

# Scalable Inference in Probabilistic Topic Models

(Online variational inference is great)

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# Information overload



As more information becomes available, it becomes more difficult to find and discover what we need.

We need new tools to help us organize, search, and understand these vast amounts of information.

# Topic modeling



Topic modeling provides methods for automatically organizing, understanding, searching, and summarizing large electronic archives.

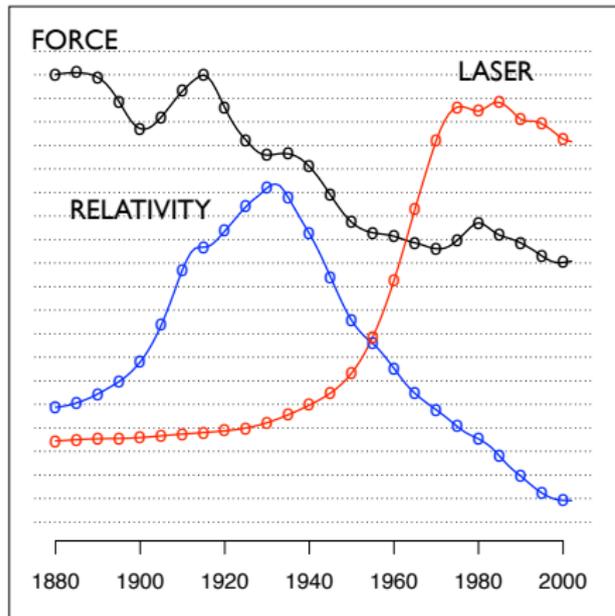
- 1 Discover the hidden themes that pervade the collection.
- 2 Annotate the documents according to those themes.
- 3 Use annotations to organize, summarize, and search the texts.

# Discover topics from a corpus

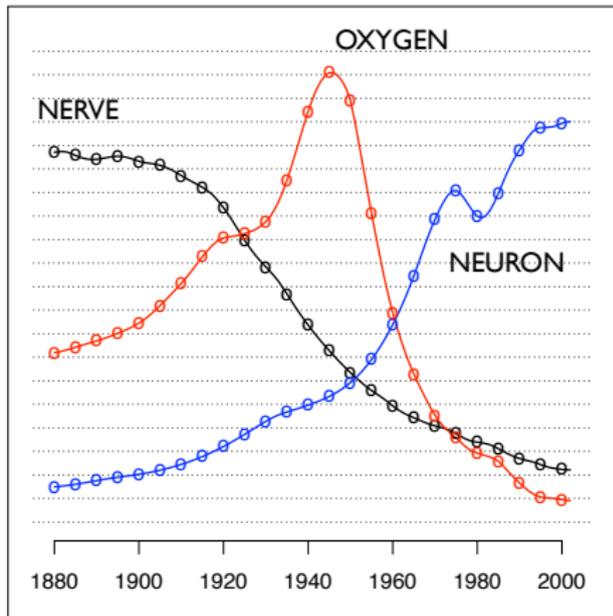
|             |              |              |             |
|-------------|--------------|--------------|-------------|
| human       | evolution    | disease      | computer    |
| genome      | evolutionary | host         | models      |
| dna         | species      | bacteria     | information |
| 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 |

# Model the evolution of topics over time

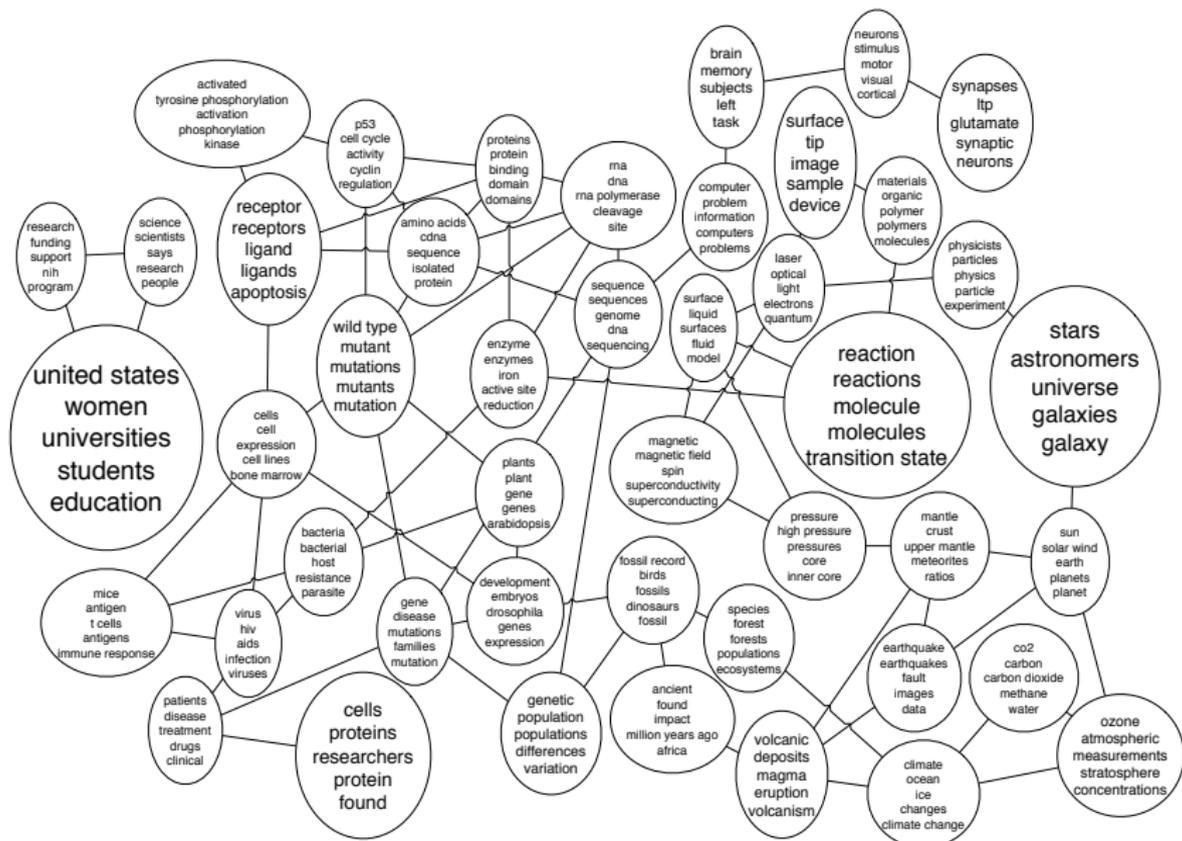
## "Theoretical Physics"



## "Neuroscience"



# Model connections between topics



# Browse and discover patterns in large data sets

Original article

Topic-based browser

Related articles

## Automatic Analysis, Theme Generation, and Summarization of Machine-Readable Texts

Gerard Salton, James Allan, Chris Buckley,

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Many kinds of texts are currently available in machine-readable form and are amenable to automatic processing. Because the available databases are large and cover many different subject areas, automatic aids must be provided to users interested in accessing the data. It has been suggested that links be placed between related pieces of text, connecting, for example, particular text paragraphs to other paragraphs covering related subject matter. Such a linked text structure, often called hypertext, makes it possible for the reader to start with particular text passages and use the linked structure to find related text elements (1). Unfortunately, until now, viable methods for automatically building large hypertext structures and for using such structures in a sophisticated way have not been available. Here we give methods for constructing text relation maps and for using text relations to access and use text databases. In particular, we outline procedures for determining text themes, traversing texts selectively, and extracting summary statements that reflect text content.

### Text Analysis and Retrieval: The Smart System

The Smart system is a sophisticated text retrieval tool, developed over the past 30 years, that is based on the vector space

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model of retrieval model, all information as well as information sent by sets, or  $v$  is typically a word, associated with this action. In principle chosen from a core a thesaurus, but be constructing such for unrestricted top to derive the terms under consideration terms assigned to a text content.

Because the term for content represent introduce a term- $w$  signs high weights to and lower weights to A powerful term- $w$  kind is the well- $k$  (term frequency  $f$  frequency ( $f_i$ ) in  $p$  with a low frequency ( $f_j$ ). Such terms that which they occur fit

When all texts represented by weighted)  $D_i = (d_{i1}, d_{i2}, \dots)$  weight assigned to  $i$  similarity measure between pairs of vectors. Thus,  $g$

SCIENCE • VU3

## "Automatic Analysis, Theme Generation, and Summarization of Machine-Readable Texts" (1994)

| TOPIC                                    | PROB |
|--|------|
| data computer system information network | 0.30 |
| information library text index libraries | 0.19 |
| two three four different single          | 0.16 |

| DOCUMENT  | SCORE  |
|---|--------|
| "Global Text Matching for Information Retrieval" (1991)   | 0.2570 |
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| "Data Processing by Optical Coding" (1961)  | 0.4290 |
| "Pattern-Analyzing Memory" (1976)   | 0.4320 |
| "The Storing of Pamphlets" (1899)   | 0.4440 |
| "A Punched-Card Technique for Computing Means, Standard Deviations, and the Product-Moment Correlation Coefficient and for Listing Scattergrams" (1946) | 0.4550 |

## Global Text Matching for Information Retrieval

GERARD SALTON AND CHRIS BUCKLEY

An approach is outlined for the retrieval of natural language texts in response to multiple search requests and for the recognition of content similarities between text corpora. The proposed retrieval process is based on flexible text matching procedures carried out in a number of different text environments and is applicable to large text collections covering unrestricted subject matter. For unrestricted text environments this system appears to outperform other currently available methods.

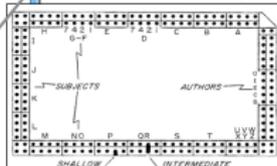


Fig. 1. The search card, showing the different modes of searching and the "2-2-2" table. Combination of these three modes can produce any number from 1 to 10. It is also possible to code numbers 1 to 10 in a 2x2x2 table and only one mode that are required to select the number desired (1). To select a given number in the 2-2-2 table, it may be necessary to modify some text.

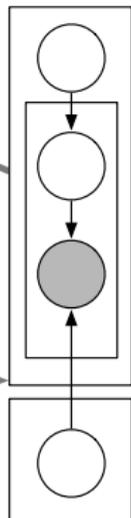
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# We need online inference



**Analyze the collection**



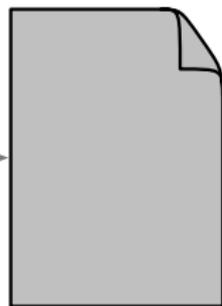
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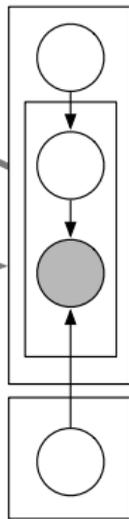
# We need online inference



*Sample one document*



*Analyze it*



*Update the model*

- Allows us to analyze millions of documents
- Lets us develop topic models on streaming collections

# This talk

- 1 Introduction to topic modeling
- 2 Online inference for topic models

# Introduction to topic modeling

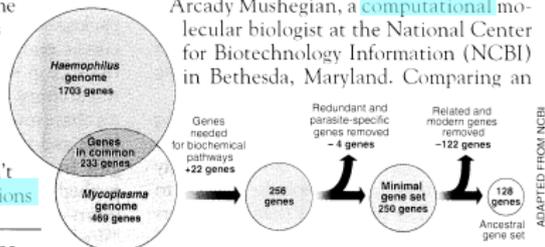
## Seeking Life's Bare (Genetic) Necessities

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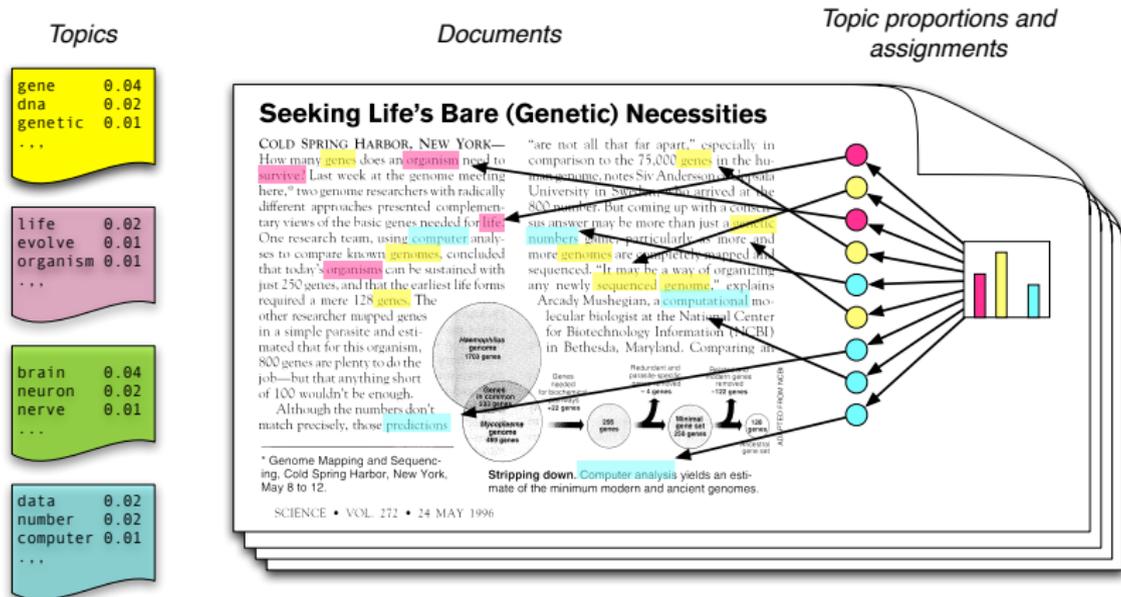
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Stripping down. Computer analysis yields an estimate of the minimum modern and ancient genomes.

SCIENCE • VOL. 272 • 24 MAY 1996

**Simple intuition:** Documents exhibit multiple topics.

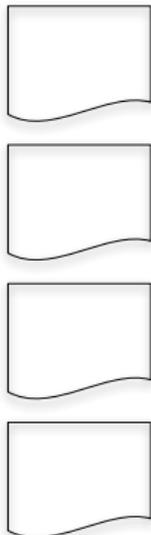
# Generative model for latent Dirichlet allocation (LDA)



- Each **topic** is a distribution over words
- Each **document** is a mixture of corpus-wide topics
- Each **word** is drawn from one of those topics

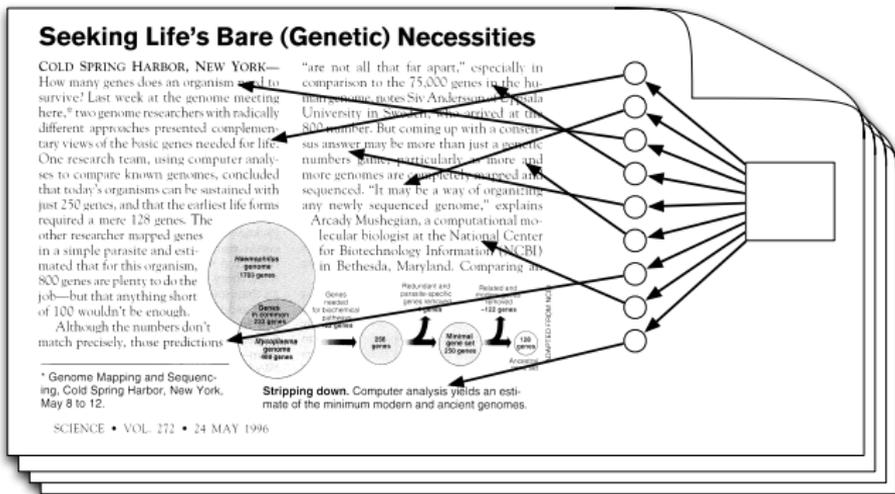
# The posterior distribution

Topics



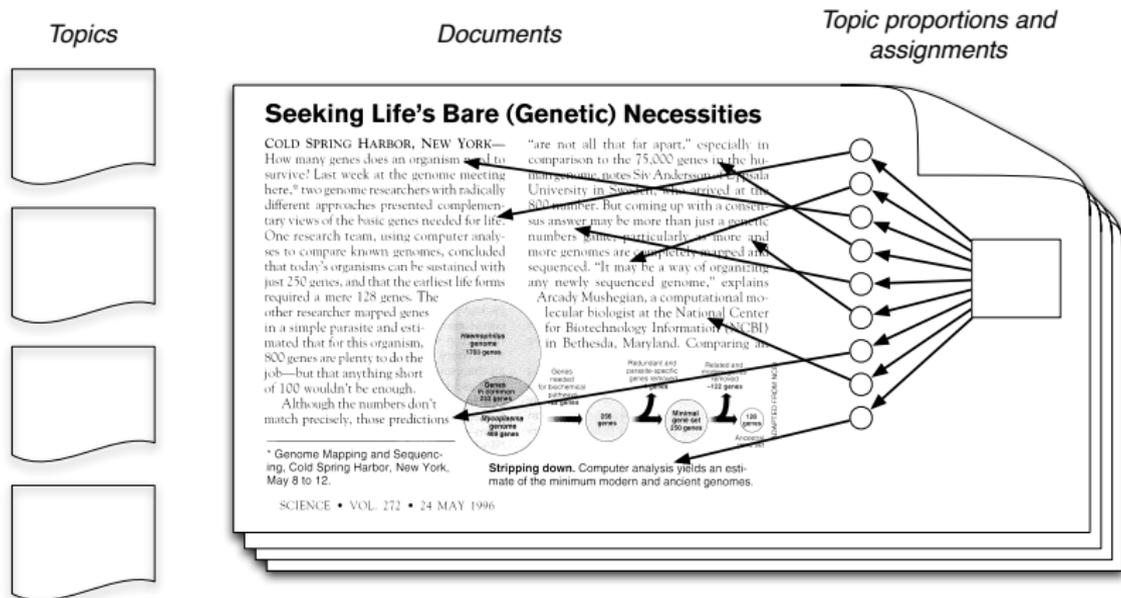
Documents

Topic proportions and assignments



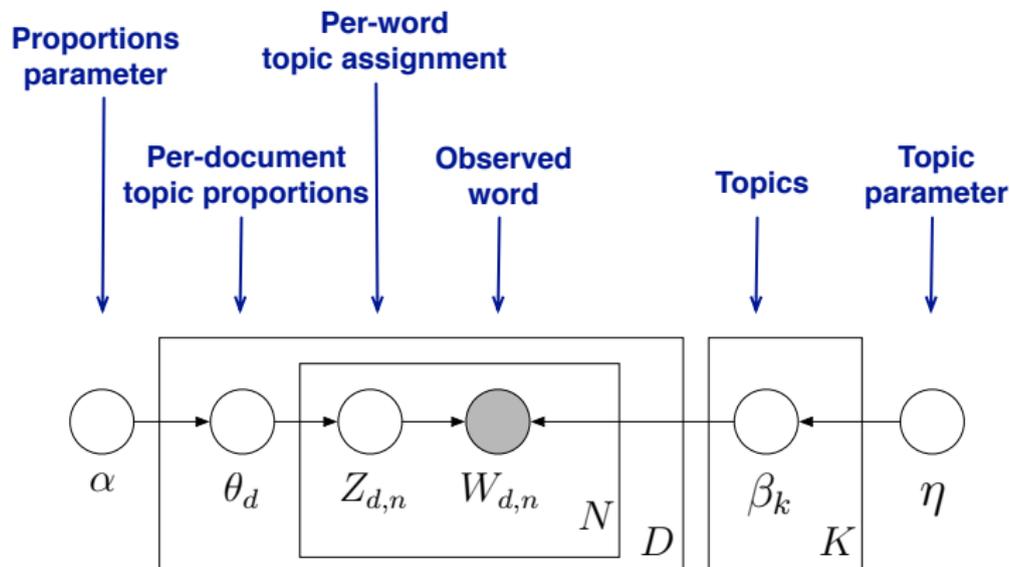
- In reality, we only observe the documents
- The other structure are **hidden variables**

# The posterior distribution



- Our goal is to **infer** the hidden variables
  - I.e., compute their distribution conditioned on the documents
- $p(\text{topics, proportions, assignments} \mid \text{documents})$

# LDA as a graphical model



- Encodes our assumptions about the data
- Helps us derive ways of computing with data
- Isolates independence assumptions, which are separate from other specific details of the model

# Example inference

## Seeking Life's Bare (Genetic) Necessities

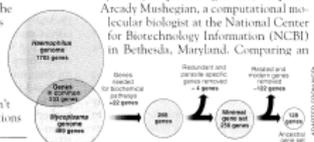
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<sup>\*</sup> Genome Mapping and Sequencing, Cold Spring Harbor, New York, May 8 to 12.

SCIENCE • VOL. 272 • 24 MAY 1996



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

- **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.

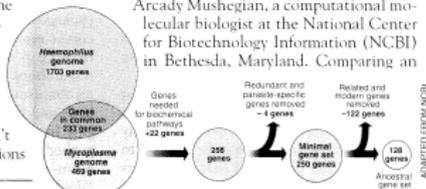
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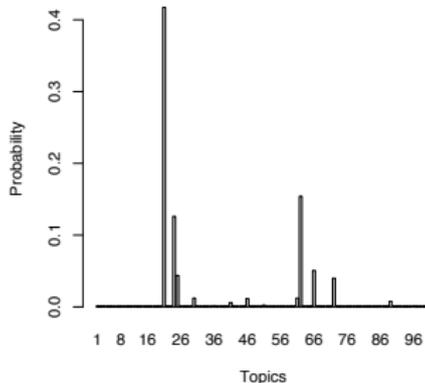
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# Example inference

|             |              |              |             |
|-------------|--------------|--------------|-------------|
| 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         |
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# Used in exploratory tools of document collections

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file:///Users/blei/doc.html

Back Forward Stop Refresh Home AutoFill Print Mail

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| TOPIC                                    | PROB |
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**FIG. 1.** The search card showing the different modes of numbering and the "2-3-1" table. Combinations of these four numbers can produce any number from 1 to 10 (15). It is also possible to code numbers 1 to 10 in a five-bit field and code area mappings are required to enter the number coded 1/3. To select a given number in the four-bit field, it may be necessary to encode more than twice.

**THE STORING OF PAMPHLETS.**

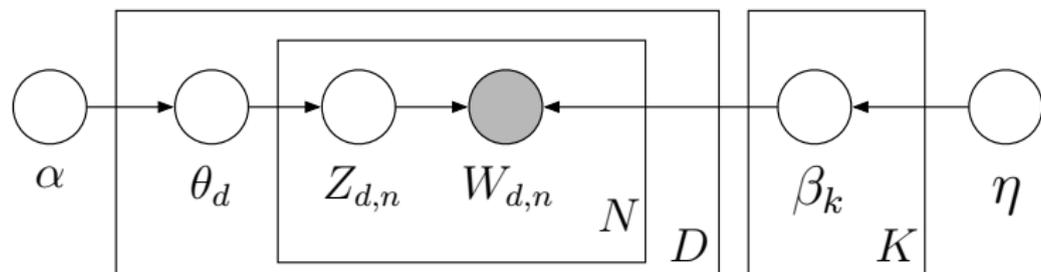
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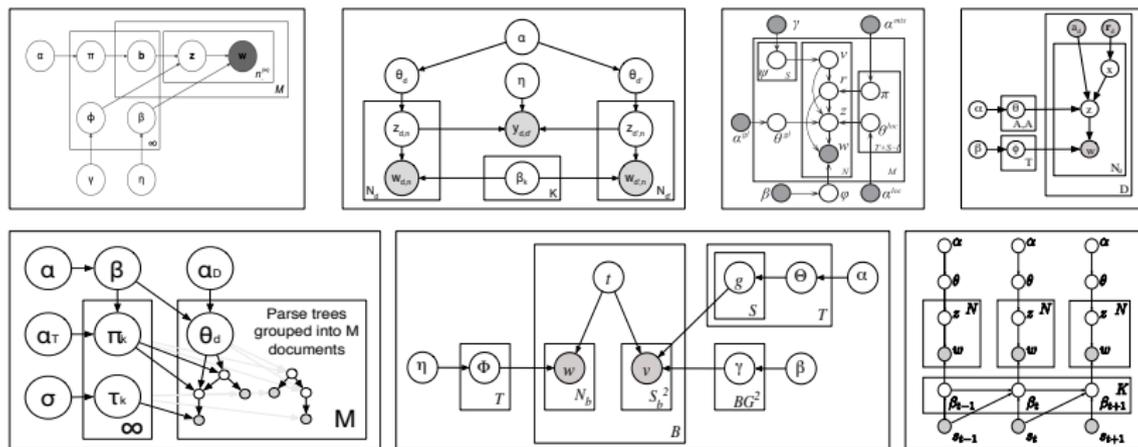
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# Summary of LDA



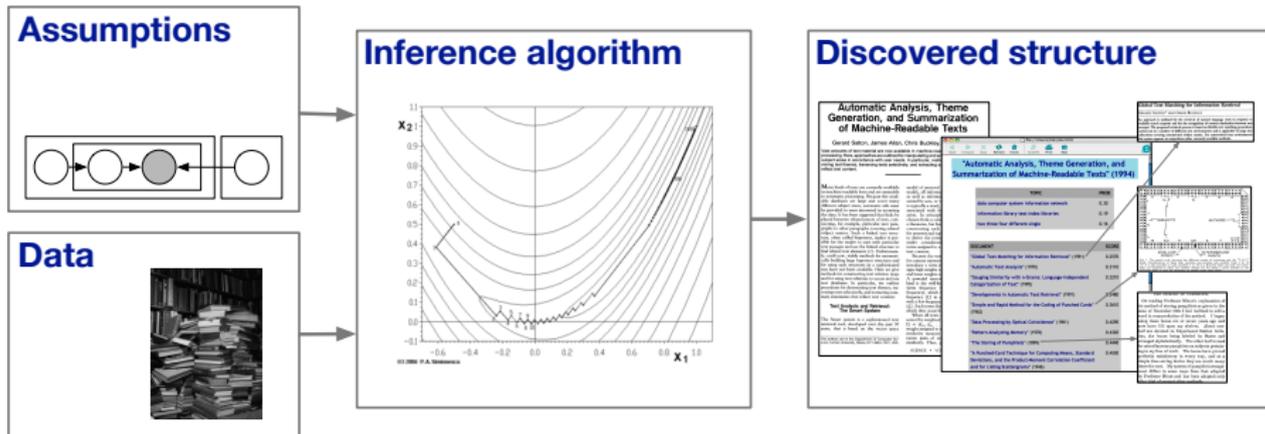
- LDA can
  - visualize the hidden thematic structure in large corpora
  - generalize new data to fit into that structure
- Builds on Deerwester et al. (1990) and Hofmann (1999)  
It is an example of a *mixed membership model* (Erosheva, 2004)  
Relates to *multinomial PCA* (Jakulin and Buntine, 2002).
- Was independently invented for genetics (Pritchard et al., 2000)

# Why develop these kinds of models?



- Organizing and finding patterns in data has become important in the sciences, humanities, industry, and culture.
- LDA can be embedded in more complicated models.
- Algorithmic improvements let us fit models to massive data.

# Bigger Picture: Probabilistic modeling



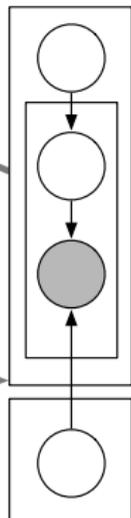
- Research in modeling separates these basic activities
- Though linked, we can work on each piece separately

# Online inference for topic models

# We need online inference



**Analyze the collection**



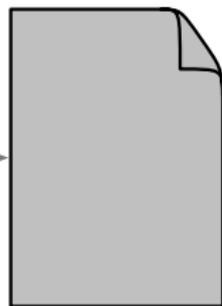
**Update the model**

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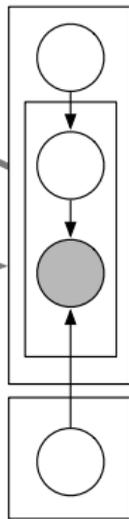
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*Sample one document*



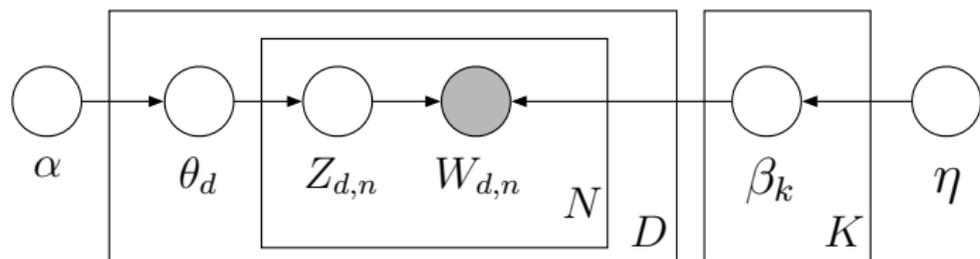
*Analyze it*



*Update the model*

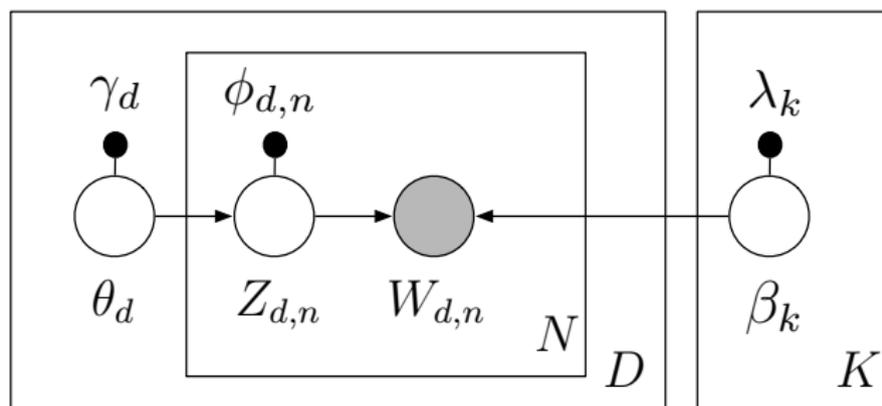
- Allows us to analyze millions of documents
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# Computation with LDA



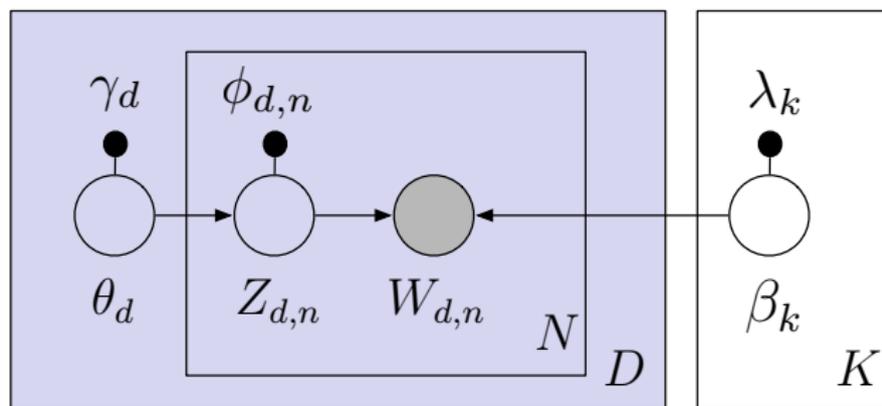
- Our goal is to compute the *posterior*, the conditional distribution of the hidden variables given the documents.
- We will build on *variational inference*.
  - Posit a parameterized distribution  $q$  over hidden variables.
  - Optimize to make  $q$  close (in KL) to the posterior.

## Batch variational inference for LDA



- The *mean field distribution* places a variational parameter on each hidden variable.
- Optimize these with coordinate ascent, iteratively optimizing each parameter while holding the others fixed.

# Batch variational inference for LDA



- In the “local step” we iteratively update the parameters for each document, holding the topic parameters fixed.

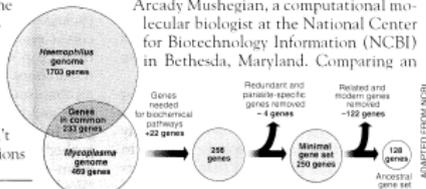
# Example inference (again)

## Seeking Life's Bare (Genetic) Necessities

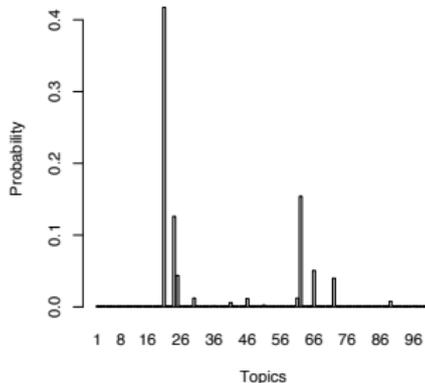
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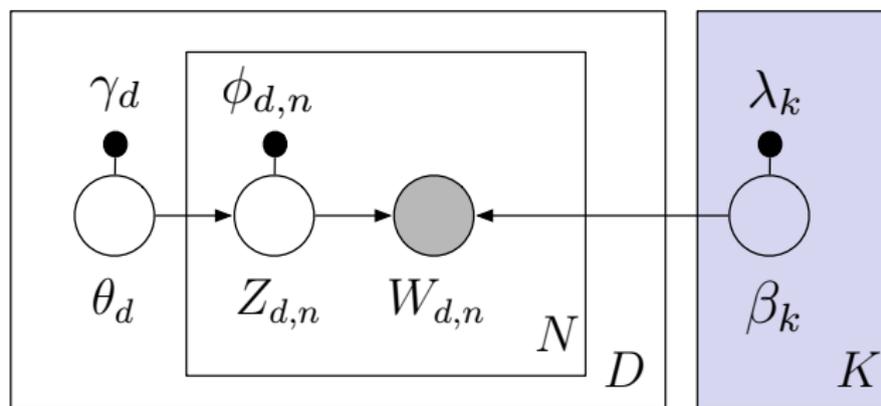


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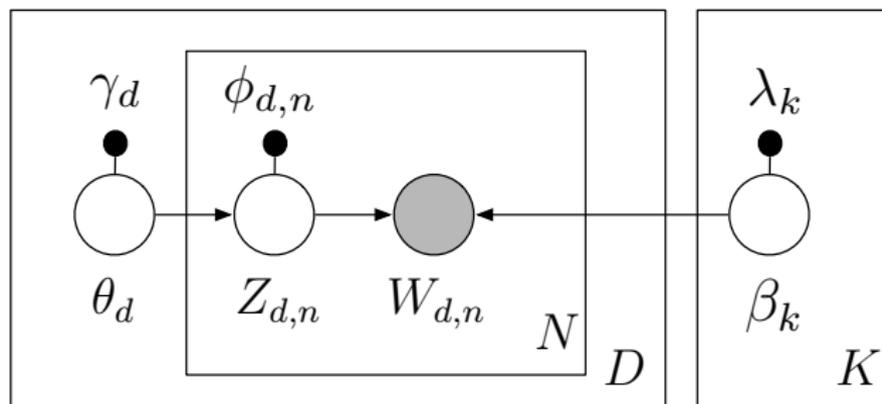


- In the “global step” we aggregate the parameters computed from the local step and update the parameters for the topics.

# Example topic inference

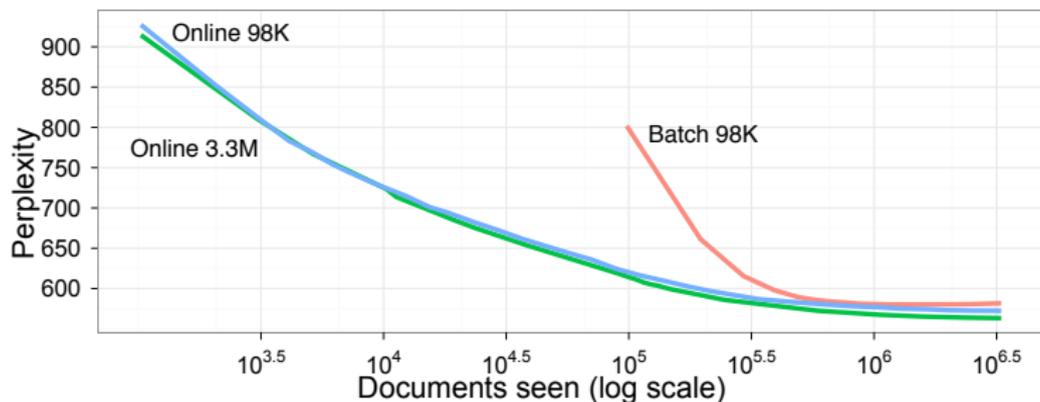
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|-------------|--------------|--------------|-------------|
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| genome      | evolutionary | host         | models      |
| dna         | species      | bacteria     | information |
| genetic     | 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 |

# Online inference for LDA



- 1 Randomly pick a document.
- 2 Perform local variational inference with the current topics.
- 3 Form “fake” topics, treating the sampled document as though it were the only document in the collection.
- 4 Update the topics to be a weighted average of the fake topics and current topics.

# Analyzing 3.3M articles from Wikipedia



| Documents analyzed | 2048  | 4096   | 8192   | 12288   | 16384   | 32768  | 49152   | 65536   |
|--------------------|---|--|--|---|---|--|---|---|
| Top eight words    | systems<br>road<br>made<br>service<br>announced<br>national<br>west<br>language | systems<br>health<br>communication<br>service<br>billion<br>language<br>care<br>road | service<br>systems<br>health<br>companies<br>market<br>communication<br>company<br>billion | service<br>systems<br>companies<br>business<br>company<br>billion<br>health<br>industry | service<br>companies<br>systems<br>business<br>company<br>industry<br>market<br>billion | business<br>service<br>companies<br>industry<br>company<br>management<br>systems<br>services | business<br>service<br>companies<br>industry<br>services<br>company<br>management<br>public | business<br>industry<br>service<br>companies<br>services<br>company<br>management<br>public |

# Why does this work?

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## A STOCHASTIC APPROXIMATION METHOD<sup>1</sup>

BY HERBERT ROBBINS AND SUTTON MONRO

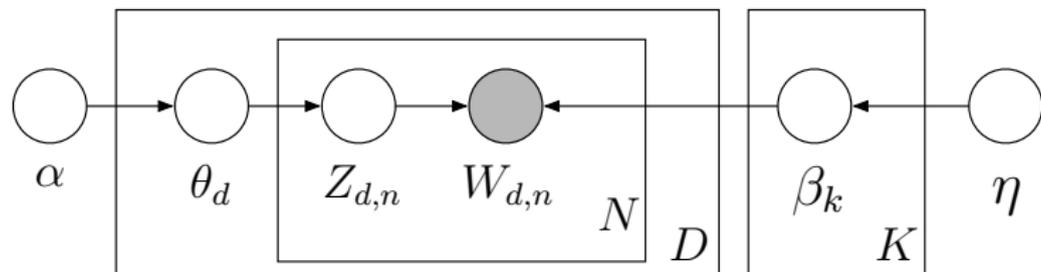
*University of North Carolina*

**1. Summary.** Let  $M(x)$  denote the expected value at level  $x$  of the response to a certain experiment.  $M(x)$  is assumed to be a monotone function of  $x$  but is unknown to the experimenter, and it is desired to find the solution  $x = \theta$  of the equation  $M(x) = \alpha$ , where  $\alpha$  is a given constant. We give a method for making successive experiments at levels  $x_1, x_2, \dots$  in such a way that  $x_n$  will tend to  $\theta$  in probability.

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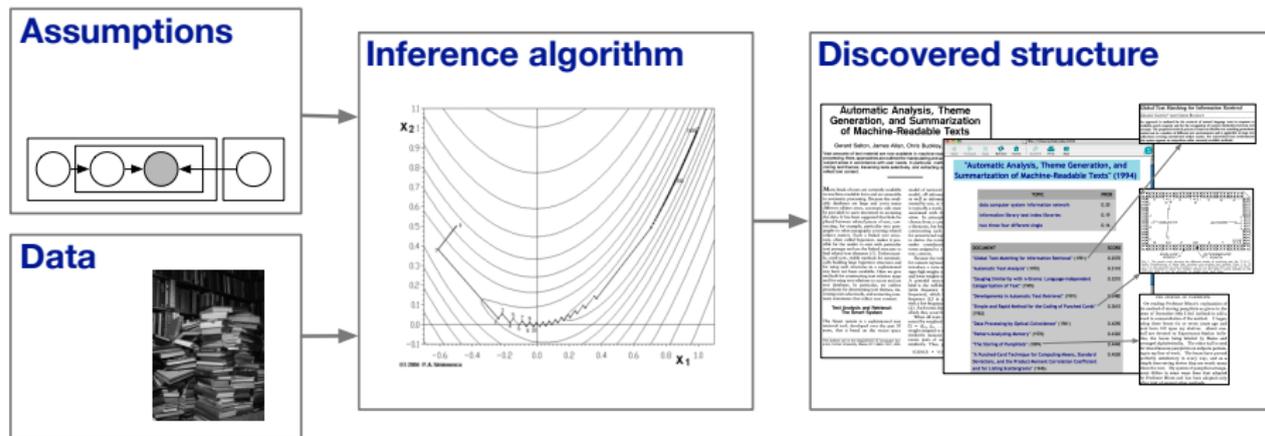
- Why waste time with the real gradient, when a cheaper noisy estimate of the gradient will do (Robbins and Monro, 1951)?
- Idea: Follow a noisy estimate of the gradient with a step-size.
- By decreasing the step-size according to a certain schedule, we guarantee convergence to a local optimum.
- See Hoffman et al. (2010) and Sato (2001).

# Summary



- Hierarchical Bayesian models of text are a powerful way to explore, summarize and search large archives of documents.
- Algorithmic advances in approximate posterior inference let us apply complex models to large real-world data sets.

# Online inference is promising



- Stochastic variational methods are a general way to approximate a posterior with massive/streaming data.
- Powerful algorithm for topic modeling, and can be adapted hierarchical models for many types of data.
- Software and papers: [www.cs.princeton.edu/~blei/](http://www.cs.princeton.edu/~blei/)

# Open research directions

- **Model diagnostics and model checking**  
Which model should I choose for which task? How does this problem change in the face of streaming data?
- **Interfaces and “downstream” applications of topic modeling**  
What can I do with an annotated corpus? What can I do with a changing approximate posterior?
- **Theoretical understanding of approximate inference**  
What do we know about variational inference from either the statistical or learning perspective?

“We should seek out unfamiliar summaries of observational material, and establish their useful properties... And still more novelty can come from finding, and evading, still deeper lying constraints.”  
(J. Tukey, *The Future of Data Analysis*, 1962)

# On-line variational inference for LDA

- 1: Define  $\rho_t \triangleq (\tau_0 + t)^{-\kappa}$
- 2: Initialize  $\lambda$  randomly.
- 3: **for**  $t = 0$  to  $\infty$  **do**
- 4:   Choose a random document  $w_t$
- 5:   Initialize  $\gamma_{tk} = 1$ . (The constant 1 is arbitrary.)
- 6:   **repeat**
- 7:     Set  $\phi_{t,n} \propto \exp\{\mathbb{E}_q[\log \theta_t] + \mathbb{E}_q[\log \beta_{\cdot, w_n}]\}$
- 8:     Set  $\gamma_t = \alpha + \sum_n \phi_{t,n}$
- 9:     **until**  $\frac{1}{K} \sum_k |\text{change in } \gamma_{t,k}| < \epsilon$
- 10:   Compute  $\tilde{\lambda}_k = \eta + D \sum_{n \sim w_t} \phi_{t,n}$
- 11:   Set  $\lambda_k = (1 - \rho_t)\lambda_k + \rho_t \tilde{\lambda}_k$ .
- 12: **end for**