

# Distributional Semantics

Sean Simpson

(some slides from Marine Carpuat, Nathan Schneider)

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# Topics

- **Lexical Semantics**

- Word Similarity
- Distributional Hypothesis
- Vector Representations
- Evaluation

- **Document Semantics**

- Topic Modeling

# Lexical Semantics

# Semantic similarity: Intuition

- Identify word closest to target:

- **Accidental**

- Abominate
- Meander
- Inadvertent
- inhibit

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# Semantic similarity: Intuition

- Identify word closest to target:

- **FedEx**

- car

- UPS

- rotate

- Navy

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# Semantic similarity: Intuition

- Identify word closest to target:

- **Millennial**

- octopus

- fork

- water

- avocado



# Semantic similarity: Intuition

- Identify word closest to target:

- **Millennial**

- octopus

- fork

- water

- avocado

# 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**

- The two concepts are close in terms of frequency
- e.g. 'inadequate' and 'sufficient'

- **World Knowledge**

- The two concepts are similar due to shared world knowledge
- e.g. 'spirit' and 'ghost'

- **Psychological**

- The two concepts are similar due to shared psychological framework
- e.g. 'money' and 'bank', or 'millennial' and 'avocado'



occur in

schema or

# 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.

# 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)

→

→ “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.

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

# 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:

		<i>subj-of, absorb</i>	<i>subj-of, adapt</i>	<i>subj-of, behave</i>	::	<i>pobj-of, inside</i>	<i>pobj-of, into</i>	::	<i>nmod-of, abnormality</i>	<i>nmod-of, anemia</i>	<i>nmod-of, architecture</i>	::	<i>obj-of, attack</i>	<i>obj-of, call</i>	<i>obj-of, come from</i>	<i>obj-of, decorate</i>	::	<i>nmod, bacteria</i>	<i>nmod, body</i>	<i>nmod, bone marrow</i>
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

$$\text{association}_{\text{PMI}}(w, f) = \log_2 \frac{P(w, f)}{P(w)P(f)}$$

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

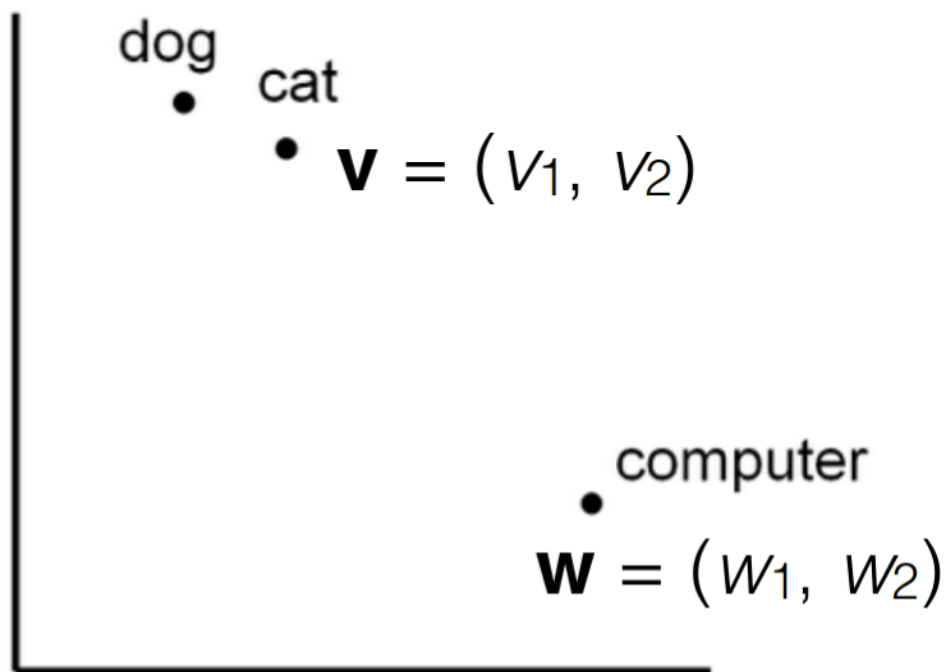
# Computing Similarity

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:

- $V = \text{'cat'}$
- $W = \text{'computer'}$

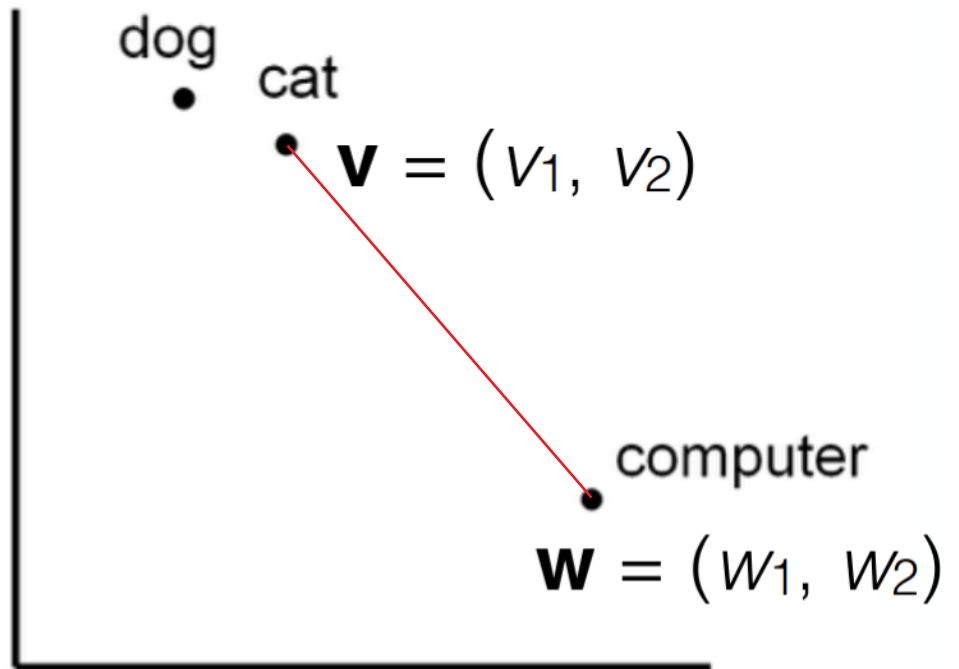


# Euclidean Distance

- **Formula:**

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

→ Can be oversensitive to extreme values

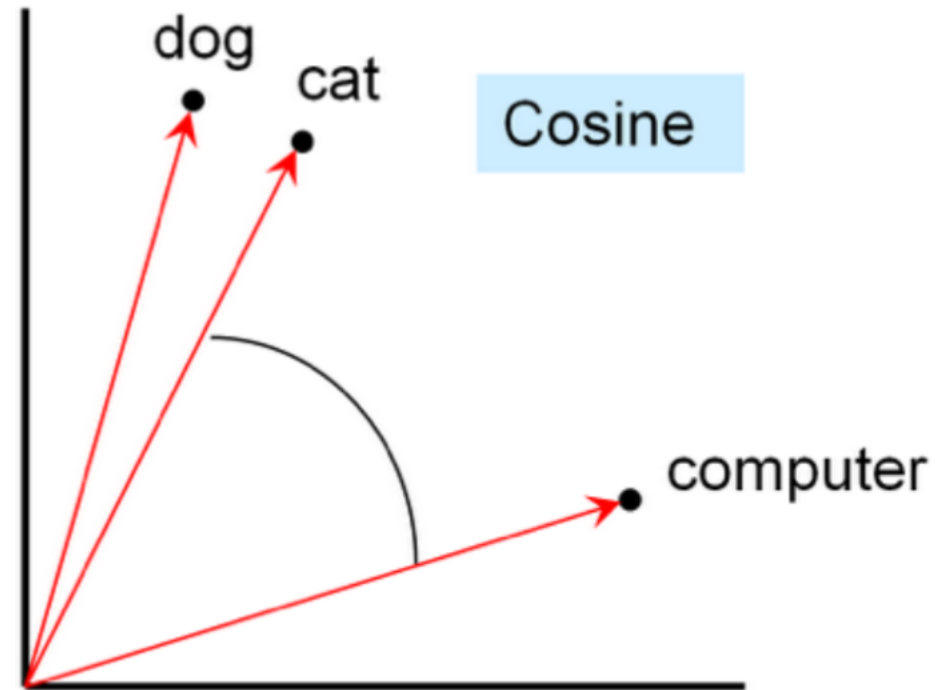


# Cosine Similarity

- **Formula:**

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

- 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

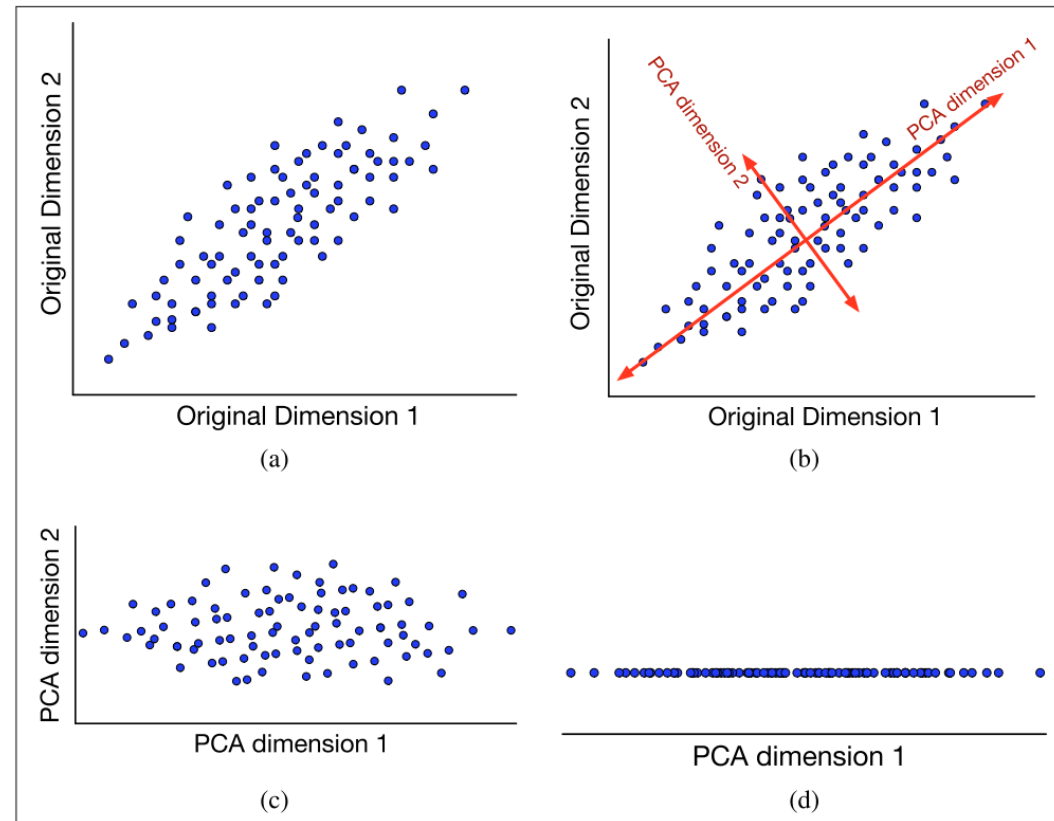
(2) Neural Language Models



# 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.

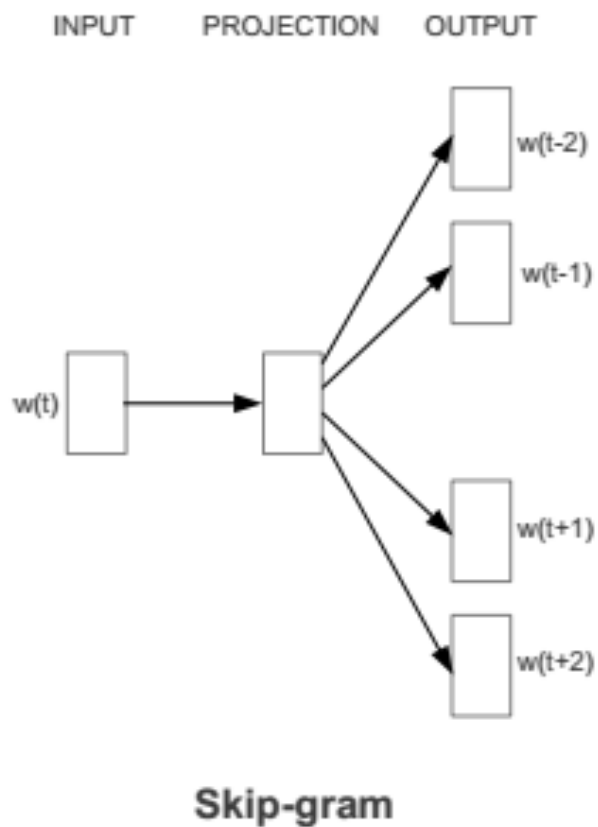
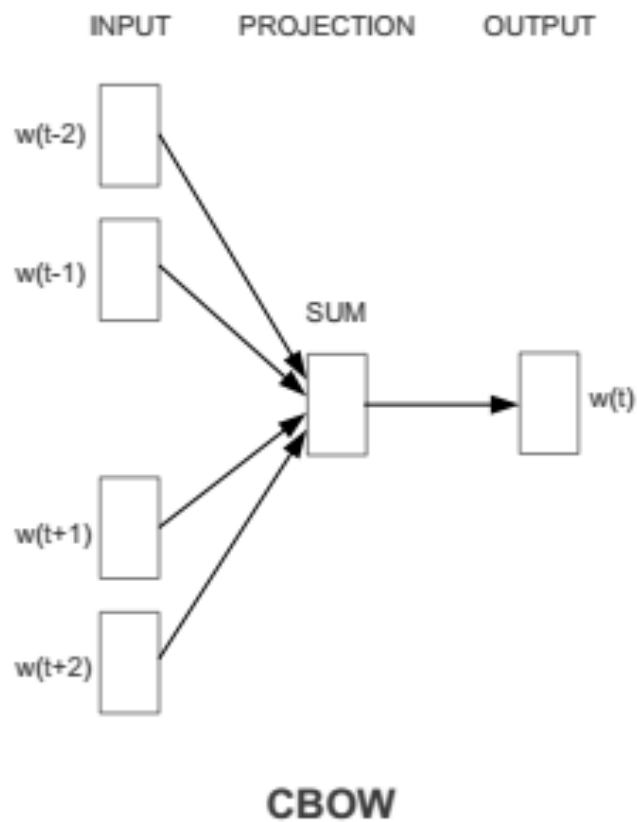
- Similar input words → similar context word prediction
- Similar input words → similar corresponding rows in the weight matrix of the trained network.

*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/ESld8LcDxIAJ>

# Properties of dense word embeddings

## Dense word embeddings encode:

- Semantic Relationships
- Syntactic Relationships

## Can probe relations between words using vector arithmetic:

- $\text{king} - \text{male} + \text{female} = ?$
- $\text{walked} - \text{walk} + \text{fly} = ?$

# 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

	<b>D1</b>	<b>D2</b>	<b>D3</b>	<b>D4</b>
<b>W1</b>	23	17	0	0
<b>W2</b>	102	0	14	24
<b>W3</b>	14	57	0	2
<b>W4</b>	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

$$\rightarrow \text{tf}(t,d) = f(t,d)$$

Idf: inverse of the proportion of docs containing the term

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

# Document-Term Matrix

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# Tf-idf weighted Document-Term Matrix

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

# Tf-idf weighted Document-Term Matrix

Word  
Vectors

	<b>D1</b>	<b>D2</b>	<b>D3</b>	<b>D4</b>
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# 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
...	

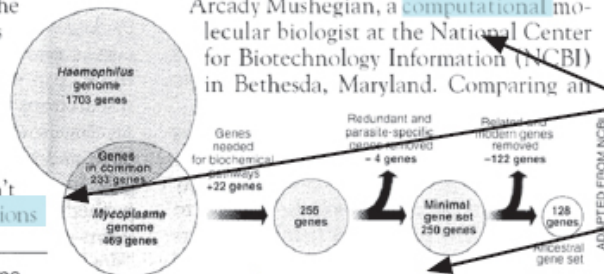
## Documents

### 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 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

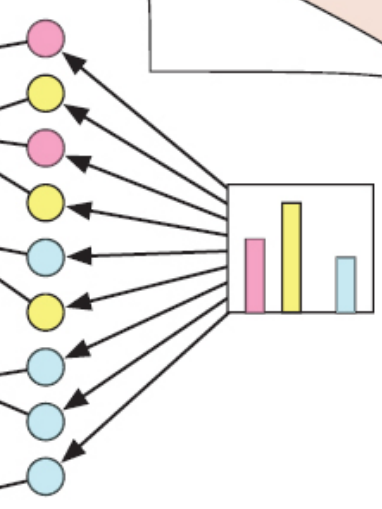


\* Genome Mapping and Sequencing, Cold Spring Harbor, New York, May 8 to 12.

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

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## Topic proportions and assignments





Questions?