

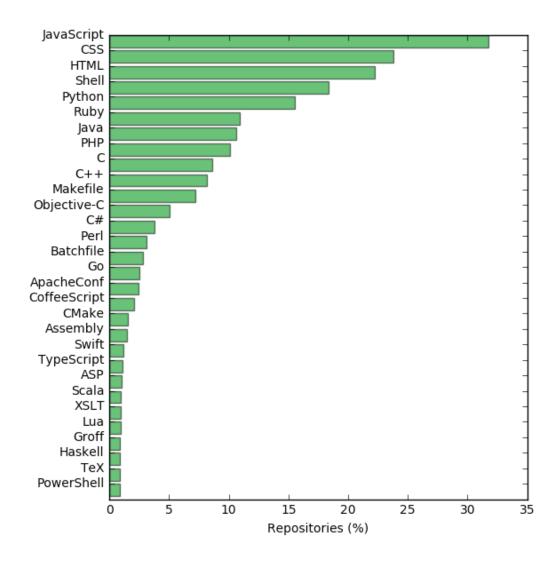
Matrix Data Visualization

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GitHub archive dataset

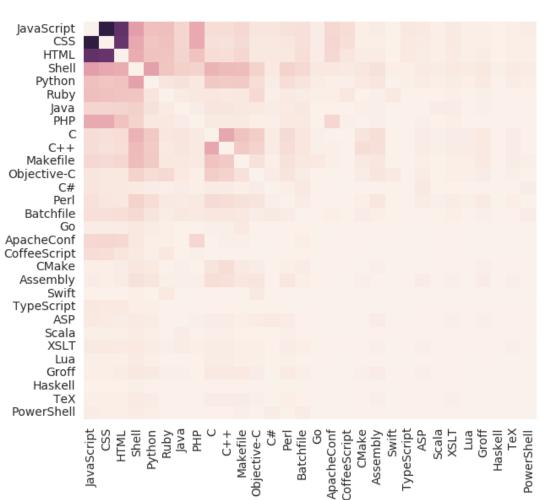
 The plot on this slide shows the percentage of repositories that use specific programming languages

 Suppose our goal is to visualize cooccurrence of pairs of programming languages in different repositories



Heatmap

- Co-occurrence of pairs of programming languages in repositories can be visualized by a heatmap
- It is important how the rows and columns are sorted to visualize any possibly existing clusters
- In this slide, the rows and columns are sorted in decreasing popularity of programming languages
 - A heuristic that for this instance reveals some clusters, but this is not necessary in general



600000

450000

300000

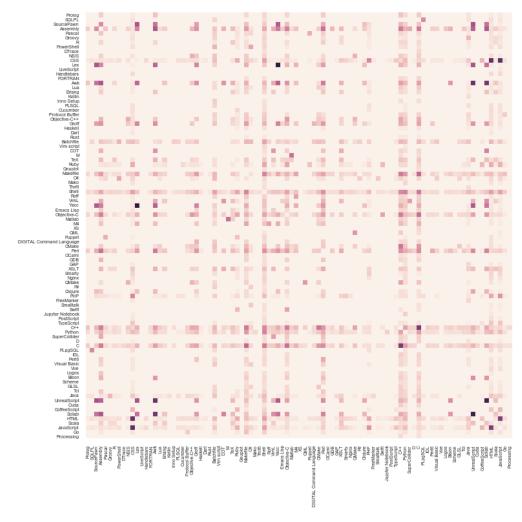
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Use case: similarity matrices

- A similarity matrix quantifies how "similar" pairs of items are
- Similarity may be defined as cosine similarity for items associated with feature vectors: for two non-null feature vectors a and b in \mathbf{R}^n , the cosine similarity is

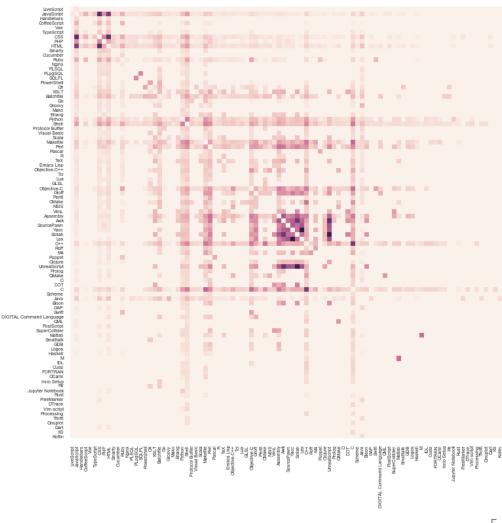
$$sim(a,b) = \frac{\sum_{i=1}^{n} a_i b_i}{\sqrt{\sum_{i=1}^{n} a_i^2} \sqrt{\sum_{i=1}^{n} b_i^2}}$$

• In our example, a feature vector associated with a programming language indicates its usage over different repositories



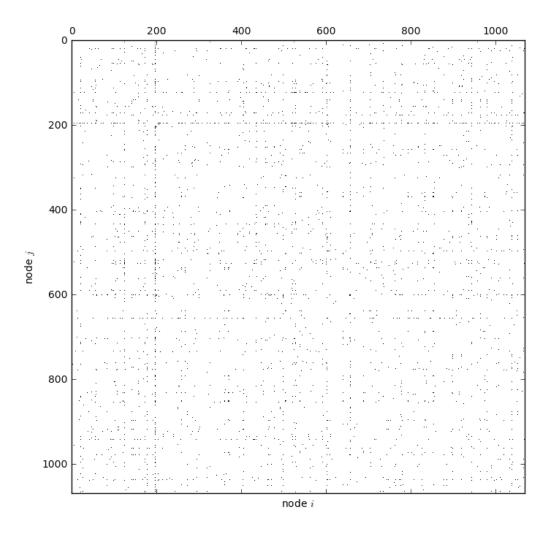
Use case: similarity matrices (cont'd)

 How can we order rows and columns of a matrix to visualize any possibly existing clusters in matrix data?



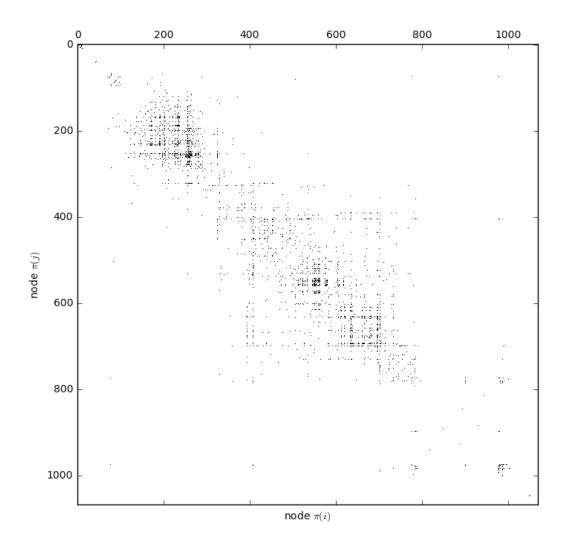
Use case: adjacency matrices

- Adjacency matrix of a graph indicates whether or not there is an edge between different pairs of nodes of the graph
- The plot in this slide shows the adjacency matrix of a graph that specifies existence of communications between Amazon Mechanical Turk workers
- Dataset source: Yin et al, The Communication Network within the Crowd, WWW 2016



Use case: adjacency matrices

- Reordered rows and columns
 - i.e. rearranged node identifiers
- The adjacency matrix with reordered rows and columns in this slide suggests existence of different communities of workers



Software modules

- Scikit-learn biclustering module
 - Scikit-learn Section 2.4 Biclustering

http://scikit-learn.org/stable/modules/biclustering.html

- from sklearn.cluster.bicluster import SpectralCoclustering
- from sklearn.cluster.bicluster import SpectralBiclustering
- R seriation package
 - https://cran.r-project.org/web/packages/seriation/index.html

Some linear algebra concepts

Eigenvalues and eigenvectors

• λ is an eigenvalue of matrix A if for some vector $x \neq 0$

$$Ax = \lambda x$$

A corresponding vector x is called an eigenvector

Laplacian matrix

- Let A be a real symmetric matrix
- The Laplacian matrix L_A is defined by

$$L_A = D_A - A$$

where D_A is a diagonal matrix with $d_{i,i} = \sum_{j=1}^n a_{i,j}$

• A is a real symmetric matrix $\Rightarrow L_A$ is a real symmetric matrix

Laplacian matrix (cont'd)

- For any real symmetrix matrix $A \in \mathbb{R}^{n \times n}$:
 - A has n eigenvectors
 - All eigenvectors of *A* are pairwise orthogonal
 - All eigenvalues of A are real
- Every Laplacian matrix has all its eigenvalues real and non-negative, which is equivalent to saying that it is positive semi-definite
- Every Laplacian matrix has the vector of all ones \boldsymbol{e} as an eigenvector corresponding to the eigenvalue zero

Fiedler value and eigenvector

- For real symmetric matrix $A \in \mathbb{R}^{n \times n}$, Fiedler value is defined as the minimum eigenvalue of the Laplacian L_A that has an eigenvector orthogonal to e
- The corresponding eigenvector is called a Fiedler eigenvector
- The Fiedler value is the optimum value of the optimization problem:

minimize
$$x^T L_A x$$

subject to $x^T e = 0$
 $x^T x = 1$

Historical remarks

- Miroslav Fiedler
- Czech Republic's mathematician
- 1926-2015
- Charles University, Prague



• M. Fiedler, Algebraic connectivity of graphs, Czehoslovak Math. J., 23(98), 1973

Laplacian matrix (cont'd)

• **Lemma**: For any real, symmetric matrix *A*:

$$x^T L_A x = \sum_{i < j} a_{i,j} (x_i - x_j)^2$$

- Laplacian matrices are closely related to graph cuts
 - Graph G = (V, E) with edge weights: edge (i, j) has weight $a_{i,j}$
 - A is the adjacency matrix of G
 - Let x takes value in $\{-1,1\}^n$ defining a vertex cut: partitioning vertices into two sets (negative and positive labeled)
 - Graph cut is defined as the sum of weights of edges whose end vertices belong to different components of the vertex cut

Seriation

Seriation

- Input: a real, symmetric matrix $A \in \mathbb{R}^{n \times n}$
 - $a_{i,j}$ interpreted as the similarity between items i and j
- Goal: find a linear ordering (permutation) of items such that similar items are placed nearby, specifically, find a permutation π^* that minimizes

$$c(\pi) = \sum_{i < j} a_{i,j} (\pi_i - \pi_j)^2$$

over the set of all possible permutations of n elements Π_n

This problem is NP hard

Fractional relaxation

• Find optimal solution to the following problem:

minimize
$$c(x)$$

subject to $x^T e = 0$
 $x^T x = 1$
 $x \in \mathbf{R}^n$

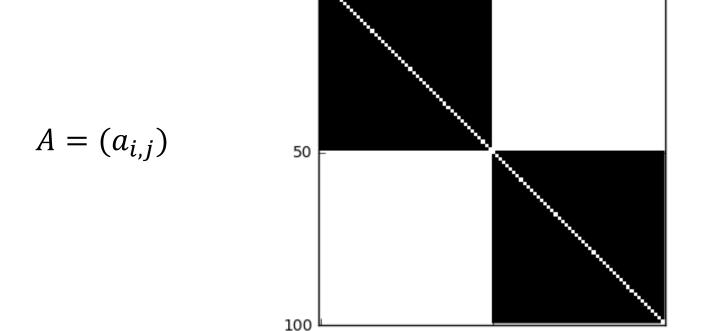
- The first constraint avoids multiplicity of solutions by adding a positive constant to each coordinate of x
- The second constraint avoids vector 0 to be a trivial solution
- The optimum solution is a Fiedler vector of A

Robinson matrices

- A matrix A is said to be a Robinson matrix (R-matrix) if, and only if,
 - *A* is symmetric
 - $a_{i,j} \le a_{i,k}$ for j < k < i and $a_{i,j} \ge a_{i,k}$ for i < j < k

- In other words, a matrix is a R-matrix if it is symmetric and it has off-diagonal elements non-decreasing by moving away from the diagonal
- A matrix A is said to be a pre-R matrix if it can be symmetrically permuted (reordering rows and columns by the same permutation) to become an R-matrix

An example of a R-matrix



50

100

- Clearly, a symmetric matrix
- The elements are decreasing as we move away from the diagonal along any row

black point if $a_{i,j} = 1$ white point if $a_{i,j} = 0$

An example R-matrix: stochastic block model

- Stochastic block model is a random graph model commonly studied in the community detection and graph clustering literature
- A stochastic block model can be defined by
 - Parameters $0 \le q \le p \le 1$
 - Set of vertices $V = \{1, 2, \dots, n\}$
 - Hidden bipartition of vertices $(S, V \setminus S)$
 - Set of edges E: for every pair of vertices (i, j) such that i < j we have

$$(i,j) \in E$$
 independently with probability =
$$\begin{cases} p & \text{if } i,j \in S \text{ or } i,j \in V \setminus S \\ q & \text{otherwise} \end{cases}$$

- A is defined as the adjacency matrix of G
- The case q=0 and p=1 is trivial when the vertex-set partition is not hidden

Fiedler vector of R-matrices

• **Theorem**: If A is a R-matrix then it has a monotone Fiedler vector.

• Proof: Atkins et al (1998)

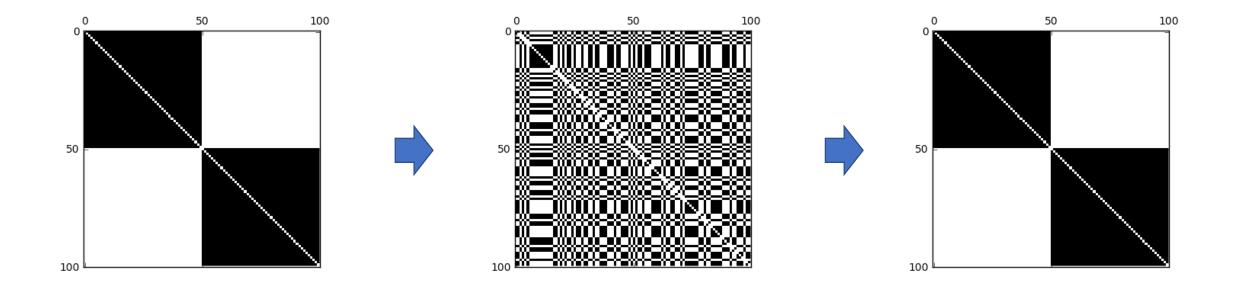
Fiedler vector of R-matrices (cont'd)

• **Theorem**: Let A be a pre-R matrix with a simple Fiedler value (i.e. unique value) and a Fiedler vector with no repeated elements. Let π_1 be the permutation sorting elements of the Fiedler vector in increasing order. Let π_2 be the permutation sorting elements of the Fiedler vector in decreasing order. Let Π_1 and Π_2 be the corresponding permutation matrices.

Then, $\Pi_1 A \Pi_1$ and $\Pi_2 A \Pi_2$ are R-matrices and not other symmetric permutation of A produces an R matrix.

- Proof: Atkins et al (1998)
- See Thm 4.7 in Atkins et al for a statement under weaker assumptions

Example 1: p = 1, q = 0

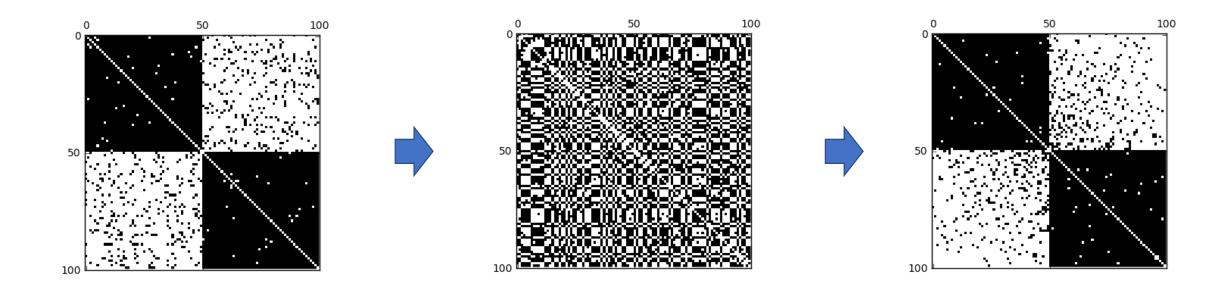


Rows and columns permuted by the same random permutation

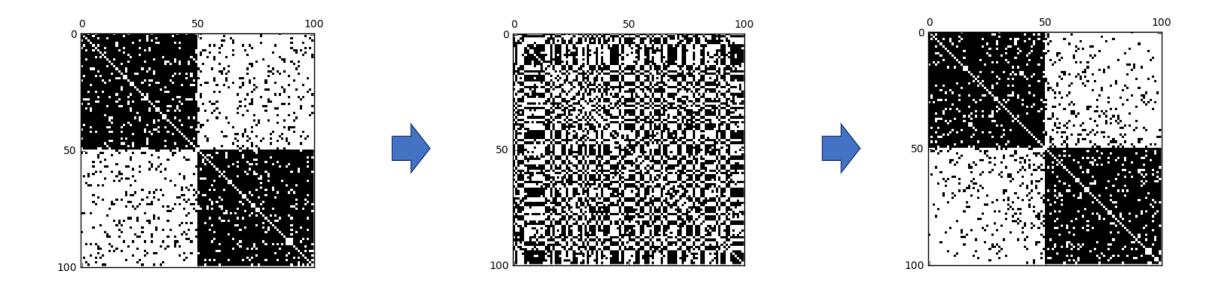
"symmetric permutation"

Rows and columns sorted in a monotonic order of the Fiedler vector elements

Example 2: p = 0.99, q = 0.01



Example 3: p = 0.9, q = 0.1



Spectral co-clustering

Graph cuts

- Let V be a set of vertices with weights $w_{i,j}$ for $i,j \in V$
- k-way partition: let $P_k(S)$ be the set of all possible partitions of S in k components
 - In particular, $(S_1, S_2) \in P_2(S)$ is referred as a bipartition
- The cut function is defined as the sum of weights of cut edges:

$$cut(V_1, V_2) = \sum_{i \in V_1, j \in V_2} w_{i,j}$$

More generally, we define

$$\operatorname{cut}(V_1, V_2, \dots, V_k) = \sum_{1 \le i < j \le k} \operatorname{cut}(V_i, V_j)$$

Graph cuts and the Laplacian matrix

• A bipartition (V_1, V_2) can be represented by a partition vector x defined as

$$x_i = \begin{cases} 1 & \text{if } i \in V_1 \\ -1 & \text{if } i \in V_2 \end{cases}$$

• Lemma: Any bipartition (V_1, V_2) and the corresponding partition vector x satisfy

$$\frac{x^T L_A x}{x^T x} = \frac{1}{n} 4 \operatorname{cut}(V_1, V_2)$$

Normalized cut function

- Define the weight of a set of vertices $S: w(S) = \sum_{i \in S} w_i$
- The normalized cut function is defined as follows:

$$Q(V_1, V_2) = \frac{\text{cut}(V_1, V_2)}{w(V_1)} + \frac{\text{cut}(V_1, V_2)}{w(V_2)}$$

- This cut function captures both sparsity of edge cuts and balancing of the component sizes
- Optimization problem formulation: minimize $Q(V_1, V_2)$ over $P_2(V)$

Special normalized cut functions

Ratio-cut

- Each vertex has a unit weight
- Amounts to looking at the eigenvalue problem: $L_A y = \lambda y$

Normalized-cut

- Each vertex weight is equal to the sum of weights of incident edges
- In this case $w(V_i) = \operatorname{cut}(V_1, V_2) + w^{int}(V_i)$ where $w^{int}(V_i) = \sum_{(u,v) \in E: u,v \in V_i} w_{u,v}$
- Amounts to the generalized eigenvalue problem : $L_A y = \lambda D_A y$

Normalized-cut function

Show that

$$Q(V_1, V_2) = 2 - \left(\frac{w^{int}(V_1)}{w(V_1)} + \frac{w^{int}(V_2)}{w(V_2)}\right)$$

 Minimizing the normalized-cut is equivalent to maximizing the proportion of edge weights that lie within each component of a vertex set partition

Generalized partition-vector representation

Let y be a generalized partition vector defined as

$$y_{i} = \begin{cases} \sqrt{\frac{w(V_{2})}{w(V_{1})}} & if \ i \in V_{1} \\ -\sqrt{\frac{w(V_{1})}{w(V_{2})}} & if \ i \in V_{2} \end{cases}$$

• Properties: (a) $y^T D_w y = w(V)$ and (b) $y^T D_w e = 0$

• Lemma:

$$\frac{y^T L_A y}{y^T D_w y} = \frac{\text{cut}(V_1, V_2)}{w(V_1)} + \frac{\text{cut}(V_1, V_2)}{w(V_2)}$$

Fractional relaxation

minimize
$$\frac{y^T L_A y}{y^T D_W y}$$
 subject to $y^T D_W e = 0$ $y \neq 0$

• **Theorem**: The solution is the eigenvector corresponding to the second smallest eigenvalue λ_2 of the generalized eigenvalue problem:

 $y \in \mathbb{R}^n$

$$L_A y = \lambda D_w y$$

• Corollary: The optimum value of the min normalized cut is $\geq \lambda_2$

Bipartite graph clustering

- Bipartite graph
 - The vertex set consists of disjoint sets of vertices L and R
 - Each edge has its vertices in L and R
- Let D_L and D_R be diagonal matrices with diagonal elements

$$(D_L)_{i,i} = \sum_{j \in R} w_{i,j} \text{ and } (D_R)_{i,i} = \sum_{j \in L} w_{j,i}$$

• For graph *G*:

$$A = \begin{pmatrix} 0 & W \\ W^T & 0 \end{pmatrix}$$
, $D_A = \begin{pmatrix} D_L & 0 \\ 0 & D_R \end{pmatrix}$ and $L_A = \begin{pmatrix} D_L & -W \\ -W^T & D_R \end{pmatrix}$

The generalized eigenvalue problem

The generalized eigenvalue problem can be written as

$$D_L x - W y = \lambda D_L x$$

- $A^T x + D_R y = \lambda D_R y$

- Assumption: W has a strictly positive element in each row and column
- Note that we can write:

$$D_L^{1/2} x - D_L^{-1/2} W y = \lambda D_L^{1/2} x$$

- $D_R^{-1/2} A^T x + D_R^{1/2} y = \lambda D_R^{1/2} y$

Change of variables

Using the change of variables

$$\widetilde{W} = D_L^{-1/2} W D_R^{-1/2}$$

$$u = D_L^{1/2} x$$

$$v = D_R^{1/2} y \text{ and}$$

$$\sigma = 1 - \lambda$$

we can write

$$\widetilde{W}v = \sigma u$$
 and $\widetilde{W}^T u = \sigma v$

Eigenvectors

• The eigenvector x_2 corresponding to the second smallest eigenvalue λ_2 of the generalized eigenvalue problem can be written as:

$$x_2 = \begin{pmatrix} D_L^{-1/2} u_2 \\ D_R^{-1/2} v_2 \end{pmatrix}$$

where u_2 and v_2 are the left and right singular vectors of \widetilde{W} corresponding to the singular value $\sigma_2=1-\lambda_2$

• We can think of u_2 to give a partition of the set of left vertices and v_2 to give a partition of the set of right vertices

Bi-clustering algorithm

- Input: W
- Compute $\widetilde{W} = D_L^{-1/2} W D_R^{-1/2}$
- Compute the left and right singular vectors u_2 and v_2 of $\widetilde W$ corresponding to the singular value $\sigma_2=1-\lambda_2$
- Partition the set of vertices in two components using k-means algorithm for input data points x_2

k-way clustering algorithm

- Given a positive integer $k \ge 2$ the goal is to partition the set of left vertices and the set of right vertices in k components
- Let $U=(u_2,u_3,\dots,u_{\ell+1})$ and $V=(v_2,v_3,\dots,v_{\ell+1})$ be ℓ the left and right singular vectors

• Let
$$(x_2, x_3, \dots, x_{\ell+1}) = \begin{pmatrix} D_L^{-1/2} U \\ D_R^{-1/2} V \end{pmatrix}$$

• Apply the k-means algorithm to the input ℓ -dimensional points

Evaluating a bi-clustering: consensus score

- The definition of the consensus score as implemented in sklearn.metrics.consensus_score
- Quantifies similarity between two input sets of biclusters
- Similarity between individual biclusters is computed
 - Default is Jaccard similarity for two sets A and B defined as $|A \cap B|/|A \cup B|$
- The best matching between sets is found using the Hungarian algorithm
- The final score is the sum of the similarities divided by the size of the larger set

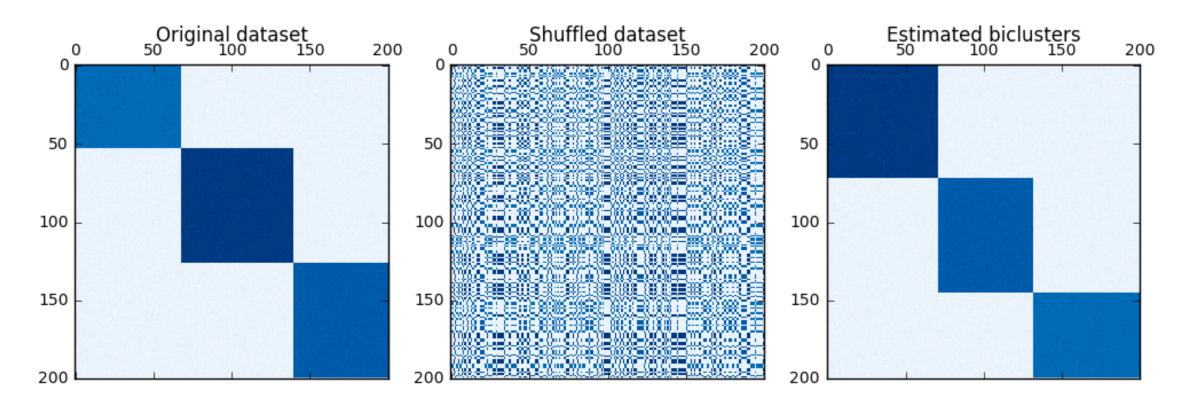
```
def consensus_score(a, b, similarity="jaccard"):
    Parameters
    a: (rows, columns)
        Tuple of row and column indicators for a set of biclusters.
    b : (rows, columns)
        Another set of biclusters like ``a``.
    similarity: string or function, optional, default: "jaccard"
        May be the string "jaccard" to use the Jaccard coefficient, or
        any function that takes four arguments, each of which is a 1d
        indicator vector: (a_rows, a_columns, b_rows, b_columns).
    if similarity == "jaccard":
        similarity = _jaccard
    matrix = _pairwise_similarity(a, b, similarity)
                                               # minimum cost assignment from sklearn.utils.linear assignment
    indices = linear_assignment(1. - matrix)
    n_a = len(a[0])
    n_b = len(b[0])
    return matrix[indices[:, 0], indices[:, 1]].sum() / max(n_a, n_b)
```

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```
def _jaccard(a_rows, a_cols, b_rows, b_cols):
    """Jaccard coefficient on the elements of the two biclusters."""
    intersection = ((a_rows * b_rows).sum() *
                    (a\_cols * b\_cols).sum())
    a_size = a_rows.sum() * a_cols.sum()
    b_size = b_rows.sum() * b_cols.sum()
    return intersection / (a_size + b_size - intersection)
def _pairwise_similarity(a, b, similarity):
    """Computes pairwise similarity matrix.
    result[i, i] is the Jaccard coefficient of a's bicluster i and b's
    bicluster j.
    1111111
    a_rows, a_cols, b_rows, b_cols = _check_rows_and_columns(a, b)
                                                                         # unpacks rows and columns
    n_a = a_{rows.shape}[0]
    n_b = b_rows.shape[0]
    result = np.array(list(list(similarity(a_rows[i], a_cols[i],
                                            b_rows[j], b_cols[j])
                                 for j in range(n_b))
                            for i in range(n_a)))
    return result
```

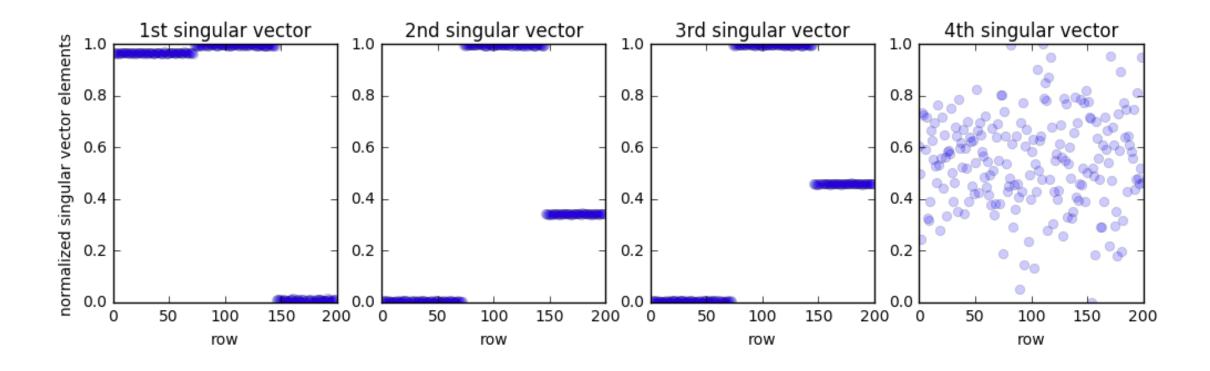
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Example



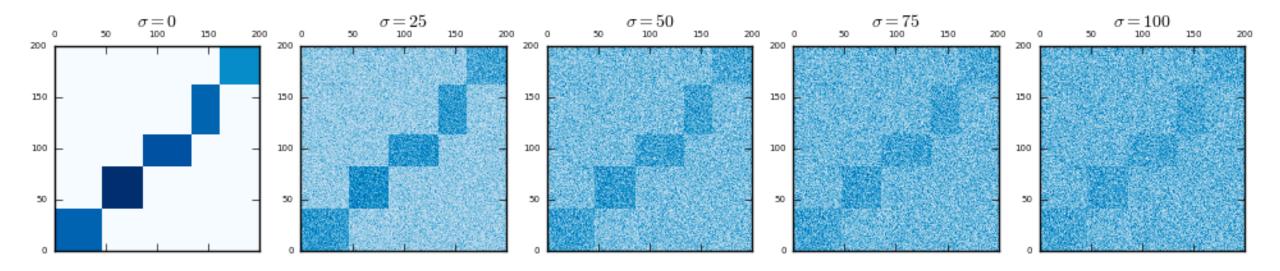
• Recovery of hidden co-clusters by spectral co-clustering

Example: singular vectors



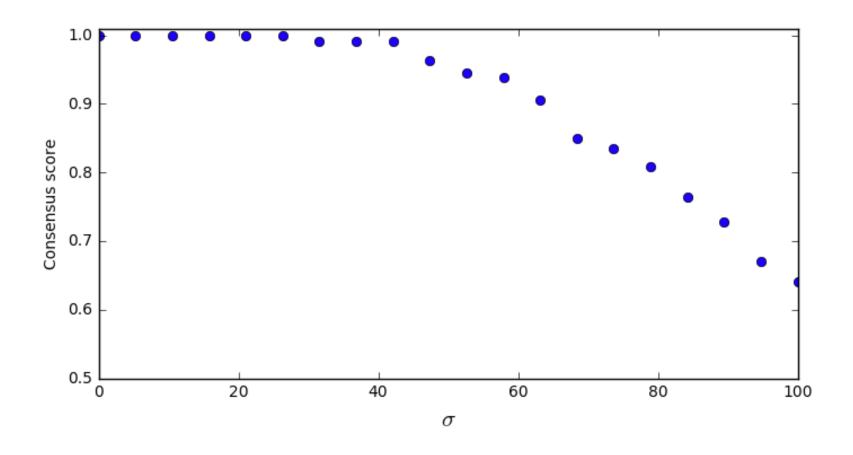
Clusters are clearly indicated by the 2nd and 3rd singular vectors

Robustness to noise



• Input matrix corrupted by noise with varying variance σ

Robustness to noise (cont'd)



• Consensus score vs standard deviation of noise

References

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