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# Dimension Reduction and Iterative Consensus Clustering

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Southeastern Clustering and Ranking Workshop

August 24, 2009



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#### **Document Clustering**

For document clustering, we create a term-document matrix, A, as follows:

Term 1 
$$A_{m \times n} = \begin{array}{c} \text{Term 1} \\ \text{Term } i \\ \text{Term } m \end{array} \left( \begin{array}{cccc} \text{Doc 1} & \text{Doc } j & \text{Doc } n \\ & & | & \\ & & | & \\ & - & - & - & f_{ij} \end{array} \right)$$

Where  $f_{i,j}$  is the frequency of term i in document j.

- Various types of term-weighting can be used in place of raw frequencies. For our experiments, we simply normalized the columns.
- Each column of A represents the coordinates of a document in the m-dimensional "term-space", where each standard basis vector represents one term from the dictionary.

Geometry of the SVD Principal Direction Divisive Partitioning

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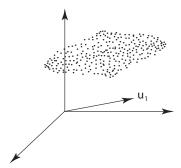
$$(\sigma_1\mathbf{u}_1,\sigma_2\mathbf{u}_2,\ldots\sigma_r\mathbf{u}_r)$$

 We'll use the columns of V<sup>T</sup> as a lower dimensional representation of the columns of A for the purposes of clustering.



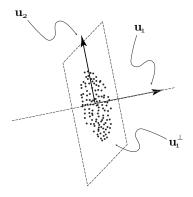
#### Geometry of Singular Vectors when A is centered

• The first left-hand singular vector,  $\mathbf{u}_1$ , of the centered matrix  $\mathbf{C} = \mathbf{A} - \mu \mathbf{e}^T$  is the direction along which the variance of the data is maximal.



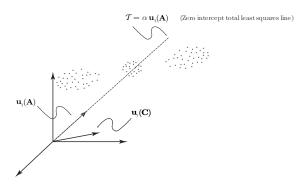
#### Geometry of Singular Vectors when A is centered

 The second left singular vector of C, u<sub>2</sub>, is the direction orthogonal to u<sub>1</sub> along which the variance is maximal.



#### Geometry of SVD when A is uncentered

 The first left singular vector of A is the direction of the least-squares line through the origin.



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- Iterative process partitions data into 2 clusters with each iteration, based upon their projection onto the direction of maximal variance.
- PDDP can be adapted to use more than just the principal singular vector.
- We will often use the results from PDDP to seed the k-means algorithm with an initial guess

#### Illustration of one iteration of PDDP

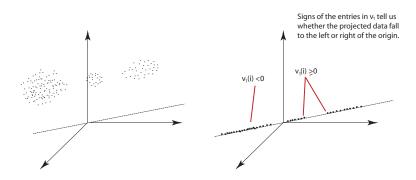


Figure: Data Cloud Projected onto the span of  $\mathbf{u}_1(\mathbf{C})$ 



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$$\mathbf{a}_{j} pprox \sum_{i=1}^{r} \mathbf{h}_{i,j} \mathbf{w}_{i}$$

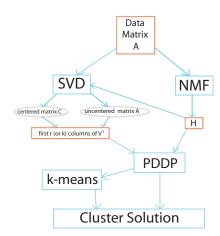


#### NMF for Dimension Reduction

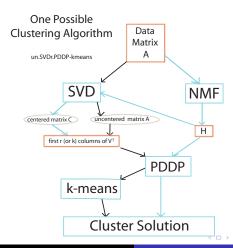
- Columns of H represent the coordinates of each document after projection into the lower dimensional "feature-space" spanned by the columns of W.
- We'll use the columns of H as a lower dimensional representation of the columns of A for the purposes of clustering.

$$\begin{pmatrix} a_1 \\ a_2 \\ a_3 \\ \vdots \\ a_m \end{pmatrix} \longrightarrow \begin{pmatrix} h_1 \\ h_2 \\ h_3 \\ \vdots \\ h_r \end{pmatrix}$$

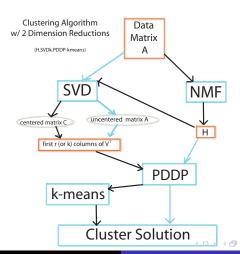
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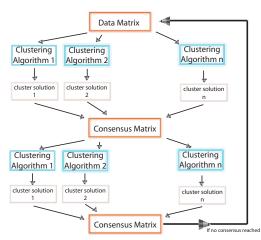
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- We sum the adjacency matrices from various algorithms to create a **consensus matrix**, **M** whose  $(i,j)^{th}$  entry reveals the number of times  $\mathbf{a}_i$  and  $\mathbf{a}_j$  were clustered together.

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- Entries in the consensus matrix that are below a certain tolerance may be changed to zero.
- This consensus matrix is then clustered using the same algorithms to see if the algorithms will agree upon a solution.



#### **Iterating the Consensus Process**



# Medlars/Cranfield/CISI - Medical and Scientific Abstracts - 4000 docs/11000 terms -k = 3 clusters

Accuracies for	Med/Cran/CISI r=k=3		n Reduction Consensus 2	to $r = 3$
NMF Basic	0.70084811	0.89771267	0.9306091	0.89719866
PDDP	0.83012079	0.89437163	0.89437163	0.89719866
PDDP-kmeans	0.96376253	0.89282961	0.89282961	0.89719866
SVDr-PDDP-kmeans	0.81624261	0.72834747	0.769211	0.89719866
un.SVDr-PDDP-kmeans	0.75970188	0.89719866	0.89719866	0.89719866
H-PDDP	0.59650475	0.89437163	0.89874068	0.89719866
H-PDDP-kmeans	0.71626831	0.89719866	0.89719866	0.89719866
H-SVDk-PDDP-kmeans	0.8234387	0.89334361	0.89334361	0.9308661
H-un.SVDk-PDDP-kmeans	0.71446929	0.9308661	0.9308661	0.89719866

#### Medlars/Cranfield/CISI

# Medlars/Cranfield/CISI - Medical and Scientific Abstracts - 4000 doc, 11000 terms - k = 3 clusters

Accuracies for Med/Cran/CISI after dimension reduction to $r = 15$						
Algorithm	<u>r=15</u>	Consensus 1	Consensus 2	Consensus 3		
NMF Basic	0	0.96530455	0.95334439	0.96453354		
PDDP	0.83012079	0.94962735	0.94962735	0.96376253		
PDDP-kmeans	0.96376253	0.96530455	0.96530455	0.96453354		
SVDr-PDDP-kmeans	0.94500129	0.71652531	0.61783603	0.73477255		
un.SVDr-PDDP-kmeans	0.78026214	0.61578001	0.92572603	0.83320483		
H-PDDP	0.86096119	0.94962735	0.97044462	0.96376253		
H-PDDP-kmeans	0.97584169	0.96530455	0.96556155	0.96453354		
H-SVDk-PDDP-kmeans	0.86533025	0.96067849	0.95451041	0.96530455		
H-un.SVDk-PDDP-kmeans	0.60164482	0.96530455	0.96453354	0.96453354		

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- Documents pertain to 4 broad topics (banking/finance, programming, science, and sport)
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- Documents were extracted automatically from the web.
  - Some long detailed articles
  - Some just list of words, addresses, or links.
  - → Noisy Data!



#### Benchmark Data - subset BCFG - k = 4 clusters

#### Cluster Accuracies for BenchmarkBCFG after Dimension Reduction to r = 4

Algorithm	<u>r=4</u>	Consensus 1	Consensus 2	Consensus 3
NMF Basic	0.62725	0.69275	0.57725	0.69425
PDDP	0.4505	0.67775	0.69325	0.69425
PDDP-kmeans	0.34025	0.69325	0.69375	0.69425
SVDr-PDDP-kmeans	0.69825	0.549	0.51575	0.69425
un.SVDr-PDDP-kmeans	0.74725	0.69475	0.6945	0.69425
H-PDDP	0.582	0.67775	0.5665	0.69425
H-PDDP-kmeans	0.65775	0.69275	0.5745	0.69425
H-SVDk-PDDP-kmeans	0.66125	0.67075	0.695	0.69425
H-un.SVDk-PDDP-kmeans	0.6825	0.69475	0.57825	0.69425

#### Benchmark Data - subset BCFG-k = 4 clusters

#### Experiment 3: Cluster Accuracies for BenchmarkBCFG after Dimension Reduction to

Algorithm	r=10	r = 10 Consensus 1	Consensus 2	Consensus 3	Consensus 5
NMF Basic		0.74725	0.75225	0.58025	0.74775
PDDP	0.4505	0.74275	0.75125	0.74775	0.74775
PDDP-kmeans	0.34025	0.75275	0.748	0.75225	0.74775
SVDr-PDDP-kmeans un.SVDr-PDDP-kmeans	0.71975 0.67325	0.5945 0.703	0.49725 0.51575	0.6395 0.52225	0.72225 0.63225
H-PDDP	0.71	0.74275	0.752	0.74775	0.74775
H-PDDP-kmeans	0.7635	0.74725	0.75225	0.58025	0.74775
H-SVDk-PDDP-kmeans	0.7255	0.736	0.748	0.7455	0.76525
H-un.SVDk-PDDP-kmeans	0.788	0.74975	0.748	0.58	0.74775

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- The choices for the size of dimension reduction, r, and the various combinations
  of algorithms produce hundreds of clusterings for the consensus approach.
- Consensus Clustering shows potential as a technique to determine a final clustering solution through many different algorithms.
- Although the final clustering solution determined through Consensus Clustering is not guaranteed to be optimal, experiments suggest that the technique provides a solution that is well above the average of the algorithms used.