Distributional Semantics

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(some slides from Marine Carpuat, Nathan Schneider)

ENLP Lecture 13

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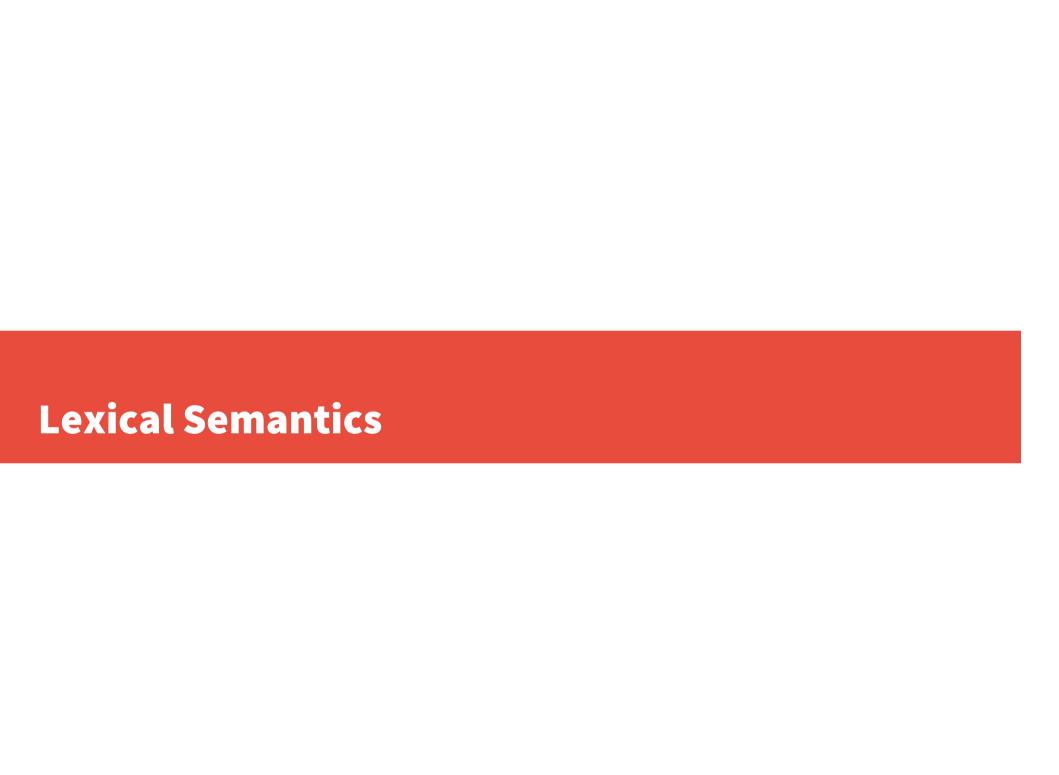
Topics

Lexical Semantics

- → Word Similarity
- → Distributional Hypothesis
- → Vector Representations
- → Evaluation

Document Semantics

→ Topic Modeling



• Identify word closest to target:

Accidental

- → Abominate
- → Meander
- → Inadvertent
- → inhibit

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FedEx

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• Identify word closest to target:

Millennial

- → octopus
- → fork
- → water
- → avocado

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Semantic Similarity

What drives semantic similarity?

Meaning

- → The two concepts are close in terms of meaning
- → e.g. 'inadvertent' and 'accidental'

World Knowledge

- → The two concepts have similar properties, often occur together, or occur in similar contexts
- → e.g. 'spinach' and 'kale,' or 'UPS' and 'FedEx'

Psychology

- → The two concepts fit together within an over-arching psychological schema or framework
- → e.g. 'money' and 'bank', or 'millennial' and 'avocado'

Semantic Similarity

What drives semantic similarity?

Meaning



ccurin

Psychol

→ The two framework

→ e.g. 'spir

schema or

→ e.g. 'money' and 'bank', or 'millennial' and 'avocado'

Automatic computation of semantic similarity

Why would such a thing be useful?

- → Semantic similarity gives us a way to generalize beyond word identities
- → Lots of practical applications
 - → Information retrieval
 - → Machine translation
 - → Ontological hierarchies
 - → Etc.

Beyond one-hot vectors

So far in this course, most of our statistical models have treated words as discrete categories.

- → No explicit relationship between "cat" and "feline" in our LMs, classifiers, HMMs
- → Equivalently, each word type in the vocabulary can be represented as an integer or as a one-hot vector
 - \rightarrow "cat" = [0 0 0 0 0 1 0 0 0 ...]
 - → "feline" = [0 0 0 0 0 0 1 0 ...]
 - → They are orthogonal; dot product is 0
 - → Length is size of the vocabulary

Distributional Hypothesis

Idea: Similar linguistic objects have similar contents (for documents, paragraphs, sentences) or contexts (for words)

→ "Differences of meaning correlates with differences of distribution" (Harris, 1970)

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→ "You shall know a word by the company it keeps!" (Firth, 1957)

Example

- → He handed her a glass of bardiwac
- → Beef dishes are made to complement the bardiwac
- → Nigel staggered to his feet, face flushed from too much bardiwac.
- → Malbec, one of the lesser-known bardiwac grapes, responds well to Australia's sunshine
- → I dined off bread and cheese and this excellent bardiwac
- → The drinks were delicious: bold bardiwac as well as light, sweet Rhenish.

Word Vectors

• A word type may be represented as a vector of features indicating the contexts in which it occurs in a corpus.

$$\vec{w} = (f_1, f_2, f_3, ..., f_N)$$

Context Features

Word Co-occurrence within a window:

	arts	boil	data	function	large	sugar	summarized	water
apricot	0	1	0	0	1	1	0	1
pineapple	0	1	0	0	1	1	0	1
digital	0	0	1	1	1	0	1	0
information	0	0	1	1	1	0	1	0

Grammatical Relations:

	subj-of, absorb	subj-of, adapt	subj-of, behave	 pobj-of, inside	pobj-of, into	 nmod-of, abnormality	nmod-of, anemia	nmod-of, architecture	 obj-of, attack	obj-of, call	obj-of, come from	obj-of, decorate	 nmod, bacteria	nmod, body	nmod, bone marrow
cell	1	1	1	16	30	3	8	1	6	11	3	2	3	2	2

Context Features

Feature Values:

- **→**Boolean
- → Raw Counts
- → Weighting Scheme (e.g. tf-idf)
- → Association Values

Association Value: Pointwise Mutual Information

 Measures how often a target word w and a feature f occur together compared to what we would expect if the two were independent

association_{PMI}
$$(w, f) = \log_2 \frac{P(w, f)}{P(w)P(f)}$$

- → PMI ranges from -inf to +inf, but negative values are generally unreliable (Jurafsky & Martin, 2017:275).
 - → Use positive PMI and clip at zero.

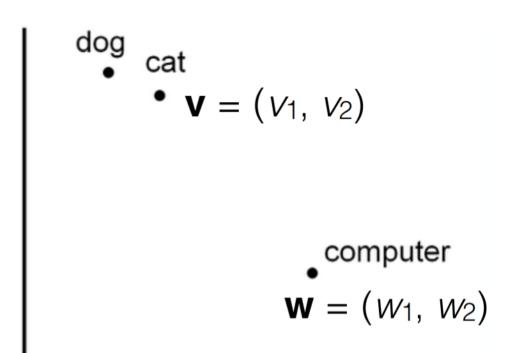
Computing Similarity

Semantic similarity boils down to computing some measure of spatial similarity between context vectors in vector space.

Words in a vector space

• In 2 dimensions:

- V = 'cat'
- W = 'computer'

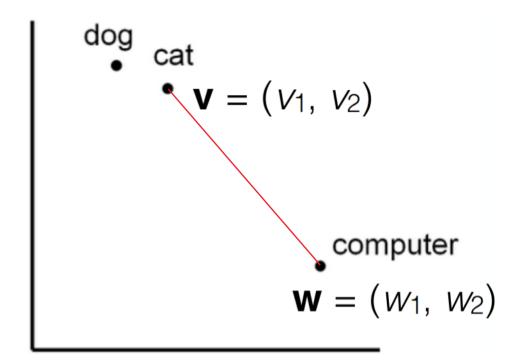


Euclidean Distance

• Formula:

$$\sqrt{\sum_i (v_i - w_i)^2}$$

→ Can be oversensitive to extreme values

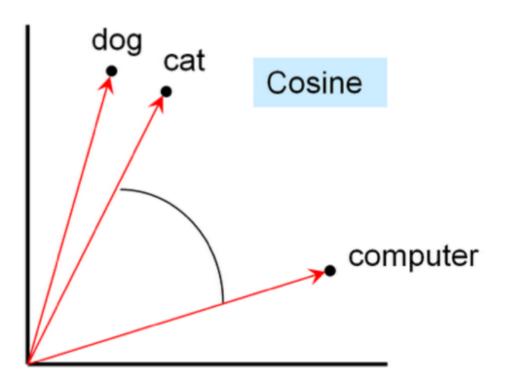


Cosine Similarity

• Formula:

$$\operatorname{sim}_{\operatorname{cosine}}(\vec{v}, \vec{w}) = \frac{\vec{v} \cdot \vec{w}}{|\vec{v}| |\vec{w}|} = \frac{\sum_{i=1}^{N} v_i \times w_i}{\sqrt{\sum_{i=1}^{N} v_i^2} \sqrt{\sum_{i=1}^{N} w_i^2}}$$

→ Typically better than Euclidean distance for vector space semantic



Vector Sparseness

- Co-occurrence based context vectors tend to very long and very sparse.
 - → len(word_vec) == len(vocab)
- **short** (dim. of around 50-300) and **dense** context vectors are usually preferable.
 - → Easier to include as features in machine learning systems
 - → Fewer parameters = better generalization & less over-fitting
 - → Better at capturing synonymy

Dense Vectors

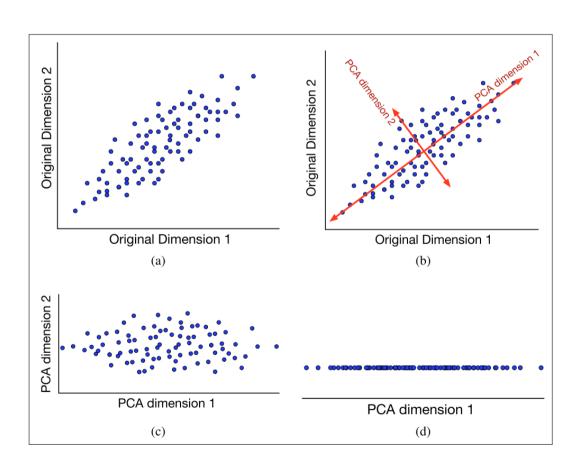
2 Main methods of producing short, dense vectors:

- (1) Dimensionality reduction
- (2) Neural Language Models

Dimensionality Reduction

Methods:

- → Principal Component Analysis (PCA)
- →t-Distributed Stochastic Neighbor Embedding (t-SNE)
- → Latent Semantic Analysis (LSA)
- →...



Neural Network Embeddings

Idea: Train a neural network to predict context words based on current current 'target' word.

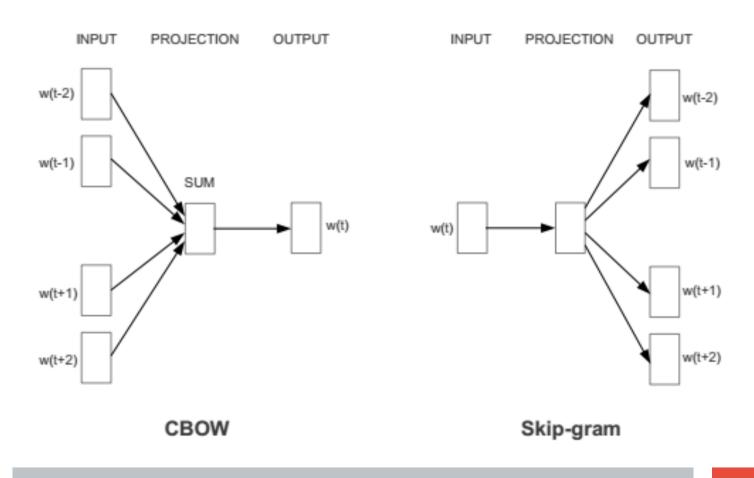
- Similar input words → similar context word prediction
- Similar input words → similar corresponding rows in the weight matrix of the trained network.

We don't actually care about context word prediction!

 Rows in the trained weight matrix become our context vectors (aka word vectors, aka word embeddings)

Neural Network Embeddings

Most popular family of methods: word2vec (Mikolov et al. 2013, Mikolov et al. 2013a)



Neural LM architectures: which to use?

- CBOW and Skip-Gram typically produce similar embeddings, but:
 - CBOW is several times faster to train, better accuracy for frequent words
 - Skip-Gram works well with small amounts of training data, and does well with representing rare words
- Mikolov: "Best practice is to try a few experiments and see what works the best for you"

https://groups.google.com/forum/#!searchin/word2vec-toolkit/c-bow/word2vec-toolkit/NLvYXU99cAM/ESId8LcDxlAJ

Properties of dense word embeddings

Dense word embeddings encode:

- → Semantic Relationships
- → Syntactic Relationships

Can probe relations between words using vector arithmetic:

- → king male + female = ?
- \rightarrow walked walk + fly = ?

Train your own word embeddings:

TensorFlow: https://www.tensorflow.org/tutorials/word2vec

Gensim: https://rare-technologies.com/word2vec-tutorial/

FastText: https://github.com/facebookresearch/fastText

Pretrained Word embeddings:

Word2Vec: https://code.google.com/archive/p/word2vec/

→ Trained on 100 billion tokens from Google News corpus

GloVe: https://nlp.stanford.edu/projects/glove/

→6B wikipedia, 42-840B tokens Common Crawl, 27B tokens Twitter

LexVec: https://github.com/alexandres/lexvec

→ 58B tokens Common Crawl, 7B tokens Wikipedia + NewsCrawl

Word embeddings: Evaluation

How to judge the quality of embeddings?

- 'Relatedness' scores for given word pairs
 - → Compare model's relatedness scores to human relatedness scores

Analogy tests

→ Find x such that x : y best resembles a sample relationship a : b

Categorization

→ Recover a known clustering of words into different categories.

Document features

• So far: Features in word-vectors can be: context counts, PMI scores, weights from neural LMs...

• Can also be features of the docs in which the words occur.

Document occurrence features are useful for topical/thematic similarity

Document-Term Matrix

	D1	D2	D3	D4
W1	23	17	0	0
W2	102	0	14	24
W3	14	57	0	2
W4	0	0	18	38

Term Frequency – Inverse Document Frequency (tf-idf)

- Common in IR tasks
- Popular method to weight term-document matrices in general

Tf: relative frequency of term in document

$$\rightarrow$$
 tf(t,d) = f(t,d)

Idf: inverse of the proportion of docs containing the term

 \rightarrow N / n_t (N = total # of docs, n_t = # of docs term t appeared in)

Document-Term Matrix

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Tf-idf weighted Document-Term Matrix

	D1	D2	D3	D4
W1	.12	.16	0	0
W2	.21	0	.13	.11
W3	.03	.22	0	.01
W4	0	0	.39	.41

Tf-idf weighted Document-Term Matrix

		D1	D2	D 3	D4
	W1	.12	.16	0	0
Word	W2	.21	0	.13	.11
Vectors	W3	.03	.22	0	.01
	W4	0	0	.39	.41

Tf-idf weighted Document-Term Matrix

Document Vectors

	D1	D2	D3	D4
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W4	0	0	.39	.41

Topic Models

Latent Dirichlet Allocation (LDA) and variants known as topic models.

- → Learned on large document collection (unsupervised)
- →Latent probabilistic clustering of words that tend to occur in the same document. Each 'topic' cluster is a distribution over words.
- →Generative Model: Each document is a sparse mixture of topics. Each word in the doc is chosen by sampling a topic from the doc-specific topic distribution, then sampling a word from that topic.

Topic Models

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

Documents

Topic proportions and assignments

Seeking Life's Bare (Genetic) Necessities

Haemophilus

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 mera 128 wares. The

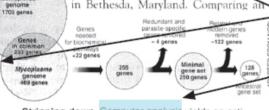
required a mere 128 genes. The other researcher mapped genes in a simple parasite and estimated that for this organism, 800 genes are plenty to do the job—but that anything short of 100 wouldn't be enough.

Although the numbers don't match precisely, those predictions

* 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 on the sala 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 mo-

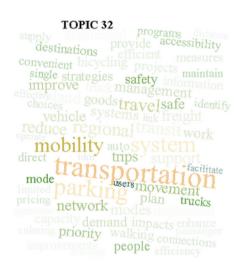
Arcady Mushegian, a computational molecular biologist at the National Center for Biotechnology Information (NCBI) in Bethesda, Maryland. Comparing an

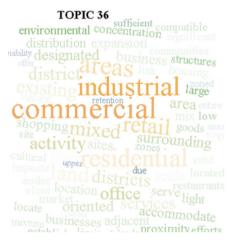


Stripping down. Computer analysis yields an estimate of the minimum modern and ancient genomes

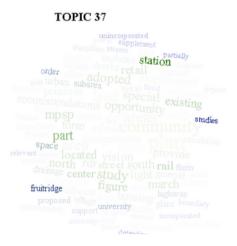
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Visualizing Topics





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Questions?