

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 by just 250 genes, and that the *Escherichia coli* genome 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 the genome," explains

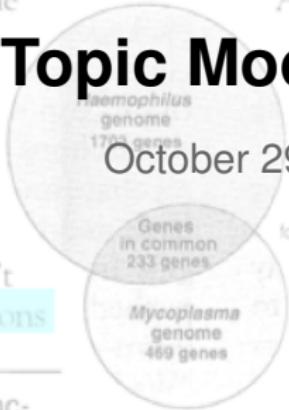
Arcady Mushegian, a computational mo-

lecular biologist at the National Center

of Biotechnology Information (NCBI) in Bethesda, Maryland. Comparing an

S&DS 265 / 565 Introductory Machine Learning

Topic Models



October 29

Genes needed
for biochemical
pathways
+22 genes

Redundant and
parasite-specific
genes removed
- 4 genes

Related and
modern genes
removed
-122 genes

256
genes

Minimal
gene set
250 genes

Ancestral
gene set
128 genes

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

Yale

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

Checkpoint

- Quiz 4 this Thursday (LMs, embeddings, Bayes, topic models)
- Assignment 4 due next Thursday
- Final exam: Monday, December 16, 2pm
- <https://registrar.yale.edu/general-information/final-exams>

Reminder: Panel discussion

Class on Tuesday, December 3:

We will have a panel discussion on

Societal issues for AI and Machine Learning

If you are interested in participating, please email
sds265@yale.edu with Subject iML panel

Bayes demo

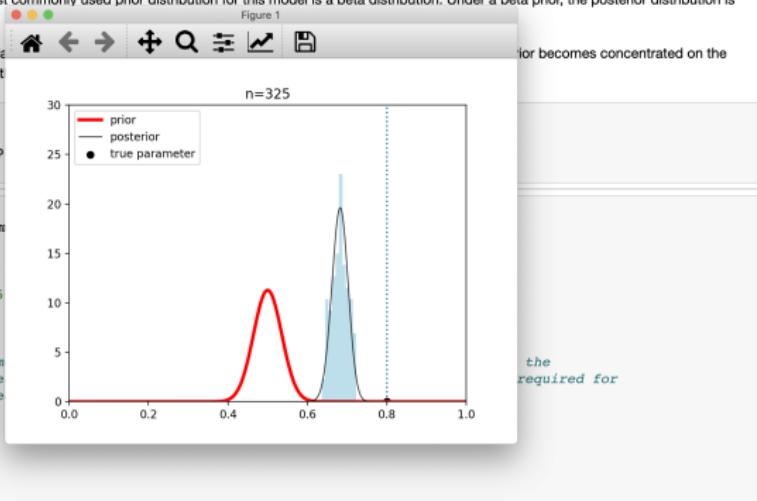
Demo code for Bayesian analysis

In this notebook we illustrate some of the basic models and priors for Bayesian inference. These concepts will be important for our discussions about "topic models."

First, we illustrate the situation where the parameter θ that we are modeling is a Bernoulli parameter. This can be thought of as the probability that flipping a certain coin comes up heads. The most commonly used prior distribution for this model is a beta distribution. Under a beta prior, the posterior distribution is again a beta distribution.

This is illustrated in the following simulation. We start with a true parameter. But as the variance of the sample size increases, the posterior distribution becomes concentrated on the true parameter.

```
In [5]: import os, gzip  
import numpy as np  
import matplotlib.pyplot as plt  
  
In [*]: %matplotlib qt  
from scipy.special import gammainc  
from scipy import random  
from scipy.stats import beta  
  
theta = np.linspace(0,1,num=5  
fig = plt.figure(1)  
plt.ion()  
  
# The following are the parameters  
# variance of the prior decreases  
# the posterior to be centered  
  
scale = 100  
a0 = scale*1  
b0 = scale*1  
  
sample_size = 100
```



the
required for

Reading

- See notes on Bayesian inference on iML site
(bayes-notes.pdf)
- Not necessary to understand everything—but you should be able to do some of the basic “coin flipping” calculations
- We’ll build on this when discussing topic models

Summary from last week

- Mixtures are latent variable models
- The mixing weight encodes a hidden variable
- Computing with mixtures uses basic probabilistic reasoning
- Bayesian inference is popular in ML
- In a Bayesian approach, the parameters are random, and the data are fixed.
- Three ingredients: Prior, likelihood, posterior

Next up: Topic models

- High level intro to topic models
- Use of latent variables, mixtures

Readings:

<http://www.cs.columbia.edu/~blei/topicmodeling.html>

A survey paper describing many of these ideas in more detail is here:

<https://www.cs.columbia.edu/~blei/papers/Blei2012.pdf>

Topic models

- Topic models automatically extract “semantic themes” from large document collections
- Based on latent variables, mixtures, and Bayesian inference
- Can be useful for a wide variety of data

Probabilistic modeling

- ① Data are assumed to be observed from a generative probabilistic process that includes hidden variables.
 - *In text, the hidden variables are the thematic structure.*
- ② Infer the hidden structure using posterior inference
 - *What are the topics that describe this collection?*
- ③ Situate new data into the estimated model.
 - *How does a new document fit into the topic structure?*

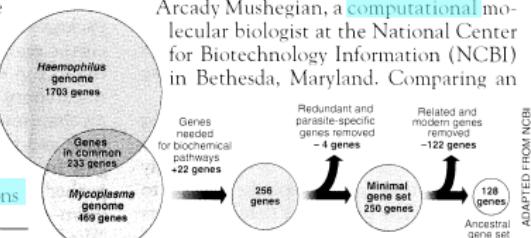
Latent Dirichlet allocation (LDA)

Seeking Life's Bare (Genetic) Necessities

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



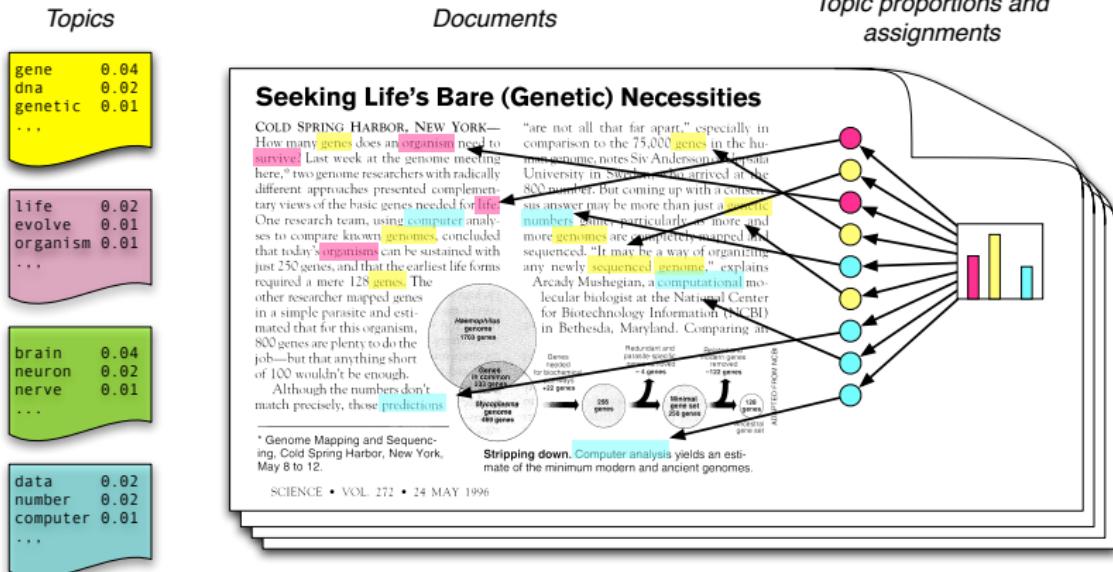
ADAPTED FROM NCBI

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

SCIENCE • VOL. 272 • 24 MAY 1996

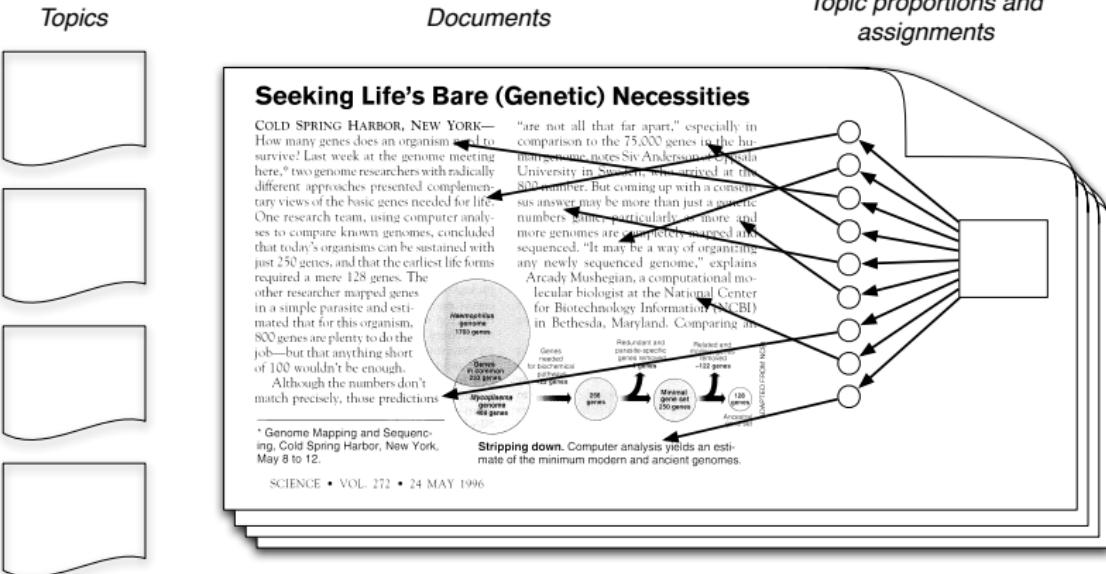
Simple intuition: Documents exhibit multiple topics.

Generative model for LDA



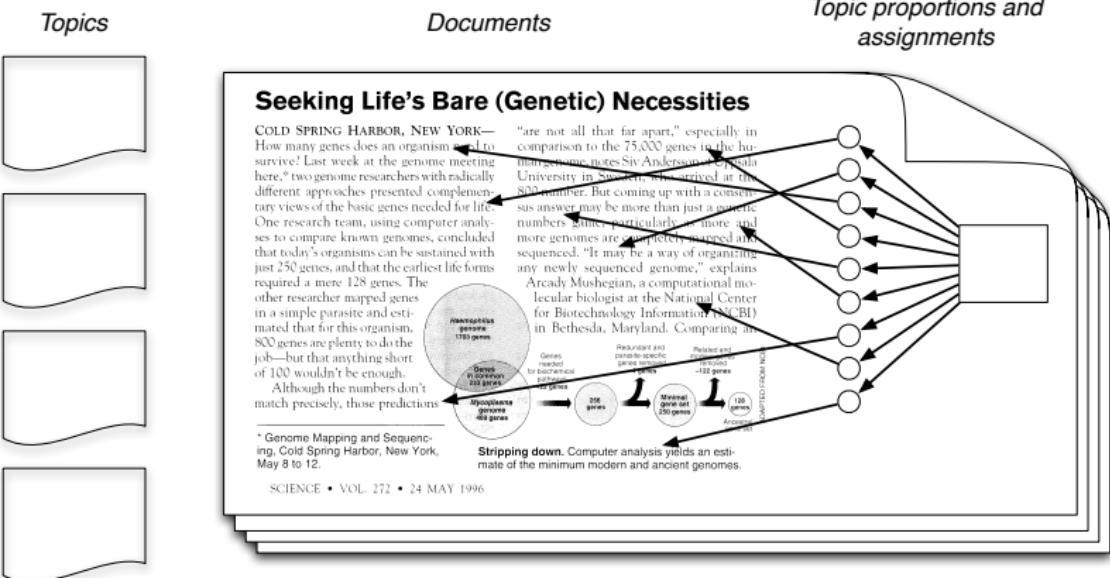
- Each **topic** is a distribution over words
- Each **document** is a mixture of corpus-wide topics
- Each **word** is drawn from one of those topics

The posterior distribution



- 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
- $$p(\text{topics, proportions, assignments} \mid \text{documents})$$

A little dicey



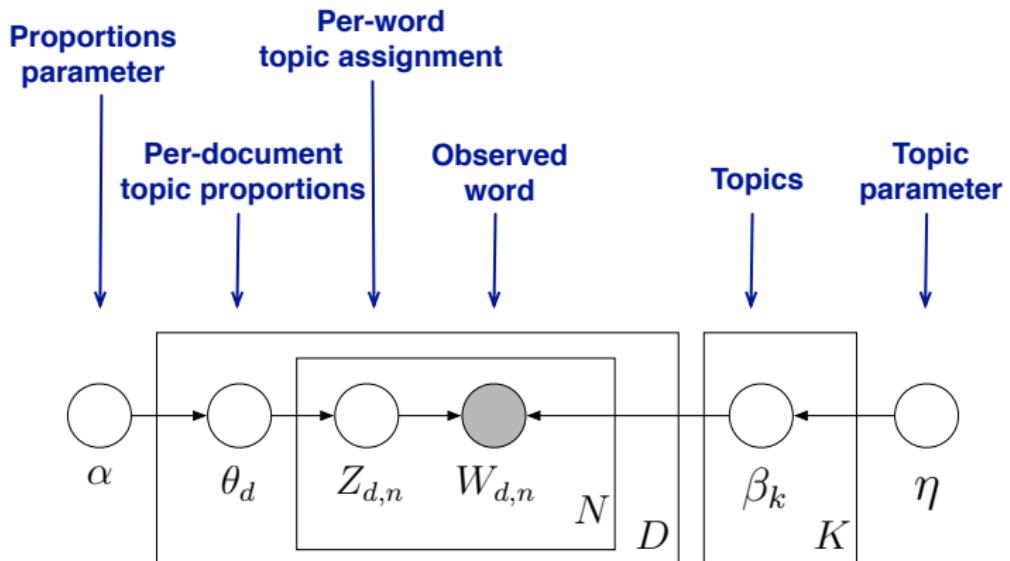
Let's illustrate this generative process

A little dicey



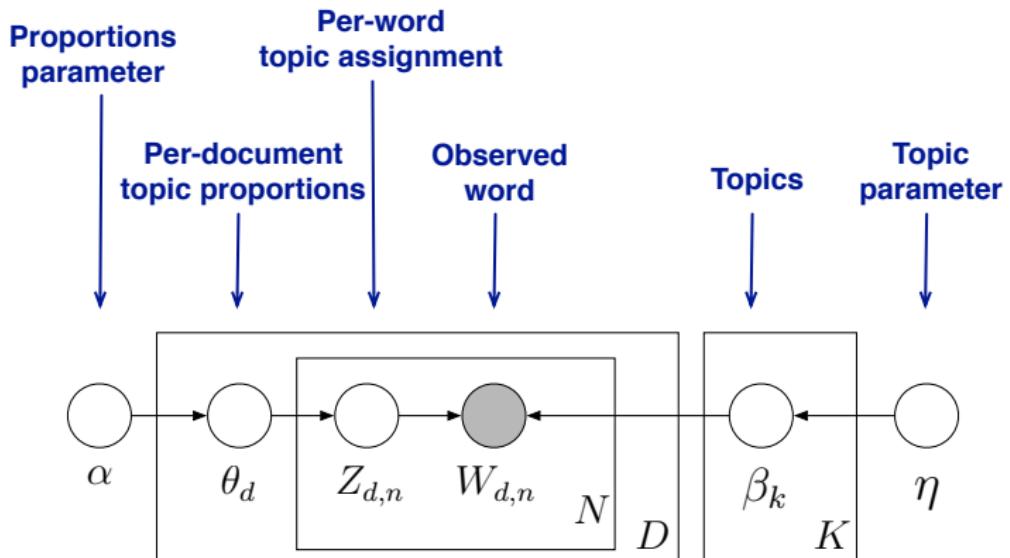
Left: Four topics β_k drawn from the prior; used across documents
Right: A distribution over topics θ ; used for a specific document

LDA as a graphical model



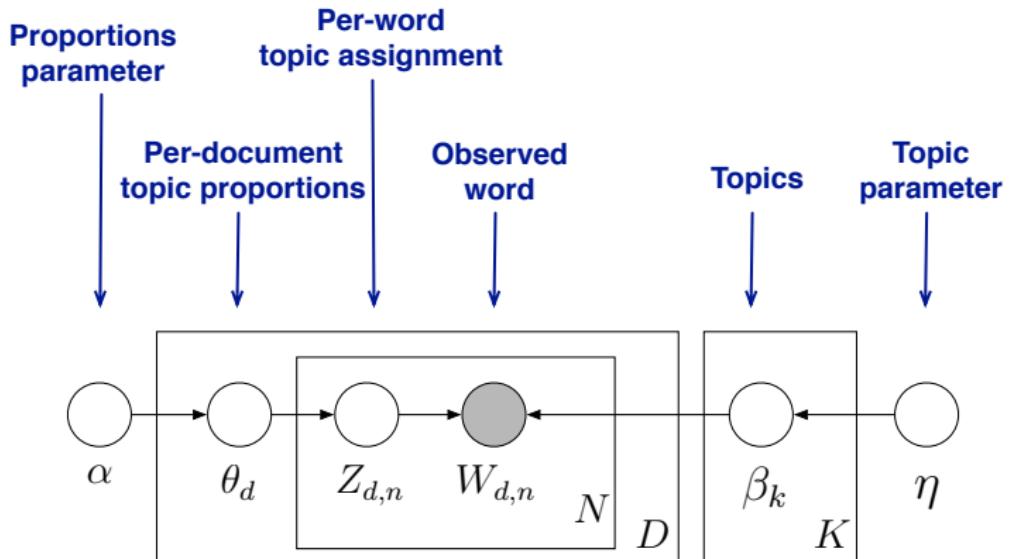
- Encodes our assumptions about the data
- Connects to algorithms for computing with data
- See *Pattern Recognition and Machine Learning* (Bishop, 2006).

LDA as a graphical model



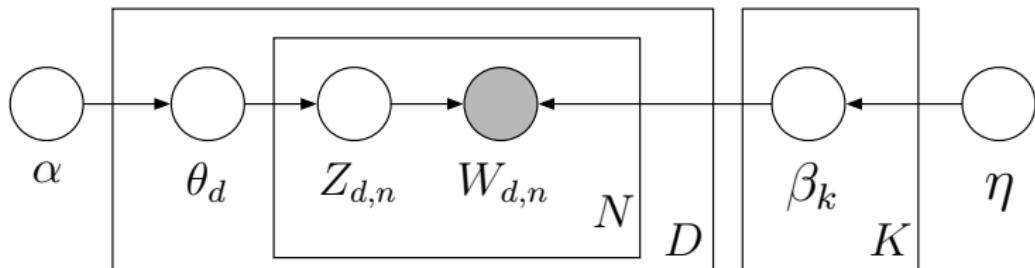
- Nodes are random variables; edges indicate dependence.
- Shaded nodes are observed.
- Plates indicate replicated variables.

LDA as a graphical model



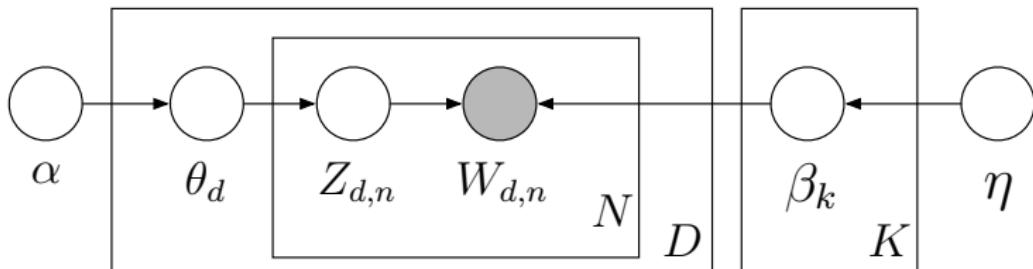
$$\prod_{i=1}^K p(\beta_i | \eta) \prod_{d=1}^D p(\theta_d | \alpha) \left(\prod_{n=1}^N p(z_{d,n} | \theta_d) p(w_{d,n} | \beta_{1:K}, z_{d,n}) \right)$$

LDA



- This joint defines a posterior.
- From a collection of documents, infer
 - Per-word topic assignment $Z_{d,n}$
 - Per-document topic proportions θ_d
 - Per-corpus topic distributions β_k
- Then use posterior expectations to perform the task at hand, e.g., information retrieval, document similarity, exploration, ...

Example inference



- **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.

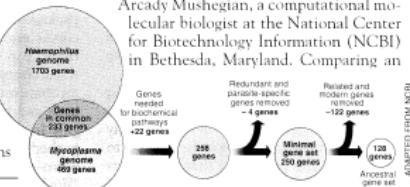
Example inference

Seeking Life's Bare (Genetic) Necessities

COLD SPRING HARBOR, NEW YORK—How many genes does an organism need to survive? Last week at the genome meeting here,⁶ 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.

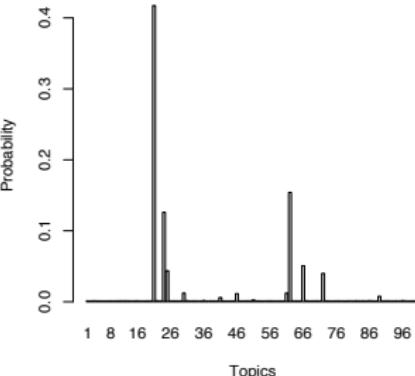
Although the numbers don't match precisely, those predictions

"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



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

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



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
sequences	common	tuberculosis	simulations

Example inference (II)

Chaotic Beetles

Charles Godfray and Michael Hassell

Ecologists have known since the pioneering work of May in the mid-1970s (1) that the population dynamics of animals and plants can be exceedingly complex. This complexity arises from two sources: The tangled web of interactions that constitute any natural community provide a myriad of different pathways for species to interact, both directly and indirectly. And even in isolated populations the nonlinear feedback processes present in all natural populations can result in complex dynamic behavior. Natural populations can show persistent oscillatory dynamics and chaos, the latter characterized by extreme sensitivity to initial conditions. If such chaotic dynamics were common in nature, then this would have important ramifications for the management and conservation of natural resources. On page 389 of this issue, Costantino *et al.* (2) provide the most

convincing evidence to date of complex dynamics and chaos in a biological population—of the flour beetle, *Tribolium castaneum* (see figure).

It has proven extremely difficult to demonstrate complex dynamics in populations in the field. By its very nature, a chaotically fluctuating population will superficially resemble a stable or cyclic population buffeted by the normal random perturbations experienced by all species. Given a long enough time series, diagnostic tools from nonlinear mathematics can be used to identify the telltale signatures of chaos. In phase space, chaotic trajectories come to lie on “strange attractors,” curious geometric objects with fractal structure and hence noninteger dimension. As they

move over the surface of the attractor, sets of adjacent trajectories are pulled apart, then stretched and folded, so that it becomes impossible to predict exact population densities into the future. The strength of the mixing that gives rise to the extreme sensitivity to initial conditions can be measured mathematically estimating the Liapunov exponent, which is positive for chaotic dynamics and nonpositive otherwise. There have been many attempts to estimate attractor dimension and Liapunov exponents from time series data, and some candidate chaotic population have been identified (some insects, rodents, and most convincingly, human childhood diseases), but the statistical difficulties preclude any broad generalization (3).

An alternative approach is to parameterize population models with data from natural populations and then compare their predictions with the dynamics in the field. This technique has been gaining popularity in recent years, helped by statistical advances in parameter estimation. Good ex-



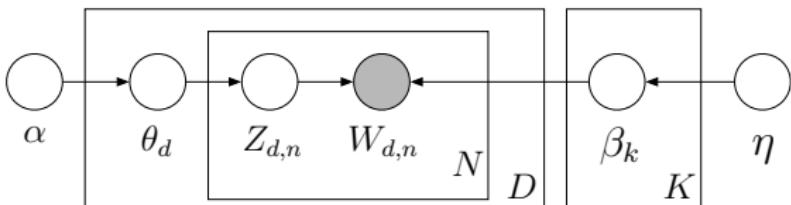
Cannibalism and chaos.
The flour beetle, *Tribolium castaneum*, exhibits chaotic population dynamics when the amount of cannibalism is altered in a mathematical model.

The authors are in the Department of Biology, Imperial College at Silwood Park, Ascot, Berks, SL5 7PZ UK. E-mail: m.hassell@ic.ac.uk

Example inference (II)

problem	model	selection	species
problems	rate	male	forest
mathematical	constant	males	ecology
number	distribution	females	fish
new	time	sex	ecological
mathematics	number	species	conservation
university	size	female	diversity
two	values	evolution	population
first	value	populations	natural
numbers	average	population	ecosystems
work	rates	sexual	populations
time	data	behavior	endangered
mathematicians	density	evolutionary	tropical
chaos	measured	genetic	forests
chaotic	models	reproductive	ecosystem

Posterior inference for LDA



- There is a large literature on approximating the posterior.
- We will focus on
 - Gibbs sampling
 - Mean-field variational methods (batch and online)



Markov chain Monte Carlo

- Construct a **Markov chain** on the hidden variables, whose limiting distribution is the posterior.
- Collect **independent samples** from that distribution; approximate the posterior with them
- In **Gibbs sampling** the chain is defined by the conditional distribution of each hidden variable given observations and the current setting of the other hidden variables.

Approximate inference

- We'll talk a bit about Gibbs sampling
- Variational inference saved for Intermediate Machine Learning (S&DS 365, IML)

Idea behind Gibbs sampling

- Only the assignments $Z_{n,d}$ are needed
- From these we can infer the proportions θ_d (per document)
- And the topics β_k (per corpus)
- The following slides indicate how in a toy example

Idea behind Gibbs sampling

At each time step in the algorithm, we have an assignment $Z_{n,d}$ of a topic to each word $w_{n,d}$ in every document d

Repeat forever:

- Select a word $w_{n,d}$
- Holding all of the other assignments $Z_{n',d'}$ fixed, calculate the probability distribution over $Z_{n,d}$ for that word
- Sample from that distribution to get a (potentially new) assignment $Z_{n,d}$

Toy example: 3 topics, 3 docs

w	z	w	z	w	z
meth	2	drug	3	inning	1
father	1	baseball	2	mother	3
divorce	3	hit	1	son	1
drug	1	inning	2	hit	2
illegal	1	steroids	1	baseball	3

Toy example: 3 topics, 3 docs

w	z	w	z	w	z
meth	1	drug	1	inning	1
father	2	baseball	2	mother	1
divorce	2	hit	2	son	2
drug	1	inning	3	hit	3
illegal	3	steroids	1	baseball	2

Toy example: 3 topics, 3 docs

w	z	w	z	w	z
meth	1	drug	1	inning	2
father	3	baseball	2	mother	3
divorce	3	hit	2	son	3
drug	1	inning	2	hit	2
illegal	1	steroids	1	baseball	2

Extensions

Modeling richer assumptions

- Correlated topic model
- Dynamic topic model

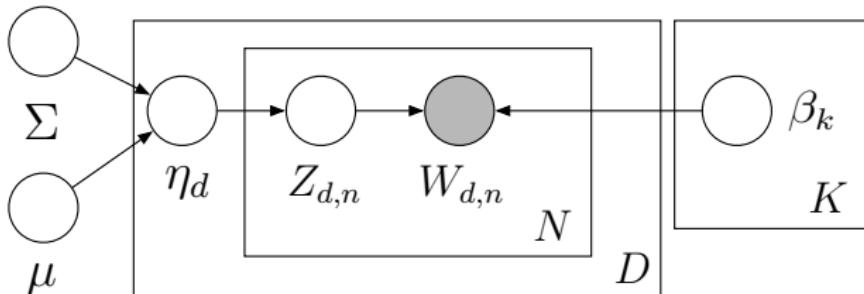
Shortcoming of the Dirichlet

- Dirichlet for topic proportions:

$$p(\theta | \alpha) \propto \prod_{j=1}^k \theta_j^{\alpha_j - 1}$$

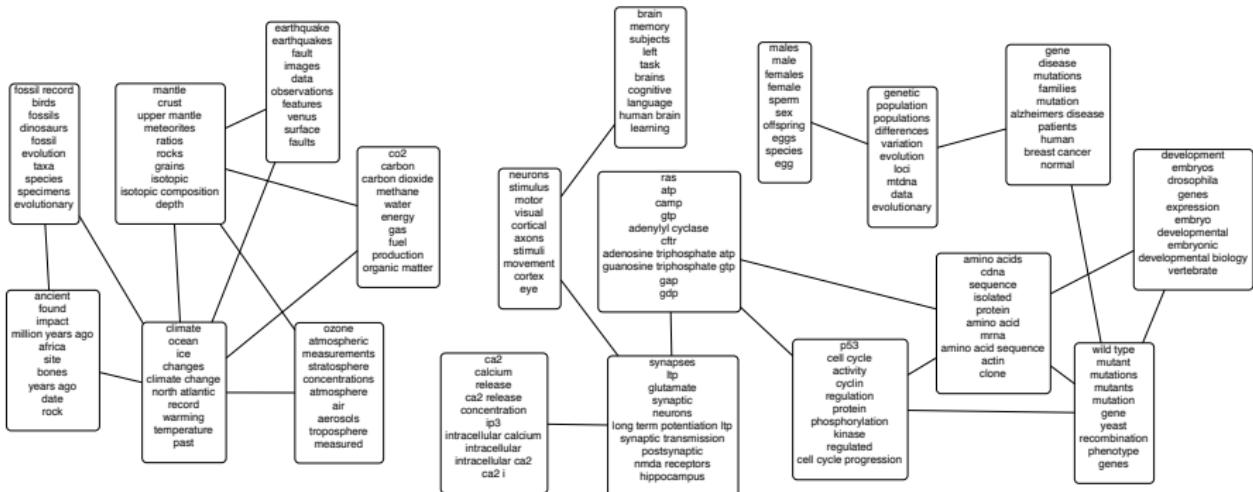
- Near independence of components makes it an unrealistic model
 - ▶ An article about *fossil fuels* is more likely to also be about *geology* than about *genetics*

Correlated topic model

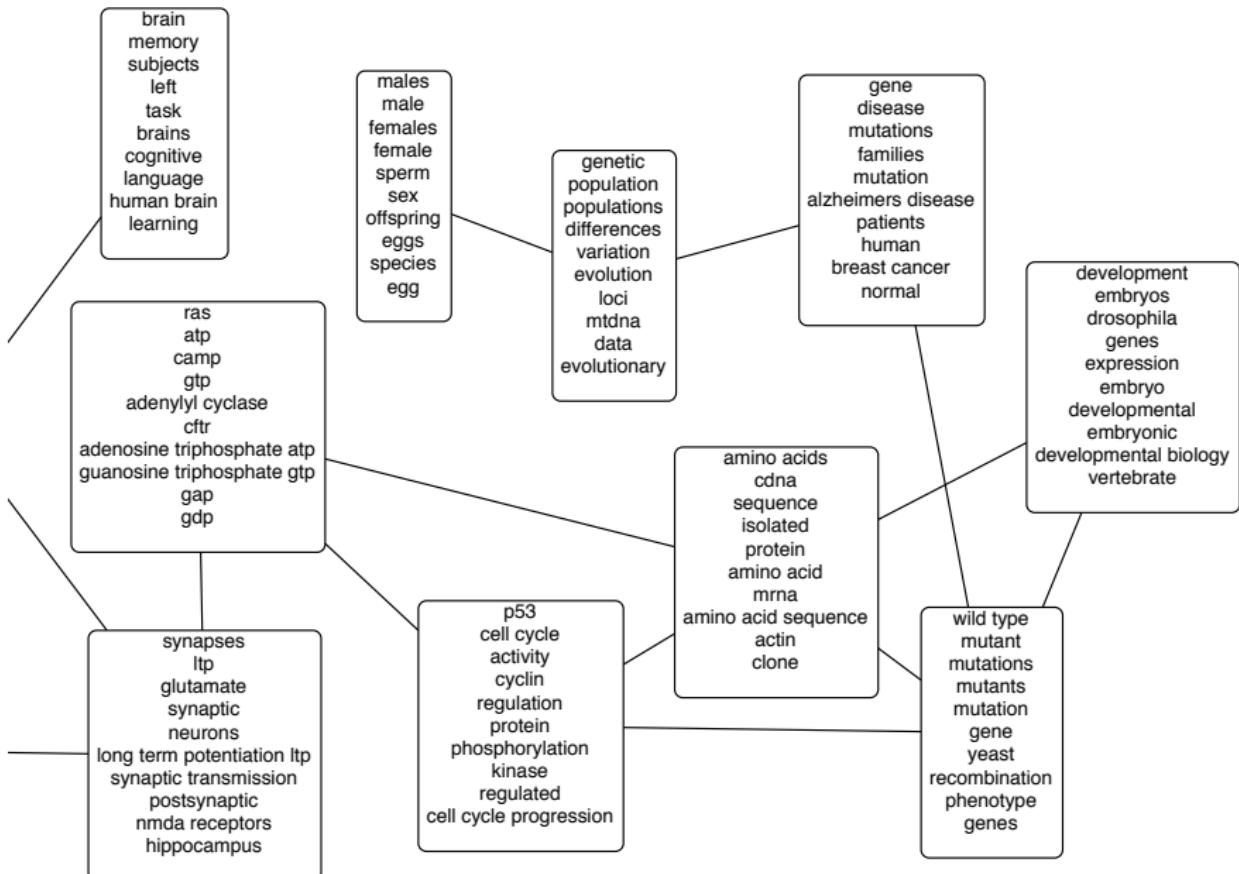


- Draw topic proportions from a logistic normal.
- Useful for:
 - ▶ providing a “map” of topics and how they are related;
 - ▶ better prediction via correlated topics.
- Sacrifice conjugacy: Posterior over θ does not have same form

Topic graphs



Topic graphs



Modeling Evolution of Topics

- In LDA, document order doesn't matter
- The topics should *evolve* over time
 - ▶ “Cleaning Birds” (1883)
 - ▶ “Interspecific Brood Parasitism in Blackbirds (Icterinae): A Phylogenetic Perspective” (1992)
- Many document collections have such dynamics: emails, query logs, news articles, etc.

Science 1893 ⇒ Science 1976

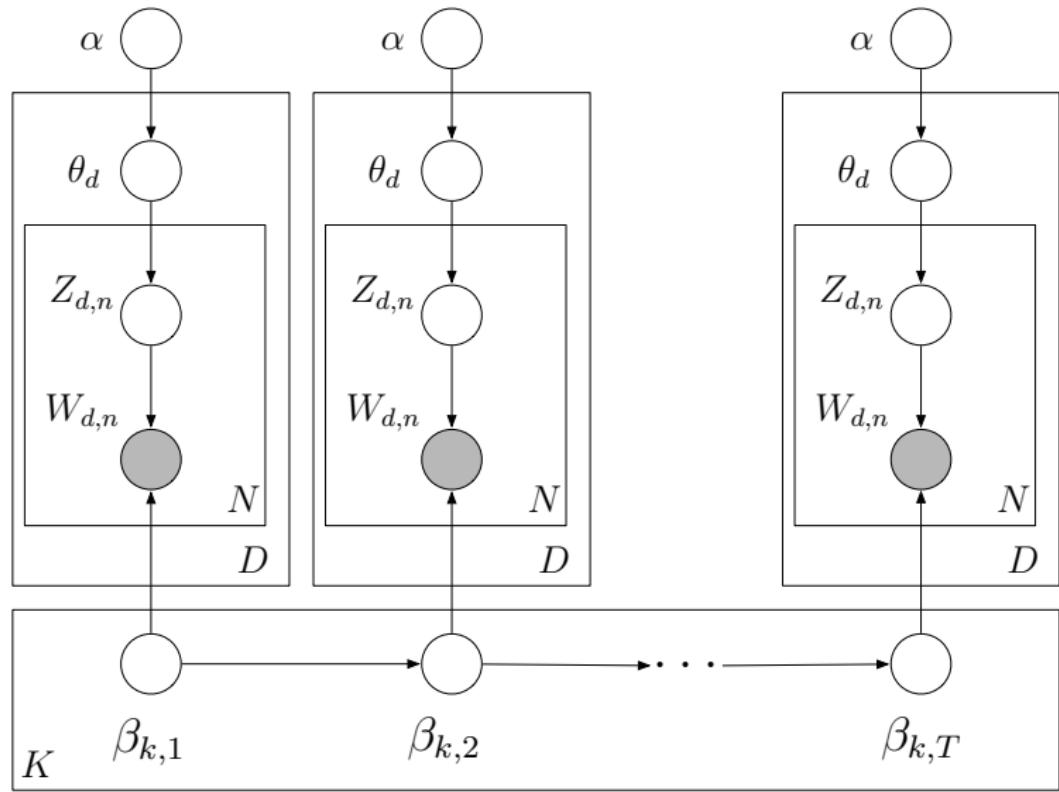
Administration	Limnology	Astronomy	Psychology
association	water	observatory	mind
meeting	lake	observations	nature
american	sea	stars	say
committee	waters	time	science
congress	lakes	made	psychology
members	gulf	astronomical	work
held	great	comet	knowledge
international	depth	star	truth
meetings	river	observed	religion
section	stream	telescope	human

Administration	Limnology	Astronomy	Psychology
house	water	mass	human
congress	concentrations	radio	attempts
science	mercury	objects	theory
bill	fish	astronomy	learning
nsf	samples	xray	ideas
president	soil	stars	new
budget	lake	astronomical	memory
office	ppm	sources	psychology
committee	concentration	observations	behavior
new	waters	observatory	complex

Time series topic model

1. Allow topics evolve between time slices
3. For each document in the current time slice:
 - a. Select a distribution over topics;
 - b. Generate the words from the resulting topic mixture.

Dynamic topic models



Topics drifting in time

Time-corrected document similarity

The Brain of the Orang (1880)

200

SEARCH

There is one case, which were submitted to us at the 4th of December last in connexion with the former: no objection being made we printed them in a separate paper. We have now received from Mr. Webster that the characters before us are satisfactory to him. We therefore request our readers to consider with care.

THE NAME OF THE OWNER



1

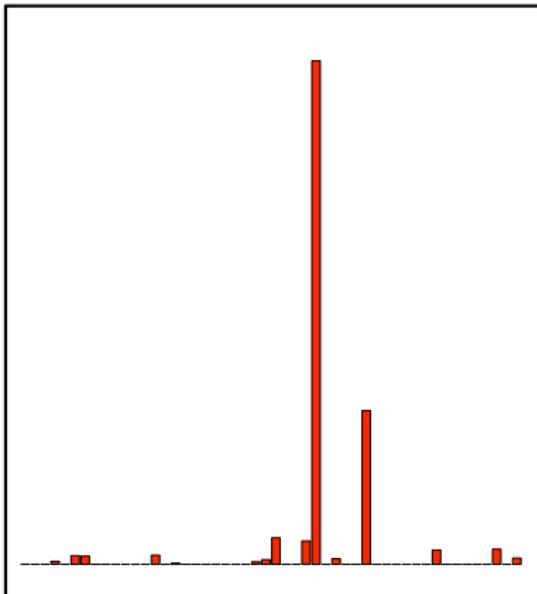
The brain of the Oxybelis, like those of many other serpents, is the same; there are certain minor differences, however, in their disposition in all three. The fissure of Sylvius in particular is more distinct, and the posterior commissure passes along the right optic nerve, instead of the anterior, as in the snake-brain in general.



6

aspiral fissure; externally it is continuous with the right lobe, as the first mesocoxal suture, anteriorly separated from the posterior central convolution or coenonympha than is max, by a fissure which runs parallel with the central fissure. This is in the Otago, which also fissure running parallel with the postcoxal, which divides the upper parital lobule into lobe and max positions. The postcoxal, or the space on the max side of the parital lobe between the post- and

• Florida Proceedings of the Academy of Natural Sciences, Phila., etc.



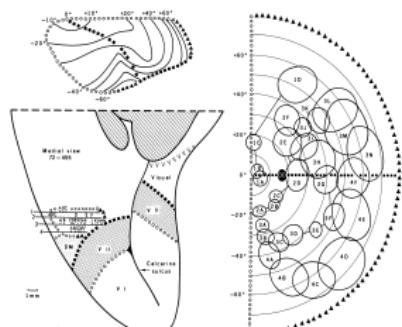
Time-corrected document similarity

Representation of the Visual Field on the Medial Wall of Occipital-Parietal Cortex in the Owl Monkey (1976)

present by recording responses of the medial occipital cortex were plotted with描记technique using techniques in five owl monkeys (2). The monkeys were anesthetized, killed, and prepared for recording. Tissue and pterygomastoid incisions were used to expose the medial occipital cortex or occasionally from single resections it was possible to expose the parietal cortex. The surface of exposed parietal cortex, that is, the surface of the medial occipital cortex, was covered with a thin layer of a translucent plastic hemisphere centered in front of the contralateral eye. A circular white disk was projected onto the plane hemispherical screen with the method of Fernald and Chase (5). The preferred eye usually was

covered with a opaque shield. Electrode tracks and recording sites were extracted from histological sections and photographs of the intact brain.

In all experiments, this form of our most complete mapping of the visual field area, has obtained in the other four experiments, was used to map the visual field organization. Tungsten penetrations were made at an angle of approximately 45° to the surface of the exposed medial occipital cortex in a distance of approximately 1 mm from the center of the receptive field. In all experiments, we found that the receptive fields recorded adjacent to the medial wall of the calcarine fissure were located near the lower margin border with the medial wall of the lateral occipital margin and in the lower quadrant and projected in a broad loop in the periphery toward the contralateral eye. As shown in the maps in Figs. 1 and 2, the occlusion border between the dorsomedial and the medial wall of the lateral occipital margin was located in the lower quadrant near the ventral margin about 30° to 40° from the center (6). Thus, as is shown in Fig. 1 and



Exploring the UN General Debates with Dynamic Topic Models



Luke Lefebvre [Follow](#)
Oct 17, 2018 · 11 min read



Credit: [Vladislav Klapin on Unsplash](#)

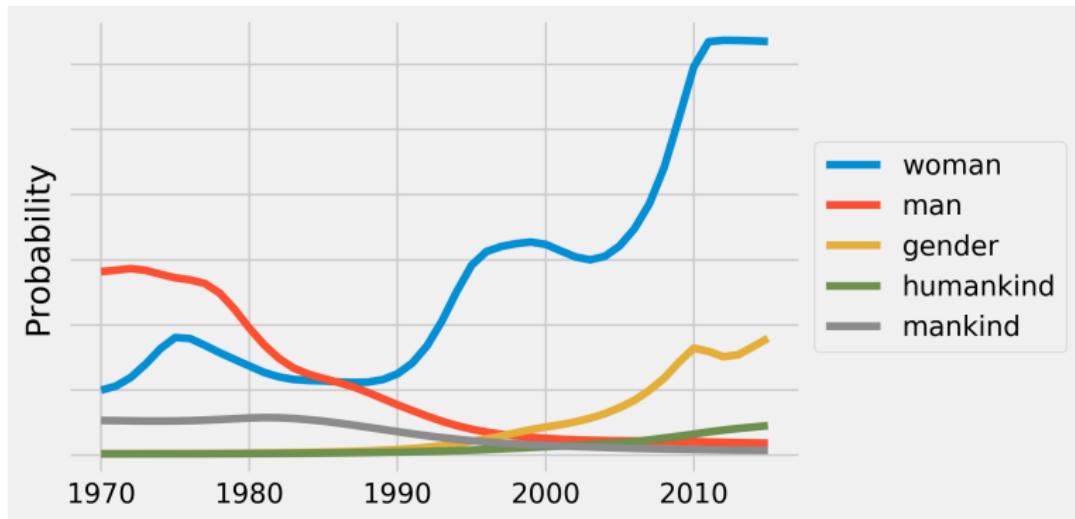
<https://towardsdatascience.com/>

[exploring-the-un-general-debates-with-dynamic-topic-models-72dc0e307696](https://towardsdatascience.com/exploring-the-un-general-debates-with-dynamic-topic-models-72dc0e307696)

Human rights

	1970	1980	1990	2000	2010
0	right	right	right	right	right
1	human	human	human	human	human
2	people	people	freedom	law	law
3	international	freedom	people	democracy	woman
4	principle	international	democracy	respect	freedom
5	justice	political	respect	international	respect
6	freedom	principle	law	people	people
7	law	respect	international	freedom	democracy
8	state	justice	principle	principle	rule
9	must	social	state	must	international

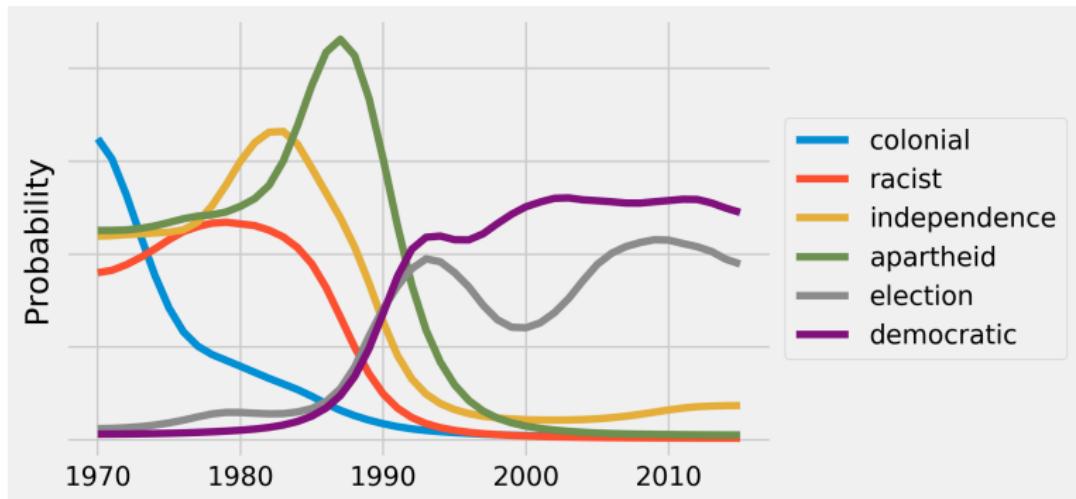
Human rights



Apartheid

	1970	1980	1990	2000	2010
0	africa	africa	africa	african	african
1	african	south	south	peace	country
2	south	african	african	africa	government
3	colonial	namibia	apartheid	country	africa
4	people	people	people	government	people
5	regime	regime	government	community	peace
6	southern	independence	country	democratic	political
7	government	apartheid	namibia	international	community
8	territory	racist	community	republic	democratic
9	apartheid	southern	process	effort	national

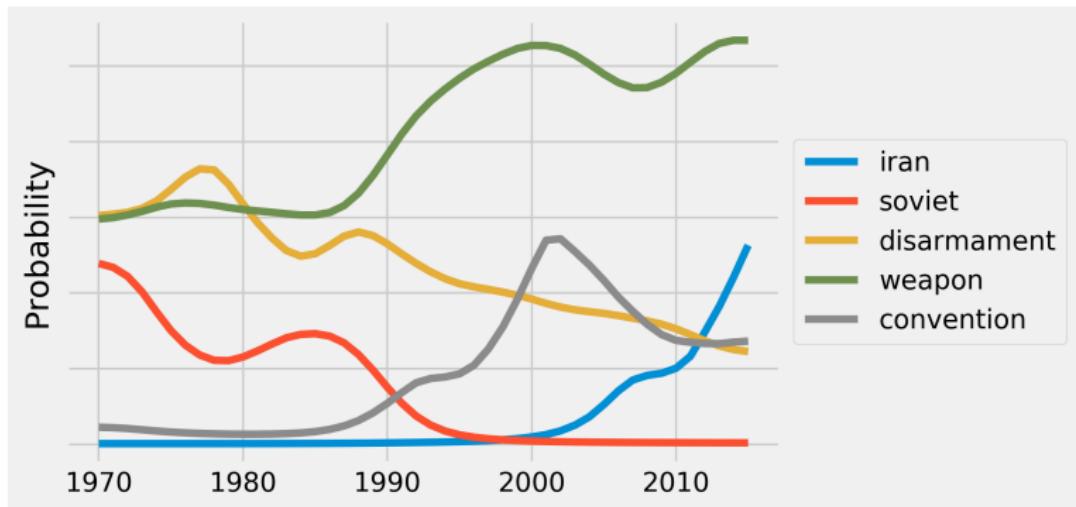
Apartheid



Nuclear arms

	1970	1980	1990	2000	2010
0	nuclear	nuclear	nuclear	weapon	nuclear
1	disarmament	disarmament	weapon	nuclear	weapon
2	weapon	weapon	disarmament	convention	non
3	soviet	arm	treaty	arm	proliferation
4	arm	state	arm	treaty	arm
5	treaty	race	state	disarmament	treaty
6	union	military	chemical	proliferation	international
7	agreement	treaty	agreement	international	disarmament
8	power	soviet	proliferation	non	convention
9	state	power	soviet	destruction	state

Nuclear arms



Topic modeling for equations

Topic	Generated Equations
Quantum physics	<ul style="list-style-type: none">$E = \hbar \frac{\partial^2 S}{\partial t^2} \left(\frac{\partial \varphi}{\partial c} \right) - \frac{k}{\hbar^2} \frac{\partial B}{\partial t} (t + \partial_t \delta).$$\Psi_{\text{pr}} = \sum_{\mathbf{l}} (\psi_{\mathbf{r}+\uparrow} - \psi_{\mathbf{r}\downarrow}^\dagger) + \sum_{\mathbf{r}'} (\psi_{\mathbf{r}',\uparrow}^\dagger - \psi_{\mathbf{r}'\downarrow} \sigma^\dagger).$
Particle physics	<ul style="list-style-type: none">$\mathcal{H} = \frac{1}{4} (\partial_\mu \phi)^2 + 2m \phi_\nu(\phi) + \frac{1}{2} m^2(\phi) (1 - \phi^2)^2.$$m_{\text{eff}}(M) = 1.4 \cdot 10^{-13} \text{ GeV}.$
Relativity	<ul style="list-style-type: none">$\mathcal{M} = \frac{1}{2} g^{\mu\nu} (f_{\mu\nu,\mu} - g_{\mu\nu,\nu} + g_{\nu\nu,b} f_{\mu,\nu}) + \frac{1}{2} g^{\mu\nu}.$$T_{\mu\nu} = \int_0^\infty ds_{\mu\nu} ds^2 + a_\mu^2 dr^2 + r^2 d\Omega^2.$

Uber Topics

From a former student:

Hi Prof. Lafferty,

I took your course last spring. I just wanted to let you know that I'm currently topic modeling at my current job at Uber!

We're using topic models at Uber to discover topics in rider feedback – when riders write comments about their driver after the trip. We're trying to find topics such as 'unprofessional driver', 'driver no-show', 'sexual harassment', etc.

Tutorials

<https://medium.com/@lettier/how-does-lda-work-ill-explain-using-emoji-108abf40fa7d>

<https://towardsdatascience.com/>

[latent-dirichlet-allocation-intuition-math-implementation-and-visualisation-63ccb616e094](https://towardsdatascience.com/latent-dirichlet-allocation-intuition-math-implementation-and-visualisation-63ccb616e094)

Summary

- Topic models automatically extract “semantic themes” from large document collections
- Use mixtures and latent variables
- Estimating Bayesian posterior done with Gibbs sampling
- Many extensions are possible