

Recommender Systems

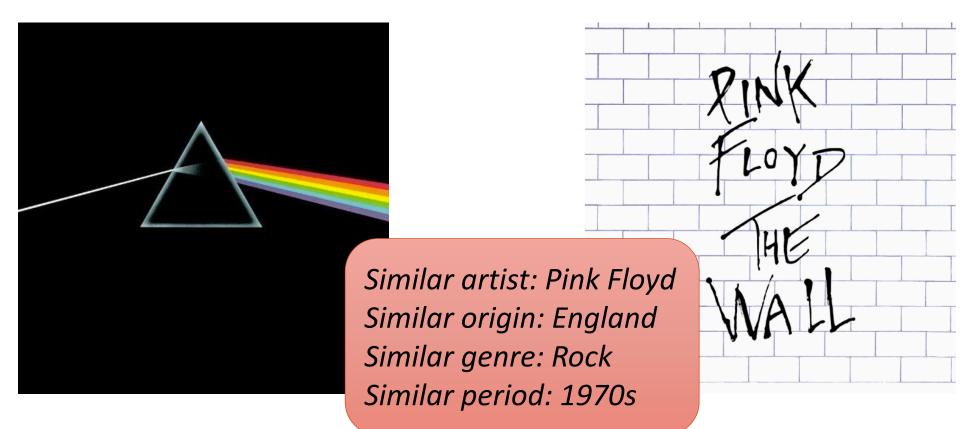
Topic Modeling

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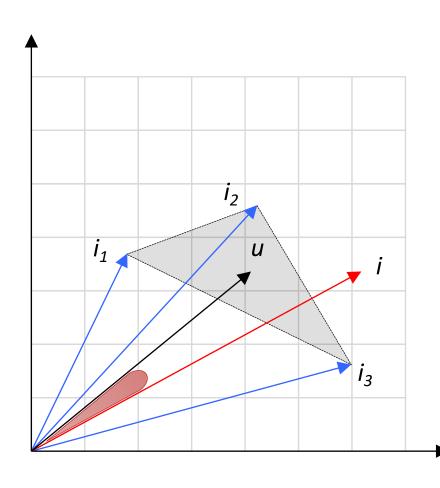
Content-based recommendation

You bought

You may like



Vector space representation



Each item is a vector

 One component for each term in the vocabulary

Each user is a vector

Some combination of item vectors

Prediction by similarity

 Cosine of the angle between the user and item vectors

The curse of dimensionality

The space of terms is very **high-dimensional!**

Problems

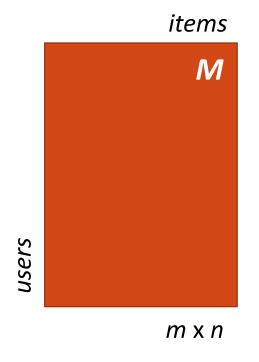
- Efficiency: it will take longer to compute similarities
- Effectiveness: it will be harder to match similar concepts

Google Web N-grams [Franz and Brants, 2006]

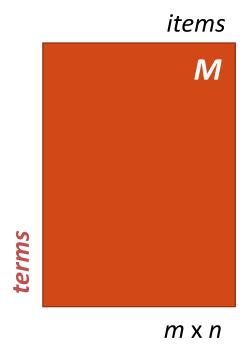
# tokens	1,024,908,267,229
# sentences	95,119,665,584
# 1-grams	13,588,391
# 2-grams	314,843,401
# 3-grams	977,069,902
# 4-grams	1,313,818,354
# 5-grams	1,176,470,663

The curse of dimensionality

Collaborative filtering

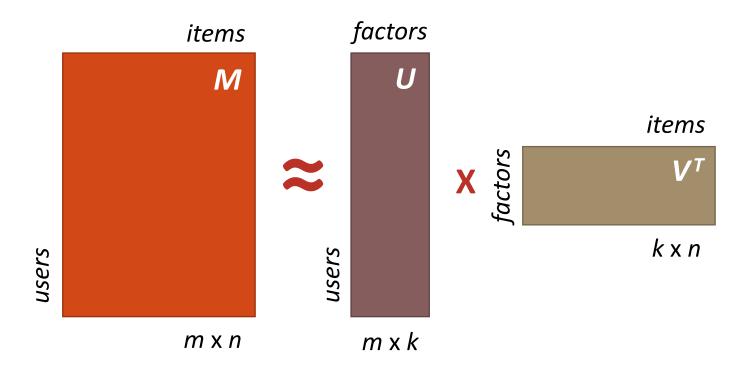


Content-based filtering



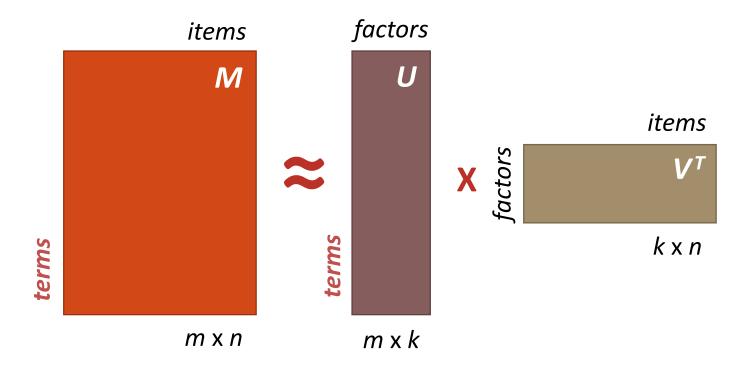
Latent semantic analysis

Collaborative filtering



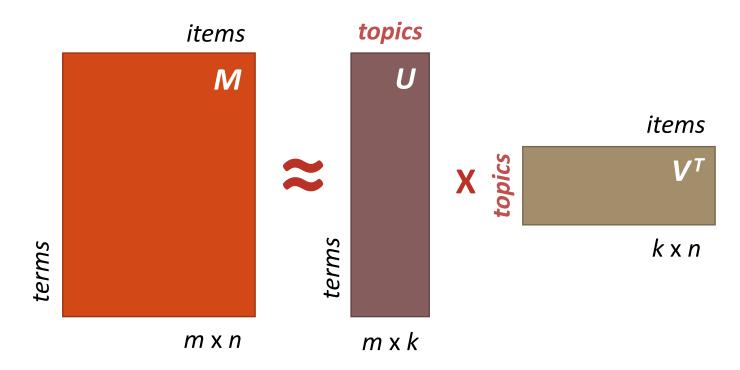
Latent semantic analysis

Content-based filtering



Latent topic modeling

Content-based filtering



Dimensionality reduction

TF-IDF [Luhn, IBM J. R&D 1957; Sparck-Jones, J. Doc. 1972; Salton and Buckley, IP&M 1988]

LSI [Deerwester et al., ASIS 1988]

pLSI [Hofmann, SIGIR 1999]

LDA [Blei et al., JMLR 2003]

Latent Dirichlet allocation (LDA)



"Imagine searching and exploring documents based on the themes that run through them.
[...] we might first find the theme that we are interested in, and then examine the documents related to that theme."

Blei, CACM 2012

Seeking Life's Bare (Genetic) Necessities

Haemophilus

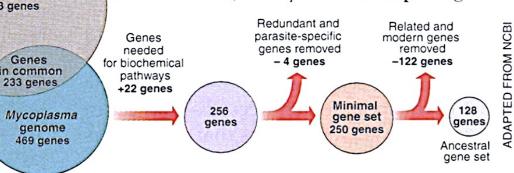
genome 1703 genes

Genes

COLD SPRING HARBOR, NEW YORK— How many genes does an organism need to survive? Last week at the genome meeting here,* two genome researchers with radically different approaches presented complementary views of the basic genes needed for life. One research team, using computer analyses to compare known genomes, concluded that today's organisms can be sustained with just 250 genes, and that the earliest life forms

required a mere 128 genes. The other researcher mapped genes in a simple parasite and estimated that for this organism, 800 genes are plenty to do the job—but that anything short of 100 wouldn't be enough.

Although the numbers don't match precisely, those predictions Arcady Mushegian, a computational molecular biologist at the National Center for Biotechnology Information (NCBI) in Bethesda, Maryland. Comparing an



Stripping down. Computer analysis yields an estimate of the minimum modern and ancient genomes.

[&]quot;are not all that far apart," especially 50 comparison to the 75,000 genes in the human genome, notes Siv Andersson of Uppsala University in Sweden, who arrived at the 800 number. But coming up with a consensus answer may be more than just a genetic numbers game, particularly as more and more genomes are completely mapped and sequenced. "It may be a way of organizing any newly sequenced genome," explains

^{*} Genome Mapping and Sequencing, Cold Spring Harbor, New York, May 8 to 12.

Latent topics

human	evolution	disease	computer
genome	evolutionary	host	models
dna	species	bacteria	information
genetic	organisms	diseases	data
genes	life	resistance	computers
sequence	origin	bacterial	system
gene	biology	new	network
molecular	groups	strains	systems
sequencing	phylogenetic	control	model
map	living	infectious	parallel
information	diversity	malaria	methods
genetics	group	parasite	networks
mapping	new	parasites	software
project	two	united	new
sequences	common	tuberculosis	simulations
"genetics"	"evolution"	"disease"	"computers"

Say you want a document with n words

- Assume there are k known topics
- Choose the document's distribution over topics
- \circ For each of the n words to be generated
 - Choose a topic from the document's topic distribution
 - Choose a word from the chosen topic

Generating *n* words

- Choose the document's topic distribution
- For each of the n words to be generated
 - Choose a topic from the document's distribution
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50% genetics 30% evolution 15% disease 5% computers

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50% genetics 30% evolution 15% disease 5% computers

"evolution"

evolution evolutionary species organisms life origin

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origin

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50% genetics 30% evolution 15% disease 5% computers

"genetics"

human genome dna genetic genes sequence

origin

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50% genetics 30% evolution 15% disease 5% computers

"computers"

computer models information data computers system

origin human

Generating *n* words

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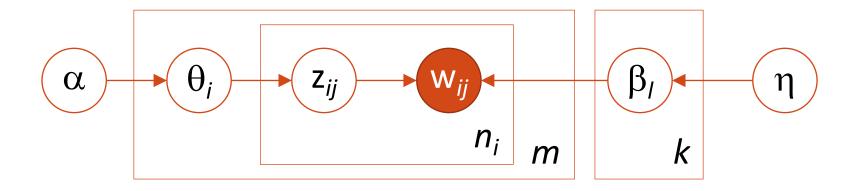
50% genetics 30% evolution 15% disease 5% computers

"computers"

computer models information data computers system

origin human models

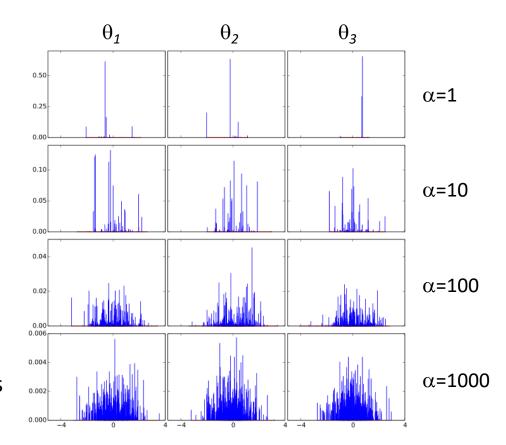
In plate notation



- θ_i : topic distribution of document *i* (of *m* documents)
 - α : parameter of the Dirichlet prior
- β_l : word distribution of topic *l* (of *k* topics)
 - η: parameter of the Dirichlet prior
- w_{ij} : j-th word in document i (with n_i words)
- z_{ij} : chosen topic of word w_{ij}

Dirichlet distribution

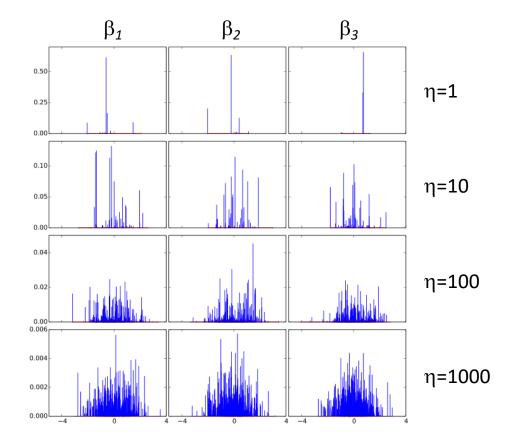
A "distribution of distributions" with concentration parameter α



Document models as topic distros

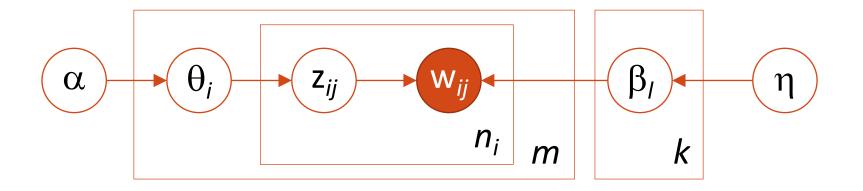
Dirichlet distribution

A "distribution of distributions" with concentration parameter β



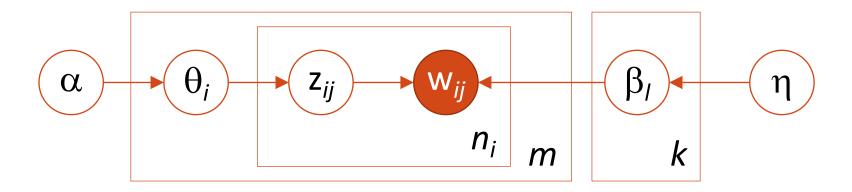
Topic models as word distros

In plate notation



- Choose $\theta_i \sim Dir(\alpha)$ for $i \in \{1, ..., m\}$
- Choose $\beta_l \sim Dir(\eta)$ for $l \in \{1, ..., k\}$
- For each document $i \in \{1, ..., m\}$
 - For each position $j \in \{1, ..., n_i\}$
 - Choose a topic $z_{ij} \sim \text{Mult}(\theta_i)$
 - Choose a word $w_{ij} \sim \text{Mult}(\beta_{z^{ij}})$

Mathematically

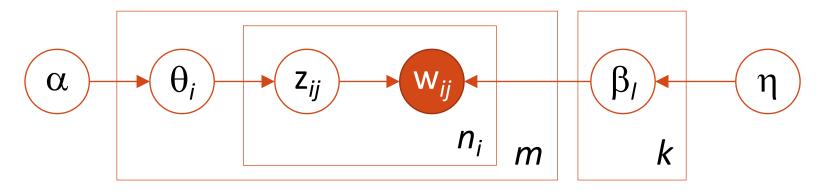


Equivalent to the following joint distribution

$$p(\beta_{1:k}, \theta_{1:m}, z_{1:m}, w_{1:m})$$

$$= \prod_{l=1}^{k} p(\beta_{l} | \eta) \prod_{i=1}^{m} p(\theta_{i} | \alpha) \left(\prod_{j=1}^{n_{i}} p(z_{ij} | \theta_{i}) p(w_{ij} | \beta_{1:k}, z_{ij}) \right)$$

Reversing the logic



In reality, we don't know the topics

- \circ Or, equivalently, the θ_i and β_l distributions
- We actually know the documents
- How to uncover the hidden topic structure?

Posterior inference

How to compute the distribution of the topic structure given the observed documents (aka the posterior)?

$$p(\beta_{1:k}, \theta_{1:m}, z_{1:m} | w_{1:m}) = \frac{p(\beta_{1:k}, \theta_{1:m}, z_{1:m}, w_{1:m})}{p(w_{1:m})}$$

Problem: computing the marginal $p(w_{1:m})$

 Intractable: would require examining every possible instantiation of the hidden variables

Consider a document-by-term matrix (tf entries)

	W_1	W_2	W_3	W_4	W_5	W_6	W_7	W_8
d_1		2		5	4			
d_2			7		1		3	
d_3	1	3		2				1
d_4						2	4	
d_5		5		6	8	2		

Randomly assign topics in $\{1, 2, ..., k\}$, say k = 3 topics

	w_1	w_2	W_3	W_4	w_5	W_6	w_7	W_8
d_1		2		5	4			
d_2			7		1		3	
d_3	1	3		2				1
d_4						2	4	
d_5		5		6	8	2		

Randomly assign topics in $\{1, 2, ..., k\}$, say k = 3 topics

	w_1	w_2	W_3	W_4	W_5	W_6	w_7	<i>W</i> ₈
d_1		2:2		5:1	4:3			
d_2			7:1		1:3		3:2	
d_3	1:3	3:2		2:2				1:3
d_4						2:3	4:1	
d_5		5:1		6:3	8:2	2:1		

Update topic counts

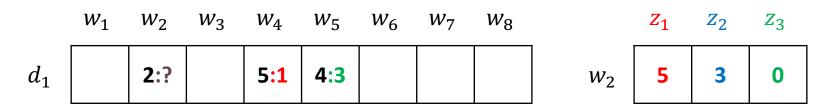
	w_1	W_2	W_3	W_4	W_5	W_6	W_7	<i>w</i> ₈
d_1		2:2		5:1	4:3			
d_2			7:1		1:3		3:2	
d_3	1:3	3:2		2:2				1:3
d_4						2:3	4:1	
d_5		5:1		6:3	8:2	2:1		

	z_1	\mathbf{z}_{2}	Z_3
w_1	0	0	1
W_2	5	5	0
W_3	7	0	0
W_4	5	2	6
•••			

	w_1	W_2	W_3	W_4	W_5	W_6	w_7	w_8		<i>z</i> ₁	z_2	Z_3
d_1		2:2		5:1	4:3				w_1	0	0	1
d_2			7:1		1:3		3:2		w_2	5	5	0
d_3	1:3	3:2		2:2				1:3	w_3	7	0	0
d_4						2:3	4:1		w_4	5	2	6
d_5		5:1		6:3	8:2	2:1						

	w_1	W_2	W_3	W_4	W_5	w_6	w_7	W_8		z_1	z_2	
d_1		2:?		5:1	4:3				W_1	0	0	
d_2			7:1		1:3		3:2		W_2	5	3	
d_3	1:3	3:2		2:2				1:3	W_3	7	0	
d_4						2:3	4:1		W_4	5	2	
d_5		5:1		6:3	8:2	2:1						

Update topic assignments one word at a time



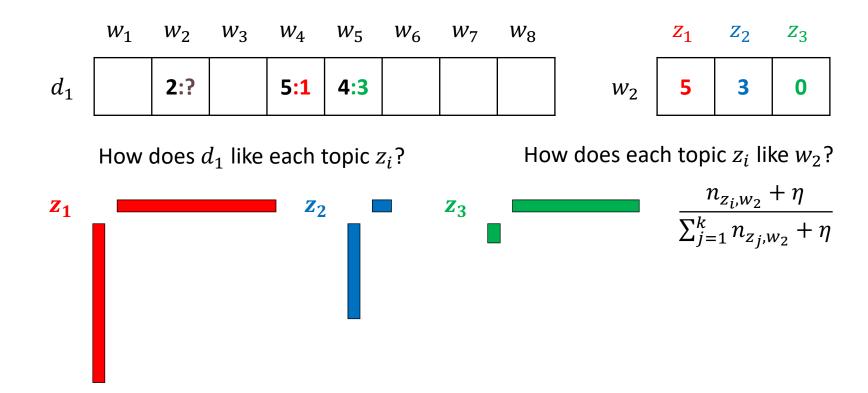
How does d_1 like each topic z_i ?

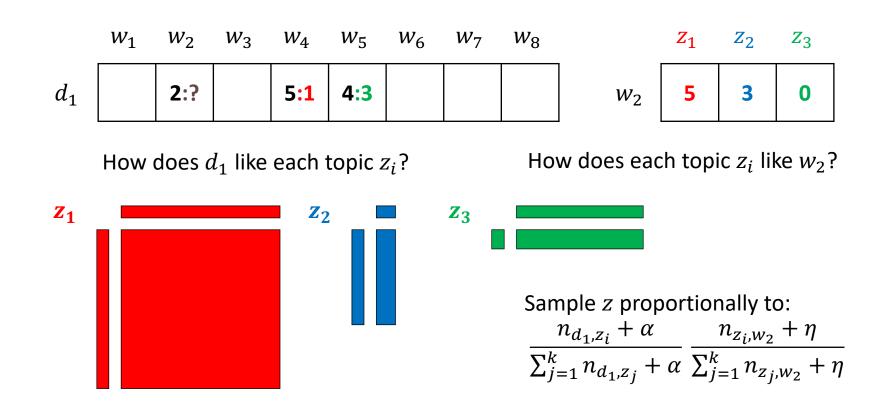
$$\frac{n_{d_1,z_i} + \alpha}{\sum_{j=1}^k n_{d_1,z_j} + \alpha}$$

$$Z_1$$

$$Z_2$$

$$Z_3$$





	w_1	W_2	W_3	W_4	w_5	W_6	w_7	w_8		z_1	z_2	<i>z</i> ₃
d_1		2:1		5:1	4:3				W_2	7	3	0

	w_1	W_2	W_3	W_4	w_5	W_6	w_7	w_8		z_1	z_2	Z_3
d_1		2:1		5:?	4:3				W_2	2	3	0

More on this?

Related courses

- Probabilistic graphical models
- Bayesian inference

How to leverage topics?

Vector space model

$$p(i|u) = \cos(\theta_u, \theta_i)$$

Item likelihood model

$$p(i|u) = \prod_{w \in i} p(w|\theta_u)^{\mathsf{tf}_{wu}}$$

Unified likelihood model

$$p(i|u) = -KL(\theta_u||\theta_i) = -p(w|\theta_u) \log \frac{p(w|\theta_u)}{p(w|\theta_i)}$$

LDA variants

Syntactic topic model

- A word or its topic is influenced by syntax
- Correlated topic model, hierarchical topic model
- Some topics resemble other topics
- Polylingual topic model
- Different languages, same topic mixtures
- Relational topic model
- Exploiting link structure

Summary

Content-based recommendation effective

Cold-start items, basket analysis

Build upon a history of research in IR

How to represent and match users and items

Still an active research area

• How to go beyond a raw content representation?

Recommending New Movies: Even a Few Ratings Are More Valuable Than Metadata

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ABSTRACT

The Netflix Prize (NP) competition gave much attention to collaborative filtering (CF) approaches. Matrix factor-

1. INTRODUCTION

The goal of recommender systems is to give personalized recommendation on items to users. Typically the recom-

We show that even 10 ratings of a new movie are more valuable than its metadata for predicting user ratings.

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ent activity of if available. plied when ering (CF)

predictor. We show that even 10 ratings of a new movie are more valuable than its metadata for predicting user ratings.

the usual vector-space model of text mining.

Our approach to connect CF and CBF methods works

References

Probabilistic topic models (CACM 2012) by David M. Blei