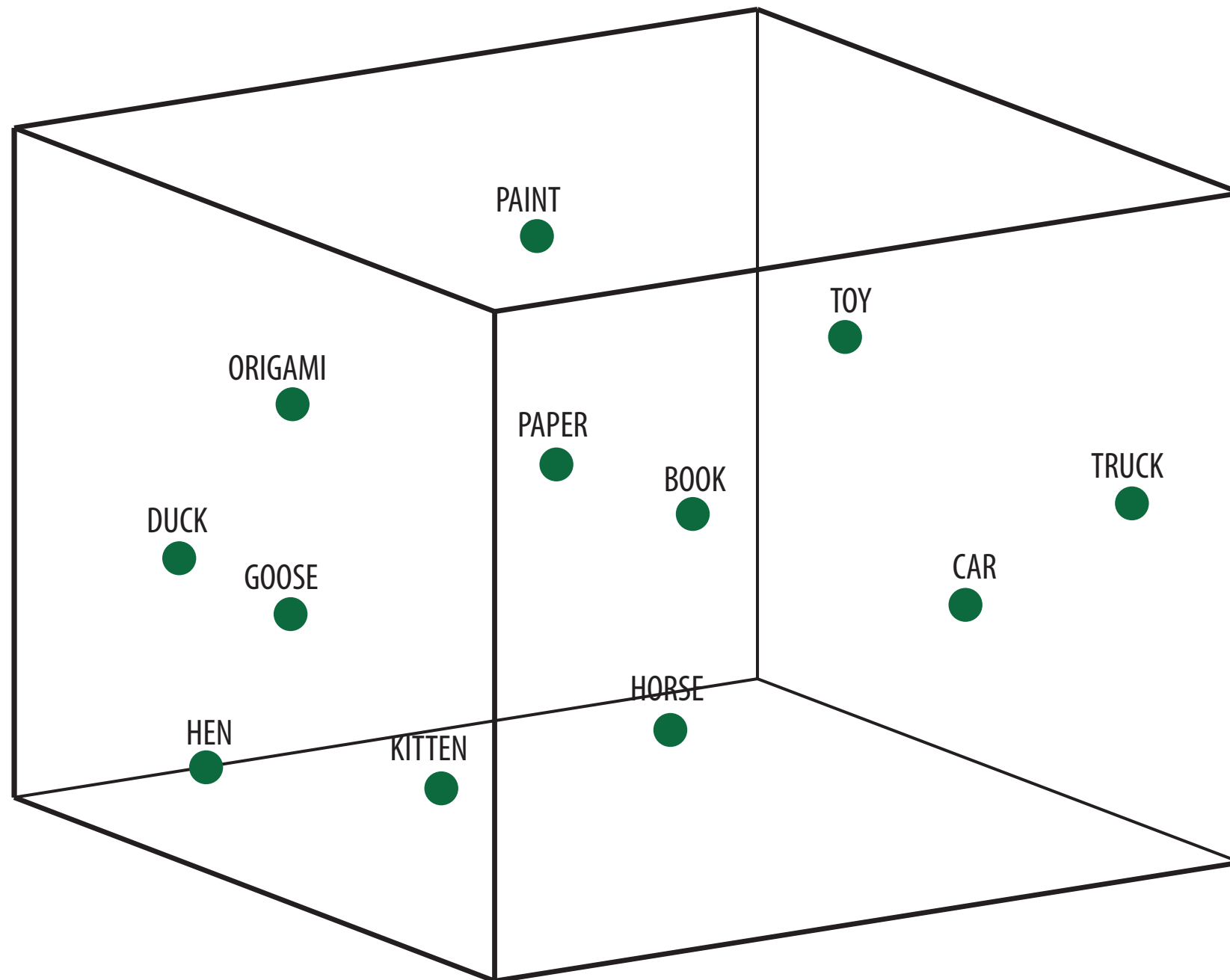


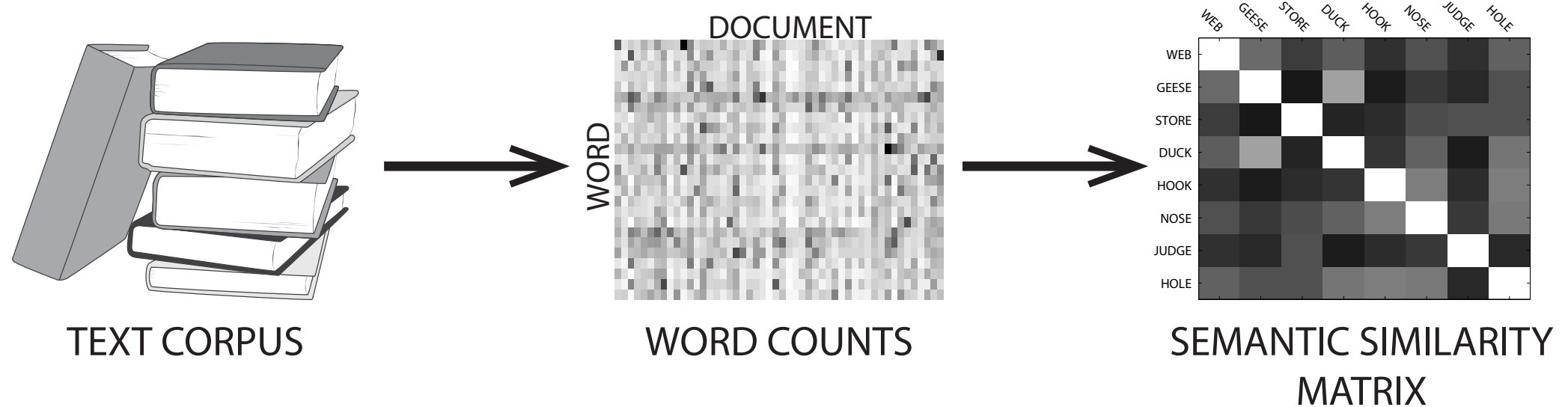
Recap

- Attribute theory
- Generalized Euclidean distance
- Distance-based similarity
- Cosine-based similarity
- Visualizing and reasoning about high-dimensional spaces

Semantic spaces



Word spaces



Topic spaces

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
...	

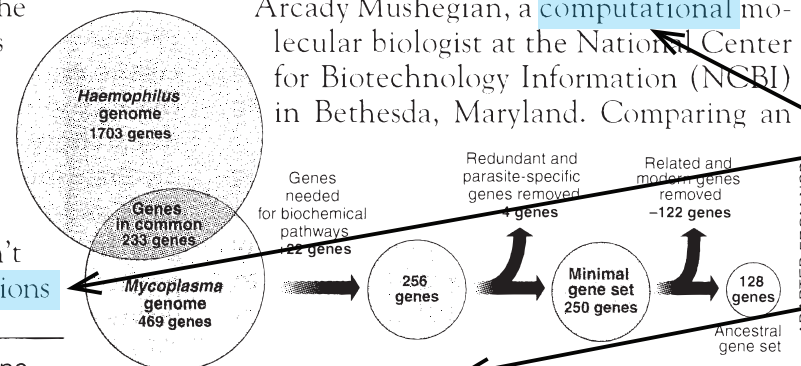
Documents

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

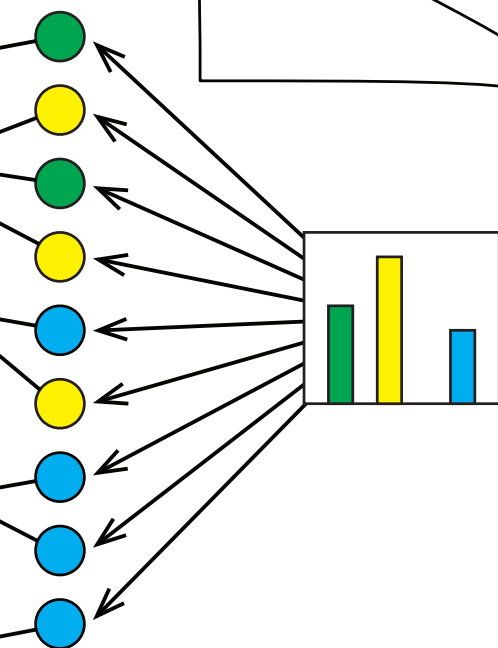


* Genome Mapping and Sequencing, Cold Spring Harbor, New York, May 8 to 12.

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

SCIENCE • VOL. 272 • 24 MAY 1996

Topic proportions and assignments



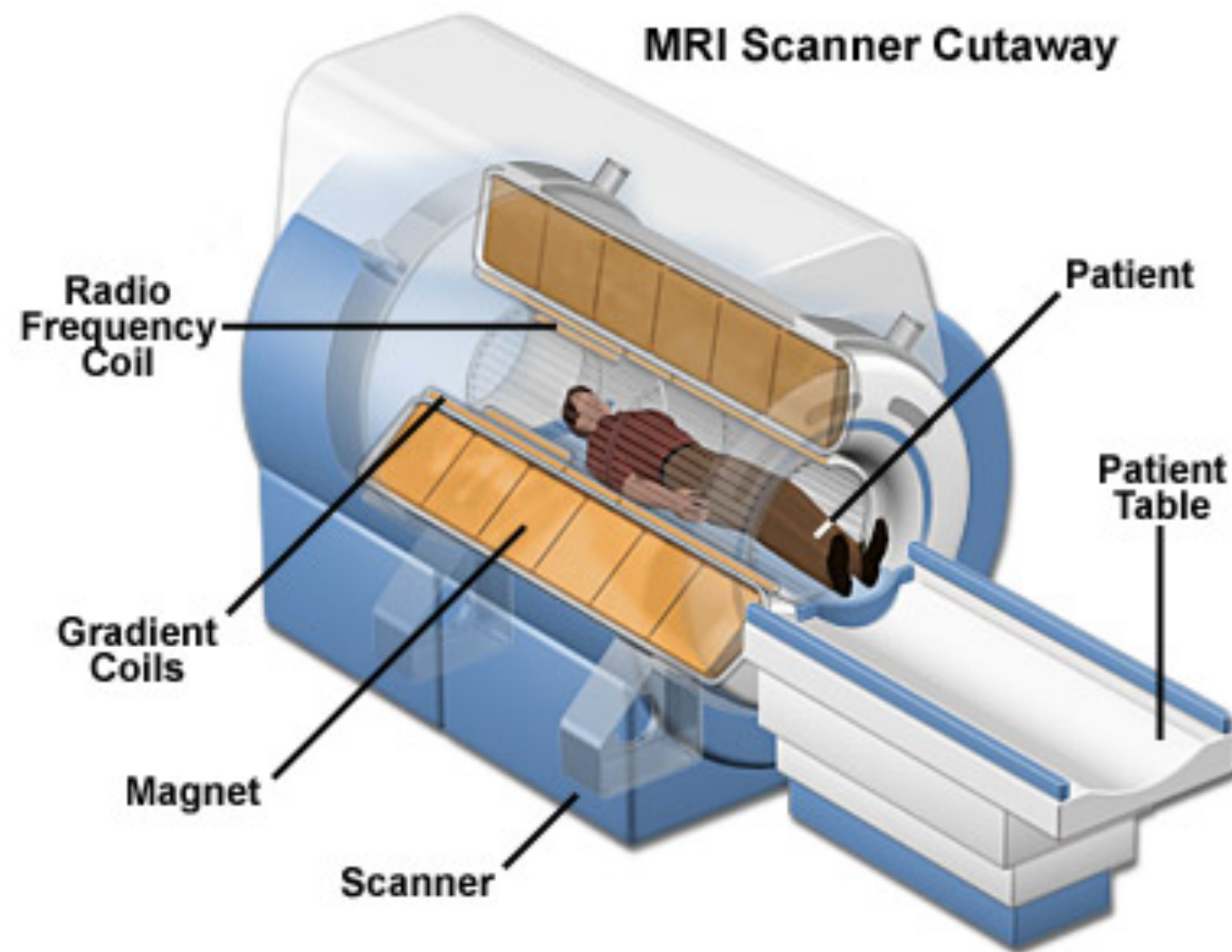
Other language models

- Psychological experiments; e.g. word association spaces (WAS; Steyvers et al., 2005)
- Detailed hand-labeled models; e.g. Princeton WordNet (Miller, 1998)
- Deep learning models

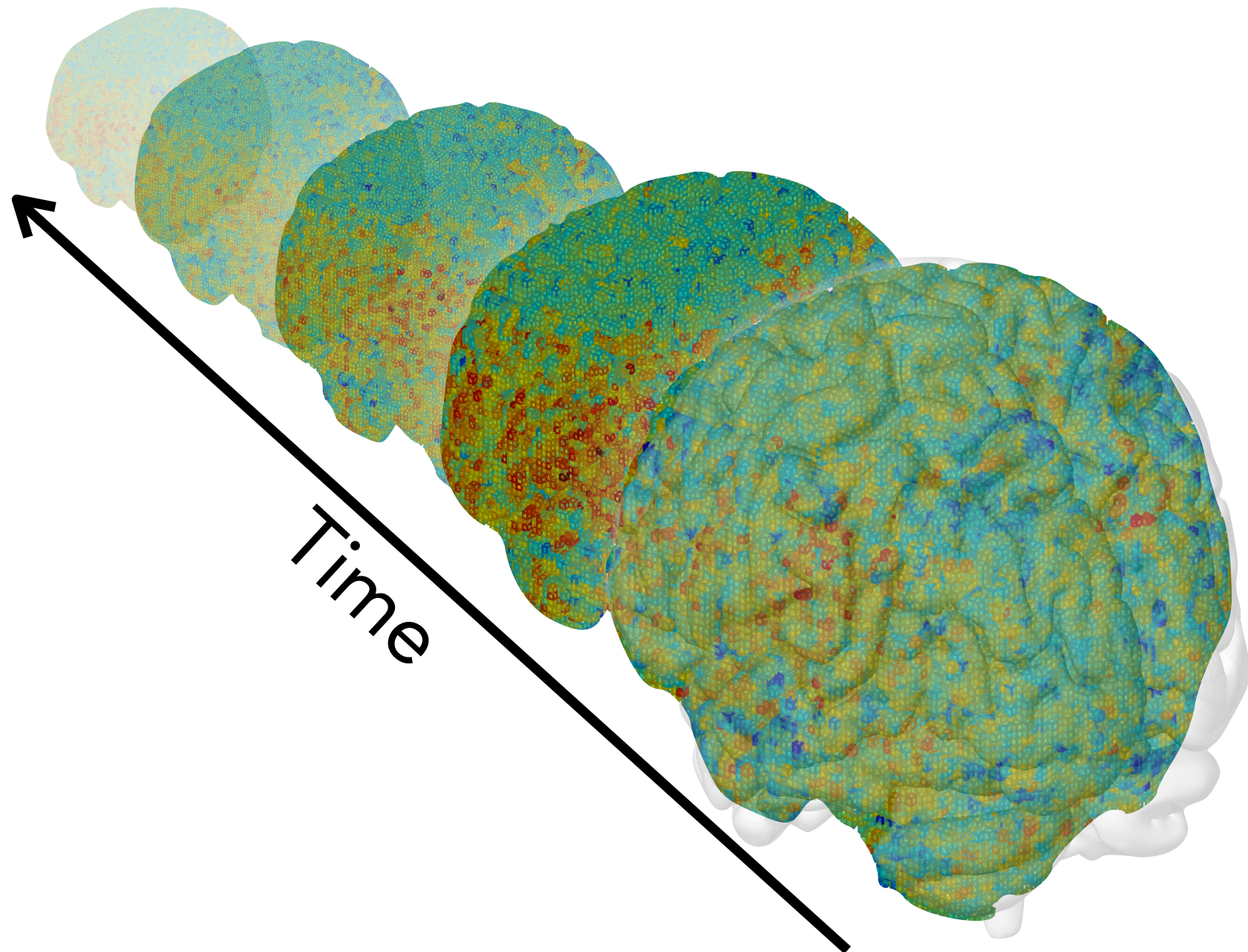
Brain spaces

- Record from people's brains during an experiment
- Summarize their brain patterns (feature vectors!)
- Idea: if our thoughts come from our brains, then similarities in brain patterns should reflect similarities in thoughts

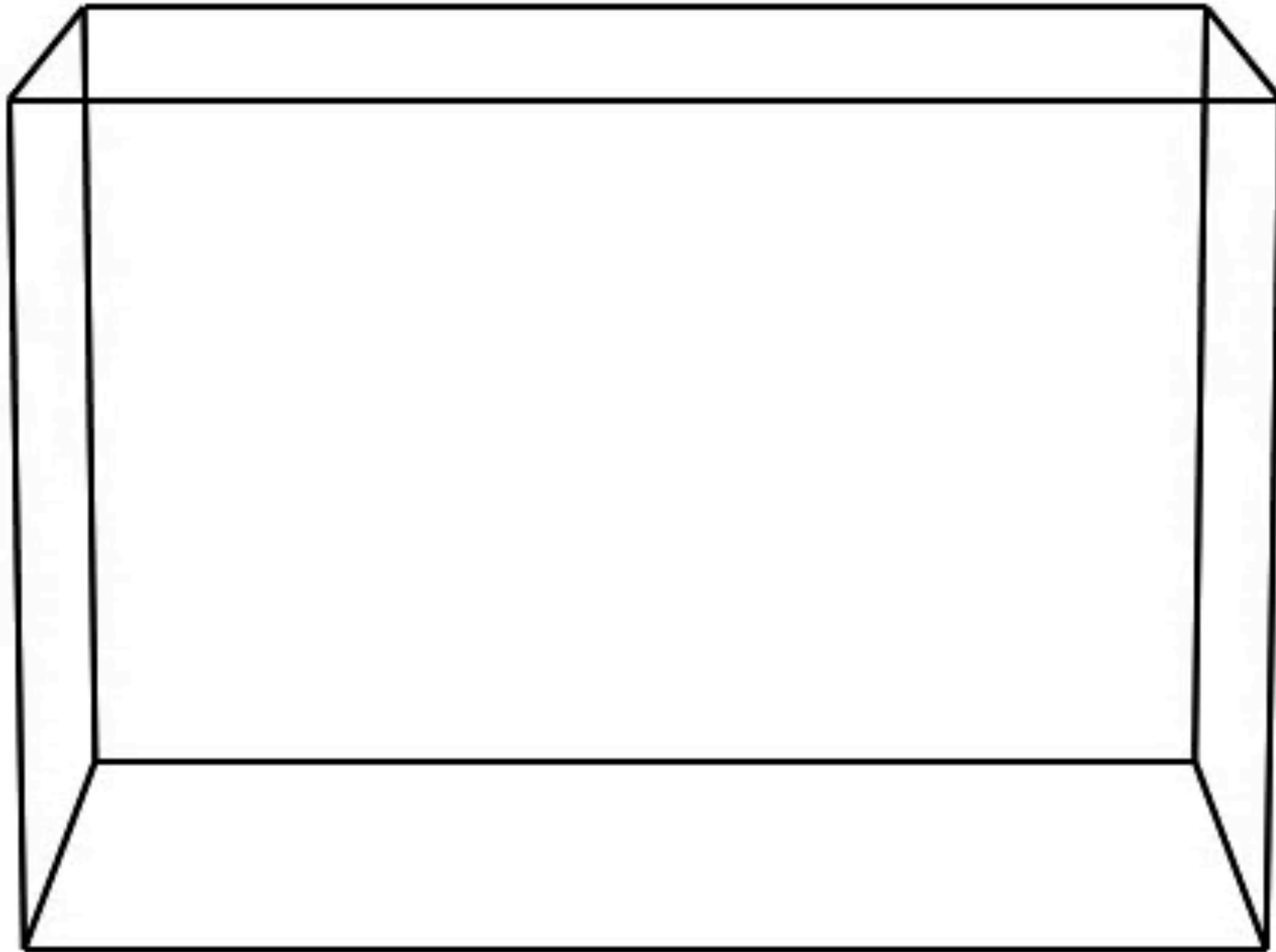
functional Magnetic Resonance Imaging (fMRI)



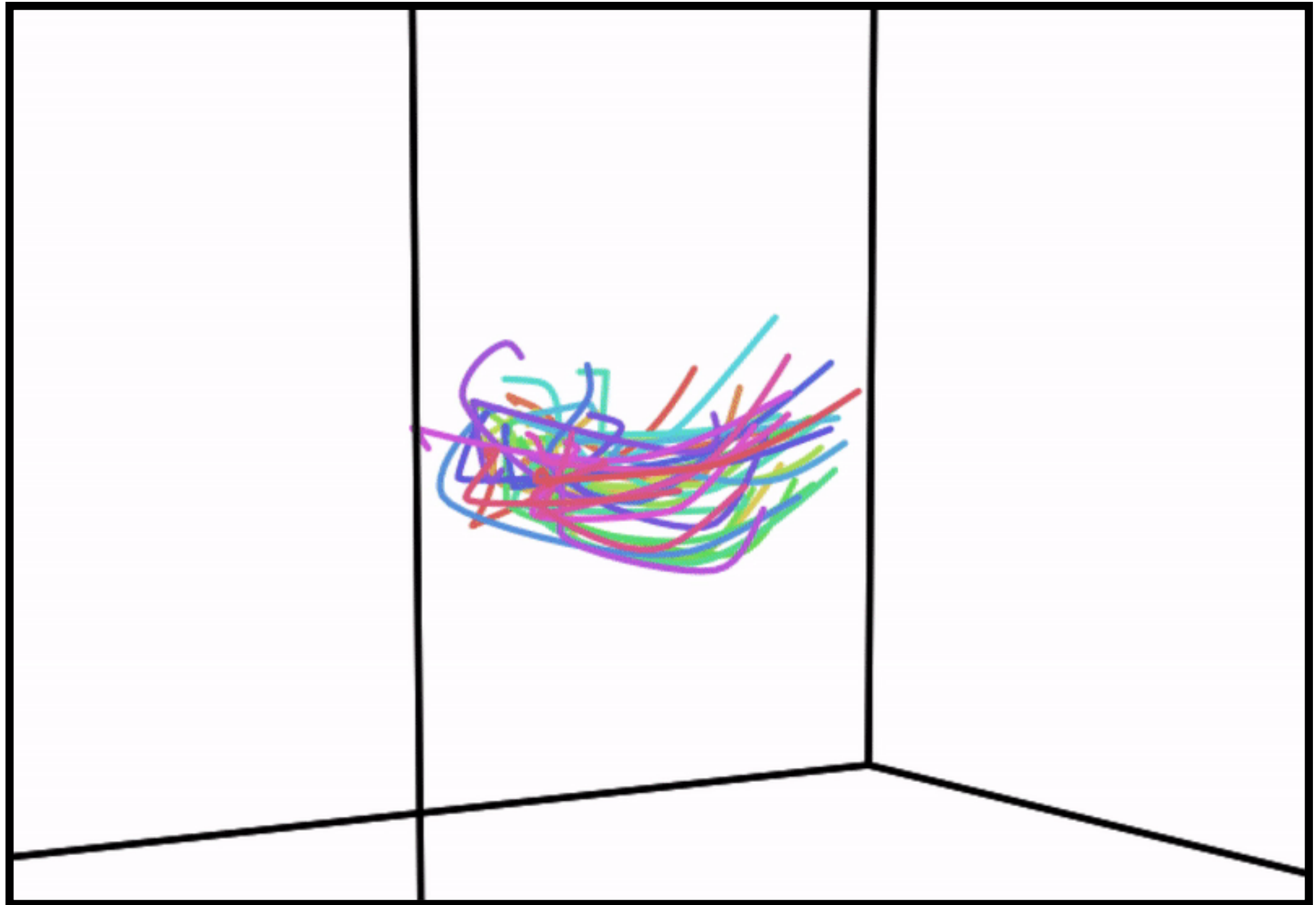
functional Magnetic Resonance Imaging (fMRI)



People watching Indiana Jones



People listening to a story



Other types of spaces

- Colors and images (pixel RGB values)
- Physical measurements (weather, geometry, velocity, voltage, etc.)
- Qualitative or quantitative properties of anything...

Laying the groundwork...

- How can we (formally) represent complex thoughts?
- Extensions of strength theory

What was “wrong” with strength theory?

- Similarity– no notion of which items are similar or how similarity affects memory
- Context– no notion of context or time
- Where does the idea of “strength” even come from?

The multiple trace hypothesis

$$M = \begin{pmatrix} m_1(1) & m_2(1) & m_3(1) \\ m_1(2) & m_2(2) & m_3(2) \\ m_1(3) & m_2(3) & m_3(3) \\ \vdots & \vdots & \vdots \\ m_1(N) & m_2(N) & m_3(N) \end{pmatrix} = (\mathbf{m}_1 \quad \mathbf{m}_2 \quad \mathbf{m}_3)$$

The multiple trace hypothesis

- Studied items get converted into vectors and stored in memory
- Test items get converted into vectors
- We can compare the test item's vector to each of the studied item's vectors
 - Remember from Chapter 2: serial search, parallel search
- Can people actually do this?

Experiment: study 2500 items

- “Visual long-term memory has a massive storage capacity for object details” – Brady et al. (2008)
- Examine **capacity** and **fidelity** of visual long-term memory
- Participants study a loooong list of items, looking for repeats (of any previously studied item)
- Then they get a series of recognition tests



















- This lasts for 5 grueling hours...
- Then participants take a 10 minute break...
- And then it's time for their memory test!









People can do this well!

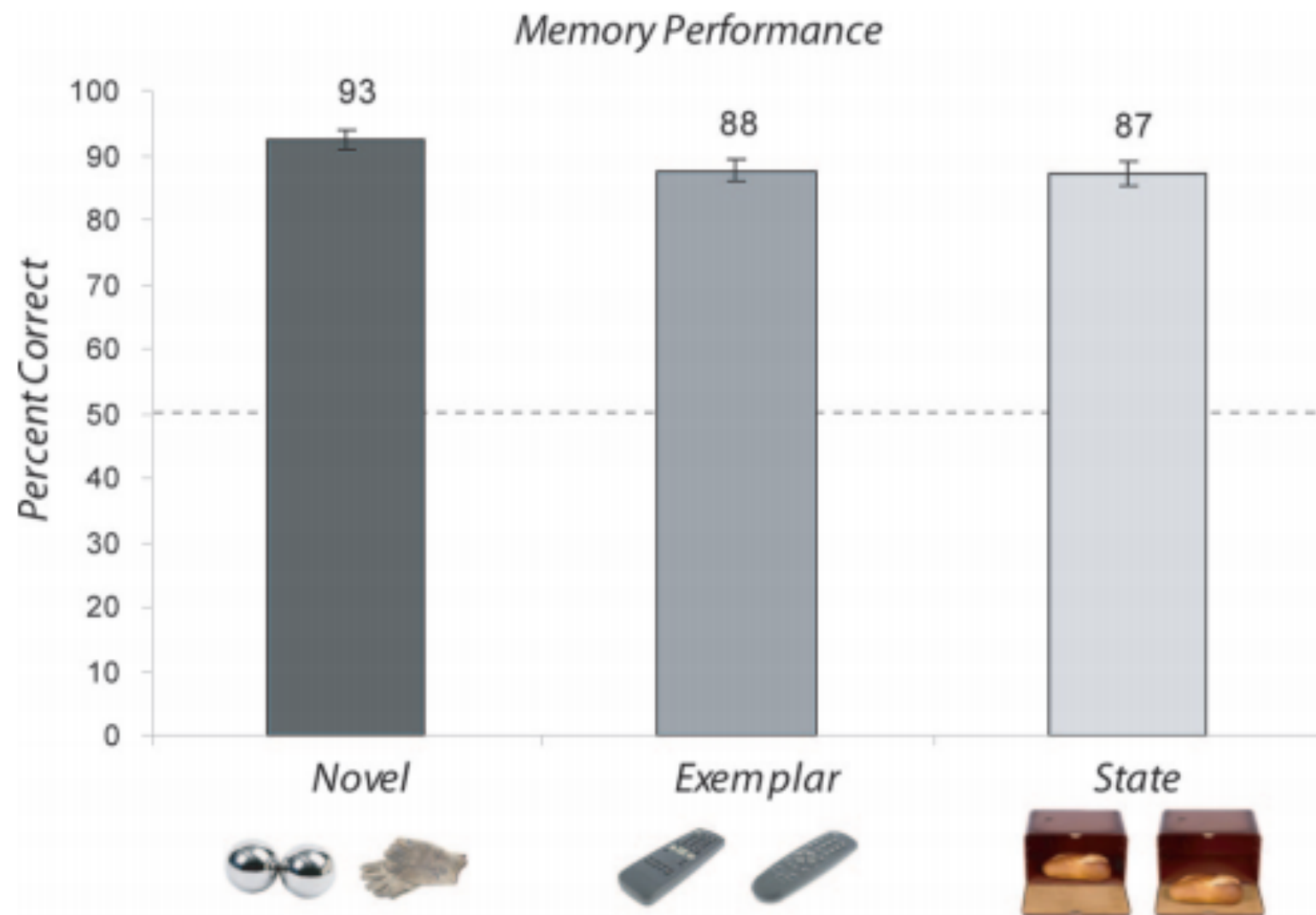
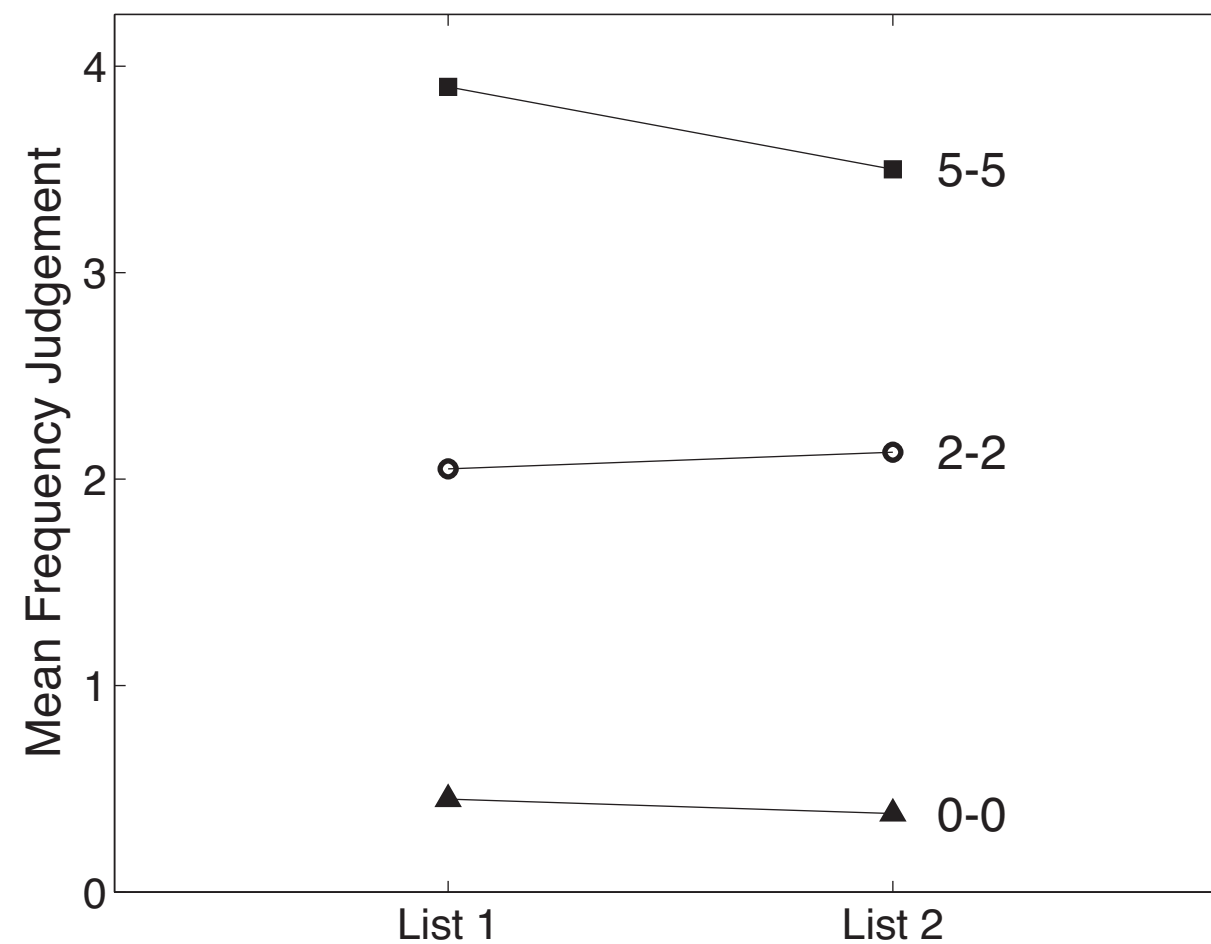


Fig. 2. Memory performance for each of the three test conditions (novel, exemplar, and state) is shown above. Error bars represent SEM. The dashed line indicates chance performance.

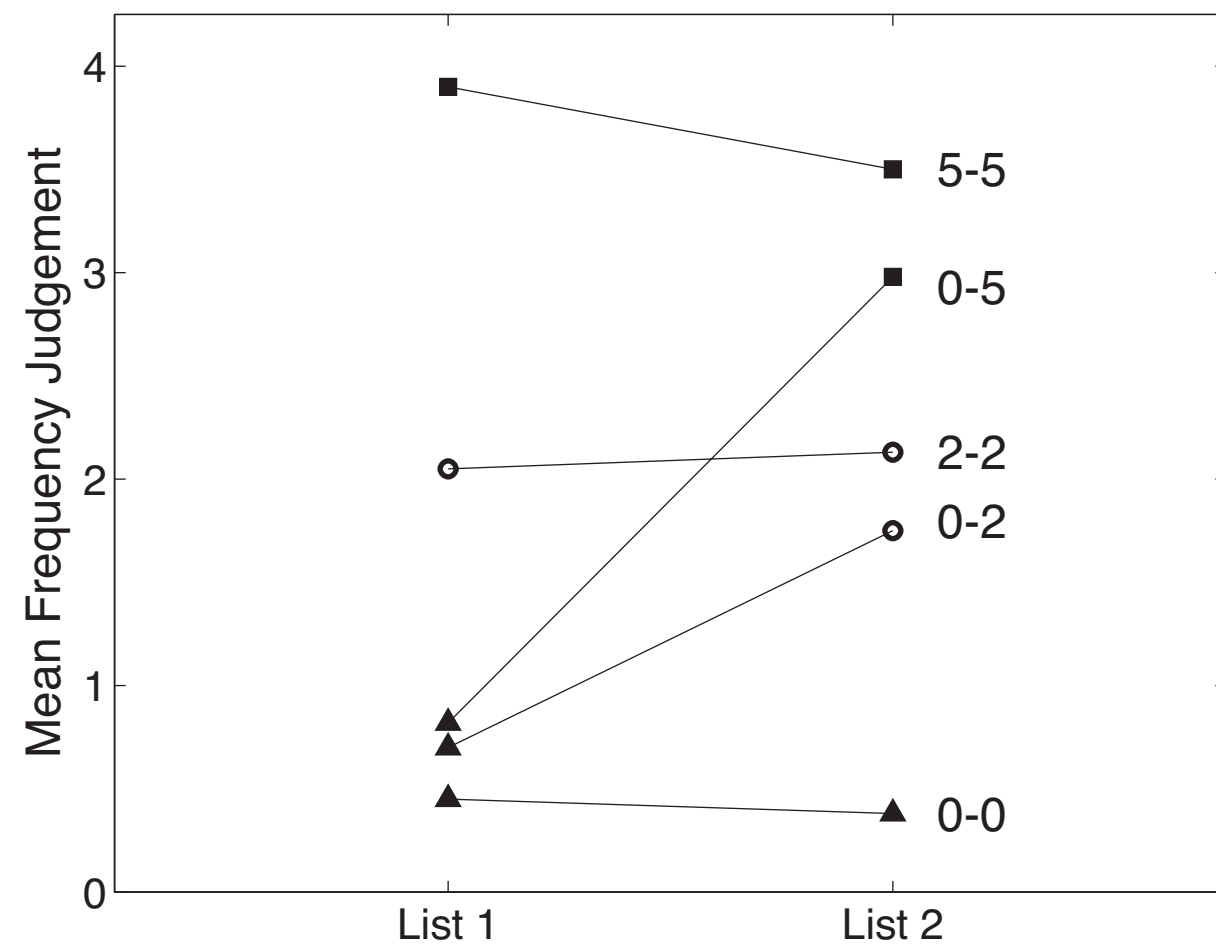
Judgment of Frequency (JOF)

- Huntsman and Block (1971)
- Two lists separated by a 5 minute break
- Each list has 104 words
 - Half are presented twice; half are presented 5 times (spaced repetitions)
- Unexpected JOF test: rate how many times you saw each item (on each list)

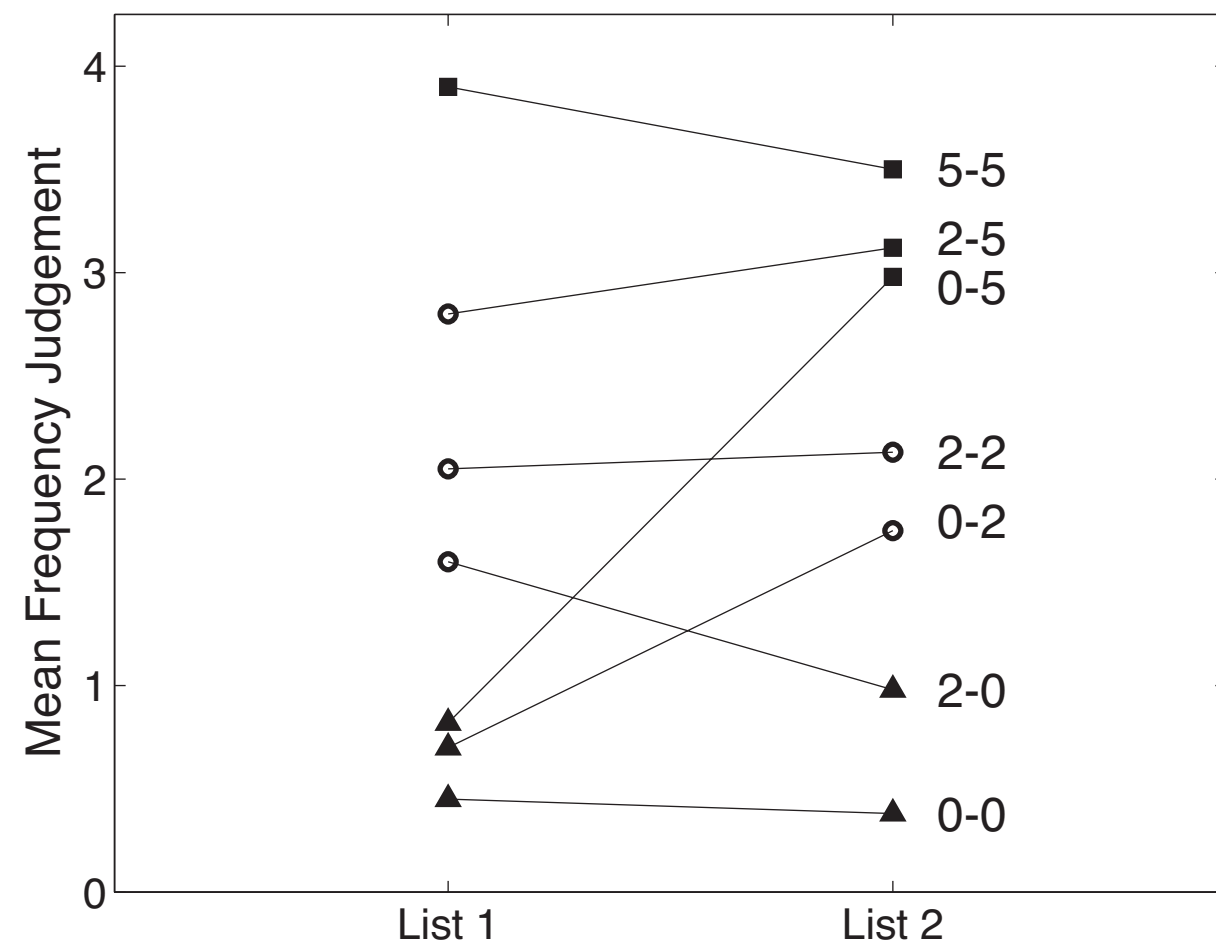
Judgment of Frequency (JOF)



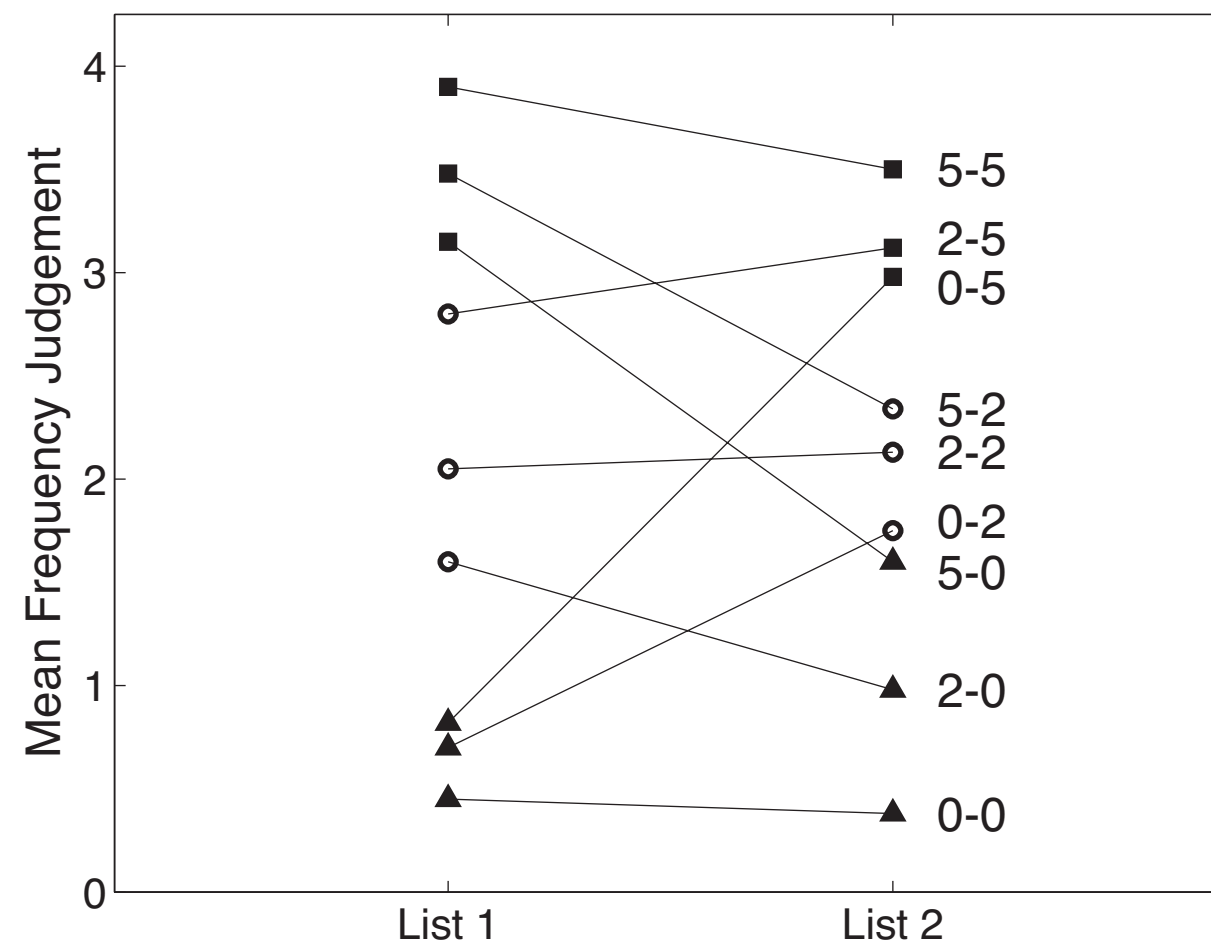
Judgment of Frequency (JOF)



Judgment of Frequency (JOF)



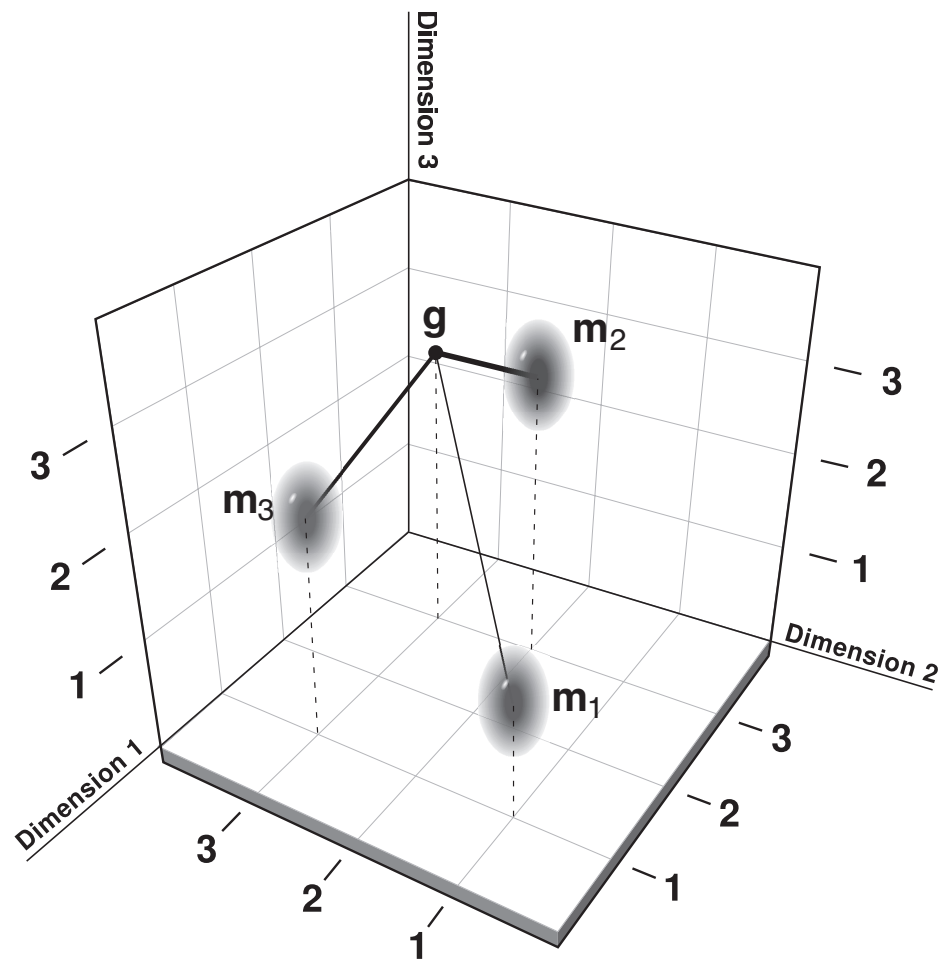
Judgment of Frequency (JOF)



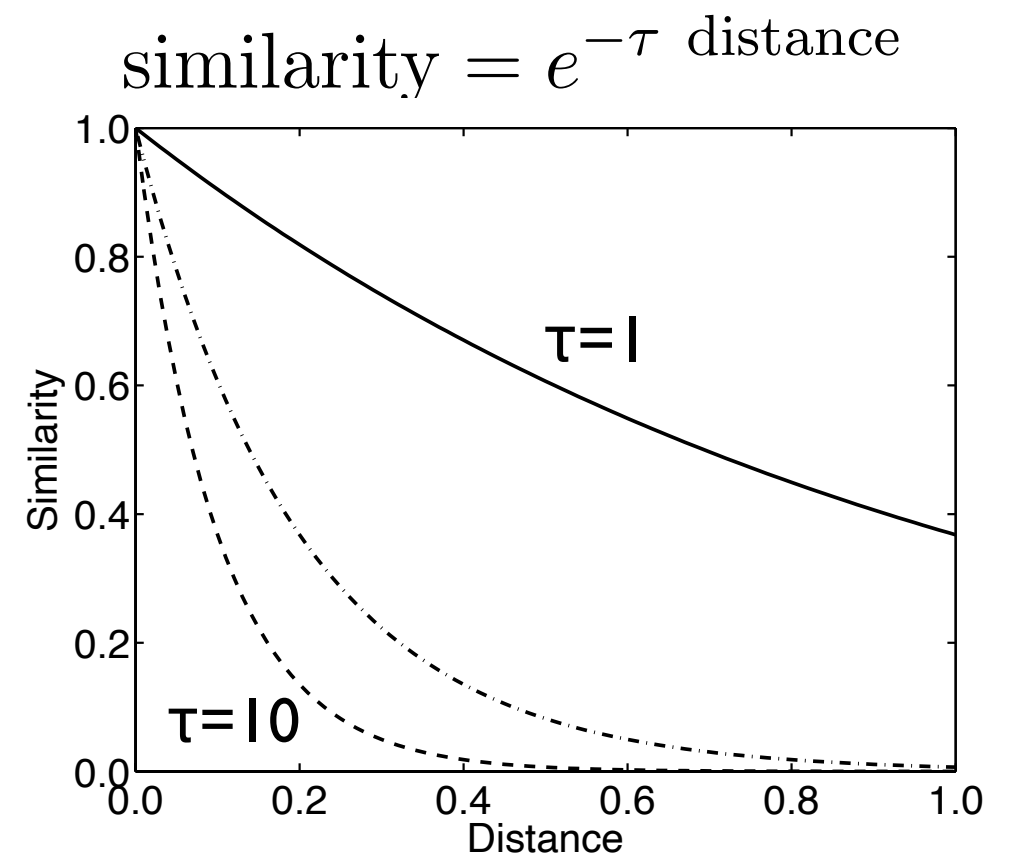
Judgment of Frequency (JOF)

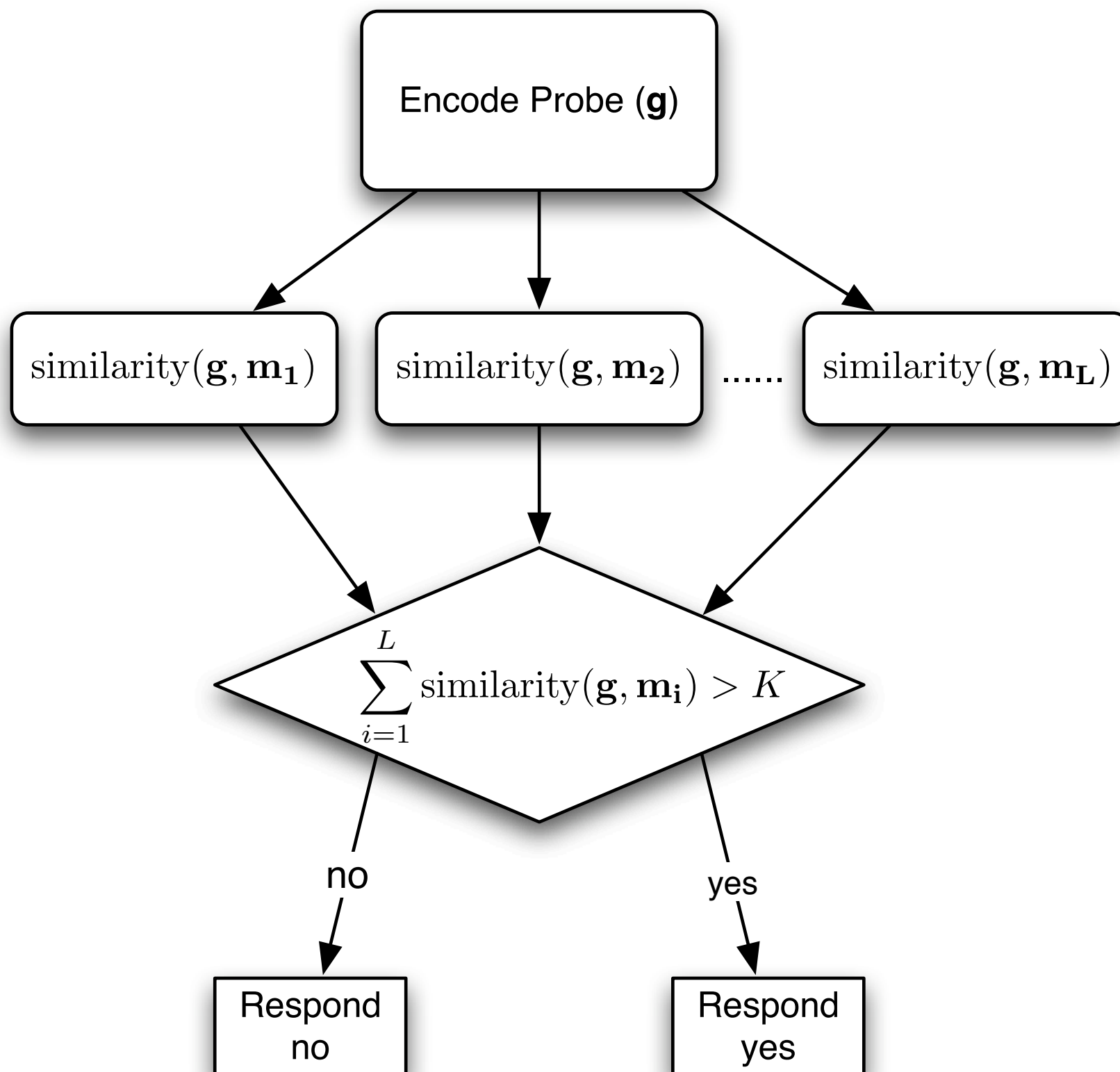
- People store multiple “copies” of each item (one per presentation?)
- Some attributes are related to the *context* (list?) in which the item was encoded
- We can gain access to this information

Summed similarity



Compute the distance between the
probe and the studied items
(Pythagorean theorem)





Following study of the list, the matrix M represents the list in memory

$$M = \begin{pmatrix} \mathbf{m}_1 & \mathbf{m}_2 & \mathbf{m}_3 & \dots & \mathbf{m}_L \end{pmatrix}$$

\mathbf{g} denotes a test item, either a target or a lure.

Similarity between \mathbf{g} and \mathbf{m}_i =

$$e^{-\tau \|\mathbf{g} - \mathbf{m}_i\|} = e^{-\tau \sqrt{\sum_{j=1}^N (g(j) - m_i(j))^2}}$$

τ determines the steepness of the exponential function.

$$P(yes) = P\left(\sum_{i=1}^L e^{-\tau} \sqrt{\sum_{j=1}^N (g(j) - m_i(j))^2} > C\right)$$

The probability of saying “yes” to a probe is equal to the probability that its summed similarity (to the items) exceeds a criterion threshold, C

Example Problem (tau=1)

stimulus	Dimension		
	x	y	z
1	3	2	3
2	1	2	3
3	3	2	3
4	2	2	2
5	1	1	2
Example Lure	3	3	3
Example Target	1	2	3

Distance to:	
Lure	Target
1	2
2.236	0
1	2
1.732	1.414
3	1.414

Similarity to:	
Lure	Target
0.37	0.14
0.11	1
0.37	.14
0.18	0.24
0.05	0.24

Summed Similarity	Lure	Target
	1.07	1.76

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	x	y	z
1	3	2	3
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