

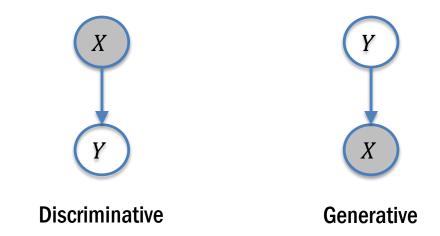
CS 6347

Lecture 21

Topic Models and LDA

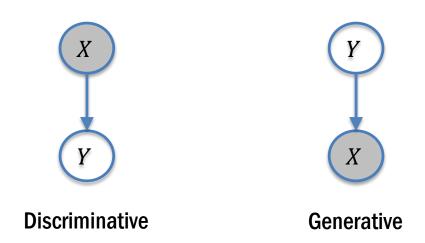
(some slides by David Blei)

 Recall that, in Bayesian networks, there could be many different, but equivalent models of the same joint distribution



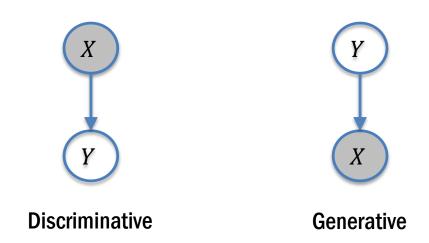
 Although these two models are equivalent (in the sense that they imply the same independence relations), they can differ significantly when it comes to inference/prediction





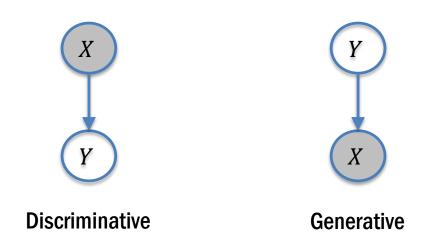
- Generative models: we can think of the observations as being generated by the latent variables
 - Start sampling at the top and work downwards
 - Examples?





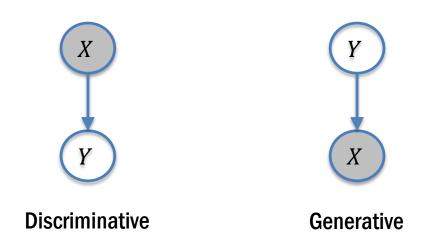
- Generative models: we can think of the observations as being generated by the latent variables
 - Start sampling at the top and work downwards
 - Examples: HMMs, naïve Bayes, LDA





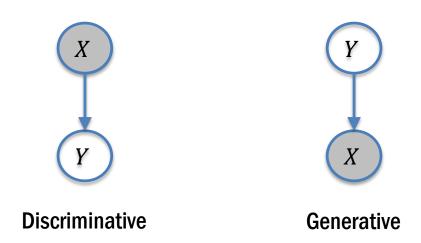
- Discriminative models: most useful for discriminating the values of the latent variables
 - Almost always used for supervised learning
 - Examples?





- Discriminative models: most useful for discriminating the values of the latent variables
 - Almost always used for supervised learning
 - Examples: CRFs





- Suppose we are only interested in the prediction task (i.e., estimating p(Y|X))
 - Discriminative model: p(X,Y) = p(X)p(Y|X)
 - Generative model: p(X,Y) = p(Y)p(X|Y)



Generative Models

- The primary advantage of generative models is that they provide a model of the data generating process
 - Could generate "new" data samples by using the model
- Topic models
 - Methods for discovering themes (topics) from a collection (e.g., books, newspapers, etc.)
 - Annotates the collection according to the discovered themes
 - Use the annotations to organize, search, summarize, etc.



Models of Text Documents

- Bag-of-words models: assume that the ordering of words in a document do not matter
 - This is typically false as certain phrases can only appear together
- Unigram model: all words in a document are drawn uniformly at random from categorical distribution
- Mixture of unigrams model: for each document, we first choose a topic z and then generate words for the document from the conditional distribution p(w|z)
 - Topics are just probability distributions over words



Topic Models

Seeking Life's Bare (Genetic) Necessities

Haemophilus

genome 1703 genes

Genes

in common

233 genes

Mycoplasma

genome

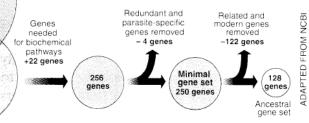
469 genes

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

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.

SCIENCE • VOL. 272 • 24 MAY 1996



[&]quot;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

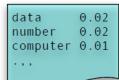
^{*} Genome Mapping and Sequencing, Cold Spring Harbor, New York, May 8 to 12.

Topics

gene 0.04 dna 0.02 genetic 0.01

life evolve	0.02
organism	0.01
. , ,	

brain	0.04
neuron	0.02
nerve 	0.01



Documents

Topic proportions and assignments

Seeking Life's Bare (Genetic) Necessities

Haemophilus

genome 1703 genes

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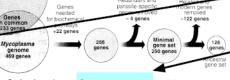
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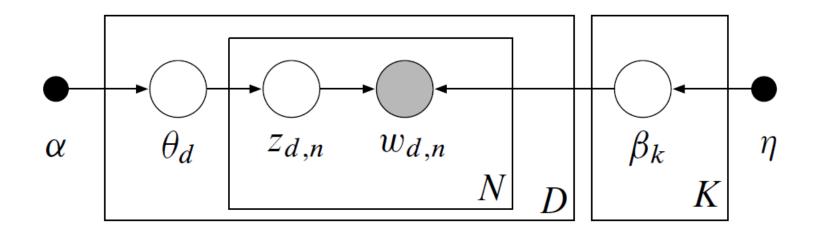
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- α and η are parameters of the prior distributions over θ and β respectively
- θ_d is the distribution of topics for document d (real vector of length K)
- β_k is the distribution of words for topic k (real vector of length V)
- $z_{d,n}$ is the topic for the nth word in the dth document
- $w_{d,n}$ is the *n*th word of the *d*th document



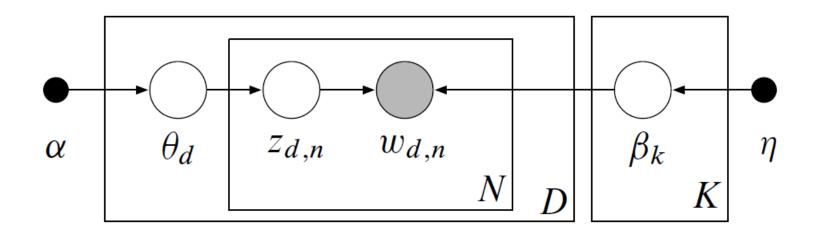
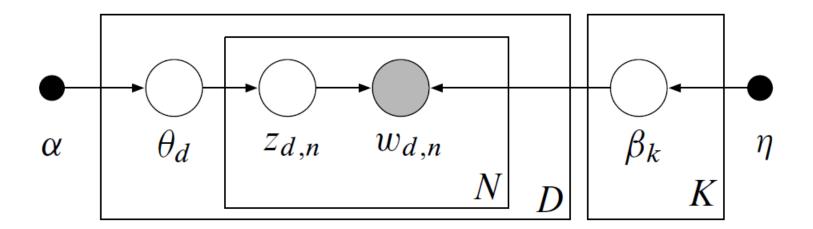


Plate notation

- There are $N \cdot D$ different variables that represent the observed words in the different documents
- There are K total topics (assumed to be known in advance)
- There are D total documents





- The only observed variables are the words in the documents
 - The topic for each word, the distribution over topics for each document, and the distribution of words per topic are all latent variables in this model



- The model contains both continuous and discrete random variables
 - $-\theta_d$ and β_k are vectors of probabilities
 - $-z_{d,n}$ is an integer in $\{1, ..., K\}$ that indicates the topic of the nth word in the dth document
 - $w_{d,n}$ is an integer in $\{1, \dots, V\}$ which indexes over all possible words



- $\theta_d \sim Dir(\alpha)$ where $Dir(\alpha)$ is the Dirichlet distribution with parameter vector $\alpha>0$
- $\beta_k \sim Dir(\eta)$ with parameter vector $\eta > 0$
- Dirichlet distribution over x_1 , ..., x_K such that x_1 , ..., $x_K \ge 0$ and $\sum_i x_i = 1$

$$f(x_1, \dots, x_K; \alpha_1, \dots, \alpha_K) \propto \prod_i x_i^{\alpha_i - 1}$$

 The Dirichlet distribution is a distribution over probability distributions over K elements



 The discrete random variables are distributed via the corresponding probability distributions

$$p(z_{d,n} = k | \theta_d) = (\theta_d)_k$$
$$p(w_{d,n} = v | z_{d,n}, \beta_1, \dots, \beta_K) = (\beta_{z_{d,n}})_m$$

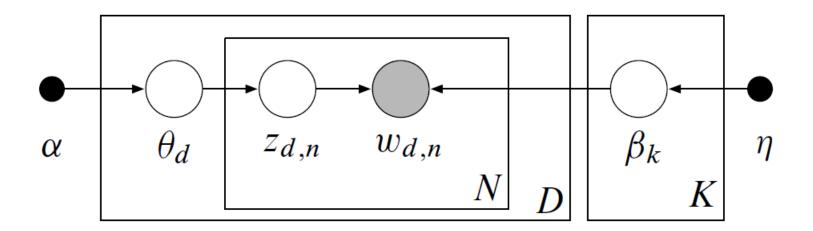
- Here, $(\theta_d)_k$ is the kth element of the vector θ_d which corresponds to the percentage of document d corresponding to topic k
- The joint distribution is then

$$p(w, z, \theta, \beta | \alpha, \eta) = \prod_{k} p(\beta_{k} | \eta) \prod_{d} \left[p(\theta_{d} | \alpha) \prod_{n} p(z_{d,n} | \theta_{d}) p(w_{d,n} | z_{d,n}, \beta) \right]$$



- LDA is a generative model
 - We can think of the words as being generated by a probabilistic process defined by the model
 - How reasonable is the generative model?





- Inference in this model is NP-hard
- Given the D documents, want to find the parameters that best maximize the joint probability
 - Can use an EM based approach called variational EM



Variational EM

 Recall that the EM algorithm constructed a lower bound using Jensen's inequality

$$l(\theta) = \sum_{k=1}^{K} \log \sum_{x_{mis_k}} p(x_{obs_k}^k, x_{mis_k} | \theta)$$

$$= \sum_{k=1}^{K} \log \sum_{x_{mis_k}} q_k(x_{mis_k}) \cdot \frac{p(x_{obs_k}^k, x_{mis_k} | \theta)}{q_k(x_{mis})}$$

$$\geq \sum_{k=1}^{K} \sum_{x_{mis_k}} q_k(x_{mis_k}) \log \frac{p(x_{obs_k}^k, x_{mis_k} | \theta)}{q_k(x_{mis_k})}$$



Variational EM

- Performing the optimization over q is equivalent to computing $p(x_{mis_k}|x_{obs_k}^k,\theta)$
- This can be intractable in practice
 - Instead, restrict q to lie in some restricted set of distributions Q
 - For example, could make a mean-field assumption

$$q(x_{mis_k}) = \prod_{i \in mis_k} q_i(x_i)$$

 The resulting algorithm only yields an approximation to the loglikelihood



EM for Topic Models

$$p(w \mid \alpha, \eta) = \int \prod_{k} p(\beta_{k} \mid \eta) \int \sum_{z} \prod_{d} \left[p(\theta_{d} \mid \alpha) \prod_{n} p(z_{d,n} \mid \theta_{d}) p(w_{d,n} \mid z_{d,n}, \beta) \right] d\theta d\beta$$

To apply variational EM, we write

$$\log p(w|\alpha,\eta) = \log \int \int \sum_{z} p(w,z,\theta,\beta|\alpha,\eta) \, d\theta d\beta$$

$$\geq q(z,\theta,\beta) \log \int \int \sum_{z} \frac{p(w,z,\theta,\beta|\alpha,\eta)}{q(z,\theta,\beta)} \, d\theta d\beta$$

where we restrict the distribution q to be of the following form

$$q(z,\theta,\beta) = \prod_{k} q(\beta_k|\eta) \prod_{d} q(\theta_d|\alpha) \prod_{n} q(z_{d,n})$$



Example of LDA

"Arts"	${ m `Budgets''}$	"Children"	"Education"
NEW	MILLION	CHILDREN	SCHOOL
FILM	TAX	WOMEN	STUDENTS
SHOW	PROGRAM	PEOPLE	SCHOOLS
MUSIC	BUDGET	CHILD	EDUCATION
MOVIE	BILLION	YEARS	TEACHERS
PLAY	FEDERAL	FAMILIES	HIGH
MUSICAL	YEAR	WORK	PUBLIC
BEST	SPENDING	PARENTS	TEACHER
ACTOR	NEW	SAYS	BENNETT
FIRST	STATE	FAMILY	MANIGAT
YORK	PLAN	WELFARE	NAMPHY
OPERA	MONEY	MEN	STATE
THEATER	PROGRAMS	PERCENT	PRESIDENT
ACTRESS	GOVERNMENT	CARE	ELEMENTARY
LOVE	CONGRESS	LIFE	HAITI

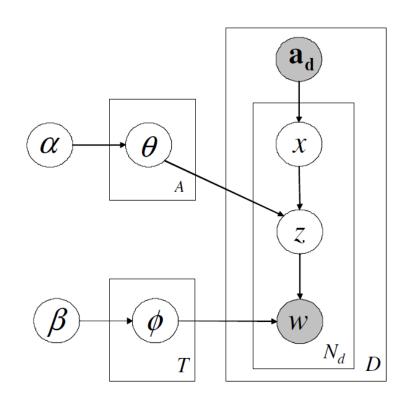


Example of LDA

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.



Extensions of LDA



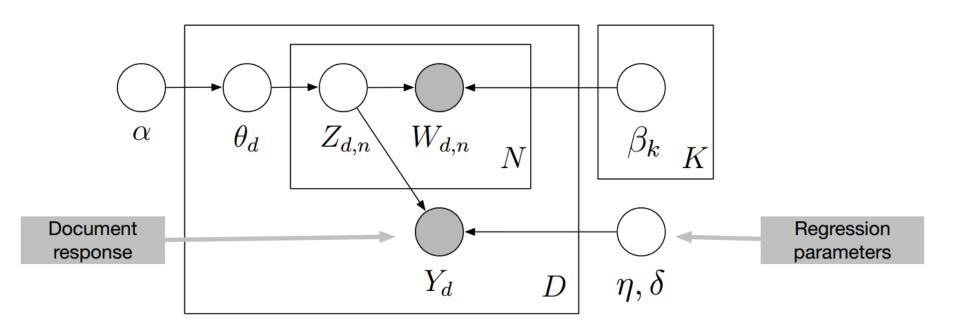
The Author-Topic Model for Authors and Documents Rosen-Zvi et al.

Author– Topic model

- $-a_d$ is the group of authors for the dth document
- $-x_{d,n}$ is the author of the nth word of the dth document
- $-\theta_a$ is the topic distribution for author a
- $-z_{d,n}$ is the topic for the nth word of the dth document



Extensions of LDA



- Label Y_d for each document represents a value to be predicted from the document
 - E.g., number of stars for each document in a corpus of movie reviews

