Data Mining and Matrices 06 – Non-Negative Matrix Factorization

Rainer Gemulla, Pauli Miettinen

May 23, 2013

Non-Negative Datasets

Some datasets are intrinsically non-negative:

- Counters (e.g., no. occurrences of each word in a text document)
- Quantities (e.g., amount of each ingredient in a chemical experiment)
- Intensities (e.g., intensity of each color in an image)

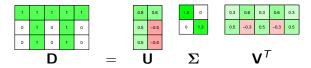
The corresponding data matrix ${\boldsymbol{\mathsf{D}}}$ has only non-negative values.

- Decompositions such as SVD and SDD may involve negative values in factors and components
- Negative values describe the absence of something
- Often no natural interpretation

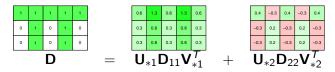
Can we find a decomposition that is more natural to non-negative data?

Example (SVD)

Consider the following "bridge" matrix and its truncated SVD:



Here are the corresponding components:



Negative values make interpretation unnatural or difficult.

Outline





3 Probabilistic Latent Semantic Analysis



Non-Negative Matrix Factorization (NMF)

Definition (Non-negative matrix factorization, basic form)

Given a non-negative matrix $\mathbf{D} \in \mathbb{R}^{m imes n}_+$, a non-negative matrix factorization of rank k is

 $\mathbf{D} \approx \mathbf{LR},$

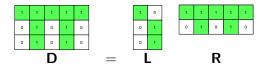
where $\mathbf{L} \in \mathbb{R}^{m \times r}_+$ and $\mathbf{R} \in \mathbb{R}^{r \times n}_+$ are both non-negative.

- \bullet Additive decomposition: factors and components non-negative \rightarrow No cancellation effects
- Rows of **R** can be thought as "parts"
- Row of **D** obtained by mixing (or "assembling") parts in **L**
- Smallest r such that D = LR exists is called *non-negative rank* of D

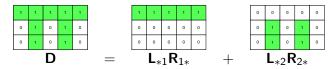
 $rank(\mathbf{D}) \leq rank_{+}(\mathbf{D}) \leq min \{ m, n \}$

Example (NMF)

Consider the following "bridge" matrix and its rank-2 NMF:



Here are the corresponding components:

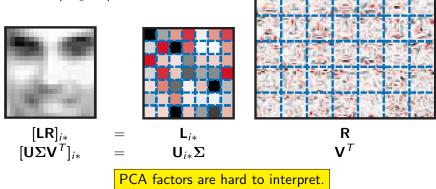


Non-negative matrix decomposition encourage a more natural, part-based representation and (sometimes) sparsity.

Decomposing faces (PCA)

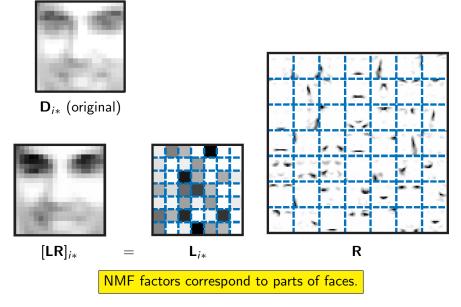


D_{*i**} (original)

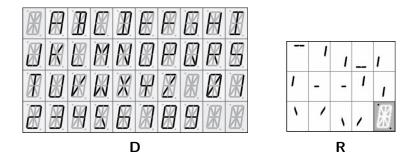


Lee and Seung, 1999.

Decomposing faces (NMF)



Decomposing digits (NMF)



NMF factors correspond to parts of digits and "background".

Some applications

- Text mining (more later)
- Bioinformatics
- Microarray analysis
- Mineral exploration
- Neuroscience
- Image understanding
- Air pollution research
- Chemometrics
- Spectral data analysis
- Linear sparse coding
- Image classification
- Clustering
- Neural learning process
- Sound recognition
- Remote sensing
- Object characterization

800 Original 10 sources (b) Typical 1000 mixtures

(c) Ten estimated components by using Fast-HALS

(d) PSNR using Beta HALS for various values of β

Figure 4.8 Illustration for (a) benchmark used in large-scale experiments with 10 nonnegative sources; (b) Typical 1000 mixtures; (c) Ten estimated components by using FAST HALS NMF from the observations matrix Y of dimension 1000 × 1000. (d) Performance expressed via the PSNR using the Beta HALS NMF algorithm for $\beta = 0.5, 1, 1.5, 2$ and 3.

• . .

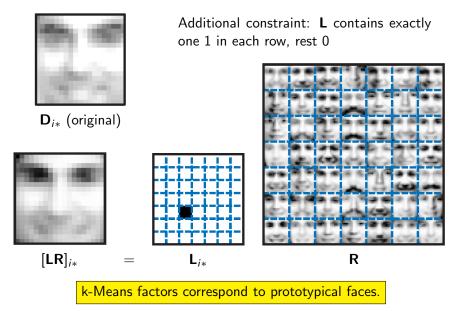
Gaussian NMF

• Gaussian NMF is the most basic form of non-negative factorizations:

$$\begin{array}{ll} \text{minimize} & \|\mathbf{D} - \mathbf{LR}\|_F^2\\ \text{s.t.} & \mathbf{L} \in \mathbb{R}_+^{m \times r}\\ & \mathbf{R} \in \mathbb{R}_+^{m \times n} \end{array}$$

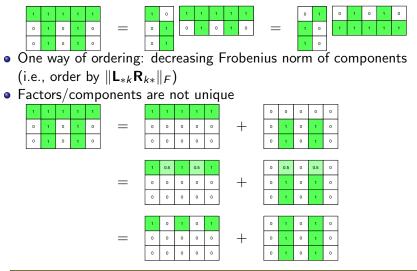
- Truncated SVD minimizes the same objective (but without non-negativity constraints)
- Many other variants exist
 - Different objective functions (e.g., KL-divergence)
 - ► Additional regularizations (e.g., *L*₁-regularization)
 - Different constraints (e.g., orthogonality of R)
 - Different compositions (e.g., 3 matrices)
 - multi-layer NMF, semi-NMF, sparse NMF, tri-NMF, symmetric NMF, orthogonal NMF, non-smooth NMF (nsNMF), overlapping NMF, convolutive NMF (CNMF), k-Means, ...

k-Means can be seen as a variant of NMF



NMF is not unique

• Factors are not "ordered"

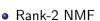


Additional constraints or regularization can encourage uniqueness.

NMF is not hierarchical

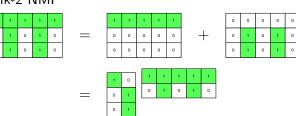
Rank-1 NMF





0

0



0.6

0.3 0.8 0.3

0.6

=

0.5

0.5

0.7

0.6

0.3

0.3 0.8 0.3 0.8 0.3

0.8

 \approx

- Best rank-k approximation may differ significantly from best rank-(k 1) approximation
- Rank influences sparsity, interpretability, and statistical fidelity
- Optimum choice of rank is not well-studied (often requires experimentation)

Outline

1 Non-Negative Matrix Factorization



3 Probabilistic Latent Semantic Analysis



NMF is difficult

We focus on minimizing $L(\mathbf{L}, \mathbf{R}) = \|\mathbf{D} - \mathbf{L}\mathbf{R}\|_{F}^{2}$.

- For varying *m*, *n*, and *r*, problem is NP-hard
- When rank(**D**) = 1 (or r = 1), can be solved in polynomial time
 - **1** Take first non-zero column of **D** as $L_{m \times 1}$
 - 2 Determine $\mathbf{R}_{1 \times n}$ entry by entry (using the fact that $\mathbf{D}_{*j} = \mathbf{L}\mathbf{R}_{1j}$)
- Problem is not convex
 - Local optimum may not correspond to global optimum
 - Generally little hope to find global optimum
- But: Problem is biconvex
 - For fixed **R**, $f(\mathbf{L}) = \|\mathbf{D} \mathbf{LR}\|_F^2$ is convex

$$\begin{split} f(\mathbf{L}) &= \sum_{i} \|\mathbf{D}_{i*} - \mathbf{L}_{i*} \mathbf{R}\|_{F}^{2} \qquad \text{(chain rule)} \\ \nabla_{\mathbf{L}_{ik}} f(\mathbf{L}) &= -2(\mathbf{D}_{i*} - \mathbf{L}_{i*} \mathbf{R}) \mathbf{R}_{k*}^{T} \qquad \text{(product rule)} \\ \nabla_{\mathbf{L}_{ik}}^{2} f(\mathbf{L}) &= 2\mathbf{R}_{k*} \mathbf{R}_{k*}^{T} \geq 0 \qquad \text{(does not depend on } \mathbf{L}) \end{split}$$

- For fixed L, $f(\mathbf{R}) = \|\mathbf{D} \mathbf{L}\mathbf{R}\|_F^2$ is convex
- Allows for efficient algorithms

General framework

- Gradient descent generally slow
- Stochastic gradient descent inappropriate
- Key approach: alternating minimization
 - 1: Pick starting point \boldsymbol{L}_0 and \boldsymbol{R}_0
 - 2: while not converged do
 - 3: Keep **R** fixed, optimize **L**
 - 4: Keep L fixed, optimize R
 - 5: end while
- Update steps 3 and 4 easier than full problem
- Also called alternating projections or (block) coordinate descent
- Starting point
 - Random
 - Multi-start initialization: try multiple random starting points, run a few epochs, continue with best
 - Based on SVD
 - ▶ ...

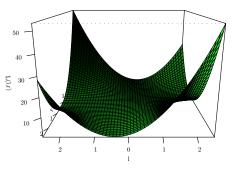
Example

Ignore non-negativity for now. Consider the regularized least-square error:

$$L(\mathbf{L}, \mathbf{R}) = \|\mathbf{D} - \mathbf{L}\mathbf{R}\|_F^2 + \lambda(\|\mathbf{L}\|_F^2 + \|\mathbf{R}\|_F^2)$$

By setting m = n = r = 1, $\mathbf{D} = (1)$ and $\lambda = 0.05$, we obtain

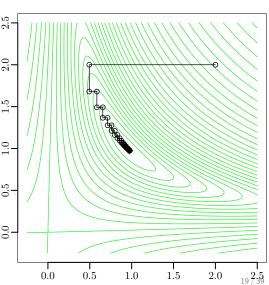
$$L(l, r) = (1 - lr)^2 + 0.05(l^2 + r^2)$$



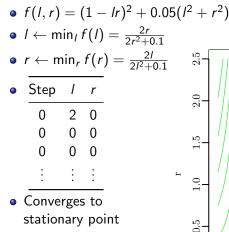
 $\begin{aligned} \nabla_{l} f(l) &= -2r(1-lr) + 0.1l \\ \nabla_{r} f(r) &= -2l(1-lr) + 0.1r \\ \text{Local optima:} \\ \left(\sqrt{\frac{19}{20}}, \sqrt{\frac{19}{20}}\right), \left(-\sqrt{\frac{19}{20}}, -\sqrt{\frac{19}{20}}\right) \\ \text{Stationary point:} (0,0) \end{aligned}$

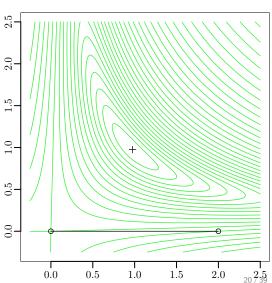
Example (ALS)

	$(r,r) = (1 - \min_l f(r))$			5(<i>1</i> ² -	$+ r^{2}$
	$-\min_r f$		1011	2.5	
• Ste	ep /	r	-	2.0	,
0	2	2	-	ç	1
1	0.49	2		LC.	
2	0.49	1.68		-	·٦ /
3	0.58	1.68		ы	/
4	0.58	1.49		1	÷- /
:	:	÷			/
10	0 0.97	0.97		0.5	;- /
• Co	nverges t	:0	-	_	
loc	al minim	um		0.0	5



Example (ALS)





Alternating non-negative least squares (ANLS)

• Uses non-negative least squares approximation of L and R:

$$\underset{\mathsf{L} \in \mathbb{R}^{m \times r}_{+}}{\operatorname{argmin}} \| \mathsf{D} - \mathsf{L} \mathsf{R} \|_{F}^{2} \quad \text{and} \quad \underset{\mathsf{R} \in \mathbb{R}^{r \times n}_{+}}{\operatorname{argmin}} \| \mathsf{D} - \mathsf{L} \mathsf{R} \|_{F}^{2}$$

- Equivalently: find non-negative least squares solution to LR = D
- Common approach: Solve unconstrained least squares problems and "remove" negative values. E.g., when columns (rows) of L (R) are linearly independent, set

$$\mathsf{L} = [\mathsf{D}\mathsf{R}^\dagger]_\epsilon$$
 and $\mathsf{R} = [\mathsf{L}^\dagger\mathsf{D}]_\epsilon$

where

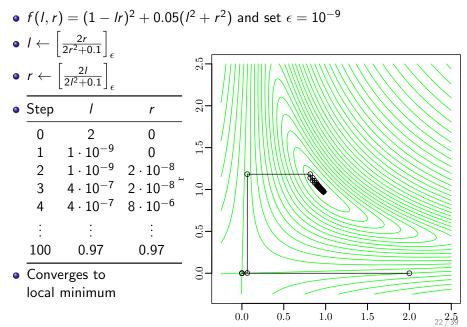
•
$$\mathbf{R}^{\dagger} = \mathbf{R}^{T} (\mathbf{R}\mathbf{R}^{T})^{-1}$$
 is the right pseudo-inverse of **R**

• $\mathbf{L}^{\dagger} = (\mathbf{L}^{T} \mathbf{L})^{-1} \mathbf{L}^{T}$ is the left pseudo-inverse of \mathbf{L}

• $[a]_{\epsilon} = \max\{\epsilon, a\}$ for $\epsilon = 0$ or some small constant (e.g., $\epsilon = 10^{-9}$)

- Difficult to analyze due to non-linear update steps
- Often slow convergence to a "bad" local minimum (better when regularized)

Example (ANLS)



Hierarchical alternating least squares (HALS)

- Work locally on a single factor, then proceed to next factor, and so on
- Let $\mathbf{D}^{(k)}$ be the residual matrix (error) when k-th factor is removed:

$$\mathbf{D}^{(k)} = \mathbf{D} - \mathbf{L}\mathbf{R} + \mathbf{L}_{*k}\mathbf{R}_{k*} = \mathbf{D} - \sum_{k' \neq k} \mathbf{L}_{*k'}\mathbf{R}_{k'*}$$

- HALS minimizes $\|\mathbf{D}^{(k)} \mathbf{L}_{*k}\mathbf{R}_{k*}\|_F^2$ for k = 1, 2, ..., r, 1, ...(equivalently: finds best solution for k-th factor, fixing the rest)
- In each iteration, set (once or multiple times):

$$\mathbf{L}_{*k} = \frac{1}{\|\mathbf{R}_{k*}\|_{F}^{2}} \begin{bmatrix} \mathbf{D}^{(k)} \mathbf{R}_{k*}^{T} \end{bmatrix}_{\epsilon} \text{ and } \mathbf{R}_{k*}^{T} = \frac{1}{\|\mathbf{L}_{*k}\|_{F}^{2}} \begin{bmatrix} (\mathbf{D}^{(k)})^{T} \mathbf{L}_{*k} \end{bmatrix}_{\epsilon}$$

• $\mathbf{D}^{(k)}$ can be incrementally maintained \rightarrow fast implementation $\mathbf{D}^{(k+1)} = \mathbf{D}^{(k)} + \mathbf{L}_{*k}\mathbf{R}_{k*} - \mathbf{L}_{*(k+1)}\mathbf{R}_{(k+1)*}$

- Often better performance in practice than ANLS
- Converges to stationary point when initialized with positive matrix and sufficiently small ϵ

Multiplicative updates

• Gradient descent step with step size η_{ki}

$$\mathbf{R}_{kj} \leftarrow \mathbf{R}_{kj} + \eta_{kj} ([\mathbf{L}^{\mathsf{T}} \mathbf{D}]_{kj} - [\mathbf{L}^{\mathsf{T}} \mathbf{L} \mathbf{R}]_{kj})$$

• Setting $\eta_{kj} = \frac{\mathbf{R}_{kj}}{(\mathbf{L}^T \mathbf{L} \mathbf{R})_{kj}}$, we obtain the multiplicative update rules

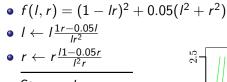
$$\mathbf{L} \leftarrow \mathbf{L} \circ \frac{\mathbf{DR}^{\,\prime}}{\mathbf{LRR}^{\,\mathcal{T}}} \quad \text{and} \quad \mathbf{R} \leftarrow \mathbf{R} \circ \frac{\mathbf{L}^{\,\prime} \, \mathbf{D}}{\mathbf{L}^{\,\mathcal{T}} \mathbf{LR}},$$

where multiplication (\circ) and division are element-wise

- \bullet Does not necessarily find optimum L (or R), but can be shown to never increase loss
- Faster than ANLS (no computation of pseudo-inverse), easy to implement and parallelize
- Zeros in factors are problematic (divisions become undefined)

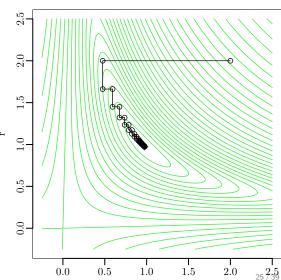
$$\mathbf{L} \leftarrow \mathbf{L} \circ \frac{[\mathbf{DR}^T]_{\epsilon}}{\mathbf{LRR}^T + \epsilon} \quad \text{and} \quad \mathbf{R} \leftarrow \mathbf{R} \circ \frac{[\mathbf{L}^T \mathbf{D}]_{\epsilon}}{\mathbf{L}^T \mathbf{LR} + \epsilon}$$

Example (multiplicative updates)



٩	Step	1	r
	0	2	2
	1	0.48	2
	2	0.48	1.66
	3	0.59	1.66
	4	0.58	1.45
	÷	÷	÷
	100	0.97	0.97

• Converges to local minimum



Outline

1 Non-Negative Matrix Factorization







Topic modeling

• Consider a document-word matrix constructed from some corpus

		air	water	pollution	democrat	republican
	doc 1	(3	2	8	0	0)
	doc 2	1	4	12	0	0
$\tilde{D} =$	$\operatorname{doc} 3$	0	0	0	10	11
	$\operatorname{doc} 4$	0	0	0	8	5
	$\begin{array}{c} \mathrm{doc}\ 1\\ \mathrm{doc}\ 2\\ \mathrm{doc}\ 3\\ \mathrm{doc}\ 4\\ \mathrm{doc}\ 5 \end{array}$	$\setminus 1$	1	1	1	1 /

- Documents seem to talk about two "topics"
 - Environment (with words air, water, and pollution)
 - Ongress (with words democrat and republican)

Can we automatically detect topics in documents?

A probabilistic viewpoint

• Let's normalize such that the entries sum to unity

		air	water	pollution	democrat	republican
	doc 1	/ 0.04	0.03	0.12	0.00	0.00
	doc 2 $$	0.01	0.06	0.12 0.17 0.00	0.00	0.00
$\mathbf{D} =$	$\operatorname{doc} 3$	0.00	0.00	0.00	0.14	0.16
	$\operatorname{doc} 4$	0.00	0.00	0.00 0.01	0.12	0.07
	doc 5	0.01	0.01	0.01	0.01	0.015 /

• Put all words in an urn and draw. The probability to draw word *w* from document *d* is given by

 $P(d, w) = \mathbf{D}_{dw}$

- Matrix **D** can represent any probability distribution
- pLSA tries to find a distribution that is "close" to **D** but exposes information about topics

Probabilistic latent semantic analysis (pLSA)

Definition (pLSA, NMF formulation)

Given a rank r, find matrices L, Σ , and R such that

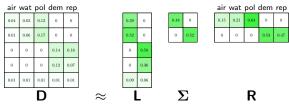
$\textbf{D}\approx\textbf{L}\boldsymbol{\Sigma}\textbf{R}$

where

- L_{m×r} is a non-negative, column-stochastic matrix (columns sum to unity),
- $\Sigma_{r imes r}$ is a non-negative, diagonal matrix that sums to unity, and
- $\mathbf{R}_{r \times n}$ is a non-negative, row-stochastic matrix (rows sum to unity).
- $\, \bullet \, \approx$ is usually taken to be the (generalized) KL divergence
- Additional regularization or tempering necessary to avoid overfitting

Example

• pLSA factorization of example matrix



- Rank r corresponds to number of topics
- Σ_{kk} corresponds to overall frequency of topic k
- L_{dk} corresponds to contribution of document d to topic k
- \mathbf{R}_{kw} corresponds to frequency of word w in topic k
- pLSA constraints allow for probabilistic interpretation $P(d, w) \approx [L\Sigma R]_{dw} = \sum_{k} \Sigma_{kk} L_{dk} R_{kw} = \sum_{k} P(k) P(d \mid k) P(w \mid k)$
- pLSA model imposes conditional independence constraints
 → restricted space of distributions

Another example

Concepts (10 of 128) extracted from Science Magazine articles (12K)

universe	0.0439	drug	0.0672	cells	0.0675	sequence	0.0818	years	0.156
galaxies	0.0375	patients	0.0493	stem	0.0478	sequences	0.0493	million	0.0556
clusters	0.0279	drugs	0.0444	human	0.0421	genome	0.033	ago	0.045
matter	0.0233	clinical	0.0346	cell	0.0309	dna	0.0257	time	0.0317
galaxy	0.0232	treatment	0.028	gene	0.025	sequencing	0.0172	age	0.0243
cluster	0.0214	trials	0.0277	tissue	0.0185	map	0.0123	year	0.024
cosmic	0.0137	therapy	0.0213	cloning	0.0169	genes	0.0122	record	0.0238
dark	0.0131	trial	0.0164	transfer	0.0155	chromosome	0.0119	early	0.0233
light	0.0109	disease	0.0157	blood	0.0113	regions	0.0119	billion	0.0177
density	0.01	medical	0.00997	embryos	0.0111	human	0.0111	history	0.0148
bacteria	0.0983	male	0.0558	theory	0.0811	immune	0.0909	stars	0.0524
bacterial	0.0561	females	0.0541	physics	0.0782	response	0.0375	star	0.0458
resistance	0.0431	female	0.0529	physicists	0.0146	system	0.0358	astrophys	0.0237
coli	0.0381	males	0.0477	einstein	0.0142	responses	0.0322	mass	0.021
strains	0.025	sex	0.0339	university	0.013	antigen	0.0263	disk	0.0173
microbiol	0.0214	reproductive	0.0172	gravity	0.013	antigens	0.0184	black.	0.0161
microbial	0.0196	offspring	0.0168	black	0.0127	immunity	0.0176	gas	0.0149
strain	0.0165	sexual	0.0166	theories	0.01	immunology	0.0145	stellar	0.0127
salmonella	0.0163	reproduction	0.0143	aps	0.00987	antibody	0.014	astron	0.0125
resistant	0.0145	eggs	0.0138	matter	0.00954	autoimmune	0.0128	hole	0.00824
	galaxies clusters matter galaxy cluster cosmic dark light density bacteria bacteria bacterial resistance coli strains microbiol microbiol strain salmonella	galaxies 0.0375 clusters 0.0279 matter 0.0232 galaxy 0.0232 cluster 0.0214 cosmic 0.0137 dark 0.0131 light 0.0109 density 0.01 bacteria 0.0983 bacteria 0.0561 resistance 0.0431 coli 0.0321 strains 0.0214 microbial 0.0196 strain 0.0109	galaxies 0.0375 galaxies 0.0375 galaxies 0.0279 drugs drugs matter 0.0232 treatment trials clusters 0.0137 therapy trials cosmic 0.0137 therapy trial dark 0.0131 light 0.0199 density 0.01 bacteria 0.0983 bacteria 0.0983 bacteria 0.0561 females coli 0.0311 fiemale sexx microbiol 0.0214 reproductive microbial microbial 0.0165 sexual sexual	anistation 0.0375 patients 0.0493 galaxies 0.0374 drugs 0.0493 clusters 0.0279 drugs 0.0444 matter 0.0233 clinical 0.0346 galaxy 0.0234 treatment 0.028 clusters 0.0214 trials 0.0277 cosmic 0.0137 therapy 0.0213 dark 0.0137 therapy 0.0213 dark 0.0131 trial 0.0164 light 0.0109 disease 0.0157 density 0.01 male 0.0588 bacteria 0.0561 females 0.0541 resistance 0.0431 females 0.0477 strains 0.025 sex 0.0339 microbial 0.0124 reproductive 0.0172 microbial 0.0165 sexual 0.0166 salmonella 0.0165 reproductive 0.0166 <th>antex 0.0375 patients 0.0493 stem galaxies 0.0375 patients 0.0493 stem clusters 0.0279 drugs 0.0444 human matter 0.0232 clnical 0.0346 cell galaxy 0.0232 treatment 0.028 gene cluster 0.0214 trials 0.0277 tissue cosmic 0.0137 therapy 0.0213 cloring dark 0.0131 trial 0.0164 transfer hght 0.0109 disease 0.0157 blood density 0.01 medical 0.0997 embryos bacteria 0.0561 females 0.0541 physicists coli 0.0381 males 0.0477 einstein strains 0.025 sex 0.0339 university microbiol 0.0214 reproductive 0.0172 gravity microbial 0.0165 sexual<!--</th--><th>andress 0.0375 patients 0.0493 stem 0.0478 clusters 0.0279 drugs 0.0444 human 0.0421 matter 0.0232 clnical 0.0346 cell 0.0309 galaxy 0.0232 treatment 0.028 gene 0.025 cluster 0.0214 trials 0.0277 tissue 0.0185 cosmic 0.0137 therapy 0.0213 cloning 0.0169 dark 0.0131 trial 0.0164 transfer 0.0155 light 0.0109 disease 0.0157 blood 0.0113 density 0.01 medical 0.00997 embryos 0.0111 bacteria 0.0561 females 0.0541 physics 0.0782 resistance 0.0431 female 0.0529 university 0.013 microbiol 0.0214 reproductive 0.0172 gravity 0.013 microbial 0.0196</th><th>ministre 0.0375 patients 0.0493 stem 0.0478 sequences galaxies 0.0375 patients 0.0493 stem 0.0478 sequences matter 0.0233 clinical 0.0346 cell 0.0309 dna galaxy 0.0233 clinical 0.0346 cell 0.0309 dna galaxy 0.0232 treatment 0.028 gene 0.025 sequences cluster 0.0137 therapy 0.0213 cloning 0.0169 genes cosmic 0.0137 therapy 0.0213 cloning 0.0169 genes dark 0.0131 trial 0.0164 transfer 0.0155 chromosome hght 0.0109 disease 0.0157 blood 0.0111 immune bacteria 0.0561 females 0.0541 physics 0.0782 response resistance 0.0431 female 0.0529 physicist 0.0146<th>minist 0.0937 patients 0.0493 stem 0.0478 sequences 0.0493 galaxies 0.0375 patients 0.0493 stem 0.0478 sequences 0.0493 galaxies 0.0279 drugs 0.0444 human 0.0421 genome 0.033 galaxy 0.0232 tireatment 0.028 gene 0.025 sequences 0.0473 galaxy 0.0232 treatment 0.028 gene 0.025 sequencing 0.0172 cluster 0.0137 therapy 0.0213 cloning 0.0169 genes 0.0123 dark 0.0131 trial 0.0164 transfer 0.0155 chromosome 0.0119 dark 0.019 disease 0.0577 blood 0.0113 regions 0.0119 bacteria 0.0983 male 0.0584 fheory 0.0811 immune 0.0909 resistance 0.0431 female 0.0529 physicis</th><th>ministre 0.0473 ister 0.0473 sequences 0.0493 milion galaxies 0.0375 patients 0.0493 stern 0.0474 sequences 0.0493 ago matter 0.0232 clinical 0.0346 cell 0.0309 dna 0.0257 time galaxy 0.0232 treatment 0.028 gene 0.025 sequencing 0.0172 age cluster 0.0214 trials 0.0277 tissue 0.0185 map 0.0123 year cosmic 0.0137 therapy 0.0213 cloning 0.0169 genes 0.0122 record dark 0.013 trial 0.0164 transfer 0.0155 chromosome 0.0119 early hght 0.0109 disease 0.0157 blood 0.0111 human 0.0111 hustory bacteria 0.0561 females 0.0541 physics 0.0782 response 0.0375</th></th></th>	antex 0.0375 patients 0.0493 stem galaxies 0.0375 patients 0.0493 stem clusters 0.0279 drugs 0.0444 human matter 0.0232 clnical 0.0346 cell galaxy 0.0232 treatment 0.028 gene cluster 0.0214 trials 0.0277 tissue cosmic 0.0137 therapy 0.0213 cloring dark 0.0131 trial 0.0164 transfer hght 0.0109 disease 0.0157 blood density 0.01 medical 0.0997 embryos bacteria 0.0561 females 0.0541 physicists coli 0.0381 males 0.0477 einstein strains 0.025 sex 0.0339 university microbiol 0.0214 reproductive 0.0172 gravity microbial 0.0165 sexual </th <th>andress 0.0375 patients 0.0493 stem 0.0478 clusters 0.0279 drugs 0.0444 human 0.0421 matter 0.0232 clnical 0.0346 cell 0.0309 galaxy 0.0232 treatment 0.028 gene 0.025 cluster 0.0214 trials 0.0277 tissue 0.0185 cosmic 0.0137 therapy 0.0213 cloning 0.0169 dark 0.0131 trial 0.0164 transfer 0.0155 light 0.0109 disease 0.0157 blood 0.0113 density 0.01 medical 0.00997 embryos 0.0111 bacteria 0.0561 females 0.0541 physics 0.0782 resistance 0.0431 female 0.0529 university 0.013 microbiol 0.0214 reproductive 0.0172 gravity 0.013 microbial 0.0196</th> <th>ministre 0.0375 patients 0.0493 stem 0.0478 sequences galaxies 0.0375 patients 0.0493 stem 0.0478 sequences matter 0.0233 clinical 0.0346 cell 0.0309 dna galaxy 0.0233 clinical 0.0346 cell 0.0309 dna galaxy 0.0232 treatment 0.028 gene 0.025 sequences cluster 0.0137 therapy 0.0213 cloning 0.0169 genes cosmic 0.0137 therapy 0.0213 cloning 0.0169 genes dark 0.0131 trial 0.0164 transfer 0.0155 chromosome hght 0.0109 disease 0.0157 blood 0.0111 immune bacteria 0.0561 females 0.0541 physics 0.0782 response resistance 0.0431 female 0.0529 physicist 0.0146<th>minist 0.0937 patients 0.0493 stem 0.0478 sequences 0.0493 galaxies 0.0375 patients 0.0493 stem 0.0478 sequences 0.0493 galaxies 0.0279 drugs 0.0444 human 0.0421 genome 0.033 galaxy 0.0232 tireatment 0.028 gene 0.025 sequences 0.0473 galaxy 0.0232 treatment 0.028 gene 0.025 sequencing 0.0172 cluster 0.0137 therapy 0.0213 cloning 0.0169 genes 0.0123 dark 0.0131 trial 0.0164 transfer 0.0155 chromosome 0.0119 dark 0.019 disease 0.0577 blood 0.0113 regions 0.0119 bacteria 0.0983 male 0.0584 fheory 0.0811 immune 0.0909 resistance 0.0431 female 0.0529 physicis</th><th>ministre 0.0473 ister 0.0473 sequences 0.0493 milion galaxies 0.0375 patients 0.0493 stern 0.0474 sequences 0.0493 ago matter 0.0232 clinical 0.0346 cell 0.0309 dna 0.0257 time galaxy 0.0232 treatment 0.028 gene 0.025 sequencing 0.0172 age cluster 0.0214 trials 0.0277 tissue 0.0185 map 0.0123 year cosmic 0.0137 therapy 0.0213 cloning 0.0169 genes 0.0122 record dark 0.013 trial 0.0164 transfer 0.0155 chromosome 0.0119 early hght 0.0109 disease 0.0157 blood 0.0111 human 0.0111 hustory bacteria 0.0561 females 0.0541 physics 0.0782 response 0.0375</th></th>	andress 0.0375 patients 0.0493 stem 0.0478 clusters 0.0279 drugs 0.0444 human 0.0421 matter 0.0232 clnical 0.0346 cell 0.0309 galaxy 0.0232 treatment 0.028 gene 0.025 cluster 0.0214 trials 0.0277 tissue 0.0185 cosmic 0.0137 therapy 0.0213 cloning 0.0169 dark 0.0131 trial 0.0164 transfer 0.0155 light 0.0109 disease 0.0157 blood 0.0113 density 0.01 medical 0.00997 embryos 0.0111 bacteria 0.0561 females 0.0541 physics 0.0782 resistance 0.0431 female 0.0529 university 0.013 microbiol 0.0214 reproductive 0.0172 gravity 0.013 microbial 0.0196	ministre 0.0375 patients 0.0493 stem 0.0478 sequences galaxies 0.0375 patients 0.0493 stem 0.0478 sequences matter 0.0233 clinical 0.0346 cell 0.0309 dna galaxy 0.0233 clinical 0.0346 cell 0.0309 dna galaxy 0.0232 treatment 0.028 gene 0.025 sequences cluster 0.0137 therapy 0.0213 cloning 0.0169 genes cosmic 0.0137 therapy 0.0213 cloning 0.0169 genes dark 0.0131 trial 0.0164 transfer 0.0155 chromosome hght 0.0109 disease 0.0157 blood 0.0111 immune bacteria 0.0561 females 0.0541 physics 0.0782 response resistance 0.0431 female 0.0529 physicist 0.0146 <th>minist 0.0937 patients 0.0493 stem 0.0478 sequences 0.0493 galaxies 0.0375 patients 0.0493 stem 0.0478 sequences 0.0493 galaxies 0.0279 drugs 0.0444 human 0.0421 genome 0.033 galaxy 0.0232 tireatment 0.028 gene 0.025 sequences 0.0473 galaxy 0.0232 treatment 0.028 gene 0.025 sequencing 0.0172 cluster 0.0137 therapy 0.0213 cloning 0.0169 genes 0.0123 dark 0.0131 trial 0.0164 transfer 0.0155 chromosome 0.0119 dark 0.019 disease 0.0577 blood 0.0113 regions 0.0119 bacteria 0.0983 male 0.0584 fheory 0.0811 immune 0.0909 resistance 0.0431 female 0.0529 physicis</th> <th>ministre 0.0473 ister 0.0473 sequences 0.0493 milion galaxies 0.0375 patients 0.0493 stern 0.0474 sequences 0.0493 ago matter 0.0232 clinical 0.0346 cell 0.0309 dna 0.0257 time galaxy 0.0232 treatment 0.028 gene 0.025 sequencing 0.0172 age cluster 0.0214 trials 0.0277 tissue 0.0185 map 0.0123 year cosmic 0.0137 therapy 0.0213 cloning 0.0169 genes 0.0122 record dark 0.013 trial 0.0164 transfer 0.0155 chromosome 0.0119 early hght 0.0109 disease 0.0157 blood 0.0111 human 0.0111 hustory bacteria 0.0561 females 0.0541 physics 0.0782 response 0.0375</th>	minist 0.0937 patients 0.0493 stem 0.0478 sequences 0.0493 galaxies 0.0375 patients 0.0493 stem 0.0478 sequences 0.0493 galaxies 0.0279 drugs 0.0444 human 0.0421 genome 0.033 galaxy 0.0232 tireatment 0.028 gene 0.025 sequences 0.0473 galaxy 0.0232 treatment 0.028 gene 0.025 sequencing 0.0172 cluster 0.0137 therapy 0.0213 cloning 0.0169 genes 0.0123 dark 0.0131 trial 0.0164 transfer 0.0155 chromosome 0.0119 dark 0.019 disease 0.0577 blood 0.0113 regions 0.0119 bacteria 0.0983 male 0.0584 fheory 0.0811 immune 0.0909 resistance 0.0431 female 0.0529 physicis	ministre 0.0473 ister 0.0473 sequences 0.0493 milion galaxies 0.0375 patients 0.0493 stern 0.0474 sequences 0.0493 ago matter 0.0232 clinical 0.0346 cell 0.0309 dna 0.0257 time galaxy 0.0232 treatment 0.028 gene 0.025 sequencing 0.0172 age cluster 0.0214 trials 0.0277 tissue 0.0185 map 0.0123 year cosmic 0.0137 therapy 0.0213 cloning 0.0169 genes 0.0122 record dark 0.013 trial 0.0164 transfer 0.0155 chromosome 0.0119 early hght 0.0109 disease 0.0157 blood 0.0111 human 0.0111 hustory bacteria 0.0561 females 0.0541 physics 0.0782 response 0.0375

pLSA geometry

• Rewrite probabilistic formulation

$$P(d, w) = \sum_{k} P(k)P(d \mid k)P(w \mid k)$$
$$P(w \mid d) = \sum_{z} P(w \mid z)P(z \mid d)$$

- Generative process of creating a word
 - Pick a document according to P(d)
 - Select a topic acc. to P(z | d)
 - Select a word acc. to P(w | z)

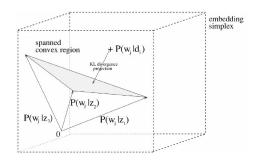


Figure 2. Sketch of the probability simplex and a convex region spanned by class-conditional probabilities in the aspect model.

Kullback-Leibler divergence (1)

- Let $\tilde{\mathbf{D}}$ be the unnormalized word-count data and denote by N total number of words
- Likelihood of seeing **D** when drawing *N* words with replacement is proportional to

$$\prod_{d=1}^{m}\prod_{w=1}^{n}P(d,w)^{\tilde{\mathsf{D}}_{dw}}$$

• pLSA maximizes the log-likelihood of seeing the data given the model

$$\log P(\tilde{\mathbf{D}} \mid \mathbf{L}, \mathbf{\Sigma}, \mathbf{R}) \propto \sum_{d=1}^{m} \sum_{w=1}^{n} \tilde{\mathbf{D}}_{dw} \log P(d, w \mid \mathbf{L}, \mathbf{\Sigma}, \mathbf{R})$$
$$\propto -\sum_{d=1}^{m} \sum_{w=1}^{n} \mathbf{D} \log \frac{1}{[\mathbf{L} \mathbf{\Sigma} \mathbf{R}]_{dw}}$$
$$= -\sum_{d=1}^{m} \sum_{w=1}^{n} \mathbf{D}_{dw} \log \frac{\mathbf{D}_{dw}}{[\mathbf{L} \mathbf{\Sigma} \mathbf{R}]_{dw}} + c_{\mathbf{D}}$$
Gaussier and Goutte, 2005. Kullback-Leibler divergence

33 / 39

Kullback-Leibler divergence (2)

• KL divergence

$$D_{KL}(\mathbf{P} \| \mathbf{Q}) = \sum_{d=1}^{m} \sum_{w=1}^{n} \mathbf{P}_{dw} \log \frac{\mathbf{P}_{dw}}{\mathbf{Q}_{dw}}$$

- Interpretation: expected number of extra bits for encoding a value drawn from ${\bf P}$ using an optimum code for distribution ${\bf Q}$
- $D_{KL}(\mathbf{P} \| \mathbf{Q}) \geq 0$
- $D_{KL}(\mathbf{P} \| \mathbf{P}) = 0$
- $D_{KL}(\mathbf{P} \| \mathbf{Q}) \neq D_{KL}(\mathbf{Q} \| \mathbf{P})$
- NMF-based pLSA algorithms minimize the generalized KL divergence

$$D_{GKL}(\tilde{\mathbf{P}} \| \tilde{\mathbf{Q}}) = \sum_{d=1}^{m} \sum_{w=1}^{n} (\tilde{\mathbf{P}}_{dw} \log \frac{\tilde{\mathbf{P}}_{dw}}{\tilde{\mathbf{Q}}_{dw}} - \tilde{\mathbf{P}}_{dw} + \tilde{\mathbf{Q}}_{dw}),$$

where $\tilde{\textbf{P}}=\tilde{\textbf{D}}$ and $\tilde{\textbf{Q}}=\textbf{L}\tilde{\boldsymbol{\Sigma}}\textbf{R}$

Multiplicative updates for GKL (w/o tempering)

- \bullet We first find a decomposition $\tilde{D}\approx\tilde{L}\tilde{R},$ where \tilde{L} and \tilde{R} are non-negative matrices
- Update rules

$$\begin{split} \tilde{\mathbf{L}} &\leftarrow \tilde{\mathbf{L}} \circ \frac{\tilde{\mathbf{D}}}{\tilde{\mathbf{L}}\tilde{\mathsf{R}}} \tilde{\mathsf{R}}^{\mathcal{T}} \operatorname{diag}(1/\operatorname{rowSums}(\tilde{\mathsf{R}})) \\ \tilde{\mathsf{R}} &\leftarrow \tilde{\mathsf{R}} \circ \operatorname{diag}(1/\operatorname{colSums}(\tilde{\mathsf{L}})) \tilde{\mathsf{L}}^{\mathcal{T}} \frac{\tilde{\mathsf{D}}}{\tilde{\mathsf{L}}\tilde{\mathsf{R}}} \end{split}$$

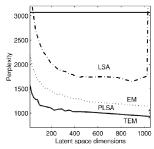
- GKL is non-increasing under these update rules
- \bullet Normalize by rescaling columns of \tilde{L} and rows of \tilde{R} to obtain

$$\begin{split} \mathbf{L} &= \tilde{\mathbf{L}} \operatorname{diag}(1/\operatorname{colSums}(\tilde{\mathbf{L}})) \\ \mathbf{R} &= \operatorname{diag}(1/\operatorname{rowSums}(\tilde{\mathbf{R}}))\tilde{\mathbf{R}} \\ \tilde{\boldsymbol{\Sigma}} &= \operatorname{diag}(\operatorname{colSums}(\tilde{\mathbf{L}}) \circ \operatorname{rowSums}(\tilde{\mathbf{R}})) \\ \mathbf{\Sigma} &= \tilde{\boldsymbol{\Sigma}} / \sum_{k} \tilde{\boldsymbol{\Sigma}}_{kk} \end{split}$$

Lee and Seung, 2001.

Applications of pLSA

- Topic modeling
- Clustering documents
- Clustering terms
- Information retrieval
 - Treat query q as a "new" document (new row in $\tilde{\mathbf{D}}$ and \mathbf{L})
 - Determine $P(k \mid q)$ by keeping Σ and **R** fixed ("fold in" the query)
 - Retrieve documents with similar topic mixture as query
 - Can deal with synonymy and polysemy
- Better generalization performance than LSA (=SVD), esp. with tempering
- In practice, outperformed by Latent Dirichlet Allocation (LDA)



Outline

1 Non-Negative Matrix Factorization



3 Probabilistic Latent Semantic Analysis



Lessons learned

- Non-negative matrix factorization (NMF) appears natural for non-negative data
- NMF encourages parts-based decomposition, interpretability, and (sometimes) sparseness
- Many variants, many applications
- Usually solved via alternating minimization algorithms
 - Alternating non-negative least squares (ANLS)
 - Projected gradient local hierarchical ALS (HALS)
 - Multiplicative updates
- pLSA is an approach to topic modeling that can be seen as an NMF

Literature

David Skillicorn

Understanding Complex Datasets: Data Mining with Matrix Decompositions (Chapter 8) Chapman and Hall, 2007

- Andrzej Cichocki, Rafal Zdunek, Anh Huy Phan, and Shun-ichi Amari Nonnegative Matrix and Tensor Factorizations: Applications to Exploratory Multi-way Data Analysis and Blind Source Separation Wiley, 2009
- Yifeng Li and Alioune Ngom The NMF MATLAB Toolbox http://cs.uwindsor.ca/~li11112c/nmf
- Renaud Gaujoux and Cathal Seoighe
 NMF R package
 http://cran.r-project.org/web/packages/NMF/index.html
- References given at bottom of slides