Efficient Spectral Clustering using Selective Similarities

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Challenges of large-scale clustering

Identifying fiber-bundles in the brain





- Lot of fibers
- > Multiple Scales
- Noisy similarities
- Computation is expensive

Diffusion spectral imaging (DSI) 250,000 fiber micro-tracks

Pairwise similarities between fiber microtracks

Collaborator: Schneider Lab at Univ. Pittsburgh, Center for Neural Basis of Cognition at CMU

Robust and Efficient Clustering

Goal: Given a noisy and incomplete pairwise similarity matrix, re-order rows/columns to infer groups with high within-cluster similarity and low between-cluster similarity.



- **Robustness:** How much **noise** can a clustering algorithm tolerate while recovering all clusters up to a desired **resolution**?
- Efficiency: How many similarity measurements and/or computation are necessary for robust clustering?

Spectral clustering



Balanced ratio-cut - Partition the graph into approximately equal size clusters such that weight of edges between them is minimized.

$$\min_{C_1, C_2} \sum_{i \in C_1, j \in C_2} W_{ij} \left(\frac{1}{|C_1|} + \frac{1}{|C_2|} \right)$$

NP Hard to solve!

<u>Spectral Clustering</u> – solves a relaxed version of the balanced graph cut.

Spectral clustering



<u>Spectral Clustering</u> - Second smallest eigenvector of the Graph Laplacian L approximates balanced cut

W : symmetric similarity matrix (n x n)

D : diagonal degree matrix $D_{ii} = \sum_{j=1}^{n} W_{ij}$

L = D – W : Graph Laplacian (unnormalized)

<u>Note:</u> L1 = D1 - W1 = 0 smallest eigenvector 1 if graph is connected.

Spectral clustering Algorithm

<u>Hierarchical Binary Spectral Clustering</u>

Compute L = D - W $v_2 \leftarrow$ second smallest eigenvector of L $C_1 = \{i : v_2(i) \ge 0\}, C_2 = \{i : v_2(i) < 0\}$ *Repeat* on each cluster



What is the price of solving this relaxation of the balanced ratio-cut problem?

Prior Justification

<u>High-level justifications</u>: Connection to graph cut, random walks on graph, electric network theory, Laplace-Beltrami operator on manifold

- don't translate to cluster recovery guarantees

<u>Perturbation analysis</u>: Eigenvectors are stable in ℓ_2 norm under small similarity perturbations

- Fraction of misclusterings $\rightarrow 0$ Ng et al (2001), Huang et al (2009)

Stochastic Block Model/ Planted Partition Model



McSherry (2001), Rohe-Chatterjee-Yu (2010), Sussman et al (2011)

probability of within-cluster edge, p > probability of between-cluster edge, q

Laplacian eigenvectors of Ultrametrics

Why should Laplacian eigenvectors of hierarchically block matrices reveal cluster structure?

<u>Ultrametric</u>: Noiseless constant block similarities.





Sharpnack, Singh (NIPS 2010)

Not low-rank or compressible!

Signal+Noise model for Hierarchical Clustering

Observed Hierarchical Similarity matrix:

 $\mathbf{W} = \mathbf{A} + \mathbf{R}$

R ~ i.i.d. zero mean, subgaussian(σ²) perturbation (includes Bernoulli)

Signal
$$\mu = \min_{\substack{(i,j) \in C}} A_{ij} - \max_{i \in C, k \notin C} A_{ik} - \eta \left(\max_{\substack{i \in C, k \notin C}} A_{ik} - \min_{\substack{i \in C, k \notin C}} A_{ik} \right)$$

Within vs between cluster similarities Cluster balance factor Cluster similarities
Signal-to-Noise Ratio, SNR = $\frac{\mu}{\sigma}$

Noise Thresholds for Spectral Clustering, NIPS 2011.

Robustness of Spectral Clustering

<u>Spectral clustering limit:</u> If

SNR
$$\left(\frac{\mu^5}{\sigma}\right)^2 \succcurlyeq \sqrt{\frac{\log n}{|C|}}$$

then, with probability > 1-1/n, **hierarchical binary spectral** clustering will exactly recover all clusters of size at least |C| in a binary hierarchy.

- Similar result for k-way partitional clustering
- SNR depends on the size of smallest cluster we want to resolve.
- Popular greedy merging strategies for hierarchical clustering such as single linkage, complete linkage or average linkage fail under this level of noise.

Minimax SNR for Clustering

 $\begin{array}{ll} \min & \max & Pr(\widehat{C}(\mathbf{W}) \neq C) \\ \text{all clusterings, } \widehat{C}(\mathbf{W}) & \mathbf{W} \text{with SNR } \mu/\sigma \end{array}$



Simulation Results

Noise threshold – two balanced clusters



Robustness: comparison with other hierarchical clustering algorithms



Efficiency of Clustering



Prior work: Can resolve clusters of size $\Omega(n)$ using O(n log n) **randomly chosen** similarities (fraction of misclusterings $\longrightarrow 0$) Hunter-Strohmer'10, Shamir-Tishby'11

Our work: Can resolve all clusters of size up to $\Omega(\log n)$ in a hierarchy using $O(n \log^2 n)$ selective similarities

Active Hierarchical Clustering



- □ Pick m objects at random
- □ Split into two (or k) clusters
- e.g. Compute $\mathbf{L}_{m} = \mathbf{D}_{m} \mathbf{W}_{m}$ $\mathbf{v}_{2} \leftarrow \text{second smallest evec}$ $C_{1} = \{i : \mathbf{v}_{2}(i) \ge 0\}$
 - $C_2 = \{i : \mathbf{v}_2(i) < 0\}$
- Assign each remaining object to the cluster with higher average similarity
- Repeat on each cluster

Efficient Active Algorithms for Hierarchical Clustering, ICML 2012 (To appear).

Active Hierarchical Clustering



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Active Hierarchical Spectral Clustering



Measurement Efficiency:

#similarities needed on each iteration = nm If clusters approx balanced, total # similarities = nm + 2 nm + 4 nm + ... $\frac{1}{2}$ $\frac{1}{4}$ = O(nm log n) = O(n log²n) if m = log n minimum possible

Computational Efficiency:

only need to compute eigenvectors of m x m matrices (log n x log n)

 $O(nm^2) = O(n \log^2 n)$ if m = log n

Active Hierarchical Spectral Clustering



Robustness Analysis:

Let $m = \log n$

- Each split succeeds with high probability if $\left(\frac{\mu}{\sigma}\right)^2 \sim \sqrt{\frac{\log n}{m}} \Rightarrow \frac{\mu}{\sigma} = \text{constant}$
- Each round of object assignments succeeds with high probability

if
$$\sigma \sqrt{\frac{\log n}{m}} < \mu \qquad \Rightarrow \frac{\mu}{\sigma} = \text{constant}$$

max of n subgaussians with scale factor σ/\sqrt{m}

• Union bound over all splits

Simulation Results



Robustness vs Efficiency Tradeoffs



Application to Evolutionary tree reconstruction



Similarity = genome sequence alignment

2048 genome sequences with 2000 base pairs (phyClust)

Non-active: Runtime 15000s, all similarities



Active Spectral Clustering

Runtime 600s, # similarities 3.5%

Thanks

Hierarchically-structured high-rank matrices can be completed using O(n log² n) selectively sampled entries!

References:

- > Noise Thresholds for Spectral Clustering, NIPS 2011.
- > Efficient Active algorithms for Hierarchical Clustering, ICML 2012.

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