Machine Learning 2

DS 4420 - Spring 2020

Topic Modeling 1

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Last time:

Clustering —> Mixture Models —> Expectation Maximization (EM)

Today: *Topic models*

Data: $\mathcal{D} = \{\mathbf{x}^{(i)}\}_{i=1}^N \text{ where } \mathbf{x}^{(i)} \in \mathbb{R}^M$

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Data: \mathcal{D} = \{\mathbf{x}^{(i)}\}_{i=1}^N \text{ where } \mathbf{x}^{(i)} \in \mathbb{R}^M Generative Story: z \sim \text{Multinomial}(\phi) \mathbf{x} \sim p_{m{	heta}}(\cdot|z)
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\begin{array}{ll} \textbf{Data:} & \mathcal{D} = \{\mathbf{x}^{(i)}\}_{i=1}^{N} \text{ where } \mathbf{x}^{(i)} \in \mathbb{R}^{M} \\ \\ \textbf{Generative Story:} & z \sim \text{Multinomial}(\phi) \\ & \mathbf{x} \sim p_{\theta}(\cdot|z) \\ \\ \textbf{Model:} & \text{Joint:} & p_{\theta,\phi}(\mathbf{x},z) = p_{\theta}(\mathbf{x}|z)p_{\phi}(z) \\ \\ & \text{Marginal:} & p_{\theta,\phi}(\mathbf{x}) = \sum_{z=1}^{K} p_{\theta}(\mathbf{x}|z)p_{\phi}(z) \end{array}
```

Data: $\mathcal{D} = \{\mathbf{x}^{(i)}\}_{i=1}^N \text{ where } \mathbf{x}^{(i)} \in \mathbb{R}^M$

Generative Story: $z \sim \text{Multinomial}(\phi)$

$$\mathbf{x} \sim p_{\boldsymbol{\theta}}(\cdot|z)$$

Model: Joint: $p_{\theta,\phi}(\mathbf{x},z) = p_{\theta}(\mathbf{x}|z)p_{\phi}(z)$

Marginal: $p_{m{ heta},m{\phi}}(\mathbf{x}) = \sum_{z=1}^K p_{m{ heta}}(\mathbf{x}|z) p_{m{\phi}}(z)$

(Marginal) Log-likelihood:

$$\ell(\boldsymbol{\theta}) = \log \prod_{i=1}^{N} p_{\boldsymbol{\theta}, \boldsymbol{\phi}}(\mathbf{x}^{(i)})$$
$$= \sum_{i=1}^{N} \log \sum_{z=1}^{K} p_{\boldsymbol{\theta}}(\mathbf{x}^{(i)}|z) p_{\boldsymbol{\phi}}(z)$$

Naive Bayes

The model

$$p(c|w_{1:N}, \pi, \theta) \propto p(c|\pi) \prod_{n=1}^{N} p(w_n|\theta_c)$$

$$p(\mathcal{D}|\theta_{1:C}, \pi) = \prod_{d=1}^{D} \left(p(c_d|\pi) \prod_{n=1}^{N} p(w_n|\theta_{c_d}) \right)$$

(Soft) EM

Initialize parameters randomly while not converged

1. E-Step:

Create one training example for each possible value of the latent variables

Weight each example according to model's confidence

Treat parameters as observed

2. M-Step:

Set the **parameters** to the values that maximizes likelihood

Treat pseudo-counts from above as observed

And for NB

For "soft" EM expected # of times

$$P(+|c) = \sum_{i}^{k} P(Z_{i} = c) \cdot Count(t in X_{i})$$
 $P(+|c) = \sum_{i}^{k} P(Z_{i} = c) \cdot IX_{i}$
 $P(+|c) = \sum_{i}^{k} P(Z_{i} = c) \cdot IX_{i}$

TOPIC MODELS



Some content borrowed from: David Blei (Columbia)

- Suppose we have a giant dataset ("corpus") of text, e.g., all of the NYTimes or all emails from a company
 - Cannot read all documents
 - But want to get a sense of what they contain



 Topic models are a way of uncovering, well, "topics" (themes) in a set of documents



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- Topic models are a way of uncovering, well, "topics" (themes) in a set of documents
- Topic models are unsupervised
- Can be viewed as a sort of soft clustering of documents into topics.





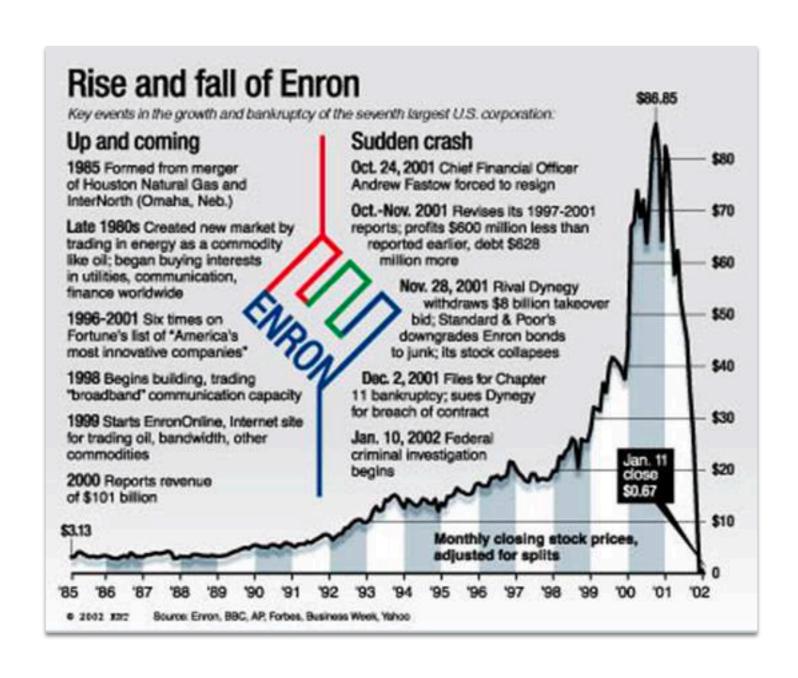
| Topic 1 | Topic 2 | Topic 3 | Topic 4 |
|--------------|----------------------------------|--|-----------------------|
| the "number" | i is | $rac{	ext{that}}{	ext{	ext{proteins}}}$ | easter ishtar |
| in | satan | the | \mathbf{a} |
| to | the | of | ${ m the}$ |
| espn | which | to | have |
| hockey | and | i | with |
| \mathbf{a} | of | if | but |
| his | metaphorical | "number" | ${f english}$ |
| as | $\stackrel{	ext{-}}{	ext{evil}}$ | you | and |
| run | there | $\hat{\mathbf{f}}$ act | is |

Example from Wallach, 2006

Key outputs

- Topics Distributions over words; we hope these are somehow thematically coherent
- Document-topics Probabilistic assignments of topics to documents

Example: Enron emails



Example: Enron emails

| Topic | Terms |
|-------|--|
| 3 | trading financial trade product price |
| 6 | gas capacity deal pipeline contract |
| 9 | state california davis power utilities |
| 14 | ferc issue order party case |
| 22 | group meeting team process plan |

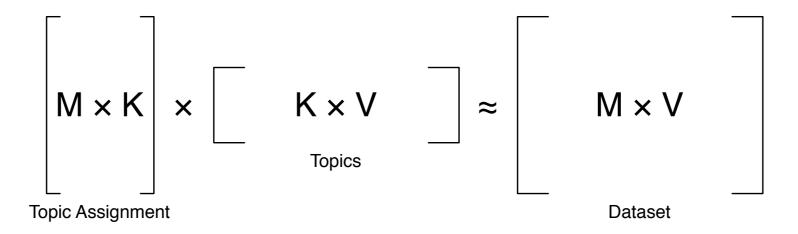
Document-topic probabilities

Yesterday, SDG&E filed a motion for adoption of an electric procurement cost recovery mechanism and for an order short-ening time for parties to file comments on the mechanism. The attached email from SDG&E contains the motion, an executive summary, and a detailed summary of their proposals and recommendations governing procurement of the net short energy requirements for SDG&E's customers. The utility requests a 15-day comment period, which means comments would have to be filed by September 10 (September 8 is a Saturday). Reply comments would be filed 10 days later.

| Topic | Probability |
|-------|-------------|
| 9 | 0.42 |
| 11 | 0.05 |
| 8 | 0.05 |

Topics as Matrix Factorization

One can view topics as a kind of matrix factorization



Topics as Matrix Factorization

One can view topics as a kind of matrix factorization

$$\begin{bmatrix}
M \times K \\
\end{bmatrix} \times \begin{bmatrix}
K \times V \\
Topics
\end{bmatrix} \approx \begin{bmatrix}
M \times V
\end{bmatrix}$$
Topic Assignment

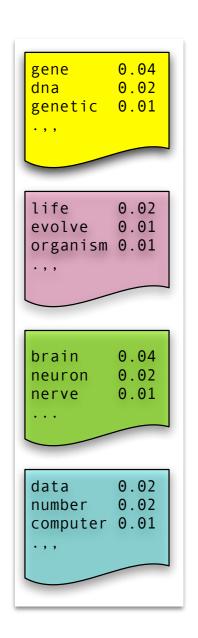
Dataset

 We will try and take a more probabilistic view, but useful to keep this in mind

Probabilistic Word Mixtures

Idea: Model text as a mixture over words (ignore order)

Seeking Life's Bare (Genetic) Necessities COLD SPRING HARBOR, NEW YORK— "are not all that far apart," especially in comparison to the 75,000 genes in the hu-How many genes does an organism need to man genome, notes Siv Andersson of Uppsala survive? Last week at the genome meeting here,* two genome researchers with radically University in Sweden, who arrived at the different approaches presented complemen-800 number. But coming up with a consentary views of the basic genes needed for life. sus answer may be more than just a genetic numbers game, particularly as more and One research team, using computer analyses to compare known genomes, concluded more genomes are completely mapped and that today's organisms can be sustained with sequenced. "It may be a way of organizing just 250 genes, and that the earliest life forms any newly sequenced genome," explains Arcady Mushegian, a computational morequired a mere 128 genes. The other researcher mapped genes lecular biologist at the National Center in a simple parasite and estifor Biotechnology Information (NCBI) Haemophilus mated that for this organism, in Bethesda, Maryland. Comparing an 1703 genes 800 genes are plenty to do the Redundant and job—but that anything short Genes parasite-specific needed aenes removed Genes in common 233 genes of 100 wouldn't be enough. for biochemical -122 genes Although the numbers don't match precisely, those predictions Mycoplasma genome Ancestral * Genome Mapping and Sequencing, Cold Spring Harbor, New York, Stripping down. Computer analysis yields an esti-May 8 to 12. mate of the minimum modern and ancient genomes.



Words: $x_n|z_n = k \sim \text{Discrete}(\boldsymbol{\beta}_k)$

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Topics: $z_n \sim \text{Discrete}(\theta)$

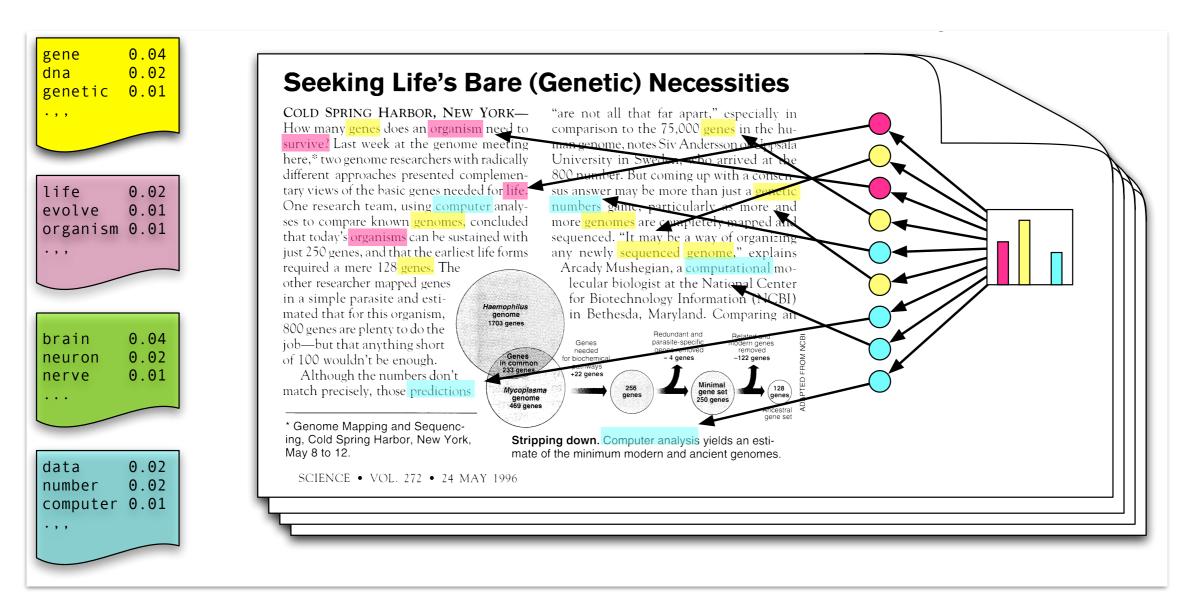
Topics (shared)

Words in Document

(mixture over topics)

Topic Proportions

(document-specific)



Idea: Model *corpus* of documents with *shared* topics

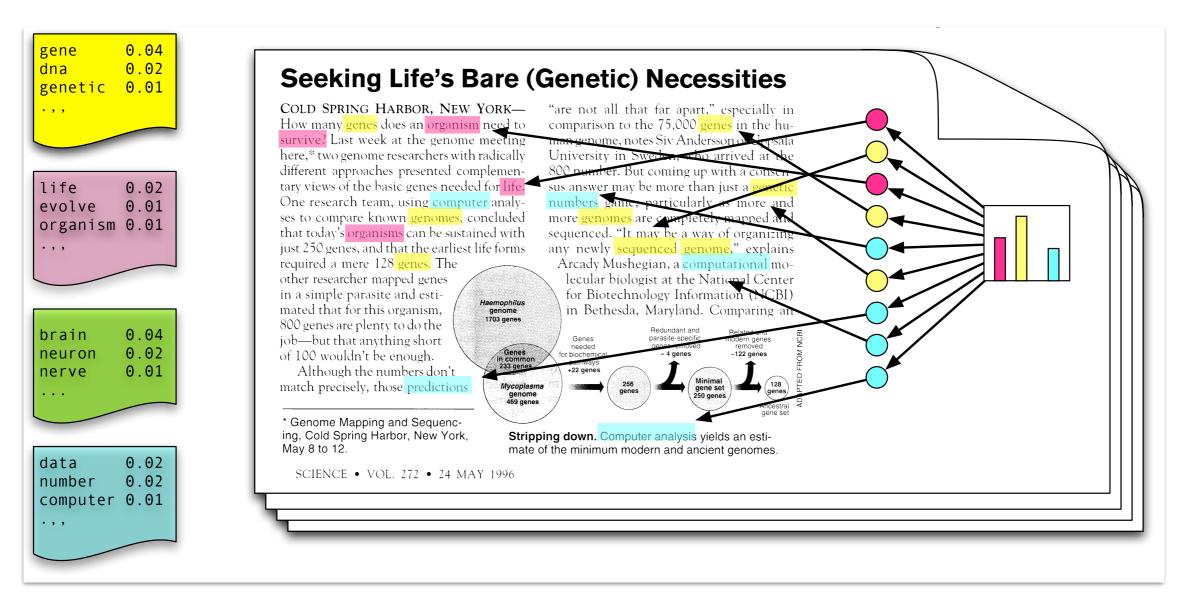
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Topic Proportions

(document-specific)



Each topic is a distribution over words

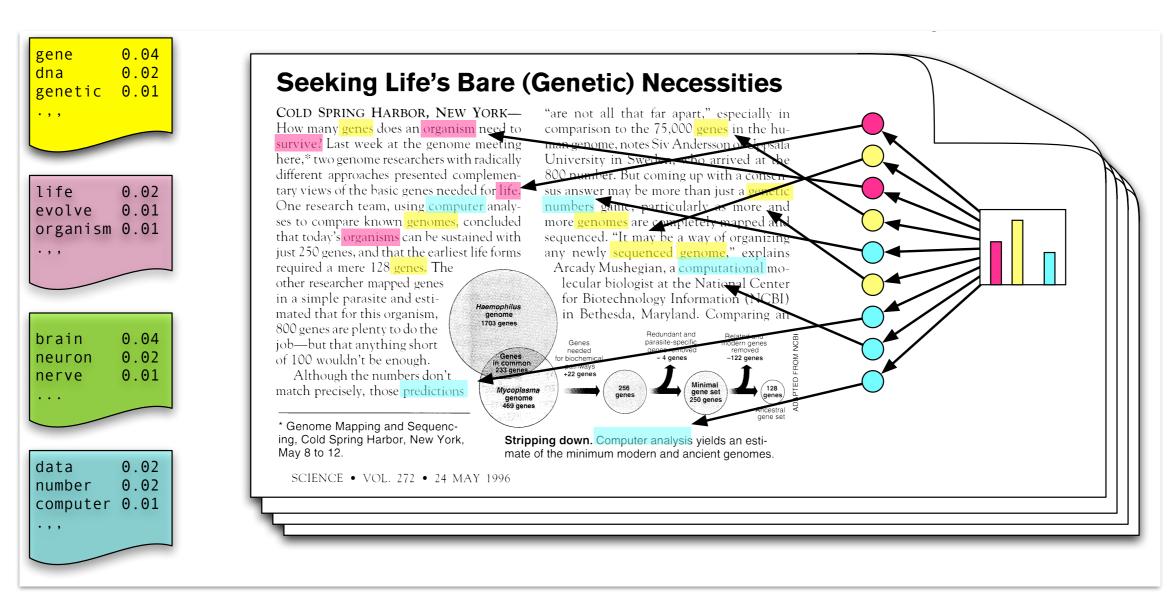
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- Each topic is a distribution over words
- Each document is a mixture over topics

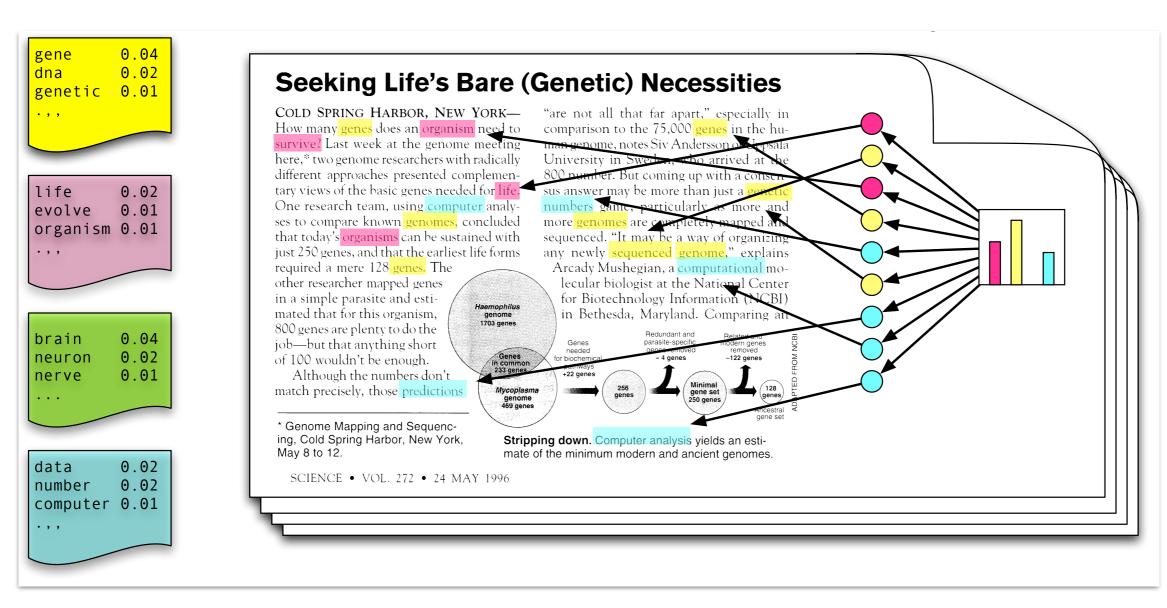
Topics (shared)

Words in Document

(mixture over topics)

Topic Proportions

(document-specific)



- Each topic is a distribution over words
- Each document is a mixture over topics
- Each word is drawn from one topic distribution

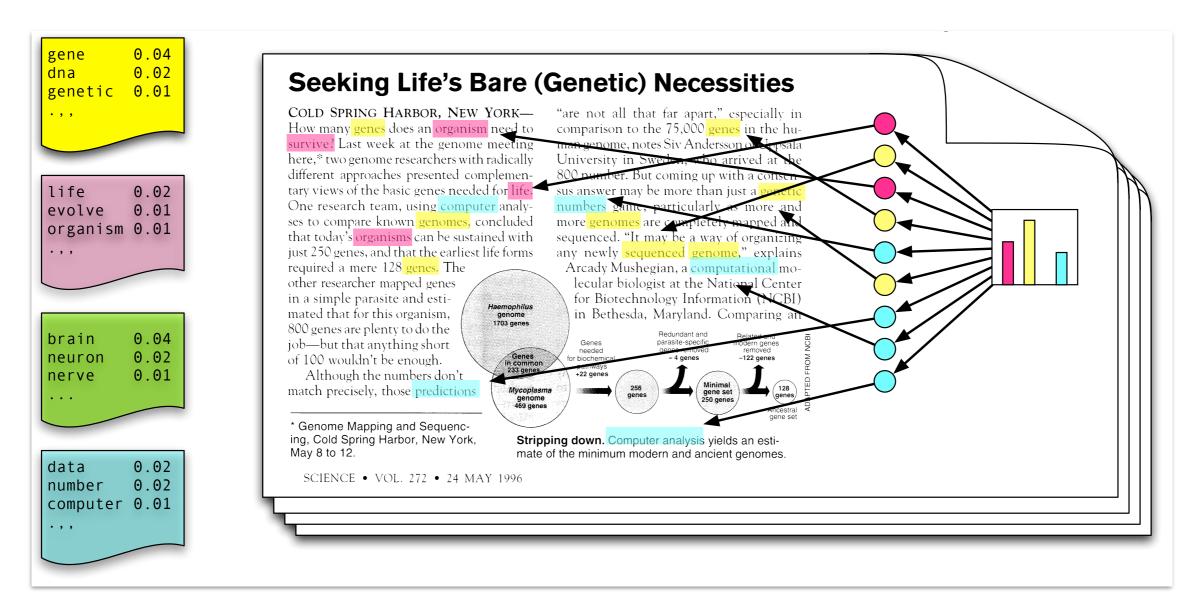
Topics (shared)

Words in Document

(mixture over topics)

Topic Proportions

(document-specific)



 $z_{dn} \sim \text{Discrete}(\theta_d)$

 $x_{dn} \mid z_{dn} = k \sim \text{Discrete}(\boldsymbol{\beta}_k)$

Each document has

Different topic proportions

LDA's view of a document

The William Randolph Hearst Foundation will give \$1.25 million to Lincoln Center, Metropolitan Opera Co., New York Philharmonic and Juilliard School. "Our board felt that we had a real opportunity to make a mark on the future of the performing arts with these grants an act every bit as important as our traditional areas of support in health, medical research, education and the social services," Hearst Foundation President Randolph A. Hearst said Monday in announcing the grants. Lincoln Center's share will be \$200,000 for its new building, which will house young artists and provide new public facilities. The Metropolitan Opera Co. and New York Philharmonic will receive \$400,000 each. The Juilliard School, where music and the performing arts are taught, will get \$250,000. The Hearst Foundation, a leading supporter of the Lincoln Center Consolidated Corporate Fund, will make its usual annual \$100,000 donation, too.

"Arts" "Budgets" "Children" "Education"

Example: Discovering scientific topics

Example Inference

human genome dna genetic genes sequence gene molecular sequencing map information genetics mapping project sequences

evolution evolutionary species organisms life origin biology groups phylogenetic living diversity group new two

common

disease host bacteria diseases resistance bacterial new strains control infectious malaria parasite parasites united tuberculosis

computer models information data computers system network systems model parallel methods networks software new simulations

Example Inference

Seeking Life's Bare (Genetic) Necessities

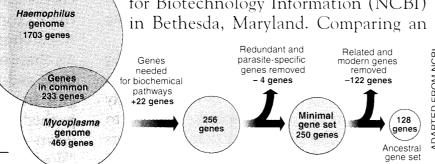
COLD SPRING HARBOR, NEW YORK— How many genes does an organism need to survive? Last week at the genome meeting here,* two genome researchers with radically different approaches presented complementary views of the basic genes needed for life. One research team, using computer analyses to compare known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

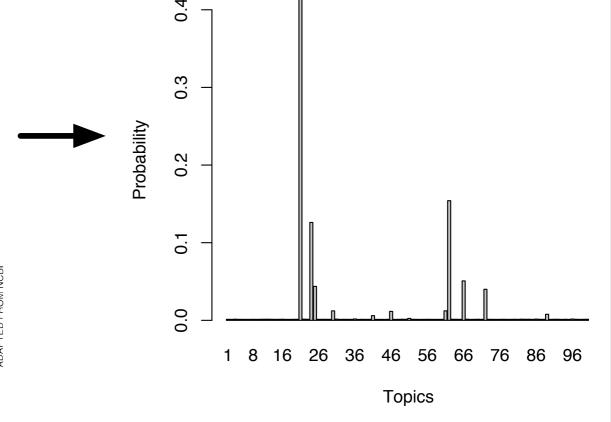
Although the numbers don't match precisely, those predictions

"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)



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.

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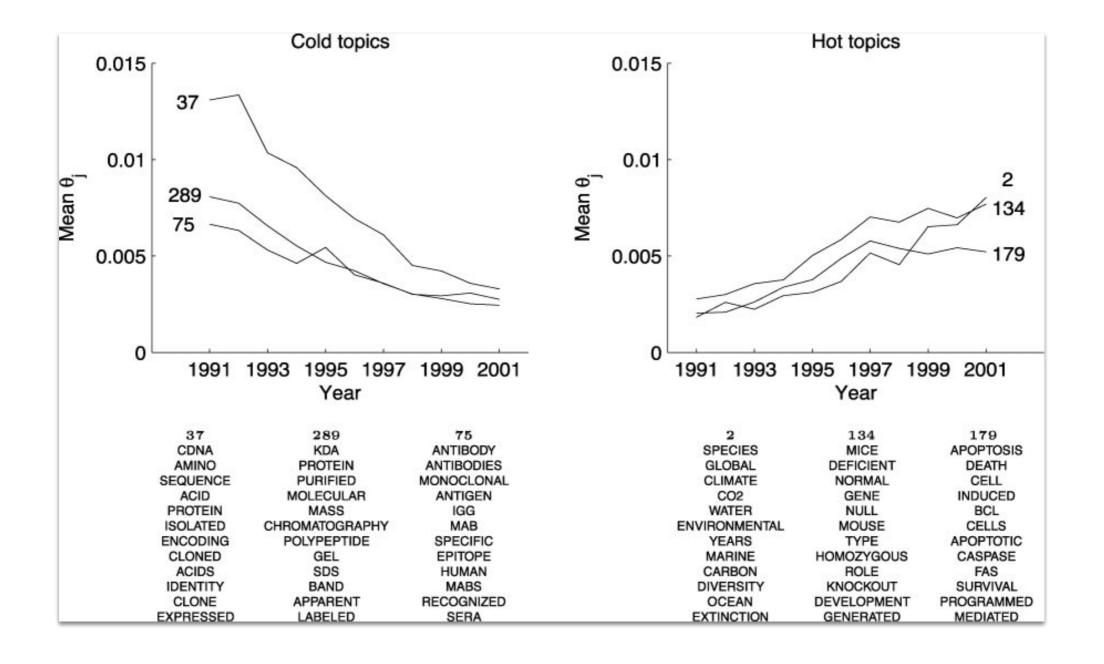
Example Inference

problem problems mathematical number new mathematics university two first numbers work time mathematicians chaos chaotic

model rate constant distribution time number size values value average rates data density measured models

selection male males females sex species female evolution populations population sexual behavior evolutionary genetic reproductive

species forest ecology fish ecological conservation diversity population natural ecosystems populations endangered tropical forests ecosystem



From Naive Bayes to Topic Models (*board*)

Likelihood

$$\log(p(\mathbf{x}_{d} \mid \boldsymbol{\beta}, \boldsymbol{\theta}_{d})) = \sum_{n} \log(p(\mathbf{x}_{dn} \mid \boldsymbol{\beta}, \boldsymbol{\theta}_{d}))$$

$$= \sum_{n} \log\left(\prod_{v} p(\mathbf{x}_{dn} = v \mid \boldsymbol{\beta}, \boldsymbol{\theta}_{d})^{I[\mathbf{x}_{dn} = v]}\right)$$

$$= \sum_{n,v} I[\mathbf{x}_{dn} = v] \log(p(\mathbf{x}_{dn} = v \mid \boldsymbol{\beta}, \boldsymbol{\theta}_{d}))$$

$$= \sum_{n,v} I[\mathbf{x}_{dn} = v] \log\left(\sum_{k} p(\mathbf{x}_{dn} = v, \mathbf{z}_{dn} = k \mid \boldsymbol{\beta}, \boldsymbol{\theta}_{d})\right)$$

$$= \sum_{n,v} I[\mathbf{x}_{dn} = v] \log\left(\sum_{k} p(\mathbf{z}_{dn} = k \mid \boldsymbol{\theta}_{d}) p(\mathbf{x}_{dn} = v \mid \mathbf{z}_{dn} = k, \boldsymbol{\beta})\right)$$

$$= \sum_{n,v} I[\mathbf{x}_{dn} = v] \log\left(\sum_{k} \boldsymbol{\theta}_{d,k} \boldsymbol{\beta}_{k,v}\right)$$

$$= \mathbf{X} \log \boldsymbol{\theta} \boldsymbol{\beta}$$

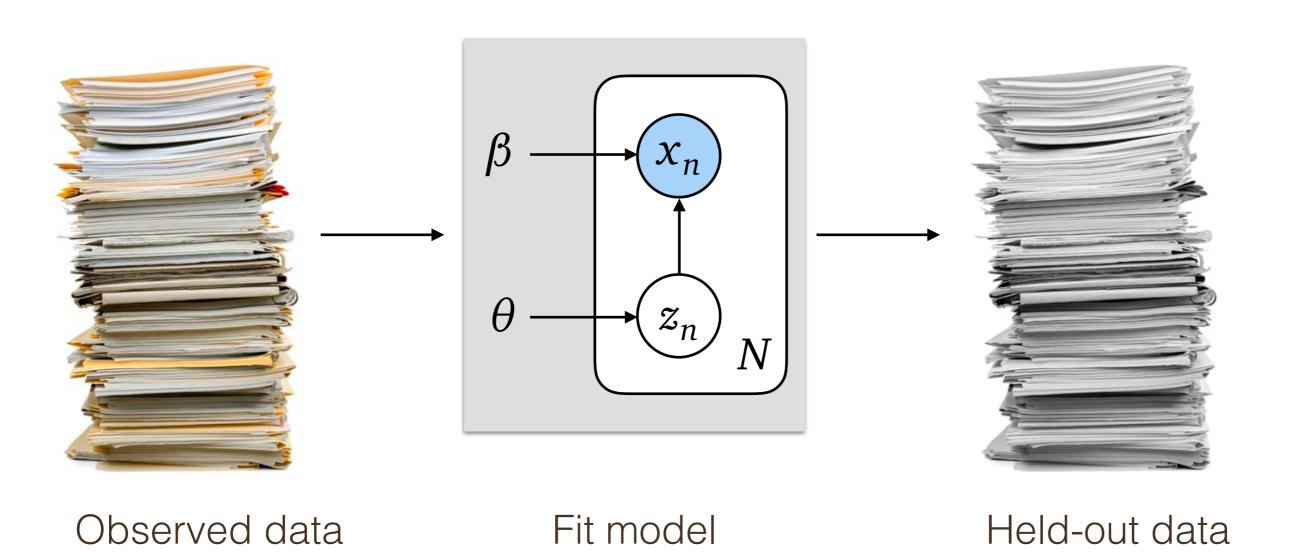
How to estimate parameters in PLSA?

Let's implement... (in class exercise)

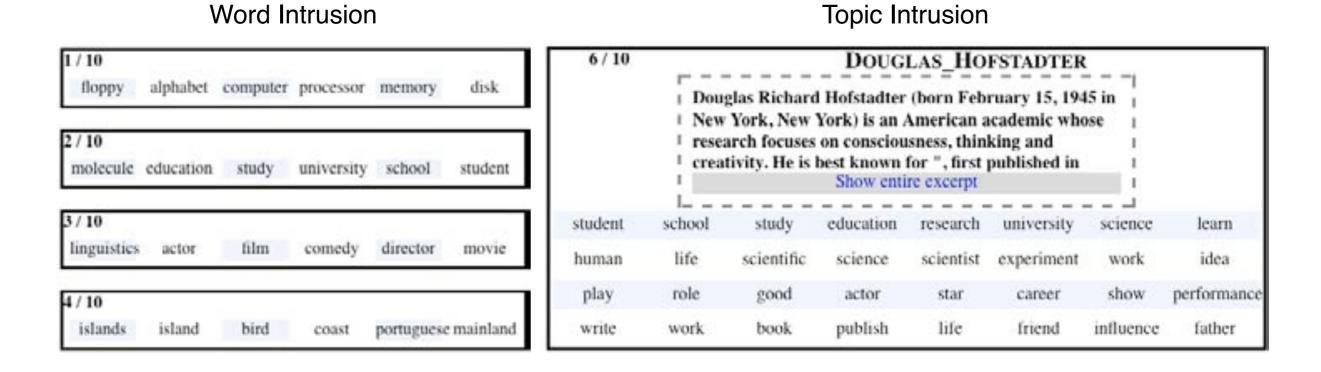
Evaluation: Are these topics any good?

 As for clustering: a bit tricky. Thoughts on how we might evaluate topics?

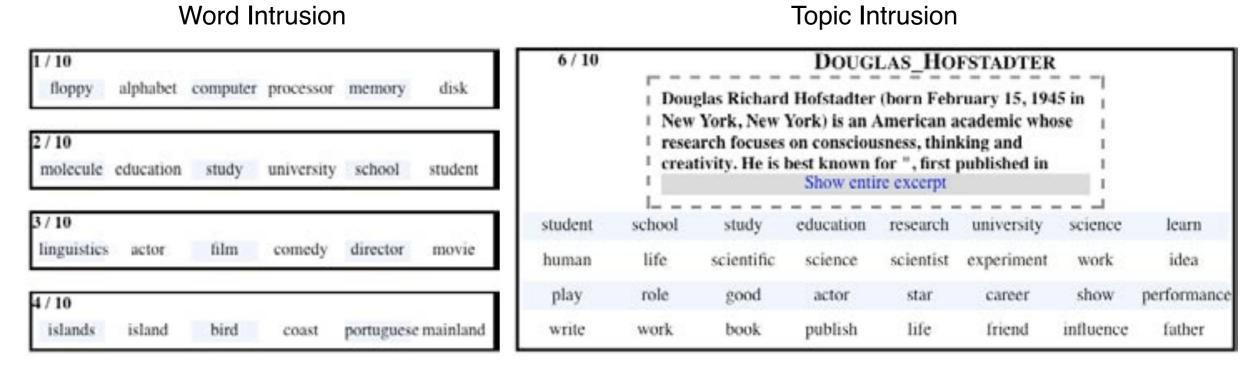
Likelihood of held-out data



"Intrusion detection"

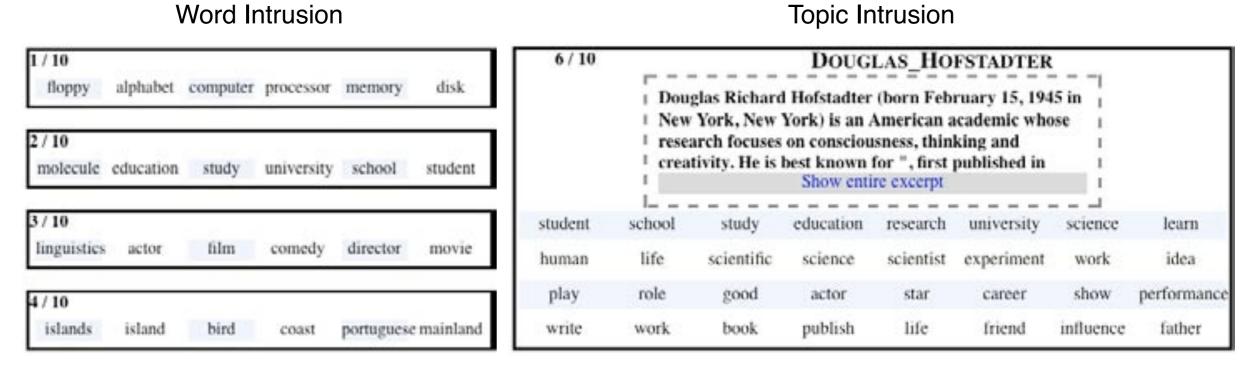


"Intrusion detection"



Which word doesn't belong?

"Intrusion detection"



Which topic doesn't belong?

Summing up

 PLSA is a simple ad-mixture model that uncovers topics (distributions over words) and soft-assigns instances to these.

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- We saw parameter estimation via Expectation-Maximization.

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- PLSA is a simple ad-mixture model that uncovers topics (distributions over words) and soft-assigns instances to these.
- We saw parameter estimation via Expectation-Maximization.
- Next time: Introducing priors into topic models Latent Dirichlet Allocation (LDA).
 - ★ This will motivate *sampling-based* estimation