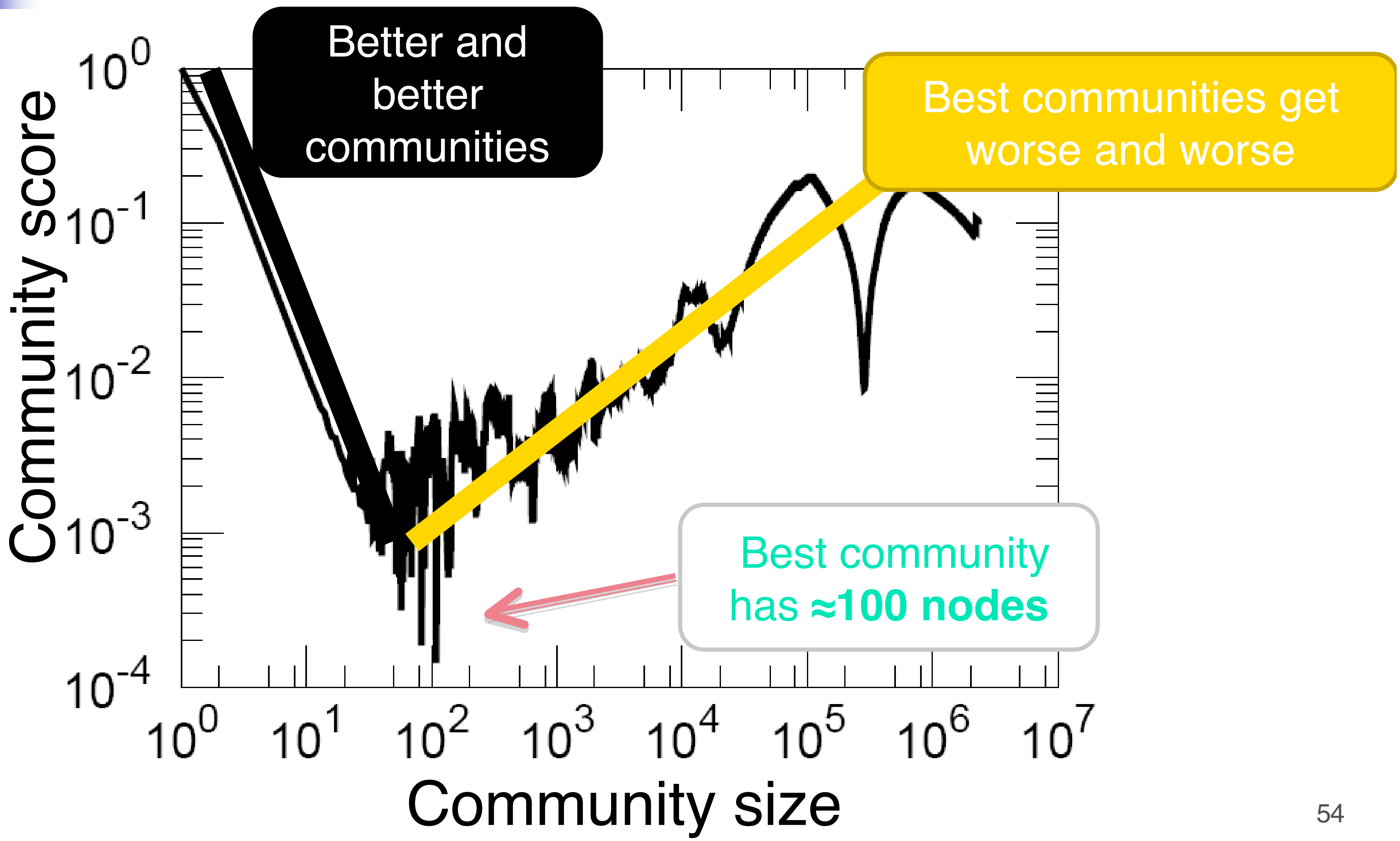


AtP-DBLP



Gnutella

NCPP: LiveJournal (N=5M, E=43M)

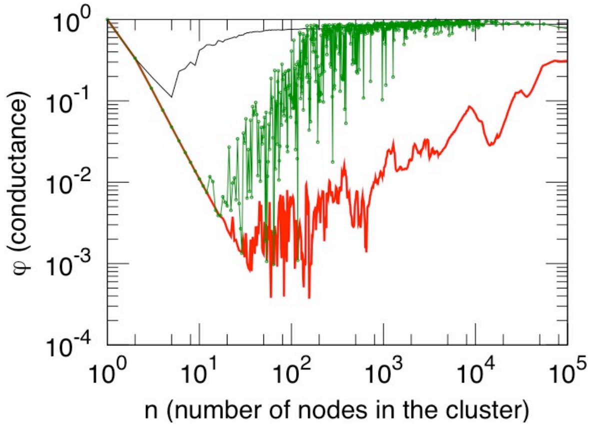


Comparison with "Ground truth" (1 of 2)

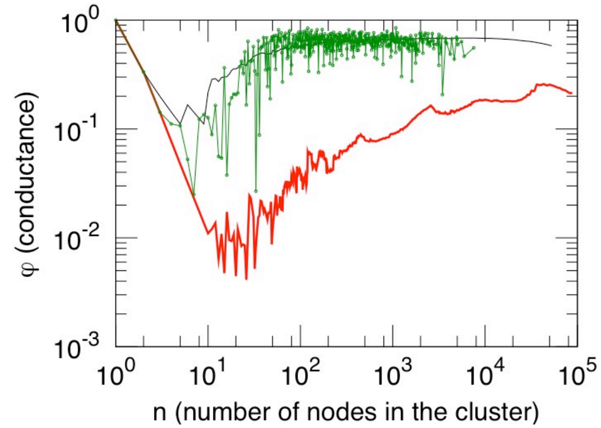
Networks with "ground truth" communities:

- LiveJournal12:
  - users create and explicitly join on-line groups
- CA-DBLP:
  - publication venues can be viewed as communities
- AmazonAllProd:
  - each item belongs to one or more hierarchically organized categories, as defined by Amazon
- AtM-IMDB:
  - countries of production and languages may be viewed as communities (thus every movie belongs to exactly one community and actors belongs to all communities to which movies in which they appeared belong)

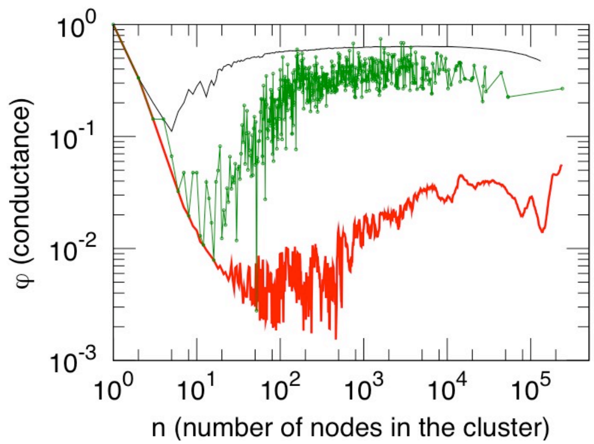
Comparison with "Ground truth" (2 of 2)



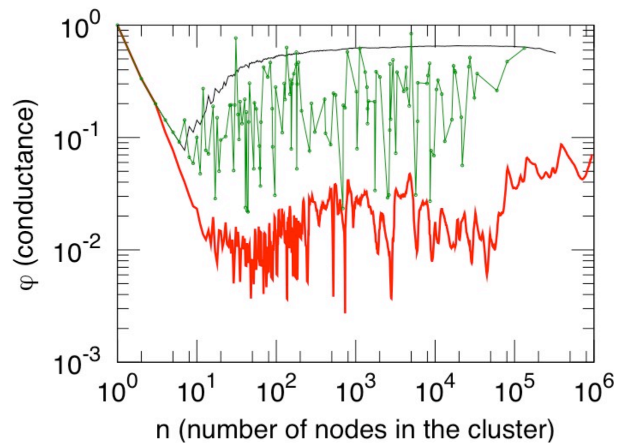
LiveJournal



CA-DBLP



AmazonAllProd



AtM-IMDB

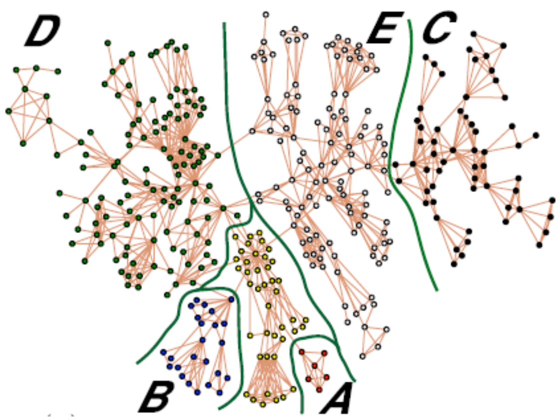
α	β
β	γ

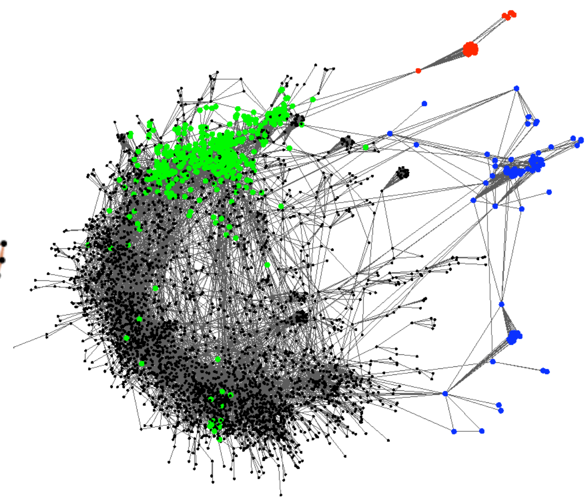
Small versus Large Networks

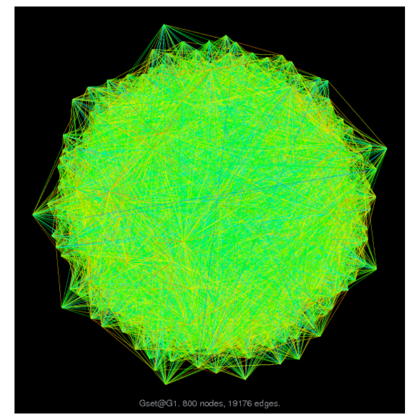
Leskovec, et al. (arXiv 2009); Mahdian-Xu 2007

- Small and large networks are very different:

(also, an expander)







E.g., fit these networks to Stochastic Kronecker Graph with "base" K=[a b; b c]:

$K_1 =$

0.99	0.17
0.17	0.82

0.99	0.55
0.55	0.15

0.2	0.2
0.2	0.2

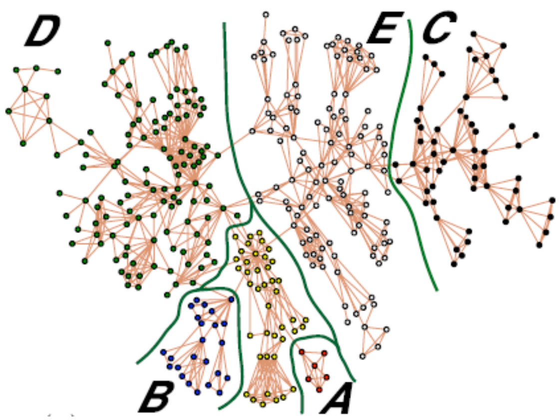
α	β
β	γ

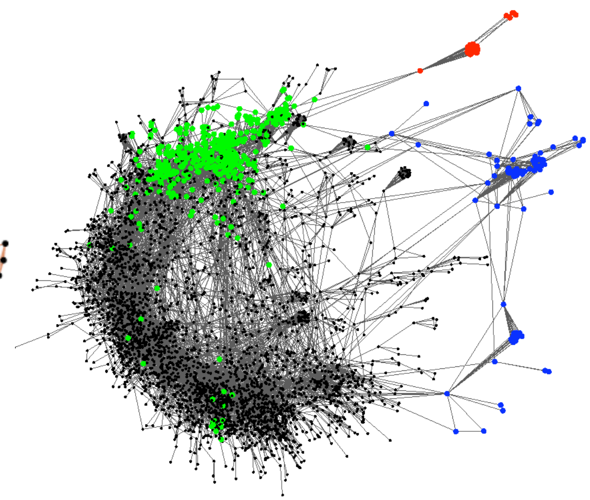
Small versus Large Networks

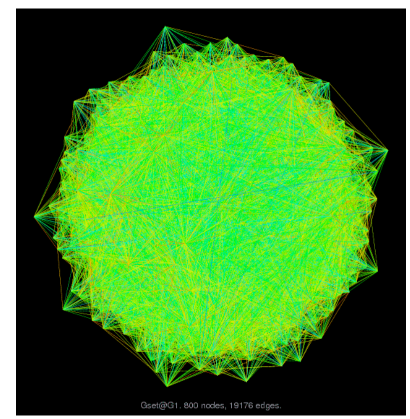
Leskovec, et al. (arXiv 2009); Mahdian-Xu 2007

- Small and large networks are very different:

(also, an expander)







E.g., fit these networks to Stochastic Kronecker Graph with "base" K=[a b; b c]:

$K_1 =$ 

Some more thoughts ...

What I just described is "obvious" ...

- There are good small clusters
- There are no good large clusters

... but not "obvious enough" that analysts don't assume otherwise *when deciding what algorithms to use*

- k-means - basically the SVD
- Spectral normalized-cuts - appropriate when SVD is
- Recursive partitioning - recursion depth is BAD if you nibble off 100 nodes out of 100,000,000 at each step

Real large-scale applications

A lot of work on large-scale data already *implicitly* uses variants of these ideas:

• Fuxman, Tsaparas, Achan, and Agrawal (2008): random walks on query-click for automatic keyword generation

• Najork, Gallapudi, and Panigraphy (2009): carefully "whittling down" neighborhood graph makes SALSA faster and better

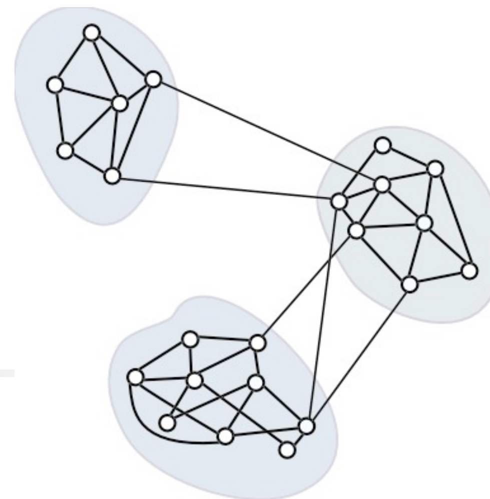
• Lu, Tsaparas, Ntoulas, and Polanyi (2010): test which page-rank-like implicit regularization models are most consistent with data

These and related methods are often very non-robust

• basically due to the structural properties described,

• since the data are different than the story you tell.

Implications more generally



Empirical results demonstrate:

• (**Good** *and* **large**) network clusters, *at least when formalized i.t.o. the inter-versus-intra bicriterion*, don't really exist in these graphs.

• *To the extent that they barely exist, existing tools are designed **not** to find them.*

This may be "obvious," but not *really* obvious enough ...

• Algorithmic tools people use, models people develop, intuitions that get encoded in seemingly-minor design decisions all assume otherwise

Drivers, e.g., funding, production, bonuses, etc bias toward "positive" results

• *Finding false positives is only going to get worse* as the data get bigger.

Conclusions (and take-home lessons)

1. Matrices and graphs are basic structures for modeling data, and many algorithms boil down to matrix/graph algorithms.
2. Often, algorithms work when they “shouldn’t,” don’t work when they “should,” and interpretation is tricky but often of interest downstream.
3. Analysts tell stories since they often have no idea of what the data “look like,” but algorithms can be used to “explore” or “probe” the data.
4. Large networks (and large data) are typically very different than small networks (and small data), but people typically implicitly assume they are the same.