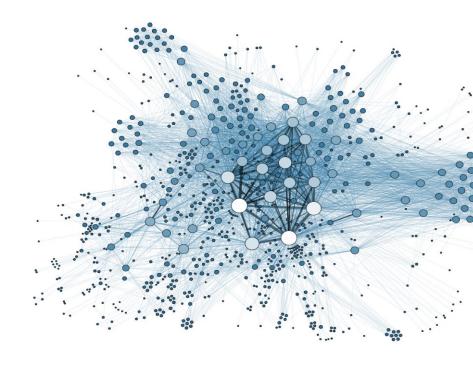


Topic Modelling

Social Media & Network Analytics



Acknowledgements

David Blei's tutorial on Topic Modelling

Overview

- Introduction and motivation for topic modelling
- Probability and statistics
- High level explanation of topic modelling
- More detailed explanation of topic modelling
 - Model
 - How to fit models (briefly)

Document Corpus







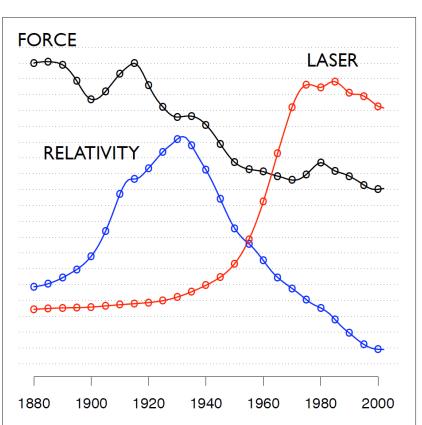
- Topic models
 - Discover hidden themes/topics that are prevalent within the corpus
 - Annotate the documents according to these topics
- Topic models can help you automatically organise, summarise and understand large electronic corpus

 Topic models is a form of exploratory analysis, unsupervised analysis

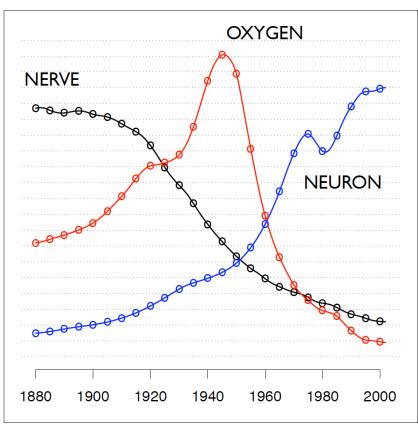


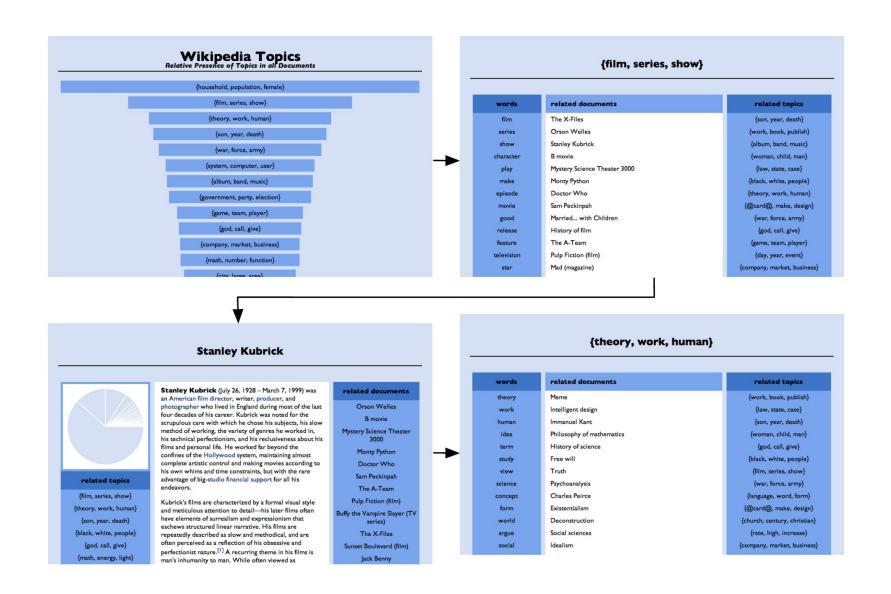
human	evolution	disease	computer
genome	evolutionary	host	models
dna	species	bacteria	information
genetic	organisms	diseases	data
genes	life	resistance	computers
sequence	origin	bacterial	system
gene	biology	new	network
molecular	groups	strains	systems
sequencing	phylogenetic	control	model
map	map living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

"Theoretical Physics"

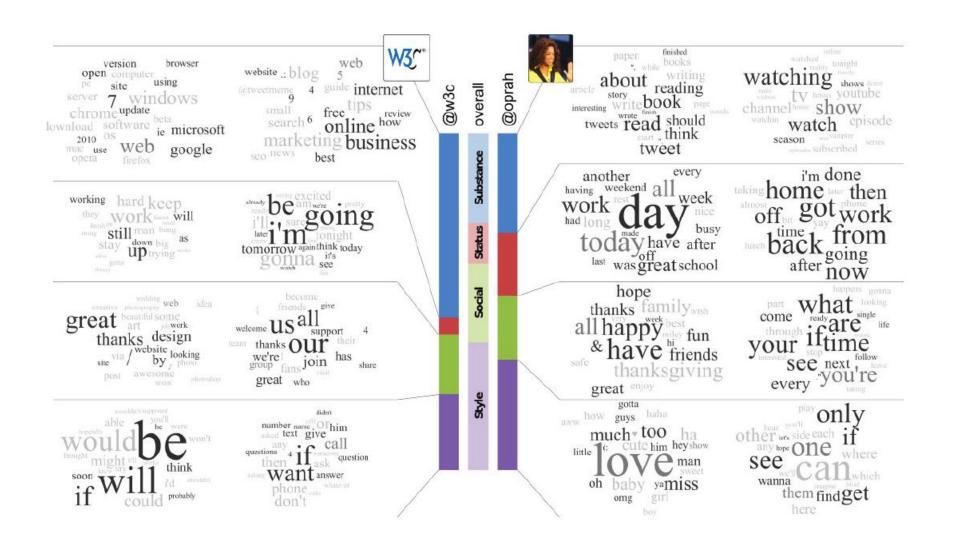


"Neuroscience"





Twitter topics



Daniel Ramage, Susan Dumais, Dan Liebling, ICWSM 2010

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Sample Space and Events

- Sample space Ω : all possible outcomes of an experiment
 - E.g., roll dice experiments: $\Omega = \{1,2,3,4,5,6\}$
 - For each $w \in \Omega$ we have a probability P(w) with:
 - $0 \le P(w) \le 1$ and $\sum_{w} P(w) = 1$
- Event E: a set of outcomes with certain probability P(E)
 - Any subset of Ω is a possible event
 - E.g., $E = \{1,2,3,4\}$ is the event that dice roll comes < 5
 - Calculate probability of an event: $P(E) = \sum_{w \in E} P(w)$
 - $P({1,2,3,4})=P(1)+P(2)+P(3)+P(4)=4/6=0.67$



Random Variables

- Not convenient for large event spaces
- Random variable is a variable that helps to describe outcomes and events:
 - Discrete: possible values from a countable domain.
 - If X is the outcome of a dice throw, then $X \in \{1,2,3,4,5,6\}$
 - Boolean random variable X ∈ {True, False}
 - X is whether a dice will come less than 5
 - X is whether the Australian PM in 2100 will be a robot
 - X is whether a patient have Ebola
 - Continuous random variable: possible values from a continuous (infinite) domain
 - X is the height of the class
 - X is how far a car travels with 50L of petrol

How to Summarise the Probabilities of P(X)?

- Prior probabilities can be described by probability distributions.
- Weather is one of Sunny, Rain, Cloudy, Snow

Weather	Sunny	Rain	Cloudy	Snow
Probabilty	0.6	0.1	0.29	0.01

- P(Weather) = < 0.6, 0.1, 0.29, 0.07
- P(Weather) follows multinomia

Need to sump up to 1!

Joint Distribution

- Instead of one random variable, the world can be described by two (or more) random variables:
 - Roll two dice, X = roll of first dice, Y = roll of second dice
 - X = sunny, Y = cold, Z = headache
- Joint probability distribution
 - Specification of probabilities for all combination of events.

	cold	~cold		cold	~cold
headache	0.108	0.012	headache	0.072	0.008
~headache	0.016	0.064	~headache	0.144	0.576

P(headache Λ sunny Λ cold) = 0.108 P(headache Λ ~sunny Λ ~cold) = 0.008

Joint Distribution

Given two random variables A and B:

Joint Distribution:

$$Pr(A = a \land B = b)$$

 $Pr(a, b)$

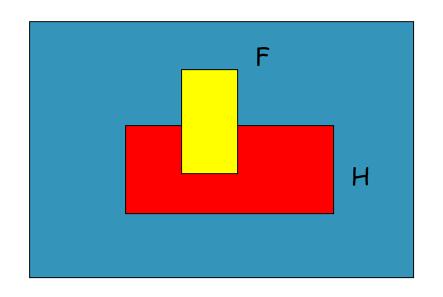
Marginisation (sumout rule):

$$Pr(A = a) = \sum_{b} Pr(A = a \land B = b)$$

$$Pr(B = b) = \sum_{a} Pr(A = a \land B = b)$$

Conditional Probability

- $Pr(A \mid B)$ = probability of A being true given that we know B
- For example: $Pr(cavity \mid toothache \land headache)$
- More general: Pr(*illness* | *symptoms*)
- Pr(A | B) fraction of worlds in which B is true that also have A true.
 H="Have headache" F="Have Flu"



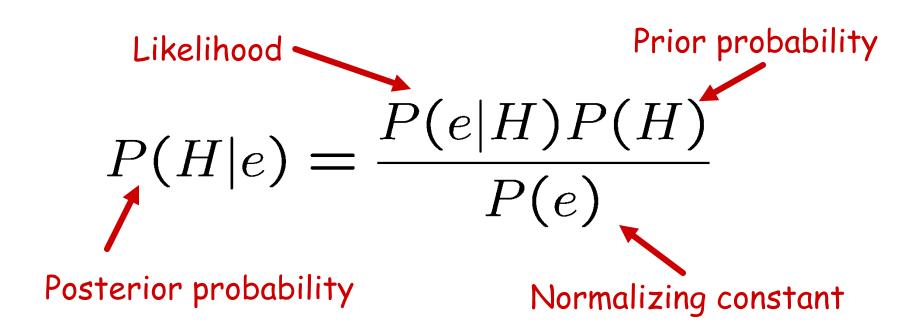
Headaches are rare and flu is rarer, but if you have the flu, then there is a 50-50 chance you will have a headache.

Bayes Rule

- Motivation: when calculating $Pr(B \mid A)$ we often know distribution $Pr(A \mid B)$
- For example:
 - A represents symptoms evidences
 - B represents illness or condition
- $P(A|B)P(B) = P(A \land B) = P(B \land A) = P(B|A)P(A)$
- Bayes rule:
 - $P(B|A) = \frac{P(A|B)P(B)}{P(A)}$

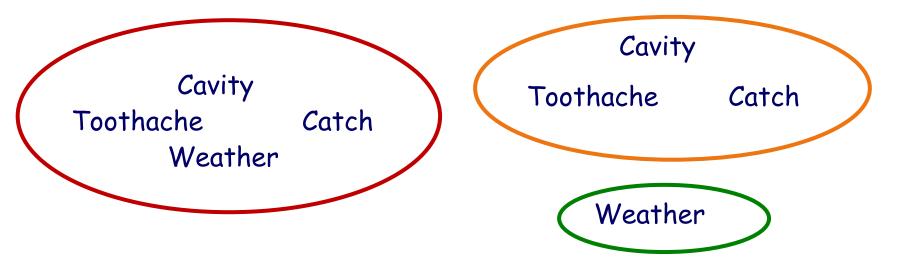
Using Bayes Rule for Inference

- Often we want to form a hypothesis about the world based on what we have observed.
- Bayes rule: allows us to state the belief given to hypothesis H, given evidence e.



Independence

A and B are independent iff
 P(A|B) = P(A) or P(B|A)=P(B) or P(A,B)=P(A)P(B)



P(Toothache, Catch, Cavity | Weather) = P(Toothache, Catch, Cavity)

P(Toothache, Catch, Cavity, Weather) = P(Toothache, Catch, Cavity) P(Weather)

What good is independence?

- Suppose (say, boolean) variables $X_1, X_2, ..., X_n$ are mutually independent
 - We can specify full joint distribution using only n parameters (linear) instead of (exponential)
- How? Simply specify $P(X_1), ..., P(X_n)$
 - $P(X_1, ..., X_n) = P(X_1)P(X_2) ... P(X_n) = \prod_{i=1}^n P(X_i)$

Conditional Independence

- Independence is very strong and hence rare ...
- Conditional independence is more common
 Consider P(catch | toothache, cavity)



depends on



but not on



```
P(catch | toothache, cavity) = P(catch | cavity)

P(catch | toothache, ¬ cavity) = P(catch | ¬ cavity)

P(Catch | Toothache, Cavity) = P(Catch | Cavity)
```

Conditional Independence

- x and y are conditionally independent given z iff
 - P(x|y,z) = P(x|z) or
 - P(y|z) = P(y|x,z) or
 - P(x,y|z) = P(x|z)P(y|z)
- e.g., learning someone's mark on SMAN exam can influence the probability you assign a specific GPA to them; but if you already knew the final grade, learning the exam mark would not influence your GPA assessment

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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

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



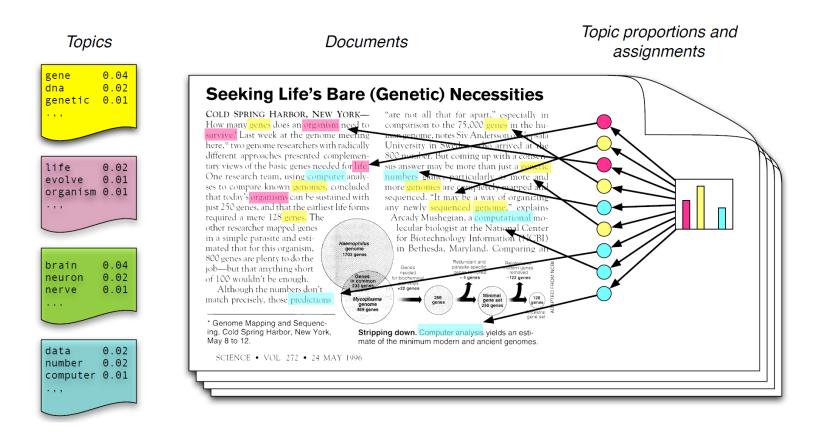
Stripping down. Computer analysis yields an estimate of the minimum modern and ancient genomes.

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

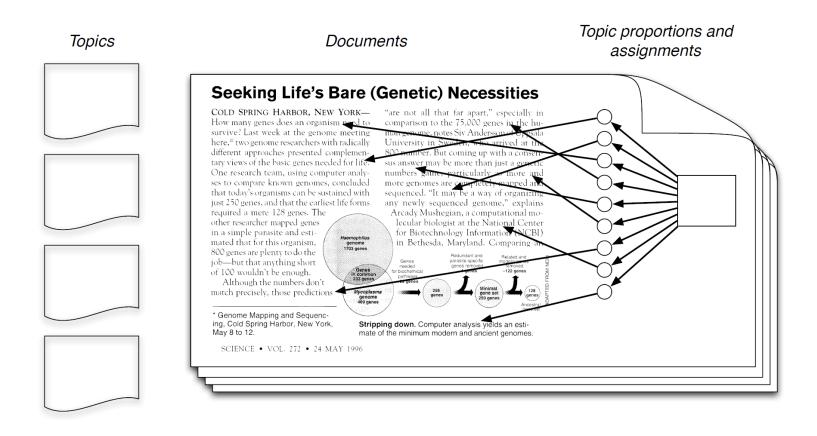
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Simple Intuition: Documents consists of multiple topics

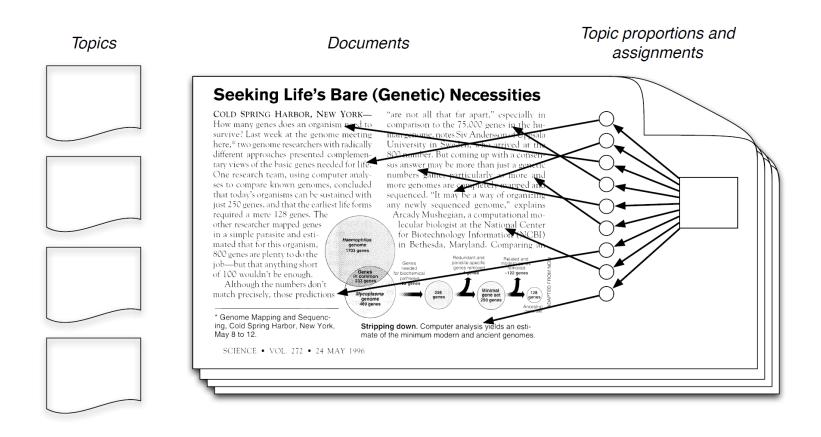
Haemophilus



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



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



- Our goal is to infer the hidden variables
- Compute their distribution conditioned on the documents p(topics, proportions, assignments | documents)

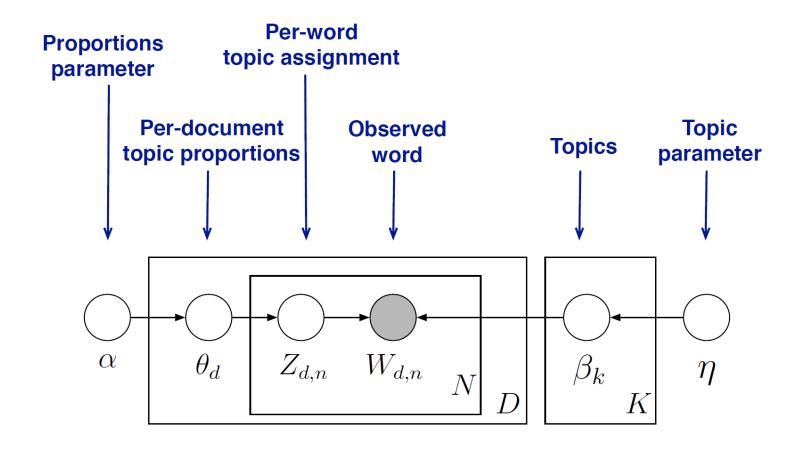
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Latent Dirichlet Analysis (LDA) Model

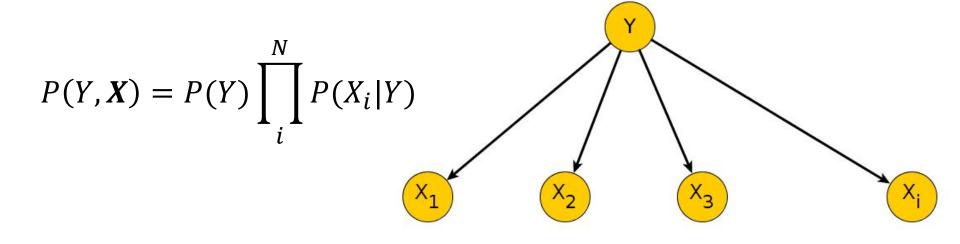
- LDA is a mixture of topics, that outputs words with certain probabilities
- It assumes a document is produced/written as follows:
 - There is K topics that have a distribution of words,
 - e.g, genetics topic, we might generate the word "gene" with probability 4%, "dna" with probability 2% and "genetics" with probability 1% etc
 - Decide on the number of words N the document will have
 - Choose a topic mixture for the document
 - E.g., if genetics and evolution topics have 30% and 20% chance appearing, you might choose the document to be 30% about genetics and 20% about evolution.
 - Generate each word w_i in the document by:
 - First picking a topic (according to the distribution we sampled above, e.g., 30% probability been genetics and 20% been evolution)
 - Using the topic selected to generate the word itself, according to the topics distribution, e.g., if we selected genetics topic, we generate the word "dna"
- Using this model, LDA starts from the words and try to infer the topics

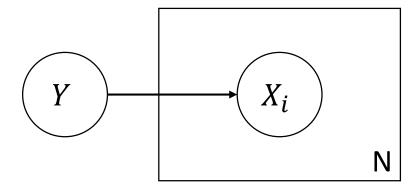
LDA model

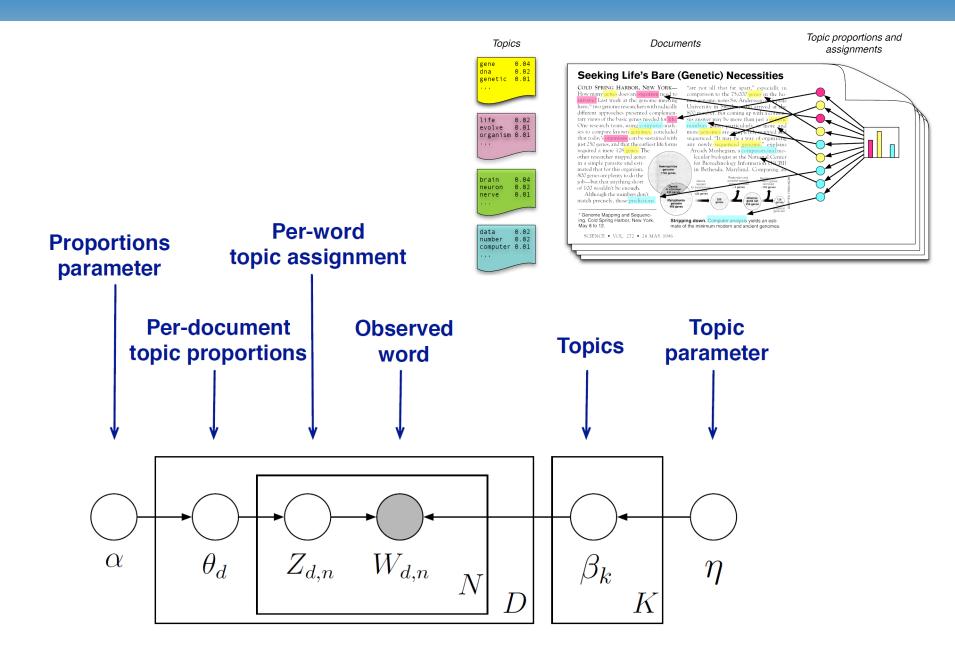


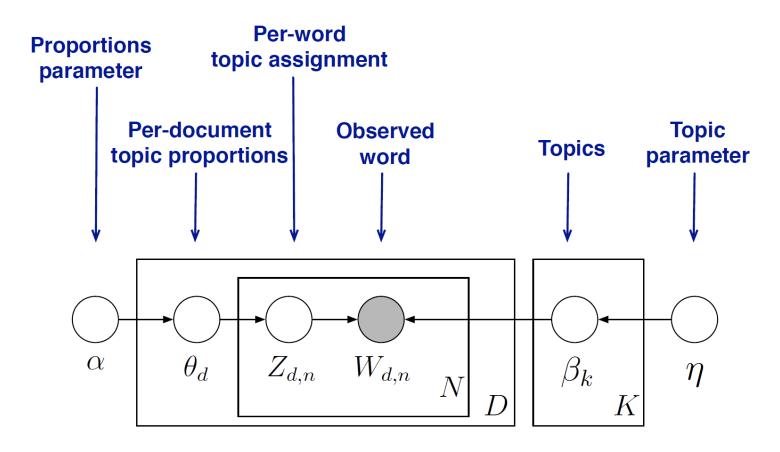
$$p(\beta_{1:K}, \theta_{1:D}, z_{1:D}, w_{1:D}) = \prod_{i=1}^{K} p(\beta_i | \eta) \prod_{d=1}^{D} p(\theta_d | \alpha) \left(\prod_{n=1}^{N} p(z_{d,n} | \theta_d) p(w_{d,n} | \beta_{1:K}, z_{d,n}) \right)$$

Plate Notation

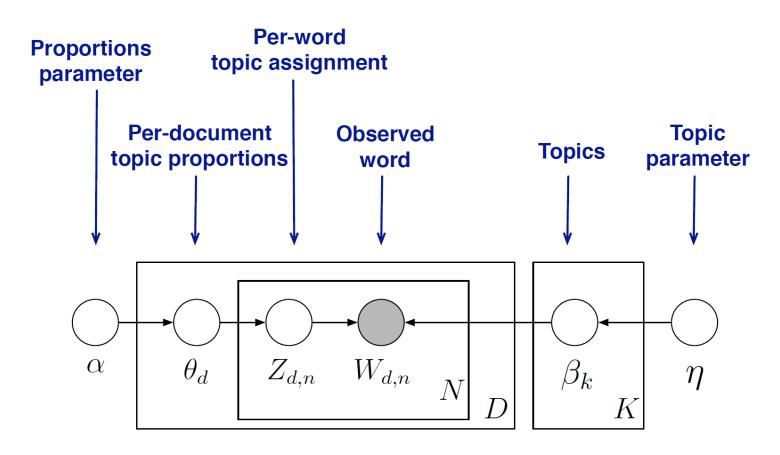




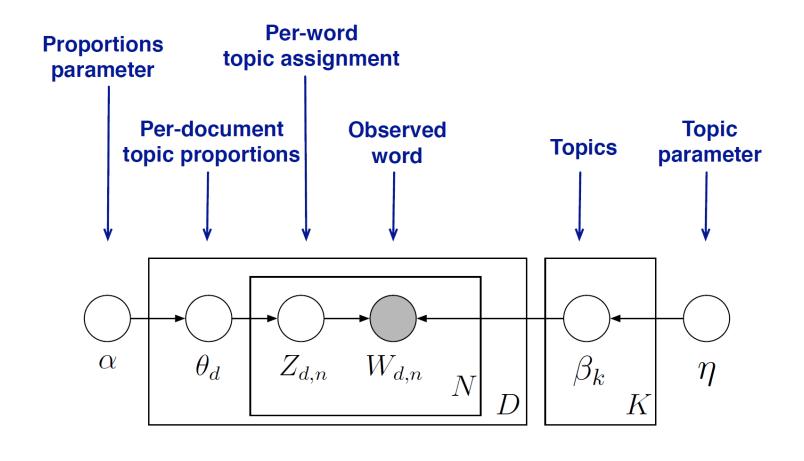




- Nodes are random variables, edges indicate dependence
- Shaded nodes are observed
- Plates indicate replicated variables



- Encodes model assumptions
- Defines a factorisation over the joint distribution
- Can use the large range of algorithmic approaches for model fitting



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



- 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

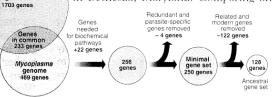
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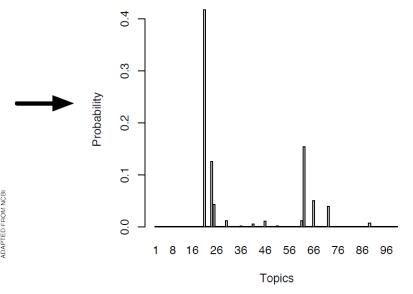
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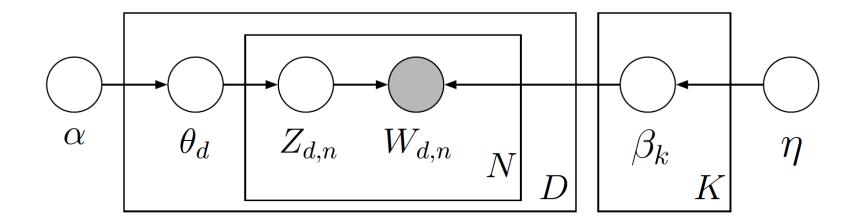
evolution	disease	computer
evolutionary	host	models
species	bacteria	information
organisms	diseases	data
life	resistance	computers
origin	bacterial	system
biology	new	network
groups	strains	systems
phylogenetic	control	model
map living		parallel
diversity	malaria	methods
group	parasite	networks
new	parasites	software
two	united	new
common	tuberculosis	simulations
	evolutionary species organisms life origin biology groups phylogenetic living diversity group new two	evolutionary host species bacteria organisms diseases life resistance origin bacterial biology new groups strains phylogenetic control living infectious diversity malaria group parasite new parasites two united

1	2	3	4	5
dna	protein	water	savs	mantle
gene	cell ' cell	climate	researchers	high
sequence	cells	atmospheric	new	earth
genes	proteins	temperature	university	pressure
sequences	receptor	global	just	seismic
human	fig	surface	science	crust
genome	binding	ocean	like	temperature
genetic	activity	carbon	work	earths
analysis	activation	atmosphere	first	lower
two	kinase	changes	years	earthquakes
6	7	8	9	10
end	time	materials	dna	disease
article	data	surface	rna .	cancer
start	two	high	transcription	patients
science	model	structure	protein	human
readers	fig	temperature	site	gene
service	system	molecules	binding	medical
news	number	chemical	sequence	studies
card	different	molecular	proteins	drug
circle	results	fig	specific	normal
letters	rate	university	sequences	drugs
11	12	13	14	15
years million	species	protein	cells	space
	evolution	structure	çell	solar
ago	population	proteins	virus	observations
age	evolutionary	two	hiv	earth
university	university	amino	infection	stars
north	populations	binding	immune	university
early	natural	acid	human	mass
fig	studies	residues	antigen	sun
evidence	genetic	molecular	infected	astronomers
record	biology	structural	viral	telescope
16	17	18	19	20
fax	cells	energy	research	neurons
manager	cell	electron	science	brain
science	gene	state	national	cells
aaas	genes	light	scientific	activity
advertising	expression	quantum	scientists	fig
sales	development	physics	new	channels
member	mutant	electrons	states	university
recruitment	mice	high	university	cortex
associate	fig	laser	united	neuronal
washington	biology	magnetic	health	visual

Why does LDA "work"?

- LDA encourages topics to have few prominent words, and documents to have few prominent topics
- It is a mixture, this find clusters (topics) of cooccurring words
- It is flexible in modelling documents of singleton topics to many topics

LDA Summary

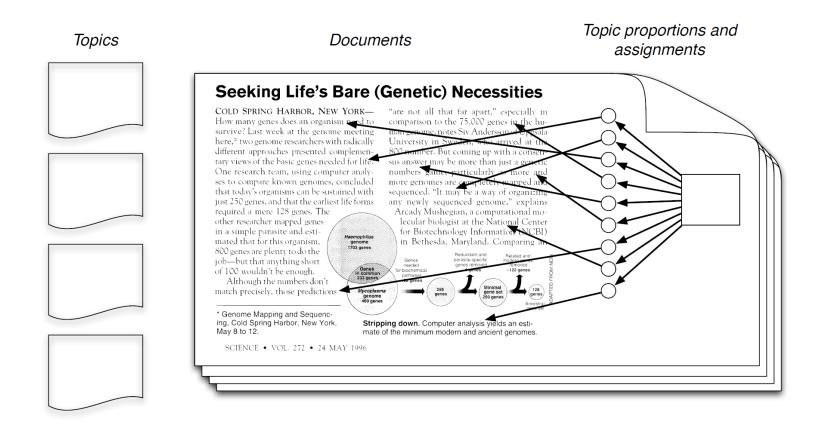


- LDA is a probabilistic model of text. It casts the problem of discovering themes/topics in large collections of documents as a posterior inference problem
- It is a mixture model
- Many more complex models built on top of LDA

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Posterior Inference



 Our goal is to compute the distribution of the hidden variables conditioned on the documents

P(topics, proportions, assignments | documents)

Inference Approaches

- Essentially alternate optimising the local and global variables
- Some examples
 - Mean field variational Methods (Blei et al, 2001, 2003)
 - Expectation propagation (Minka et al, 2002)
 - Collapsed Gibbs sampling (Griffith et al, 2002)
 - Collapsed variational inference (Teh et al, 2006)
 - Online variational inference (Hoffman et al, 2010)
 - •

Summary

- Introduced topic modelling
 - Exploratory approach
 - Find topics, particularly in large document sets
- Probabilistic model
 - Intuition and more detailed model