

A Practical Algorithm for Topic Modling with Provable Guarantees

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① Introduction

② Topic Modelling

③ Algorithm

④ Topic Recovery via Bayes' Rule

⑤ Efficiently Finding Anchor Words

⑥ Experimental Results

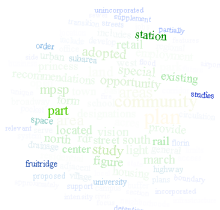
⑦ Conclusion

Information Overload



Effective Organisation





- 1 Introduction
- 2 Topic Modelling**
- 3 Algorithm
- 4 Topic Recovery via Bayes' Rule
- 5 Efficiently Finding Anchor Words
- 6 Experimental Results
- 7 Conclusion

Model of Topics

Topics

gene 0.04
dna 0.02
genetic 0.01
...

life 0.02
evolve 0.01
organism 0.01
...

brain 0.04
neuron 0.02
nerve 0.01
...

data 0.02
number 0.02
computer 0.01
...

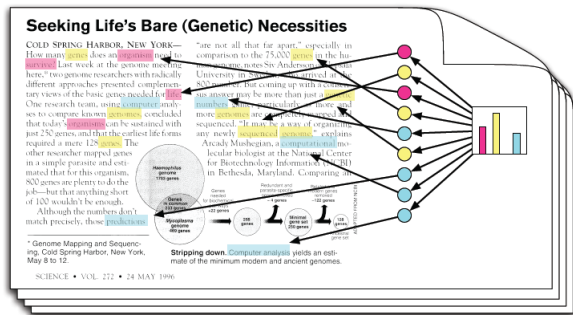
Topics are distributions over words

Model of Documents

Documents have
distribution of
topics

Documents

Topic proportions and
assignments



Topic Modelling

Topics

gene 0.04
dna 0.02
genetic 0.01
...

life 0.02
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Documents

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 Anderson, a geneticist at the University of Sydney, 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 sequenced and analyzed. "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



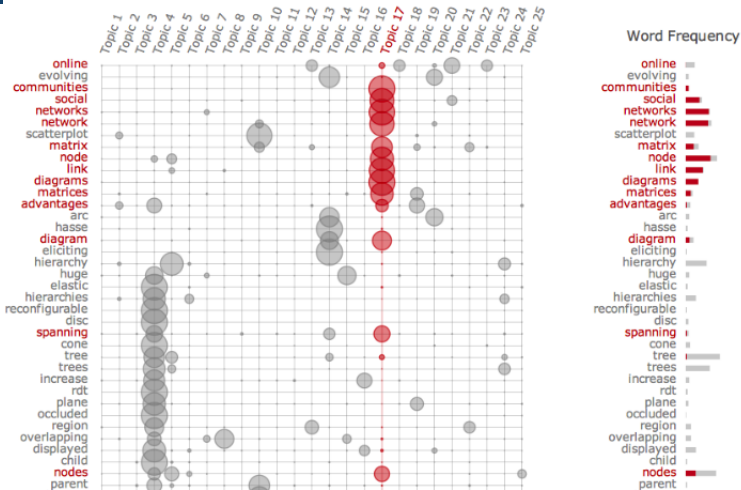
* Genome Mapping and Sequencing, Cold Spring Harbor, New York, May 8 to 12.

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

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Topic proportions and assignments

Word-topic Matrix



Aim: Find document-topic model

Steps

- Assume documents are generated by probabilistic model with unknown variables
- Infer hidden structure onto document
- Situate new document into model

Approximate Inference & Provable Guarantees

- Document-topic inference is NP-hard.
- Approximate techniques used
- Provably polynomial-time algorithms

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Algorithm

Steps

- 1 Second order moment matrix of word-word co-occurrences
- 2 Anchor word selection
- 3 Topic distribution recovery

Assumptions:

- Topics may be correlated
- Word-topic distributions are separable

Anchor Words

LDA

Contributions

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