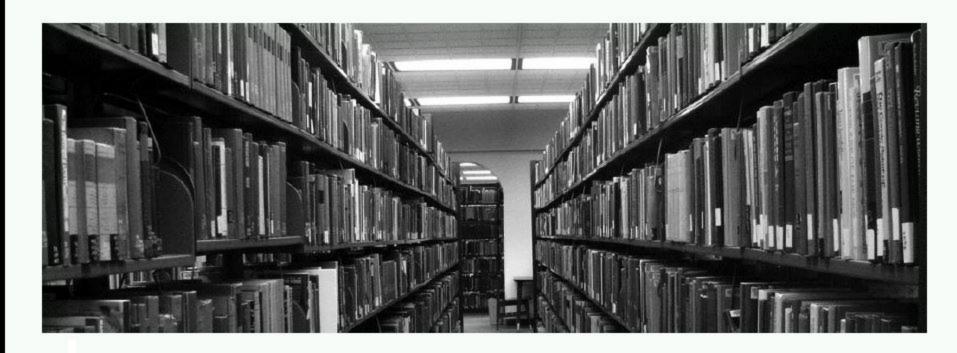
Probabilistic Topic Models and User Behavior

David M. Blei Columbia University

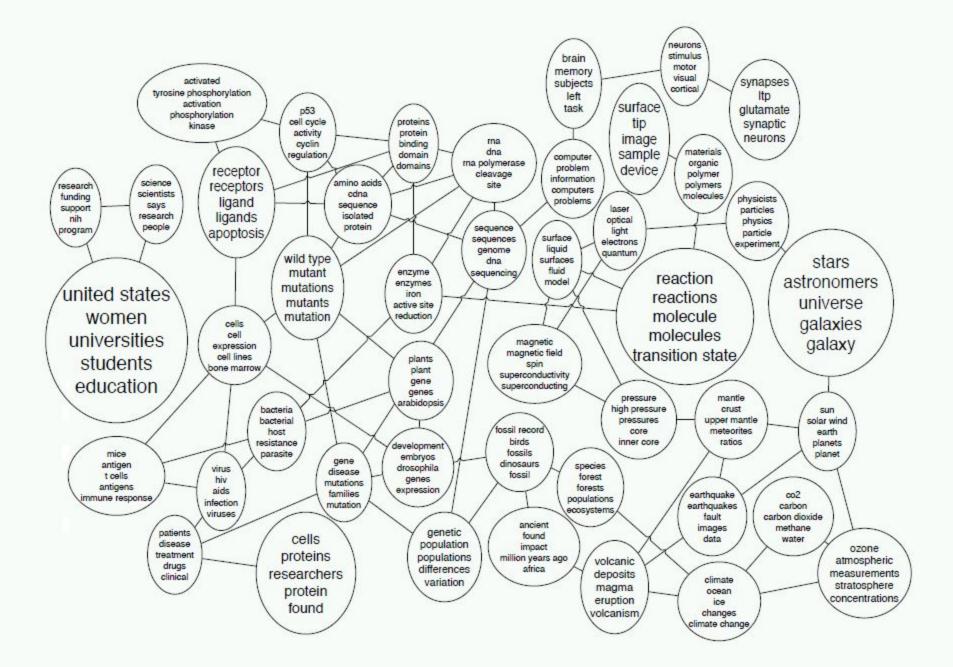


- ▶ ORGANIZE
- VISUALIZE
- **► SUMMARIZE**
- **▶ SEARCH**
- ▶ PREDICT
- UNDERSTAND



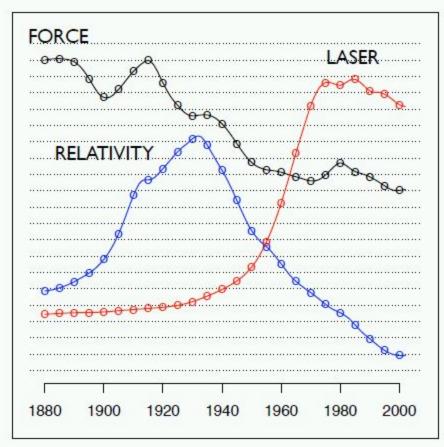
TOPIC MODELING

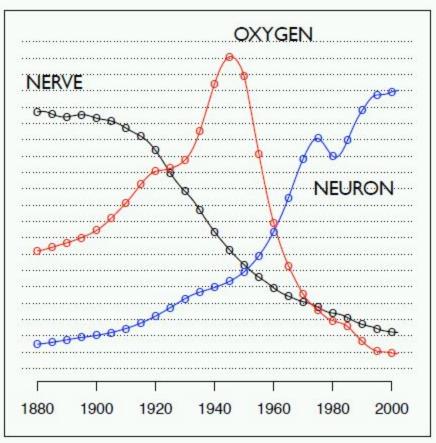
- 1. Discover the thematic structure
- 2. Annotate the documents
- 3. Use the annotations to visualize, organize, summarize, ...

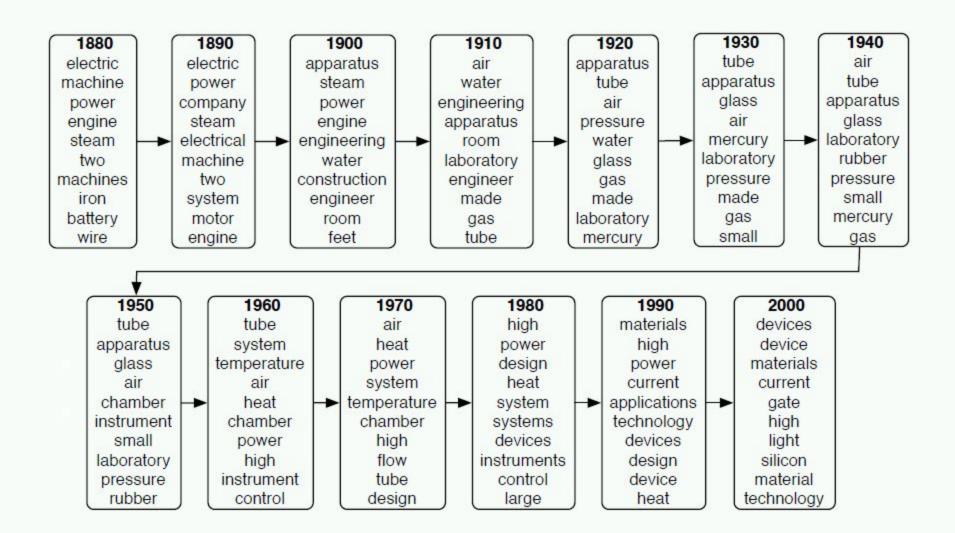


"Theoretical Physics"

"Neuroscience"









SKY WATER TREE MOUNTAIN PEOPLE



SCOTLAND WATER FLOWER HILLS TREE



SKY WATER BUILDING PEOPLE WATER



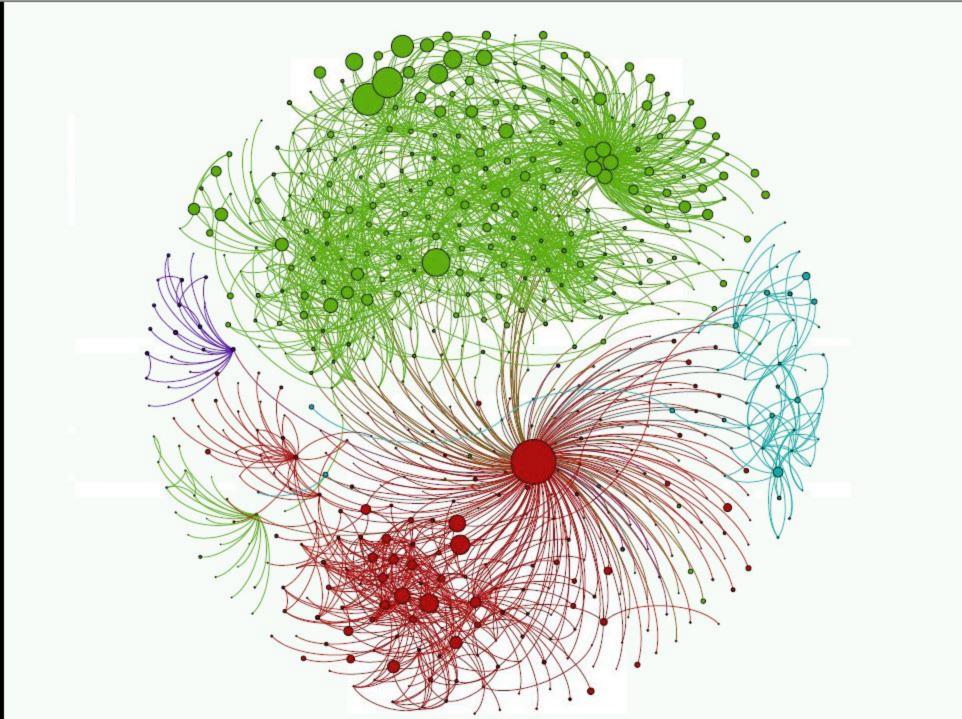
FISH WATER OCEAN
TREE CORAL

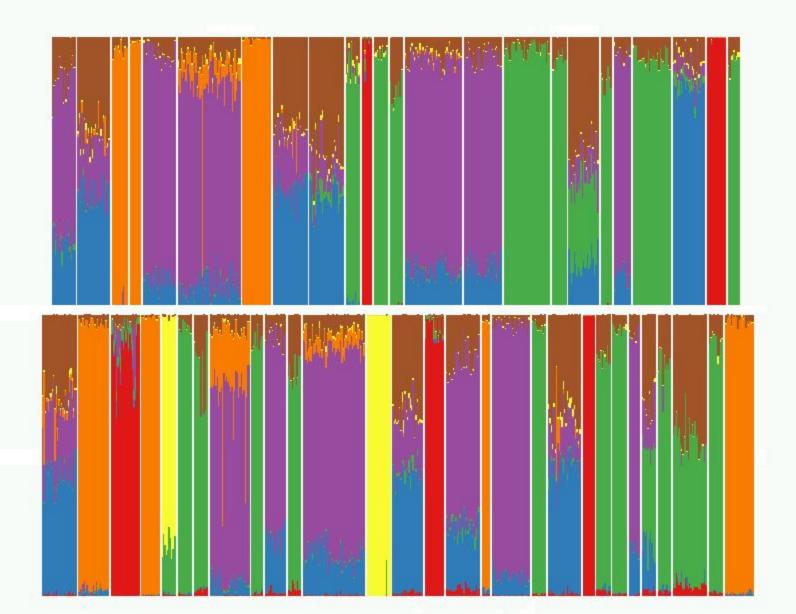


PEOPLE MARKET PATTERN TEXTILE DISPLAY

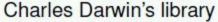


BIRDS NEST TREE BRANCH LEAVES











The NYC subway

- People read documents.
- These might be people for whom we want to form predictions.
- And, their behavior is an additional signal about the meaning of the documents and the organization of the collection.

This talk

- 1. Introduction to topic modeling
- 2. Recommendation and exploration with collaborative topic models
- 3. The bigger picture: Using probability models to solve problems with data

Seeking Life's Bare (Genetic) Necessities

Haemophilus

genome 1703 genes

Genes

233 genes.

469 genes

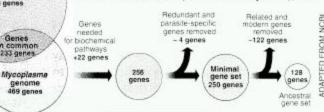
COLD SPRING HARBOR, NEW YORK-How many genes does an organism need to survive. Last week at the genome meeting here,* two genome researchers with radically different approaches presented complementary views of the basic genes needed for life. One research team, using computer analyses to compare known 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

"are not all that far apart," especially in 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

Arcady Mushegian, a computational molecular biologist at the National Center for Biotechnology Information (NCBI) in Bethesda, Maryland. Comparing an

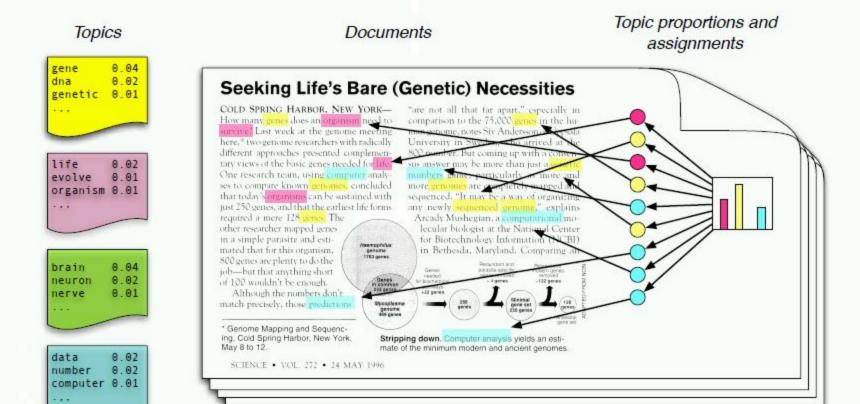


Stripping down. Computer analysis yields an estimate of the minimum modern and ancient genomes.

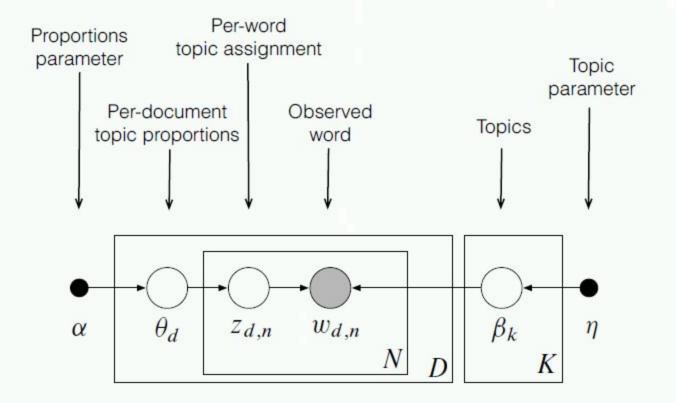
* Genome Mapping and Sequencing, Cold Spring Harbor, New York, May 8 to 12.

SCIENCE • VOL. 272 • 24 MAY 1996

Documents exhibit multiple topics.

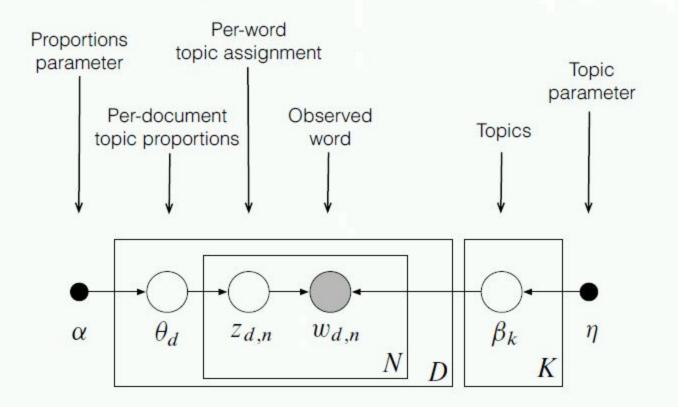


Latent Dirichlet Allocation



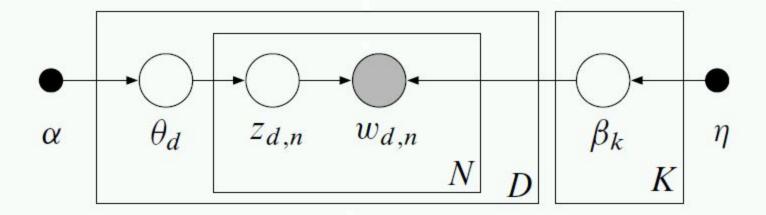
LDA as a graphical model

- Nodes are random variables; edges indicate dependence.
- Shaded nodes are observed; unshaded nodes are hidden.
- Plates indicate replicated variables.

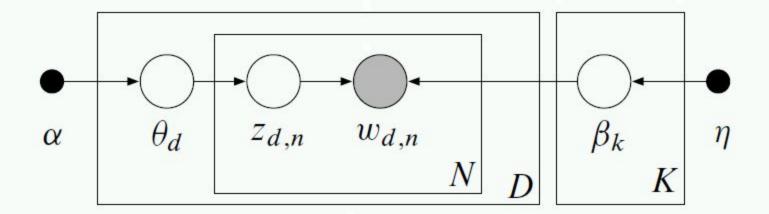


LDA as a graphical model

- Encodes independence assumptions about the variables
- Defines a factorization of the joint probability distribution
- Connects to algorithms for computing with data



- ▶ The joint defines a posterior, $p(\theta, z, \beta \mid w)$.
- From a collection of documents, infer
 - Per-word topic assignment z_{d,n}
 - Per-document topic proportions \(\theta_d \)
 - Per-corpus topic distributions β_k
- Then use posterior expectations to perform the task at hand: information retrieval, document similarity, exploration, and others.



- Mean field variational methods (Blei et al., 2001, 2003)
- Expectation propagation (Minka and Lafferty, 2002)
- Collapsed Gibbs sampling (Griffiths and Steyvers, 2002)
- Distributed sampling (Newman et al., 2008; Ahmed et al., 2012)
- Collapsed variational inference (Teh et al., 2006)
- Stochastic inference (Hoffman et al., 2010, 2013; Mimno et al., 2012)
- Factorization inference (Arora et al., 2012; Anandkumar et al., 2012)





- Data: The OCR'ed collection of Science from 1990–2000
 - 17K documents
 - 11M words
 - 20K unique terms (stop words and rare words removed)
- Model: 100-topic LDA model using variational inference.

Seeking Life's Bare (Genetic) Necessities

genome 1703 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

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* Genome Mapping and Sequenc-

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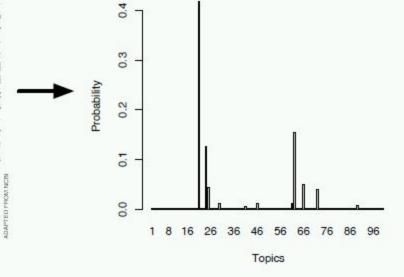
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Genee needed paratic posts of posts of

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



SCIENCE • VOL. 272 • 24 MAY 1996

Game Season Team Coach Play **Points** Games Giants Second Players Bush Campaign Clinton Republican House Party Democratic Political Democrats Senator 0 Children School Women Family

Parents

Child

Life

Says

Help

Mother

1 Stock Percent Companies Fund Market Bank Investors Funds Financial Business

House Buildings Development Space Percent Real

Life

Know

School

Street

Man

Family

Says

House

Children

Night

Building

Street

Square

Housing

0 Film Movie Show Life Television Films Director Man Story Says

0 Won Yankees Team Game Second Mets Race Season Round Run Cup League Baseball Open Game Team Play Games Win Hit

1

Church

War

Women

Life

Black

Political

Catholic

Government

Jewish

Pope

0 Art Museum Show Gallery Works Artists Street Artist **Paintings** Exhibition

0

Book

Life

Books

Novel

Story

Man

Author

House

War

Children

6 Wine Street Hotel House Room Night Place Restaurant Park Garden

Government War Military Officials Iraq Forces Iraqi Army Troops

Soldiers

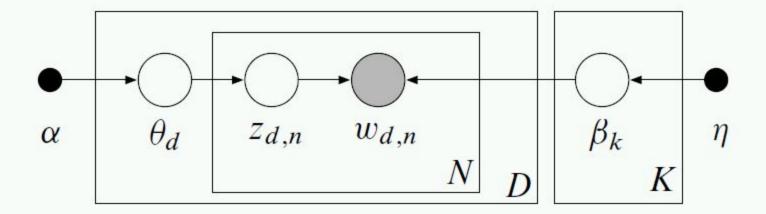
1

Police Yesterday Man Officer Officers Case Found

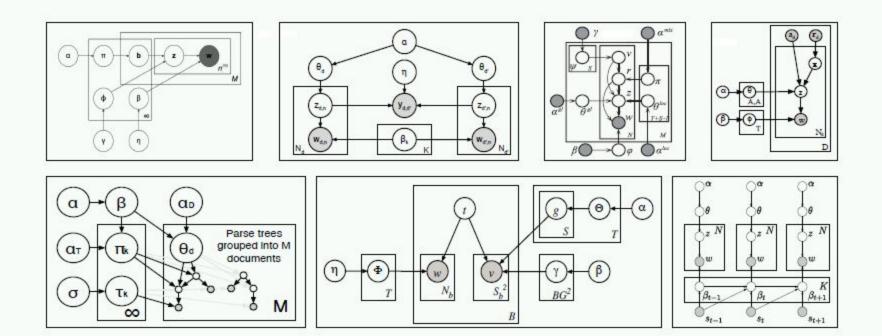
Charged

Street

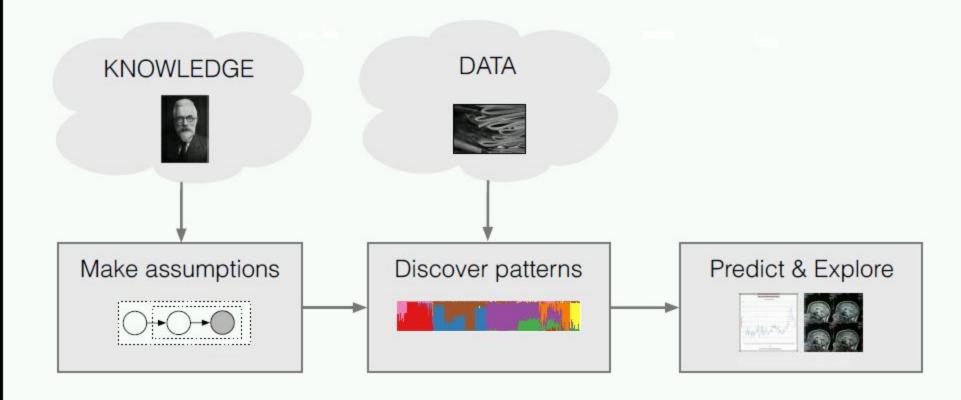
Shot



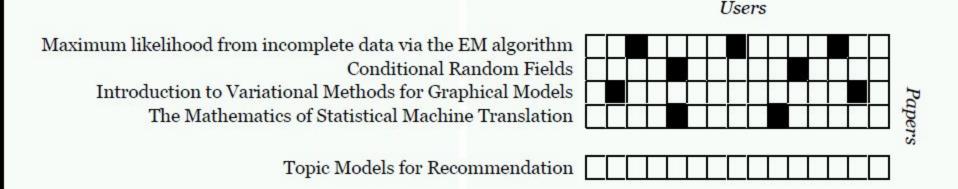
- Summary: LDA discovers themes through posterior inference.
- Other perspectives
 - Latent semantic analysis [Deerwester et al., 1990; Hofmann, 1999]
 - A mixed-membership model [Erosheva, 2004]
 - PCA and matrix factorization [Jakulin and Buntine, 2002]
 - Was independently invented for genetics [Pritchard et al., 2000]



- Organizing and finding patterns in text is important in the sciences, humanities, industry, and culture.
- LDA is a simple building block that enables many applications.
 Topic modeling is an active field of research.
- Algorithmic improvements let us fit models to massive data.
 (See VW, Gensim, Mallet, others.)

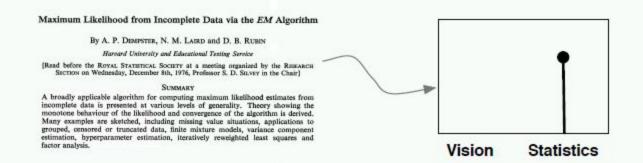


- Case study in text analysis with probability models
- Topic modeling research
 - develops new models.
 - develops new inference algorithms.
 - develops new applications, visualizations, tools.

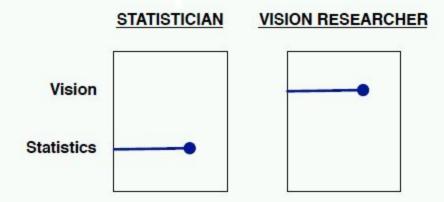


- Example: Scientists share their research libraries.
- Collaborative topic models can
 - Helps readers discover documents, old and new.
 - Describe readers in terms of topical preferences
 - Identify documents that are impactful, interdisciplinary

Consider EM (Dempster et al., 1977). We infer topics from its text:

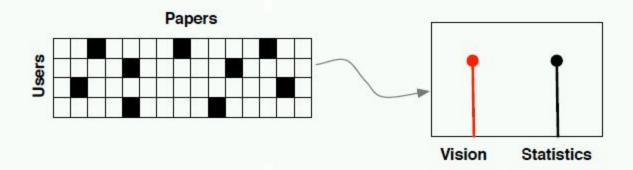


Suppose there are two types of scientists

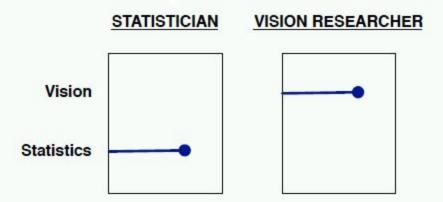


We first recommend the EM paper to statisticians.

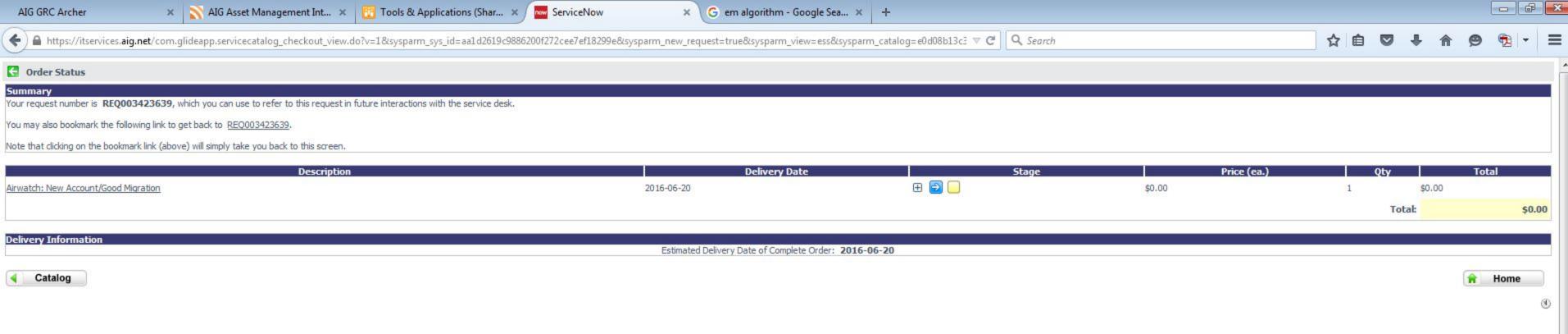
With user data, we can adjust the topics to account for who liked it:

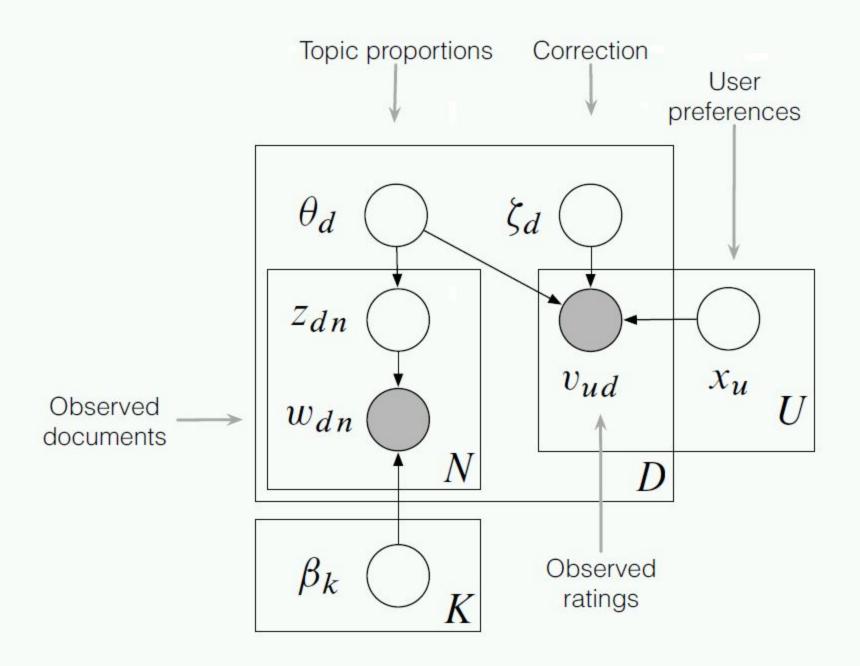


Consider again the scientists



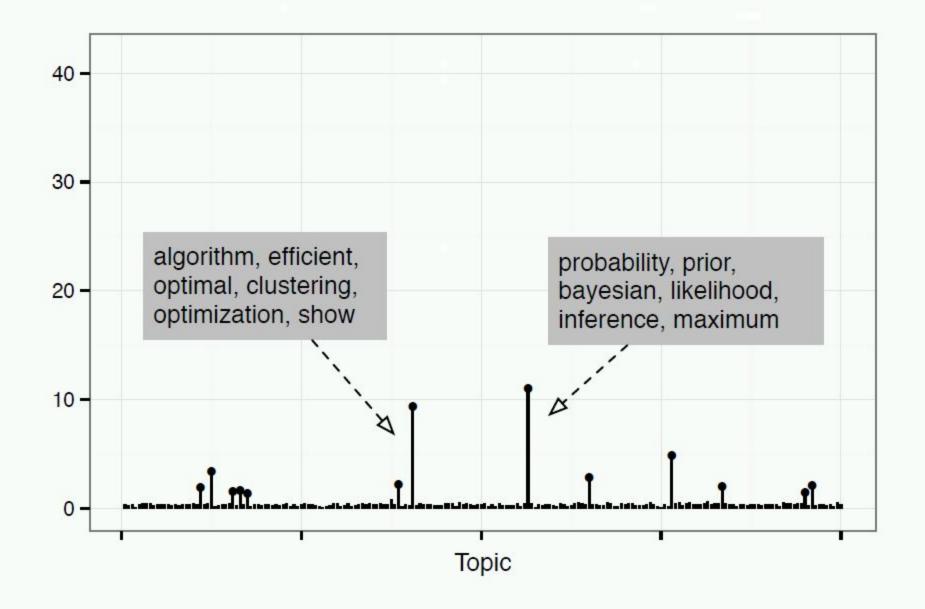
We now recommend the EM paper to vision researchers.

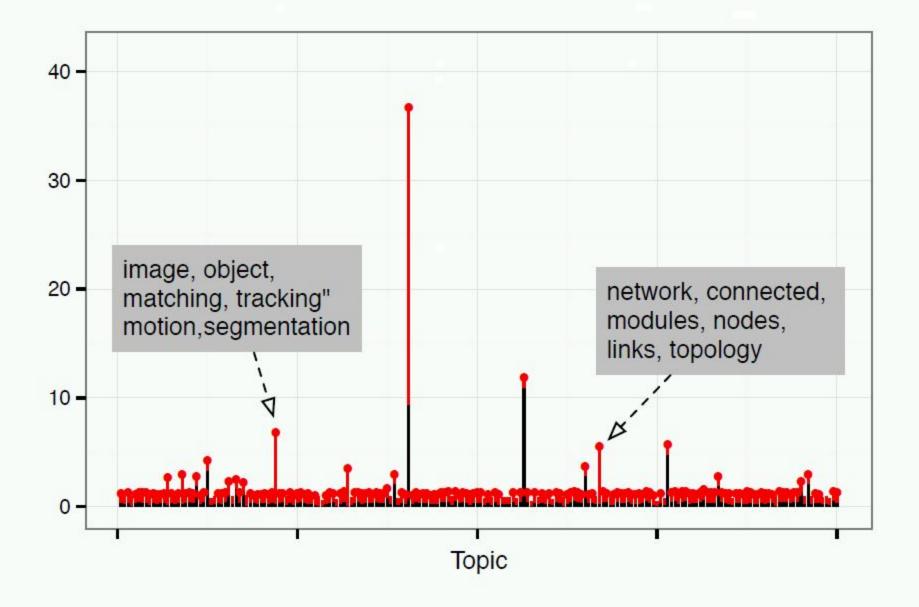




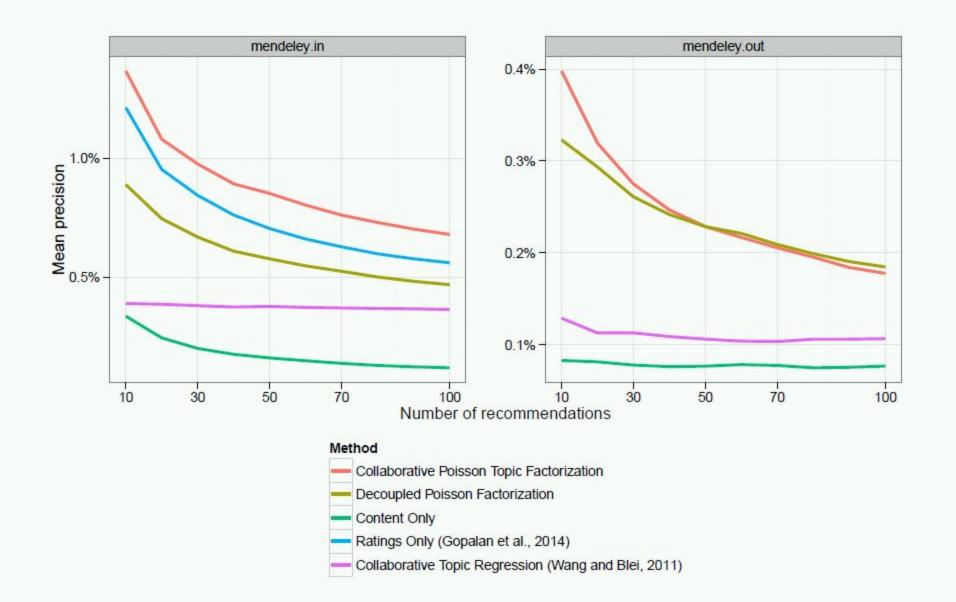


- Big data set from Mendeley.com
- The data:
 - 261K documents
 - 80K users
 - 10K vocabulary terms
 - 25M observed words
 - 5.1M entries (sparsity is 0.02%)

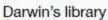


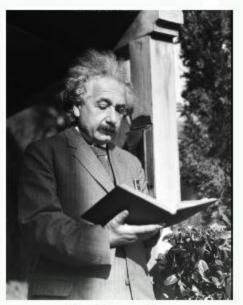


Mendeley









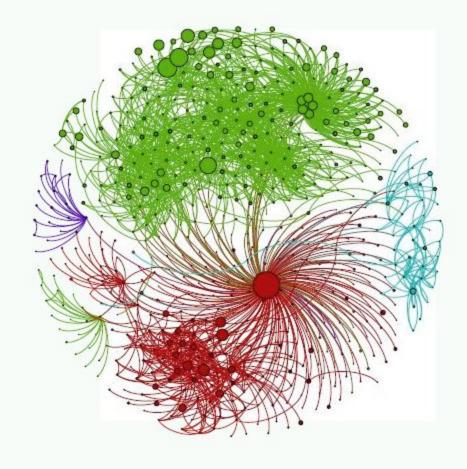
Einstein reading



Another scientist reading

- The readers also tell us about the articles.
- We can look at posterior estimates to find
 - Interdisciplinary articles
 - Influential articles within a field
 - Outside influences on a field

"Network Analysis"

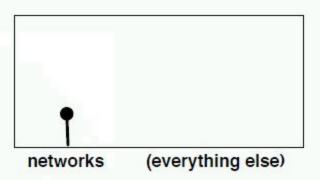


network; connected; modules; nodes; links; topology; connectivity; graph; robustness; connections; modular; world; degree; properties

Assortative mixing in networks

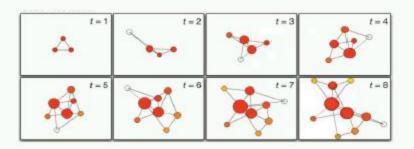
M. E. J. Newman

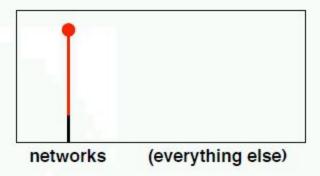
Department of Physics, University of Michigan, Ann Arbor, MI 48109-1120 and Santa Fe Institute, 1399 Hyde Park Road, Santa Fe, NM 87501



About networks

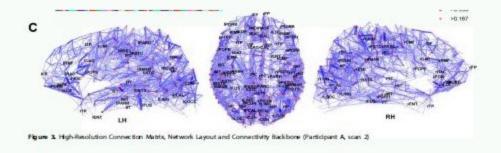
- Assortative mixing in networks (Newman, 2002)
- Mixing patterns in networks (Newman, 2002)
- Catastrophic cascade of failures in interdependent networks (Buldyrev et al., 2010)

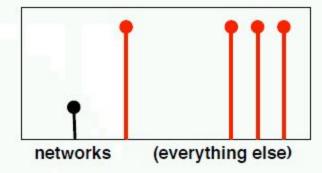




About networks; for readers of networks

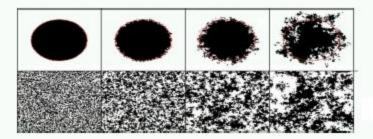
- Emergence of scaling in random networks (Barabassi and Albert, 1999)
- Statistical mechanics of complex networks (Albert and Barabassi, 2002)
- Complex networks: Structure and dynamics (Boccaletti et al., 2006)

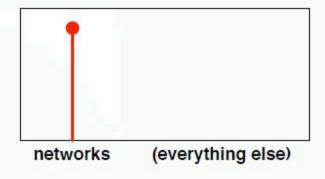




About networks; for readers of other fields

- Mapping the Structural Core of Human Cerebral Cortex (Hagmann et al., 2008)
- Network thinking in ecology and evolution (Proulx et al., 2005)
- Linked: The New Science of Networks (Barabasi, 2002)







Drag wan

Not about networks; for readers of networks

- Power-law distributions in empirical data (Clauset et al., 2009)
- Statistical physics of social dynamics (Castellano et al., 2009)
- ► The origin of bursts and heavy tails in human dynamics (Barabasi, 2005)

"Statistical Modeling"

About this field; read by users in this field

- A Bayesian analysis of some nonparametric problems
- Bayesian measures of model complexity and fit
- Monte Carlo Methods in Bayesian Computation

About this field; read by users in other fields

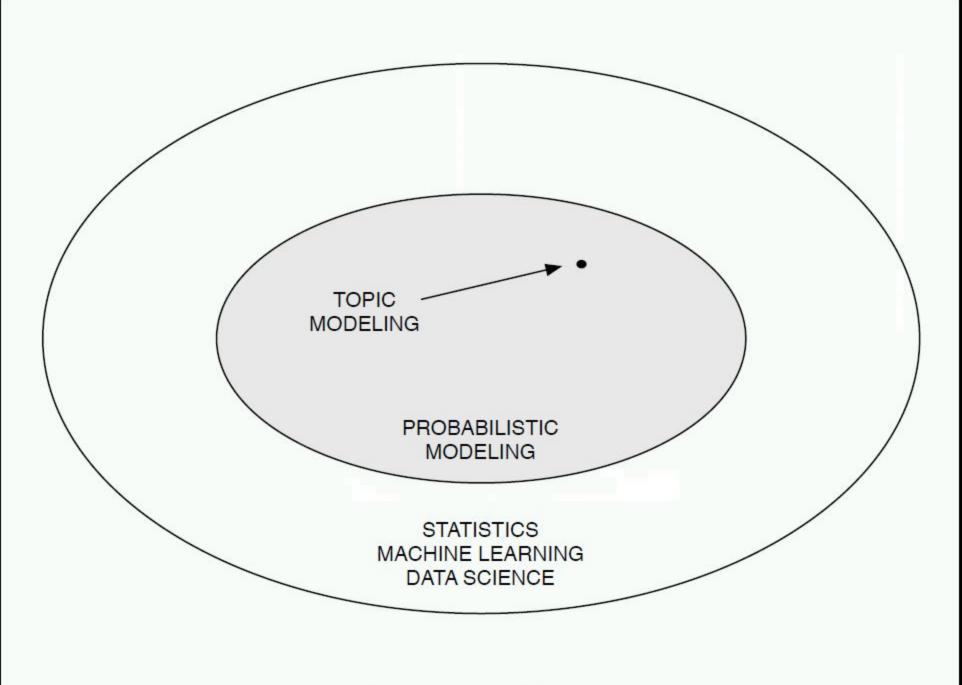
- A tutorial on HMMs and selected applications in speech recognition
- An Introduction to Bayesian Networks and Influence Diagrams
- Maximum likelihood from incomplete data via the EM algorithm

About other fields; read by users in this field

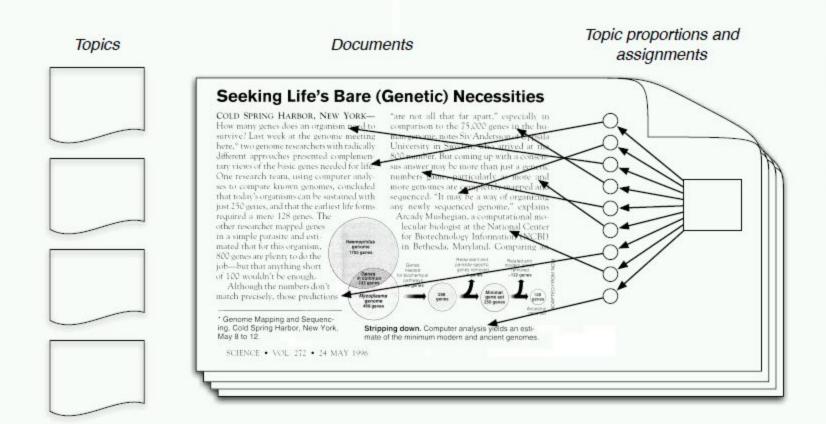
- Second Thoughts on the Bootstrap
- A guide to Eclipse and the R plug-in StatET
- Using Multivariate Statistics



- A decade of clicks on arXiv.org (2003–2013)
- ► The data:
 - 826K documents
 - 120K users
 - 14K vocabulary terms
 - 54M observed words
 - 43.6M entries (sparsity is 0.04%)



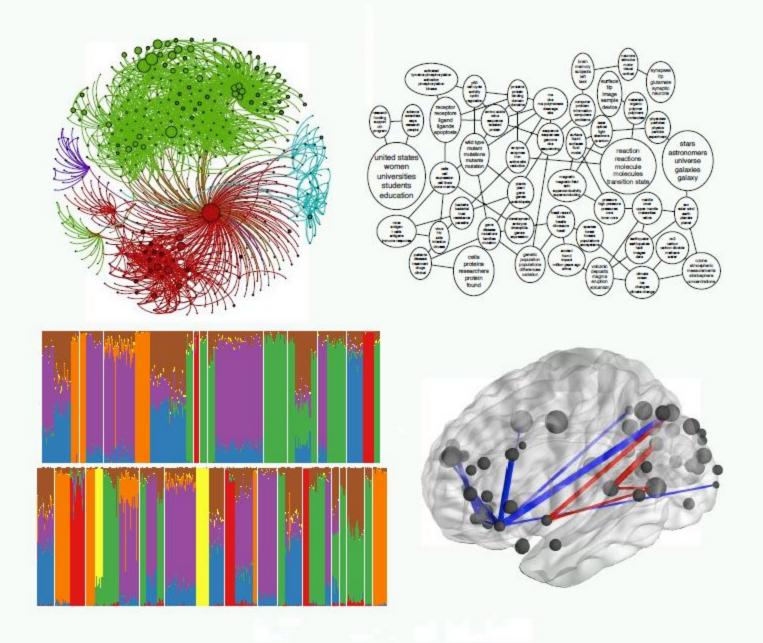
I. Assume our data come from a model with hidden patterns at work

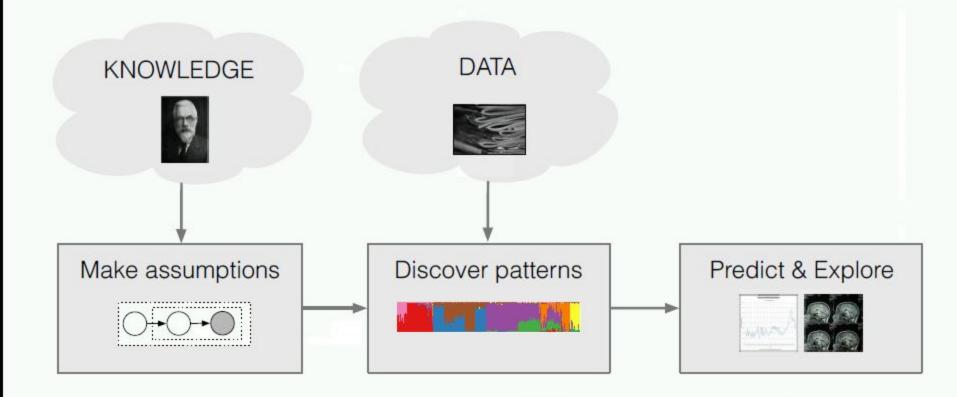


II. Discover those patterns from data

$$v^* = \arg\max_{v} \mathbb{E}_q \left[\log p(x, z, \beta \mid \alpha) \right] + \mathbb{H} \left[q(z, \beta \mid v) \right]$$

III. Use the discovered patterns to predict about and explore the data





What we need:

- Flexible and expressive components for building models
- Scalable and generic inference algorithms
- Easy to use software to stretch probabilistic modeling into new areas