

Text Data in Economics

Warwick QAPEC Summer School

5. Topic Models

Different Goals, Different Methods

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 - ▶ pursuing a known goal, e.g., predicting whether a political speech is from a Democrat or a Republican.
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- ▶ Both strategies amplify human effort, each in different ways.
- ▶ Distinctions are not clear-cut:
 - ▶ supervised learning models can be used to discover themes/patterns
 - ▶ unsupervised learning models can be used in service of prediction or known goals.

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4. Empirical analysis
 - ▶ Produce statistics or predictions with the trained model.
 - ▶ **Answer the research question.**

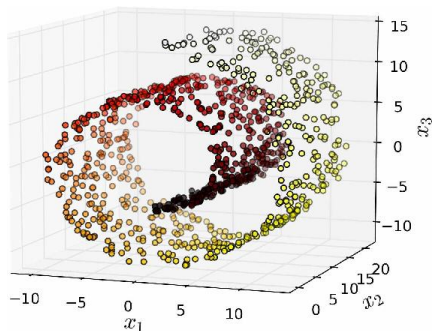
Outline

Dimensionality Reduction

Topic Models

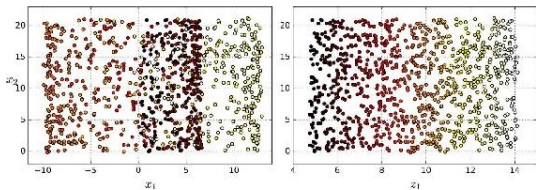
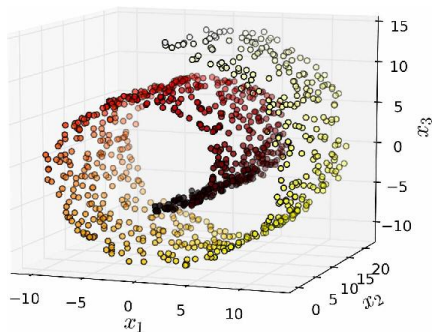
- ▶ Datasets are not distributed uniformly across the feature space.
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- ▶ **Dimensionality reduction** makes data more interpretable – for example by projecting down to two dimensions for visualization.
- ▶ improves computational tractability.
- ▶ can improve model performance.

What dimension reductions have we already tried?

The Document-Term Matrix is high-dimensional

The **document-term matrix \mathbf{X}** :

- ▶ each row d represents a **document**, while each column w represents a word (or term more generally, e.g. n-grams).
 - ▶ A matrix entry $\mathbf{X}_{[d,w]}$ quantifies the strength of association between a document and a word, generally its count or frequency

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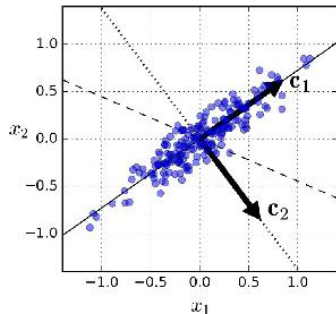
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→ \mathbf{X} often has billions of cells.

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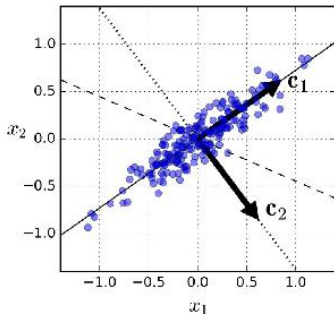
PCA (principal component analysis) / SVD (singular value decomposition)



- PCA computes the dimension in data explaining most variance.

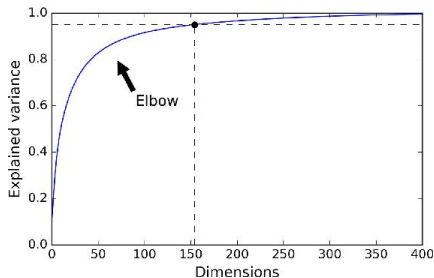
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- after the first component, subsequent components learn the (orthogonal) dimensions explaining most variance in dataset after projecting out first component.

PCA and LSA

The document-term matrix \mathbf{X} can be reduced by projecting down to first principal component dimensions.

- ▶ This is known as “latent semantic analysis”
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The document-term matrix \mathbf{X} can be reduced by projecting down to first principal component dimensions.

- ▶ This is known as “latent semantic analysis”
- ▶ Distance metrics between observations (e.g. cosine similarity) are approximately preserved.
- ▶ PCA factors are not interpretable.
 - ▶ Hoffman (1999) fixes this and puts LSA on firmer foundations by assuming a generative model of text – the word counts in a document are generated by a multinomial distribution.
 - ▶ For non-negative data (e.g. counts or frequencies), **Non-negative Matrix Factorization (NMF)** provides more interpretable factors than PCA.

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 - ▶ how observed covariates drive trends in language
 - ▶ tell a story not just about what, but how and why

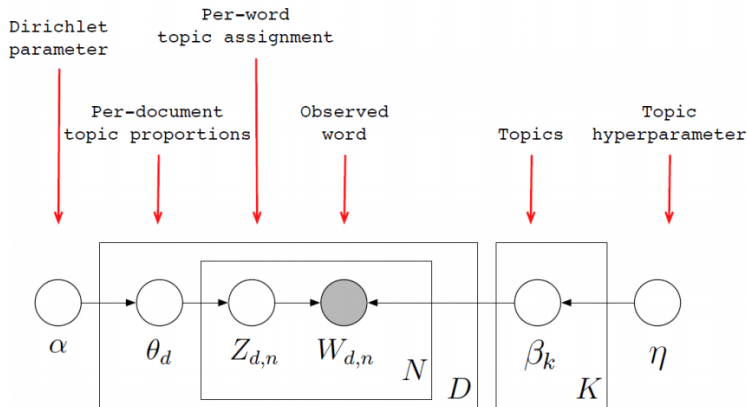
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- ▶ Social scientists use topics as a form of measurement
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 - ▶ **topic models are more interpretable** than other dimension reduction methods, such as PCA.

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- ▶ Input: $N \times M$ document-term count matrix X
- ▶ Assume: there are K topics (tunable hyperparameter, use coherence).
- ▶ Like PCA or NMF, LDA works by factorizing X into:
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Variational inference setup (Brandon Stewart slides).

```
# train LDA with 10 topics and print  
from gensim.models.ldamodel import LdaModel  
lda = LdaModel(doc_term_matrix, num_topics=10,  
               id2word = dictionary, passes=3)  
lda.show_topics(formatted=False)
```

```
# to get the topic proportions for a document, use  
# the corresponding row from the document-term matrix.  
lda[doc_term_matrix[1]]
```

ldagibbs: A command for Topic Modeling in Stata using Latent Dirichlet Allocation

Carlo Schwarz

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Coventry, United Kingdom
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```
ldagibbs varname [ , ttopics(integer) burnin_iter(integer) alpha(real)  
  beta(real) samples(integer) sampling_iter(integer) seed(integer)  
  likelihood min_char(integer) stopwords(string) name_new_var(string)  
  normalize mat_save path(string) ]
```


Seeking Life's Bare (Genetic) Necessities

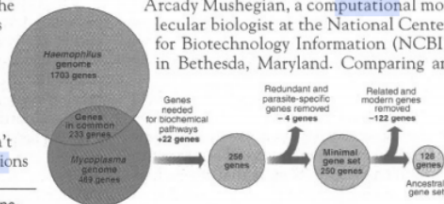
COLD SPRING HARBOR, NEW YORK—How many genes does an organism need to survive? Last week at the genome meeting here,* two genome researchers with radically different approaches presented complementary views of the basic genes needed for life. One research team, using computer analyses to compare known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

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

“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.

Image from Hanna Wallach

Using an LDA Model

Once trained, can easily get topic proportions for a corpus.

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Can then use the topic proportions as variables in a social science analysis.

- ▶ e.g., Catalinac (2016) shows that after a Japanese political reform that reduced intraparty competition, candidate platforms reduced local pork and increased national policy.

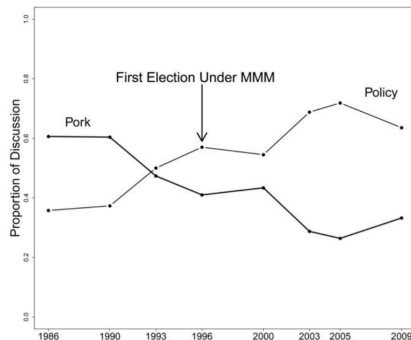


TABLE 1 A Summary of Common Assumptions and Relative Costs Across Different Methods of Discrete Text Categorization

	Method				
	<i>Reading</i>	<i>Human Coding</i>	<i>Dictionaries</i>	<i>Supervised Learning</i>	<i>Topic Model</i>
A. Assumptions					
<i>Categories are known</i>	No	Yes	Yes	Yes	No
<i>Category nesting, if any, is known</i>	No	Yes	Yes	Yes	No
<i>Relevant text features are known</i>	No	No	Yes	Yes	Yes
<i>Mapping is known</i>	No	No	Yes	No	No
<i>Coding can be automated</i>	No	No	Yes	Yes	Yes
B. Costs					
Preanalysis Costs					
<i>Person-hours spent conceptualizing</i>	Low	High	High	High	Low
<i>Level of substantive knowledge</i>	Moderate/High	High	High	High	Low
Analysis Costs					
<i>Person hours spent per text</i>	High	High	Low	Low	Low
<i>Level of substantive knowledge</i>	Moderate/High	Moderate	Low	Low	Low
Postanalysis Costs					
<i>Person-hours spent interpreting</i>	High	Low	Low	Low	Moderate
<i>Level of substantive knowledge</i>	High	High	High	High	High

Recommended: read this part of Quinn, Monroe, Colaresi, Crespin, and Radev (2010).

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Roberts, Stewart, and Tingley

STM provides two ways to include contextual information:

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- ▶ Structural topic model is not a prediction model:
 - ▶ it will tell you which topics or features correlate with an outcome, but it will not provide an in-sample or out-of-sample prediction for an outcome
- ▶ The main implementation is in R. gensim has a light-weight version called “author topic model” (see this week’s notebook).