



Representational Similarity Analysis

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Key references

frontiers in
SYSTEMS NEUROSCIENCE

ORIGINAL RESEARCH ARTICLE

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Representational similarity analysis – connecting the branches of systems neuroscience

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PLOS COMPUTATIONAL BIOLOGY

A Toolbox for Representational Similarity Analysis

Hamed Nili^{1*}, Cai Wingfield², Alexander Walther¹, Li Su^{1,3}, William Marslen-Wilson³,
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- the original RSA paper
- Cited by 1293

Decoding Neural Representational Spaces Using Multivariate Pattern Analysis

James V. Haxby,^{1,2} Andrew C. Connolly,¹ and J. Swaroop Guntupalli¹

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Annu. Rev. Neurosci. 2014. 37:435–56

Representational similarity analysis

Let's start with the following three questions:

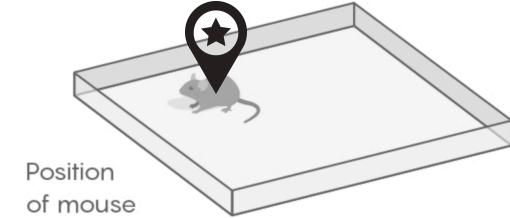
What is...

Representation?

Representational space?

Representational geometry?

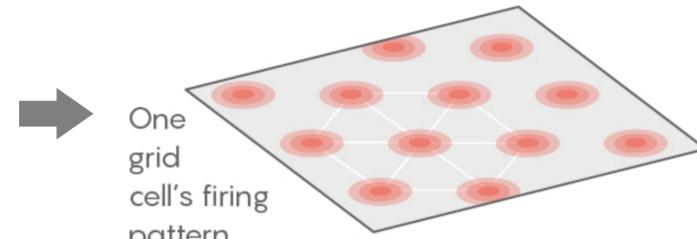
Representation



Position
of mouse



Mouse entorhinal cortex



One
grid
cell's firing
pattern

A spatial location can be represented
in very different forms across different systems



Maps

36°41'37.6"N 126°39'21.6"E
(longitude and latitude)



Computer



Binary code

Image sources:

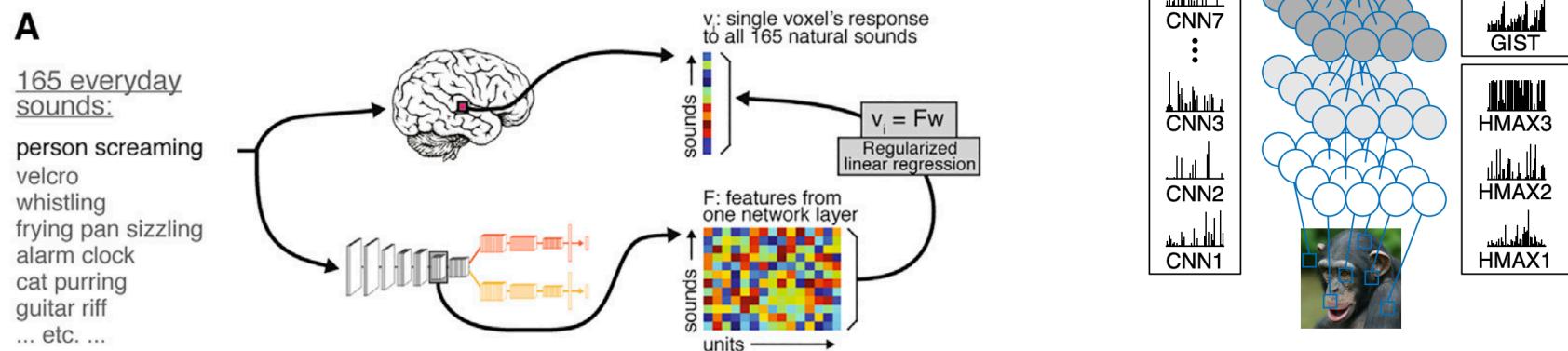
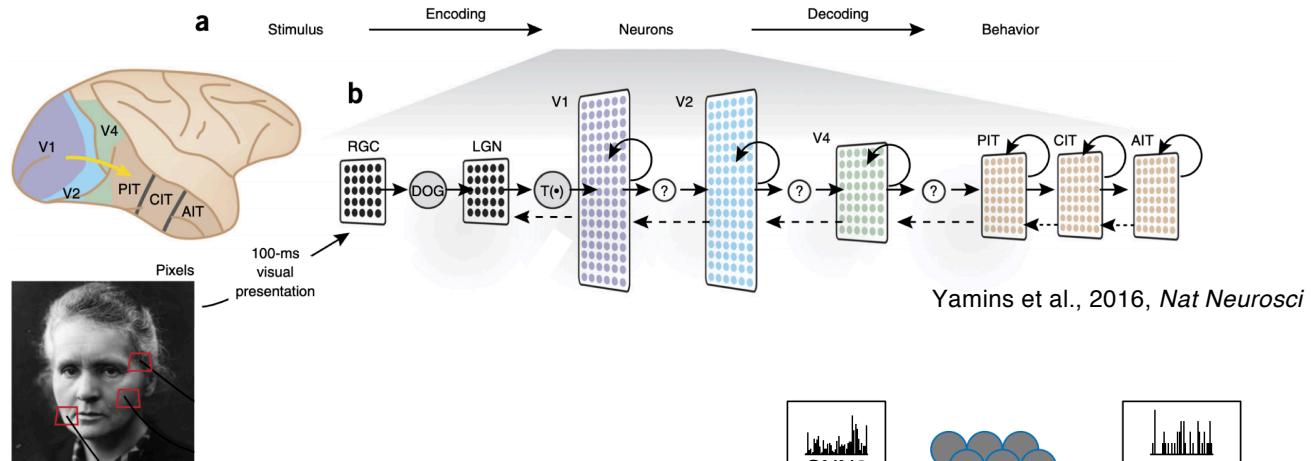
<https://www.quantamagazine.org/the-brain-maps-out-ideas-and-memories-like-spaces-20190114/>

Behrens et al., 2018, *Neuron*

Representation

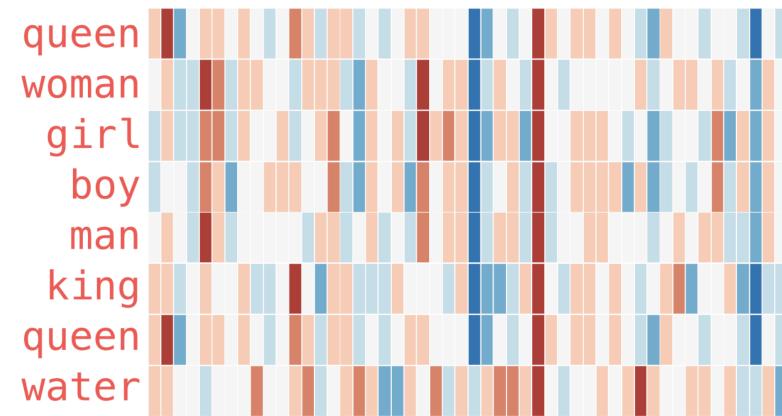
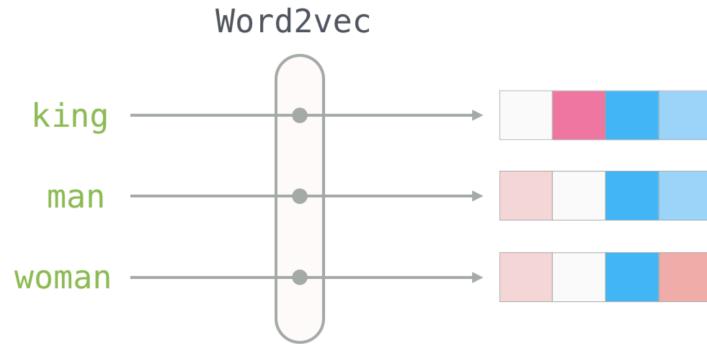
David Marr:

"A representation is a formal system for making explicit certain entities or types of information, together with a specification of how the system does this."



Embedding = Vector representation

E.g.,

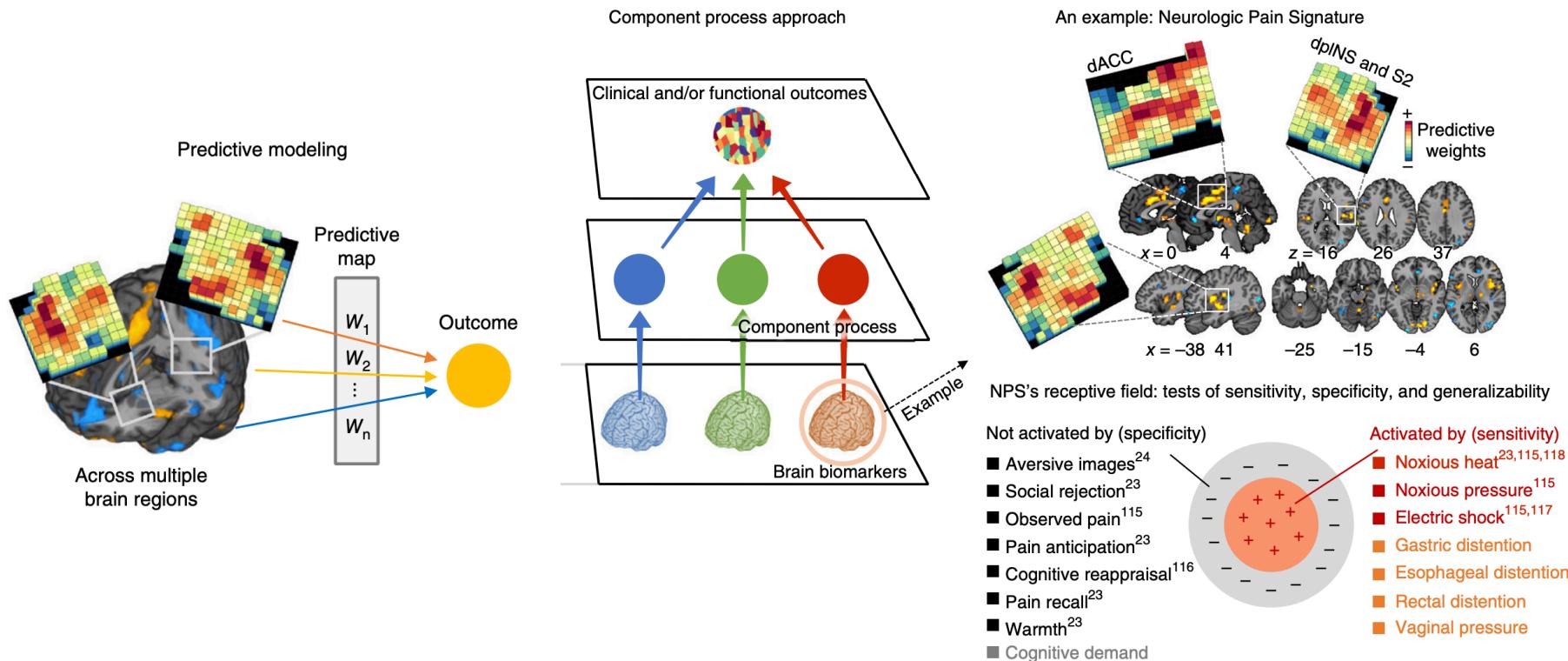


Only dimensionality reduction?
Could involve up-sampling (e.g., eye jitter)

Image sources:

<http://jalammar.github.io/illustrated-word2vec/>

Building brain biomarkers = identifying good brain representations



Woo et al., 2017, *Nat Neurosci*; Wager et al., 2013, *NEJM*

Some challenges in studying representations

1. Difficult to identify (or develop) good representations
2. Difficult to use (or compare) representations from different systems (or models)
e.g., different dimensions, different shapes, etc.

Some challenges in studying representations



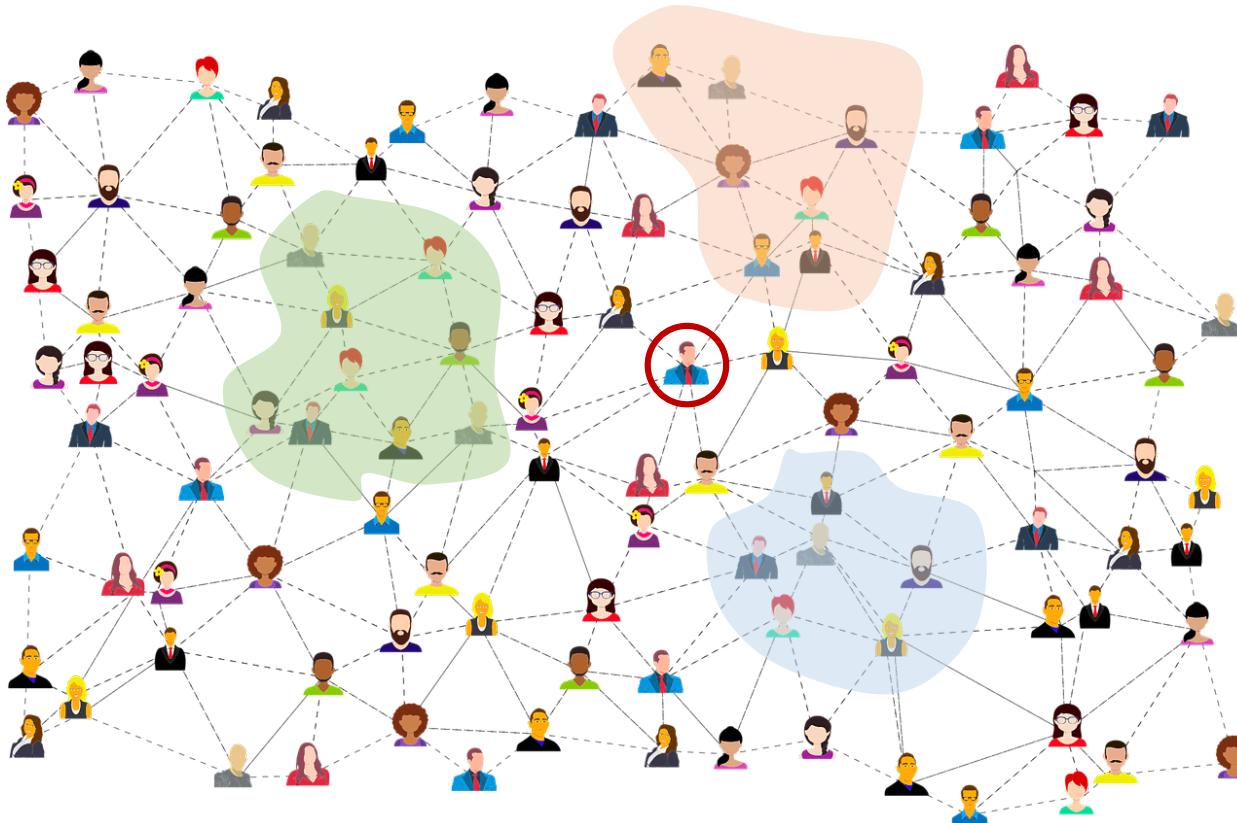
What is your representations
of people around you?

What is your (hidden) vector
representations of your
friends, family members,
colleagues, etc.??

Power? Fun? Appearance?
Knowledge? Utility? 有用的??

It is really difficult to know!

Some challenges in studying representations



An easy way around:
See how you (an internal model)
categorize (or link) people!

Compare your categories (or
links) with other people → you
may find your soulmates!

Representational similarity
analysis?

Examining the distances among
people from my point of view

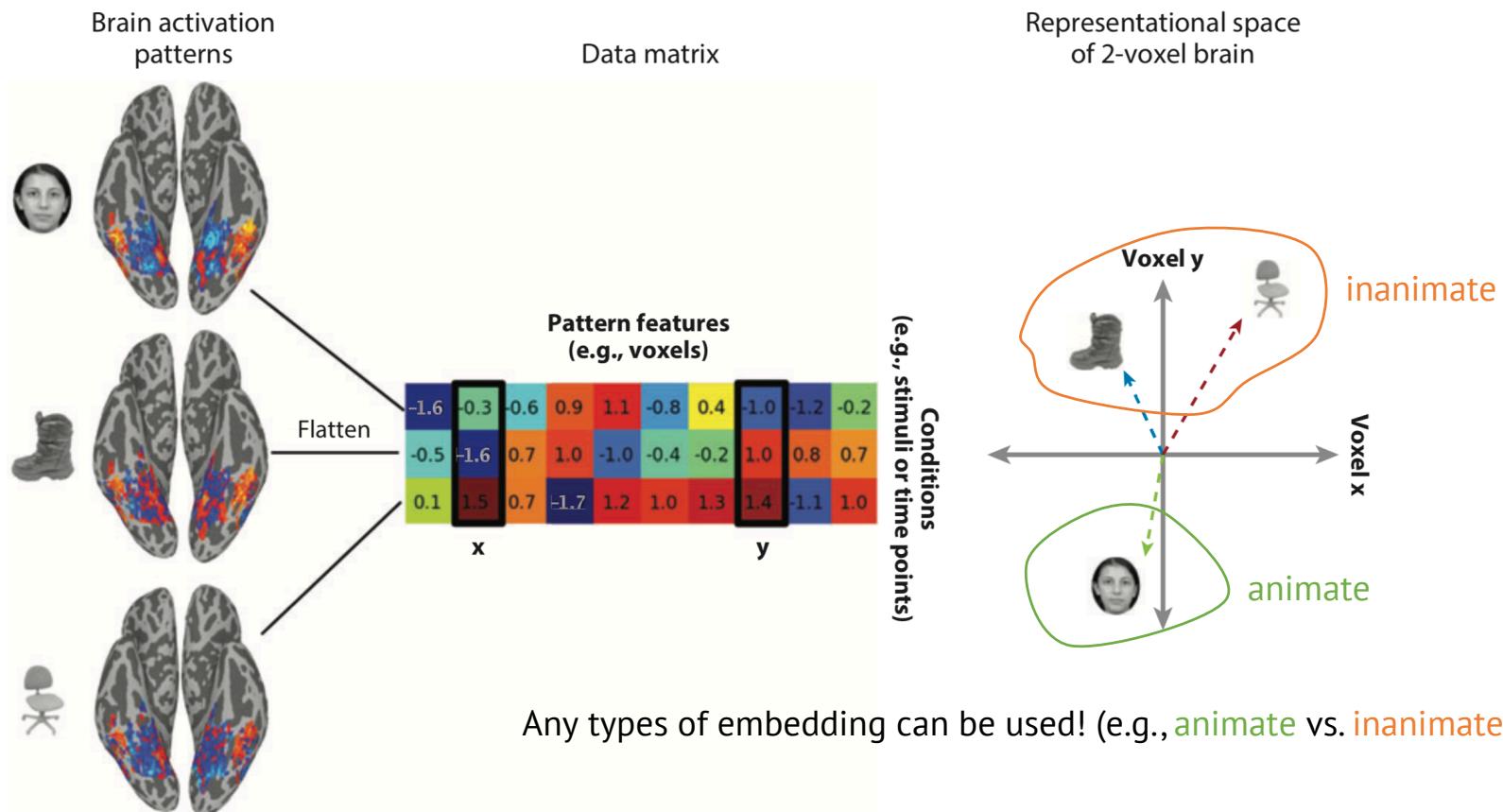
And comparing it with your
distance for people

Representational space

REPRESENTATIONAL SPACE

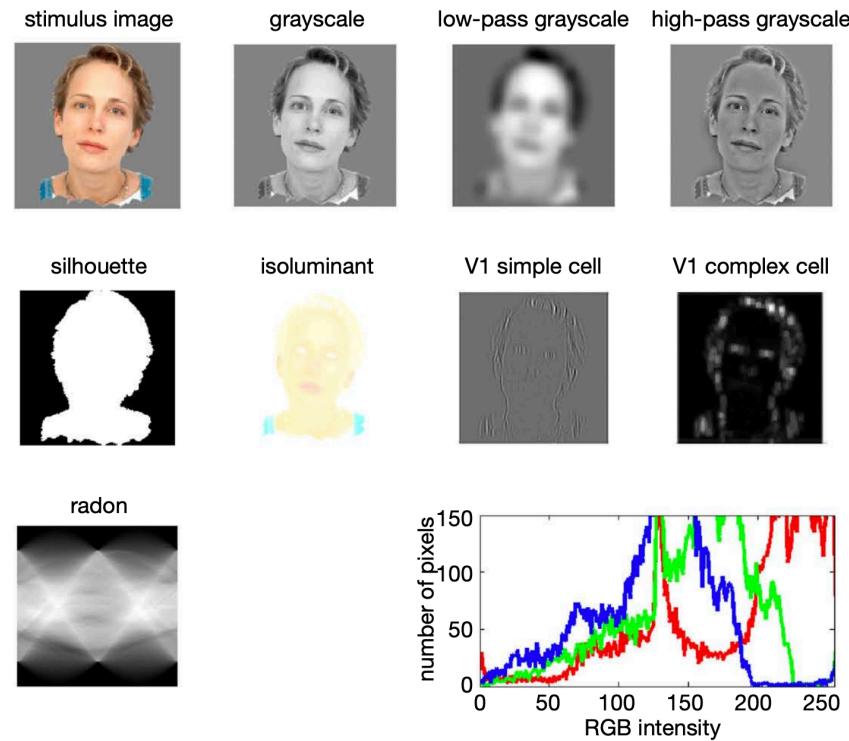
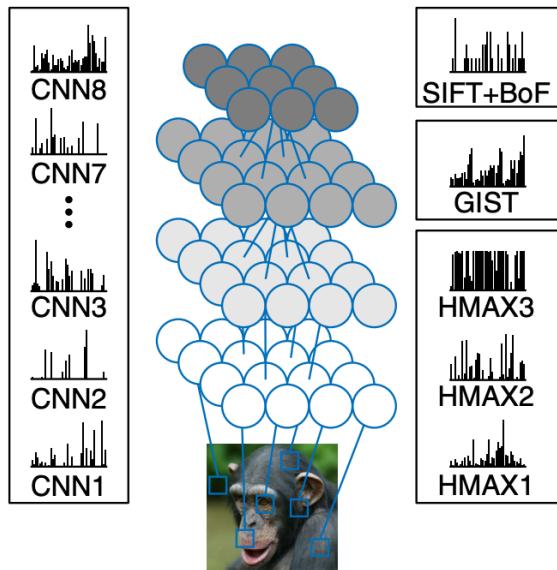
Representational space is a high-dimensional space in which each neural response or stimulus is expressed as a vector with different values for each dimension. In a neural representational space, each pattern feature is a measure of local activity, such as a voxel or a single neuron. In a stimulus representational space, each feature is a stimulus attribute, such as a physical attribute or semantic label.

Representational space



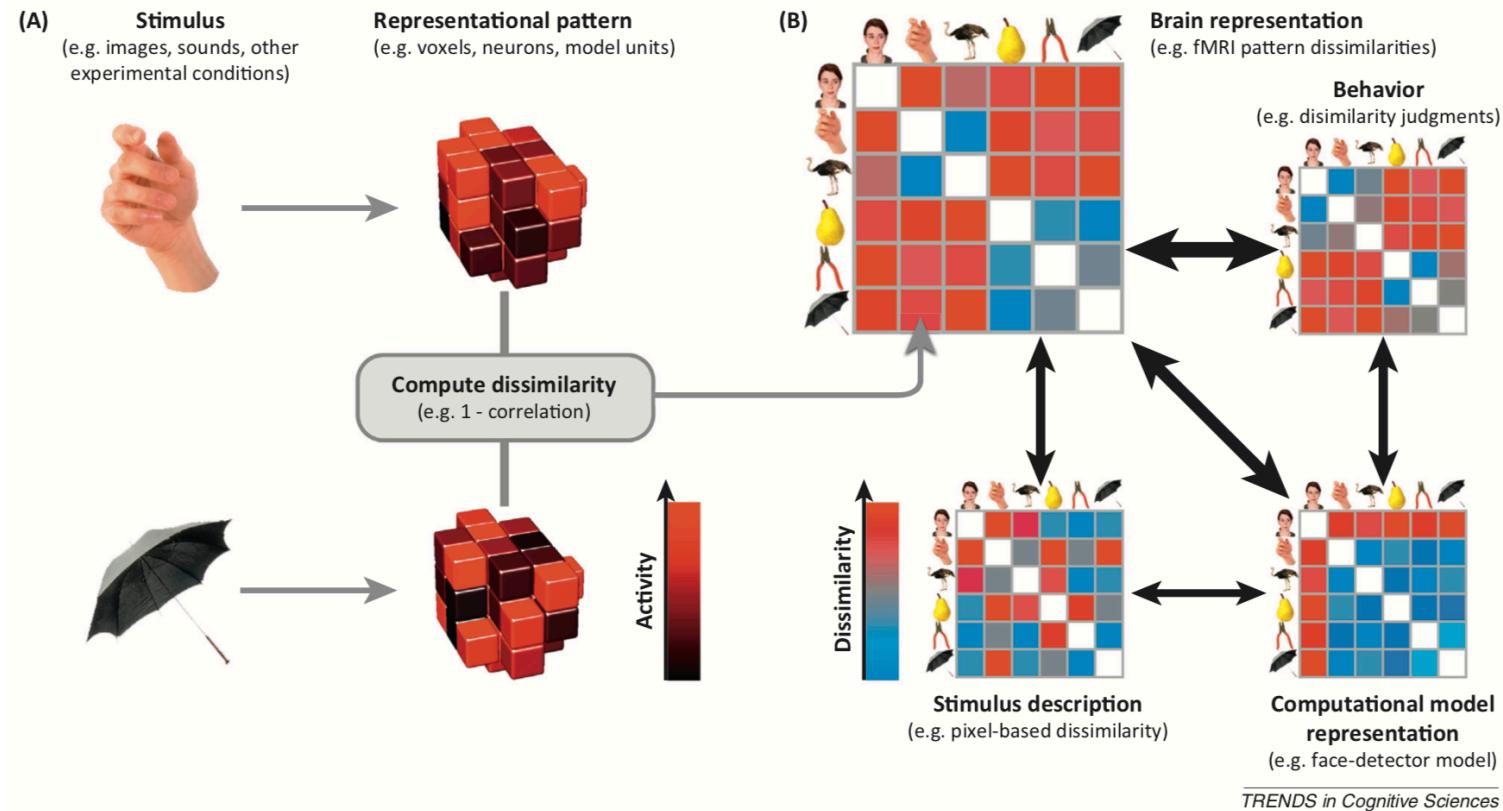
Haxby et al., 2014, *Annu Rev Neurosci*

Representational space

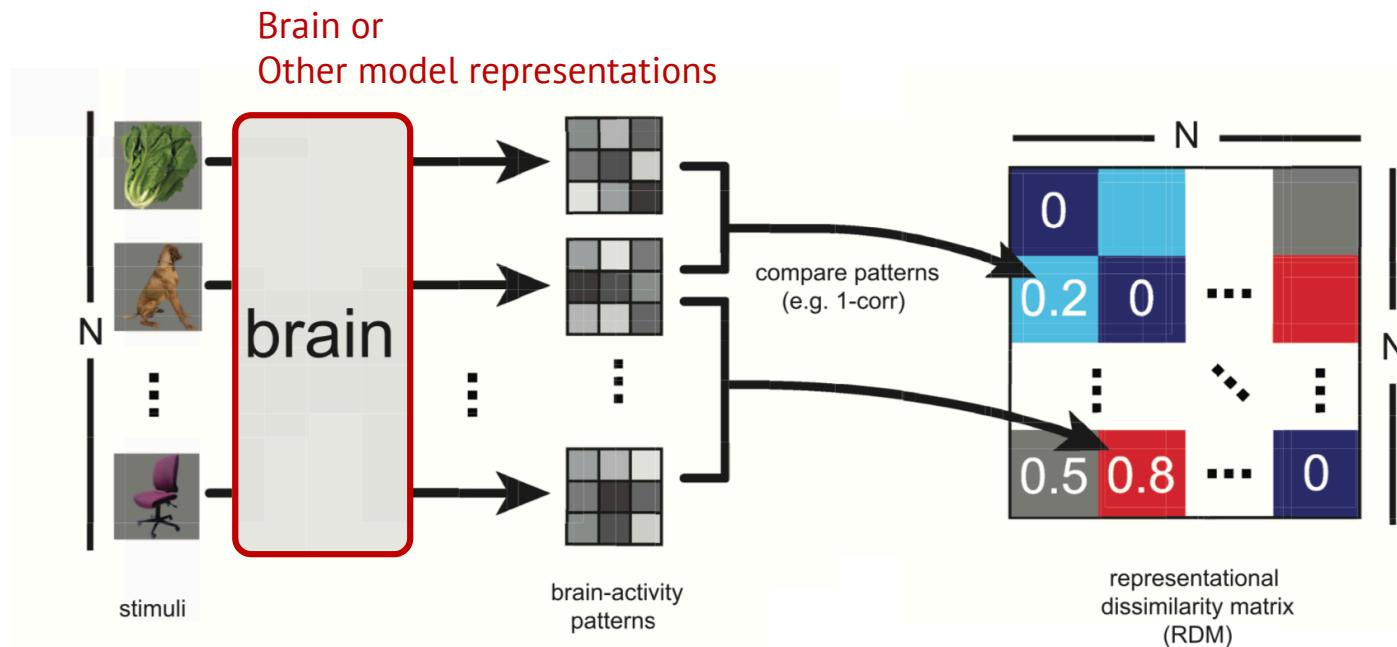


Any embeddings can be used!

Representational dissimilarity matrix

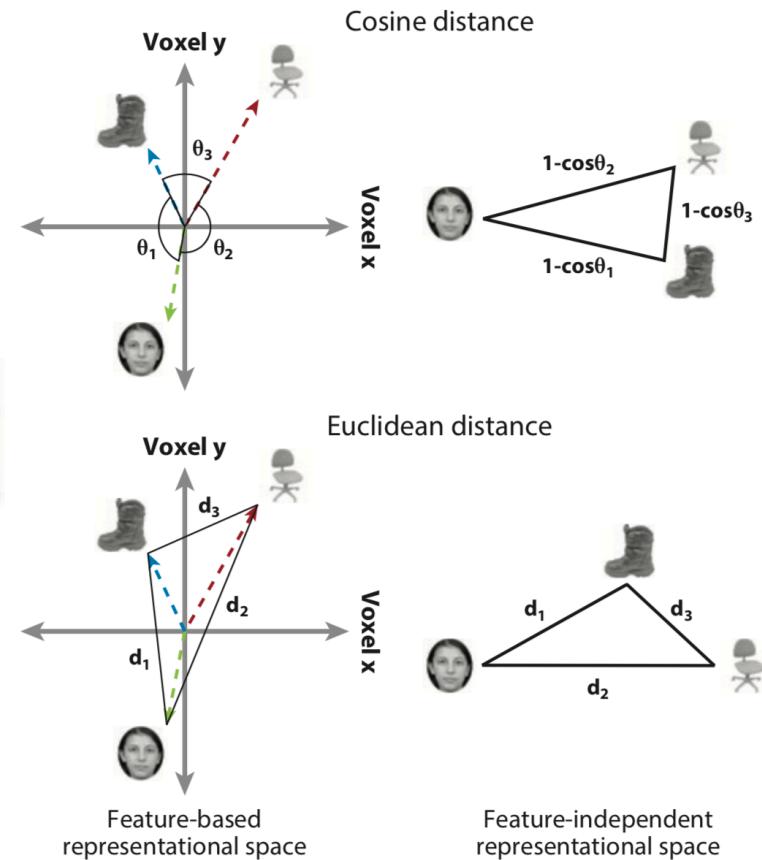
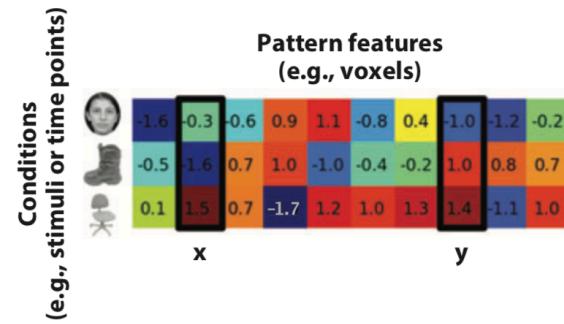


Representational dissimilarity matrix (in more detail)

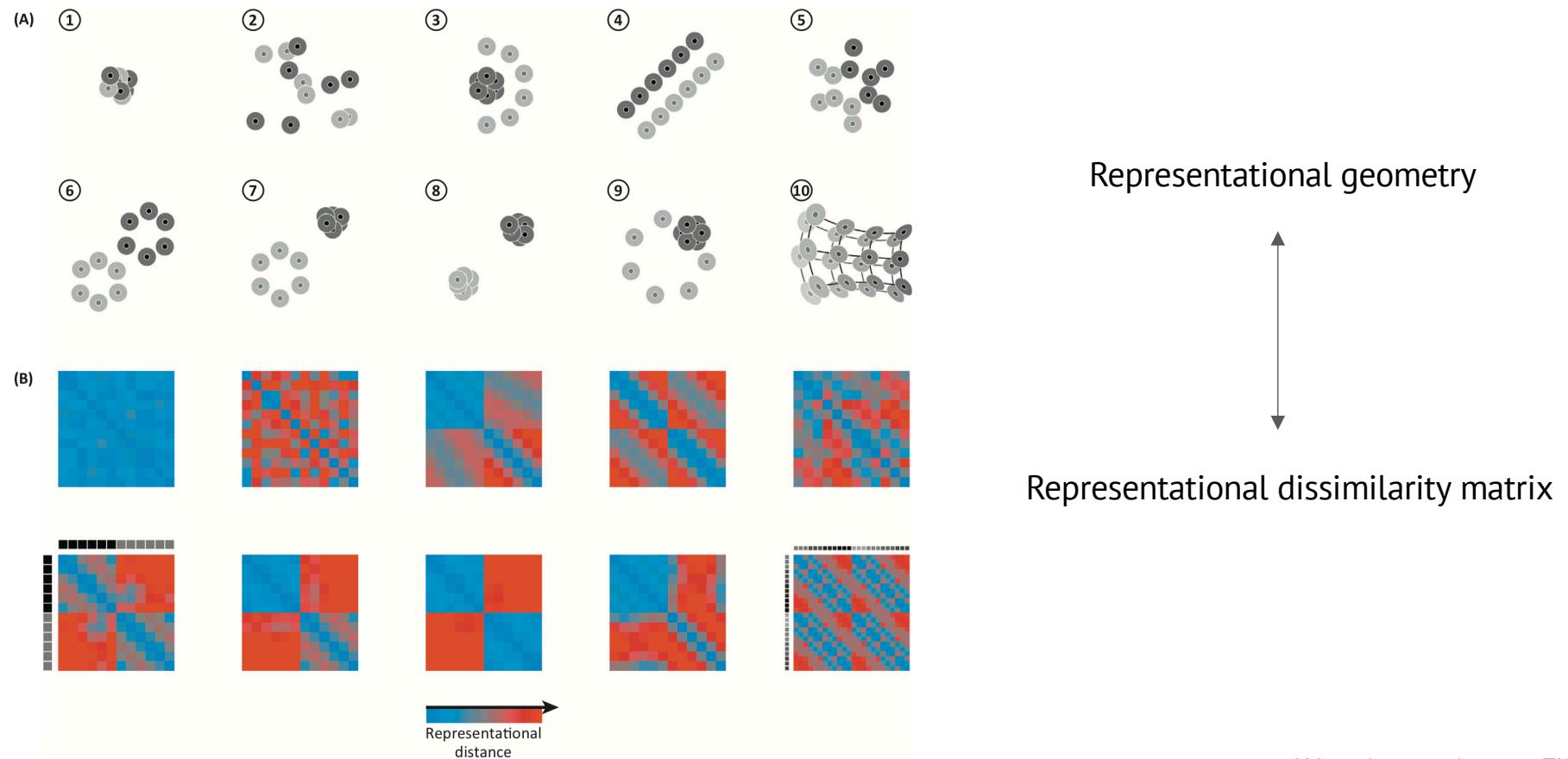


Representational dissimilarity matrix (in more detail)

Other types of distance metric can be used
(e.g., cosine, Euclidean, classification accuracy, etc.)



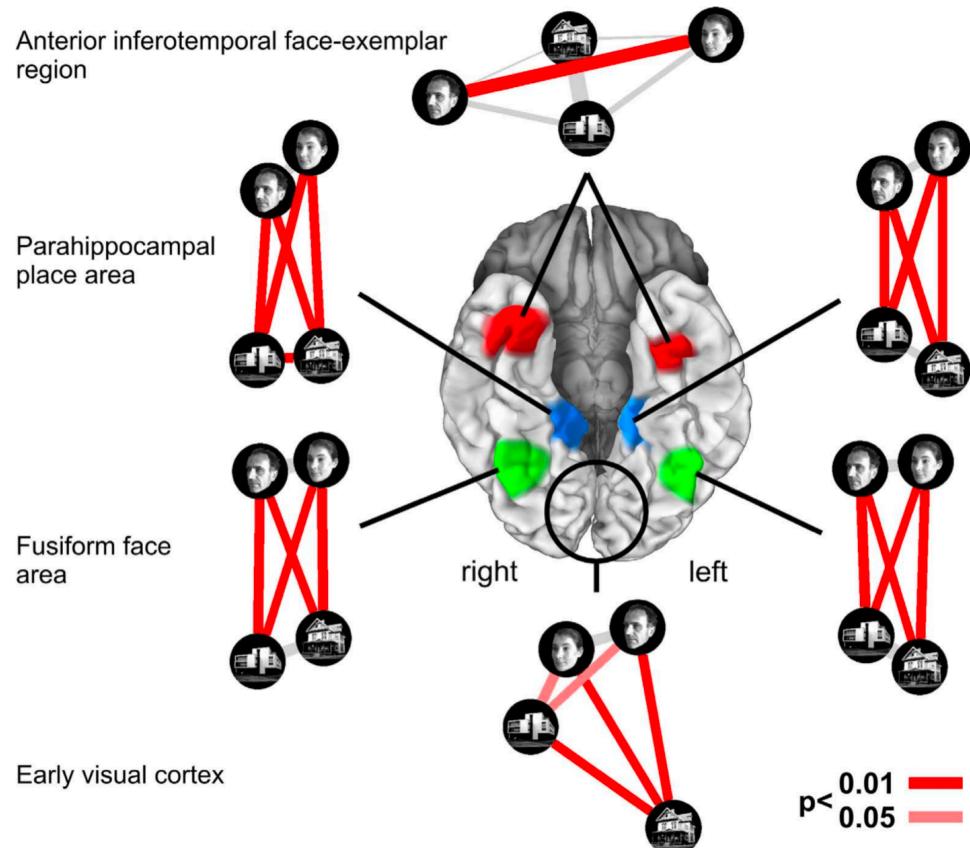
Representational dissimilarity matrix (in more detail)



TRENDS in Cognitive Sciences

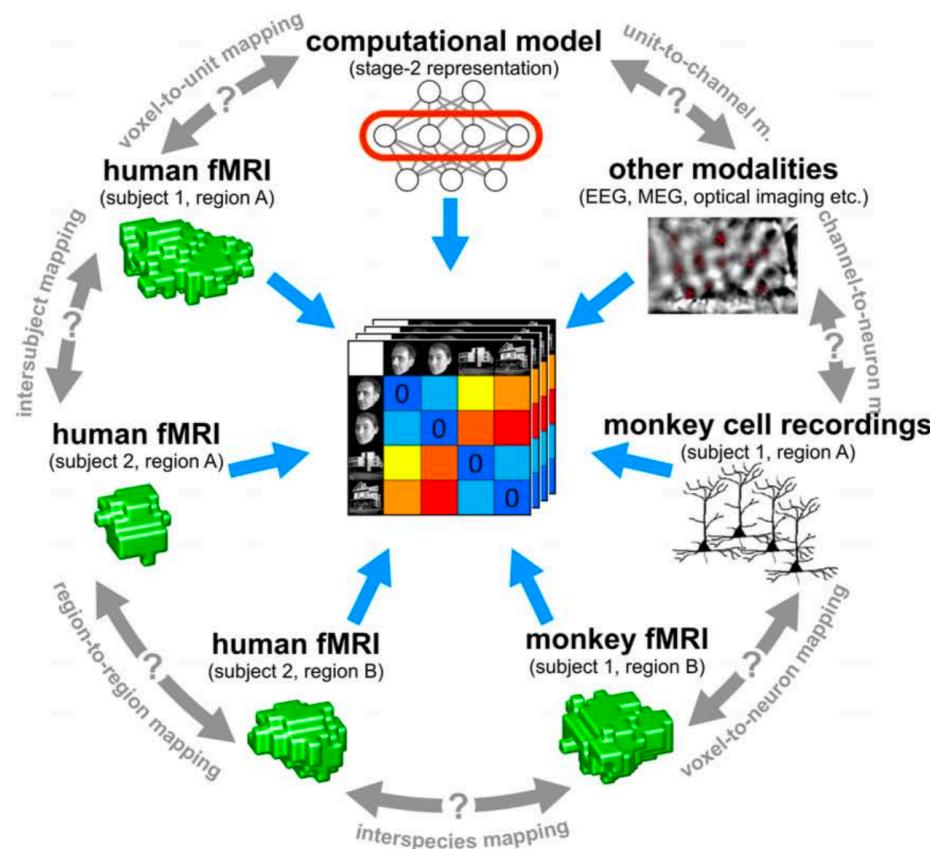
Kriegeskorte et al., 2013, TICS

Representational dissimilarity matrix (in more detail)



Different representational geometry
From different representational dissimilarity
patterns of different brain regions

Basic idea: You can compare any models/systems using RDM!



Kriegeskorte et al., 2008, *Front Sys Neurosci*

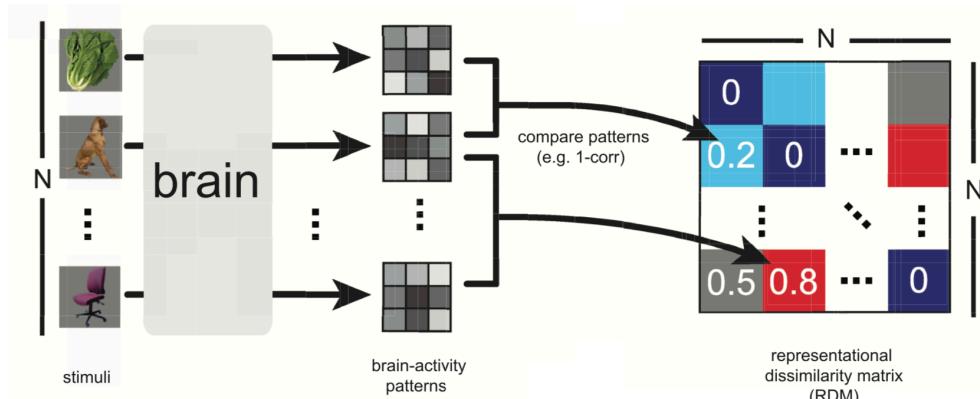
Three steps of representational similarity analysis

Step 1: Computing and visualizing RDMs

Step 2: Comparing brain and model RDMs

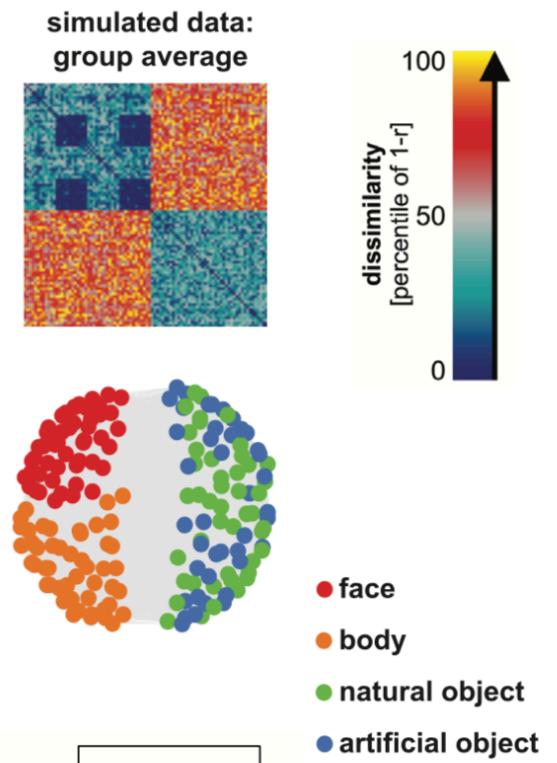
Step 3: Statistical inference

Step 1: Computing and visualizing RDMs



RDM

Dimensionality Reduction method for visualization (MDS, t-SNE, PCA, UMAP, etc.)

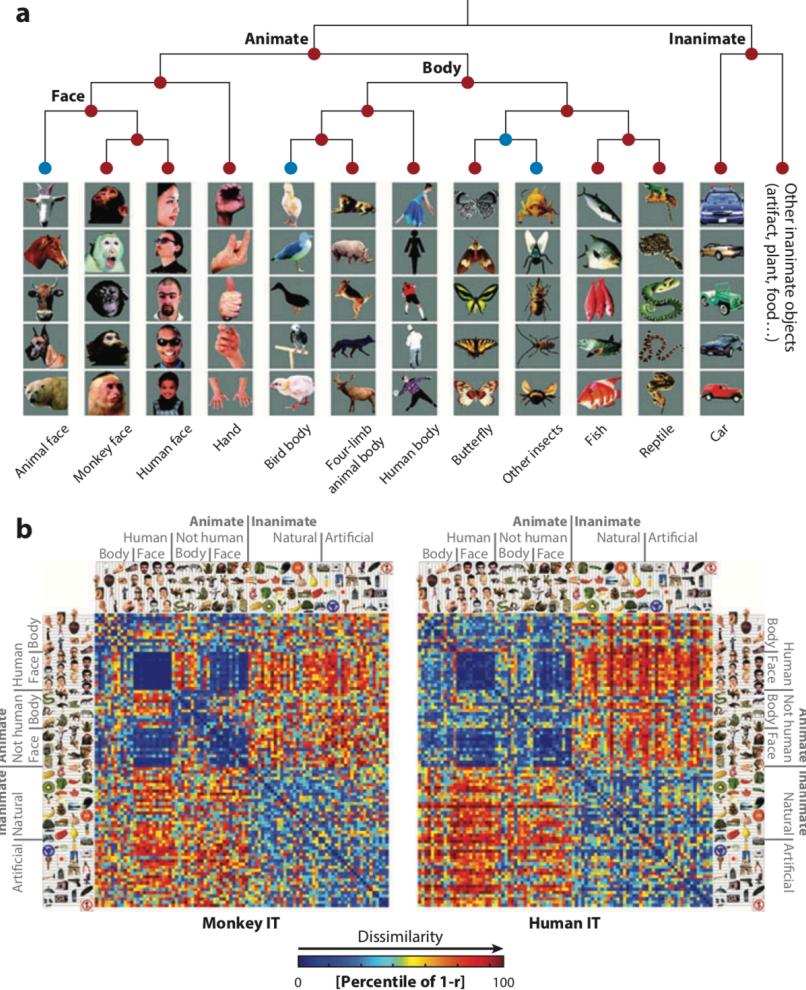


Step 1: Computing and visualizing RDMs

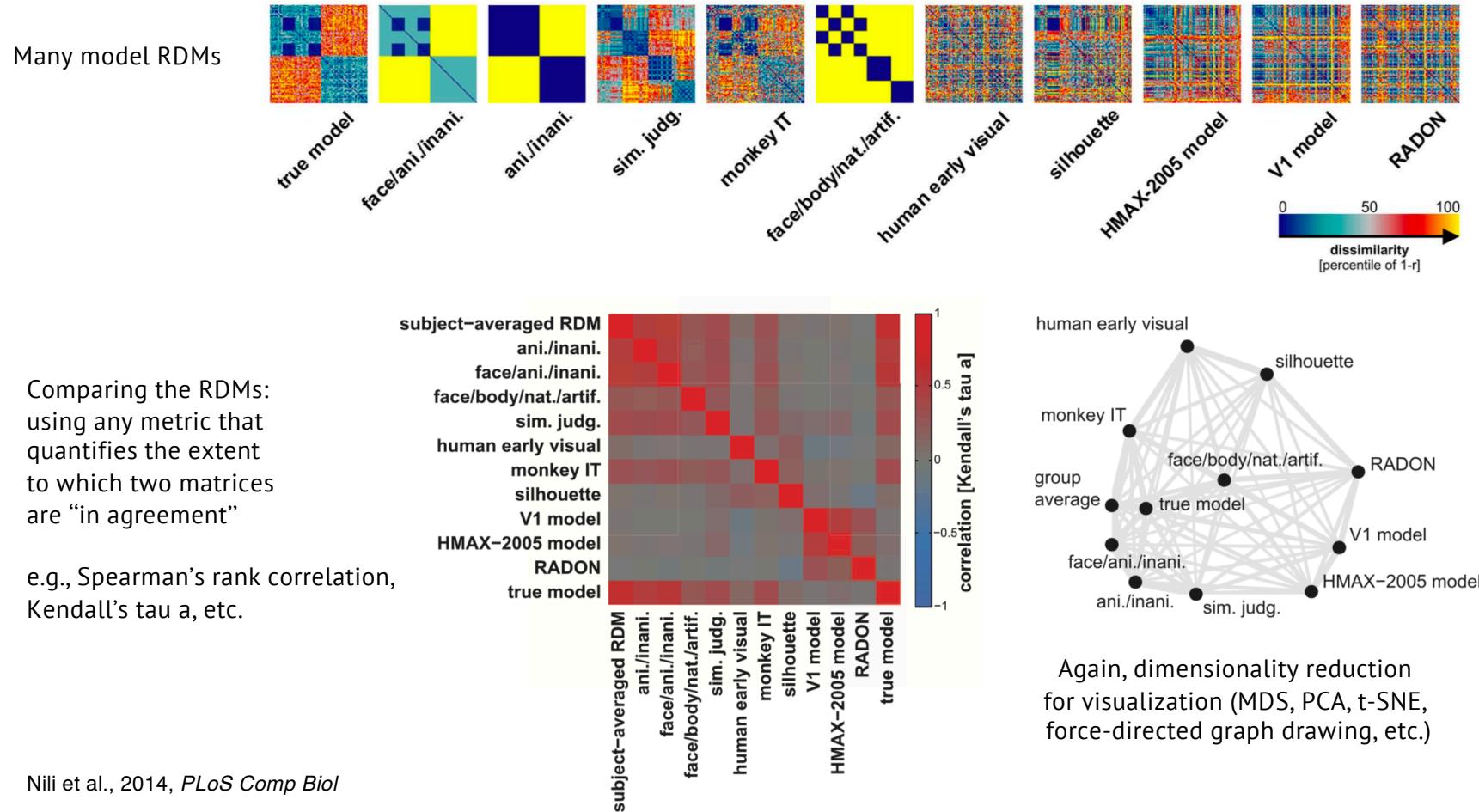
Real study examples:

Dendrogram derived from
multiple single-unit recording
in macaque inferior temporal (IT) cortex
(Kiani et al., 2007, *J. Neurophysiol.*)

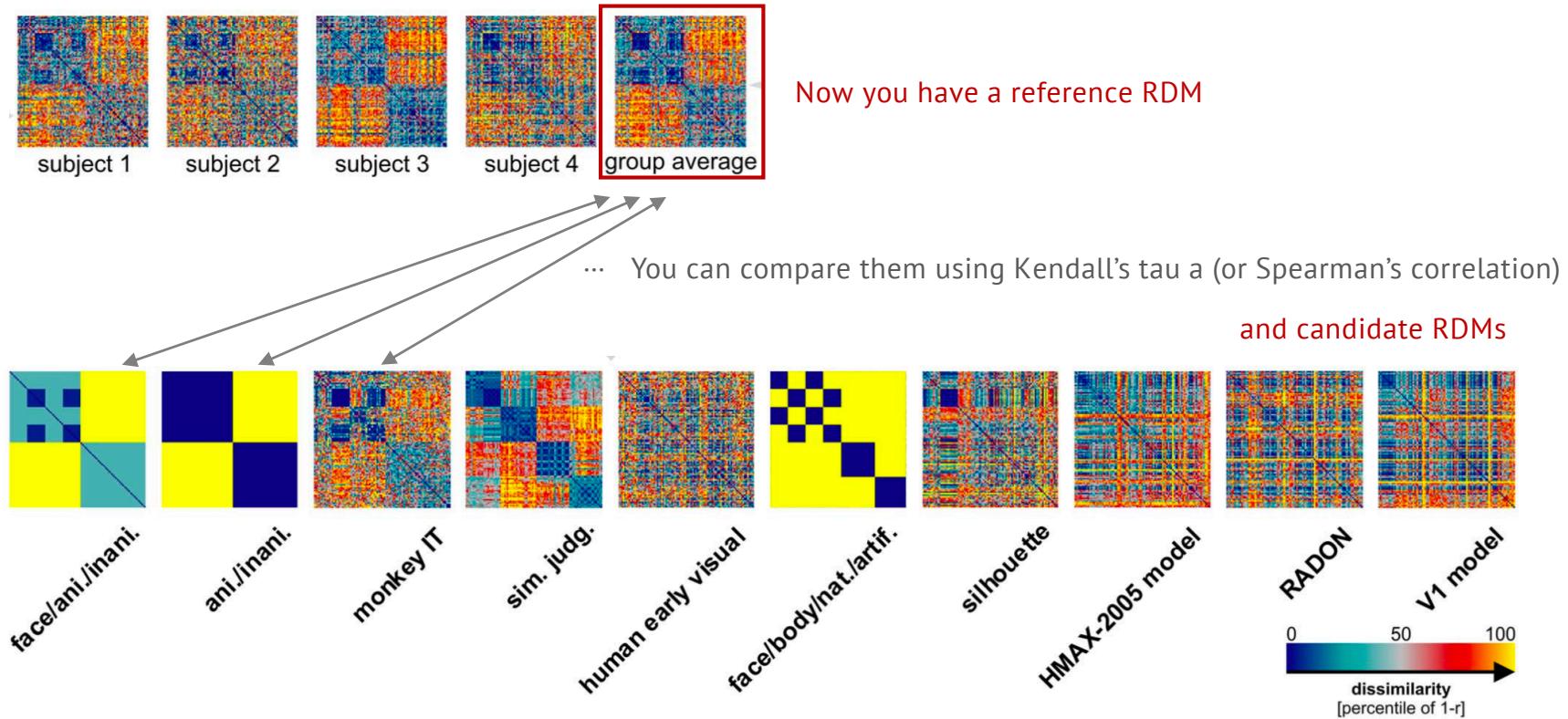
Cross-modal, cross-species comparisons of RDM
for a common set of stimuli
(Kriegeskorte et al., 2008, *Neuron*)



Step 2: Comparing brain and model RDMs

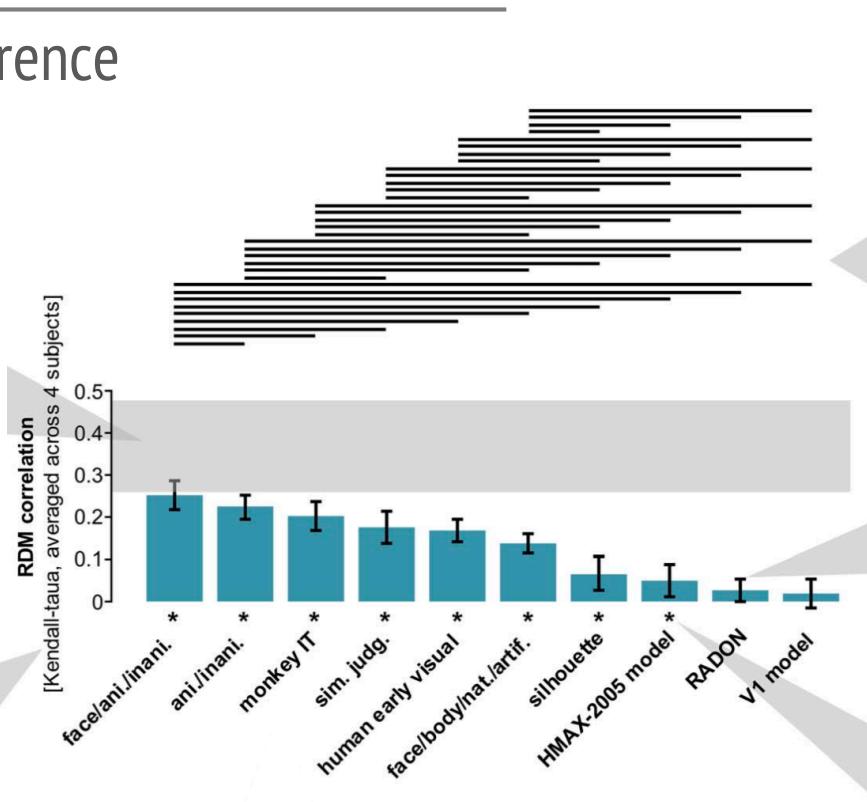


Step 3: Statistical inference



Step 3: Statistical inference

Performance is measured, as in Fig. 4, by Kendall's tau a between the reference RDM and the candidate RDMs.



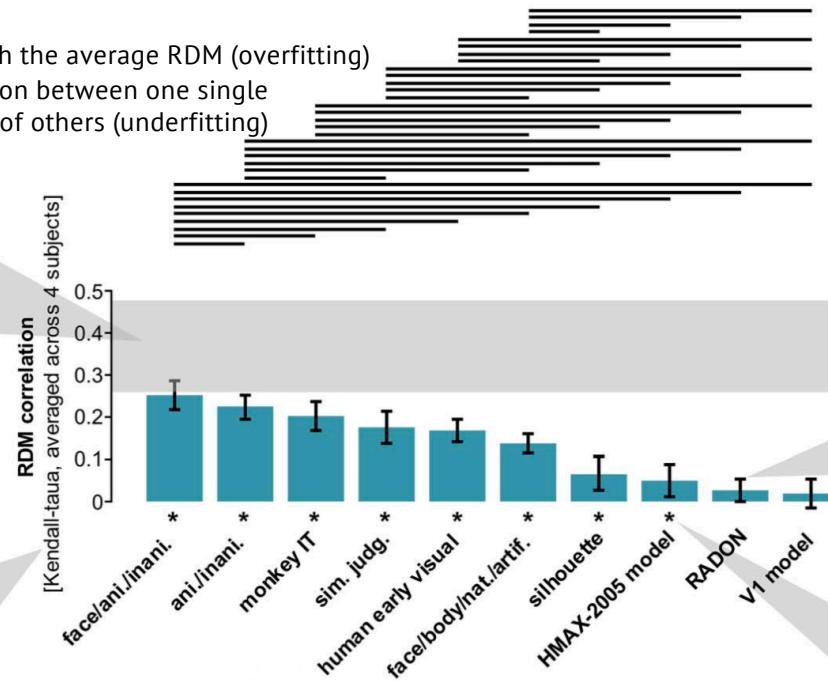
Step 3: Statistical inference

Noise ceiling:

- **Upper bound:** average correlation with the average RDM (overfitting)
- **Lower bound:** leave-one-out correlation between one single subject's RDM with the average RDM of others (underfitting)

The **noise ceiling** indicating the expected performance of the true model is much wider here than in the simulated data of Fig. 4. This reflects the fact that only 4 subjects entered this analysis, and the representation of human IT is thus much less precisely defined.

Performance is measured, as in Fig. 4, by Kendall's tau a between the reference RDM and the candidate RDMs.



Pairwise comparisons are based on bootstrap resampling of the stimulus set. This procedure simulates the variability of the estimates across random samples of stimuli (from an imaginary population of stimuli). Multiple testing is accounted for by controlling the expected FDR at 0.05.

Error bars indicate the standard error of the mean based on the bootstrap resampling of the stimulus set.

Each candidate RDM's relatedness to the reference RDM is now tested using a stimulus-label randomization test, which does not require multiple subjects. This time stars instead of p values were chosen to indicate significance. Multiple testing was accounted by controlling the expected FDR at 0.05.

Other analysis options (from Nili et al.):

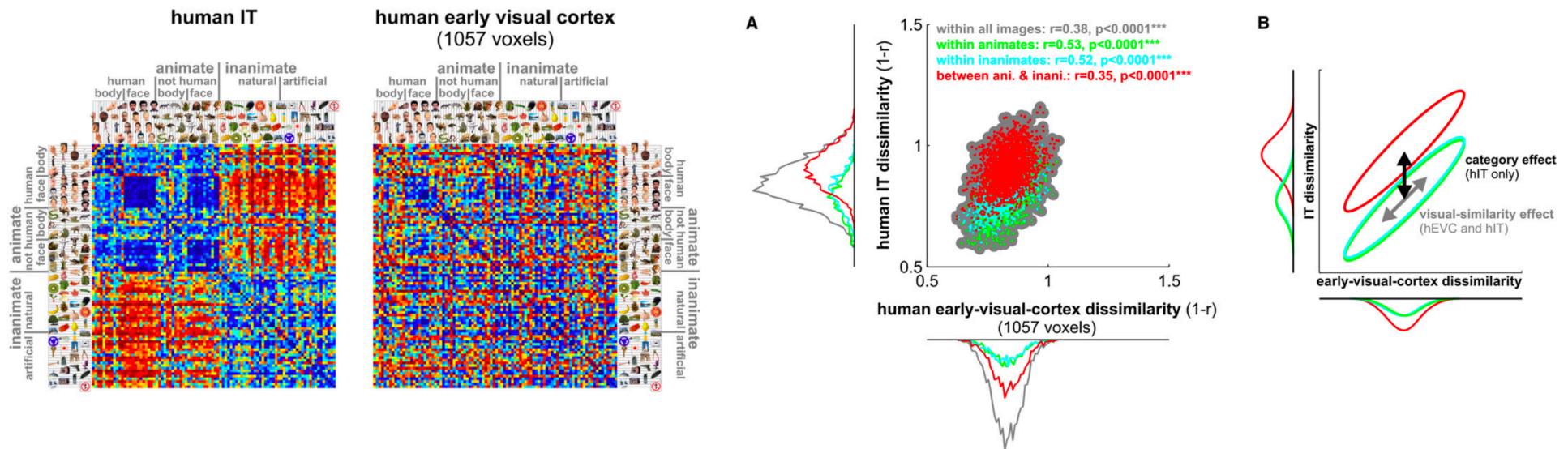
1. **Representational connectivity:** Comparing brain RDMs among different regions
2. **Searchlight RSA:** Each region serves as a model
3. Use **classification performance** as a distance metric

Other RSA options

Other analysis options

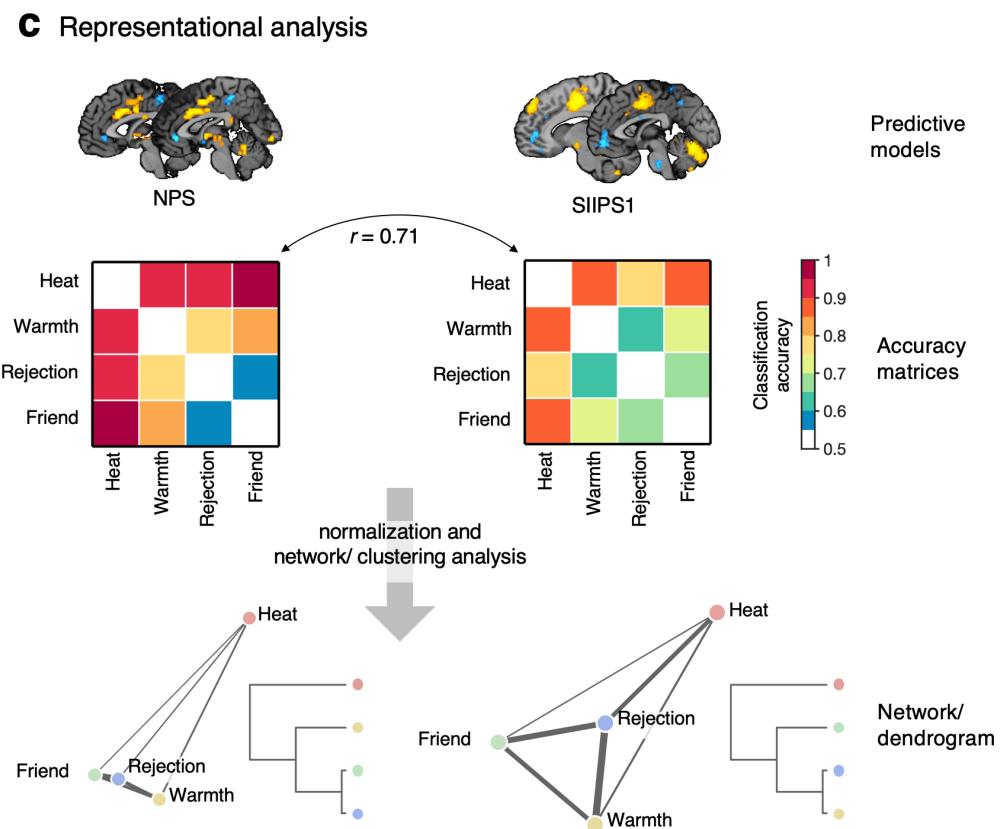
1. Representational connectivity: Comparing brain RDMs among different regions
2. Use classification performance as a distance metric
3. Searchlight RSA: Each region serves as a model
4. Conducting RSA in the GLM context

Example: 1. Representational connectivity



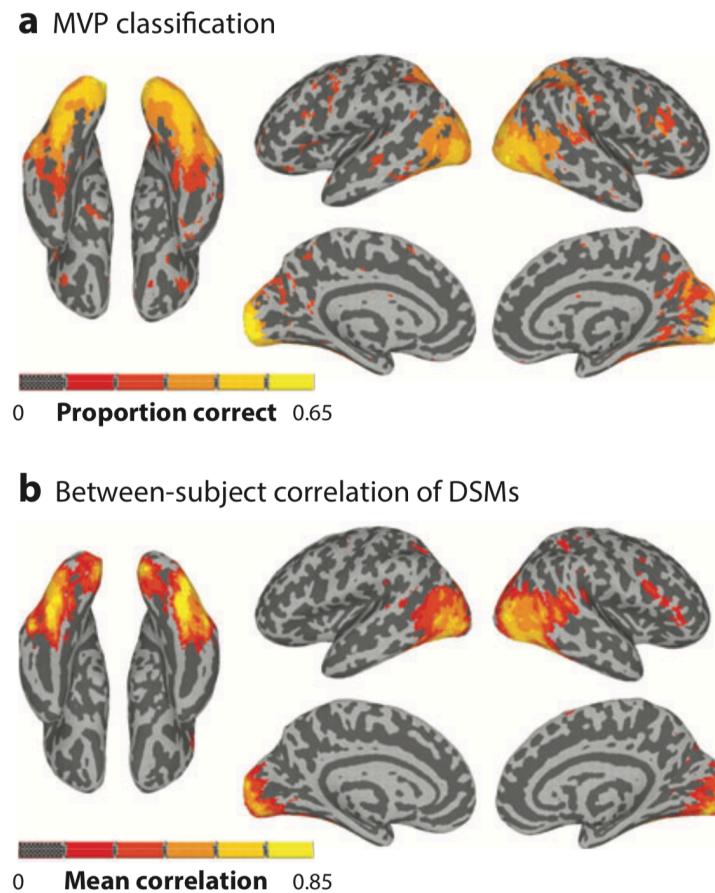
Kriegeskorte et al., 2008, *Neuron*

Example: 2. Accuracy as distance



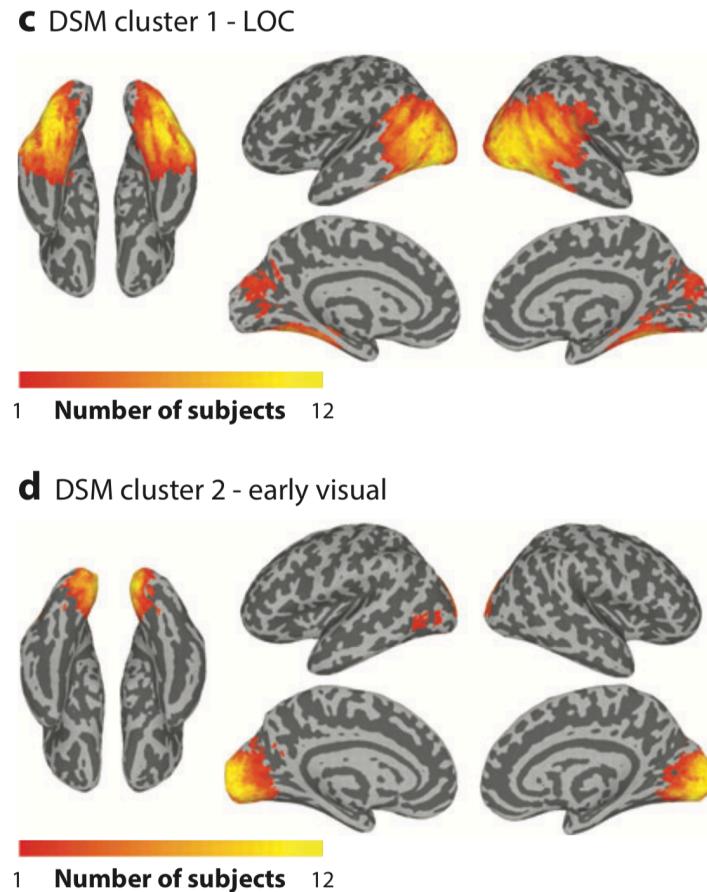
Example: 3. Searchlight RSA

In addition to the MVPA, we can calculate the RDM (in this figure, DSM) for each person, and see between-subject consistency of the RDMs

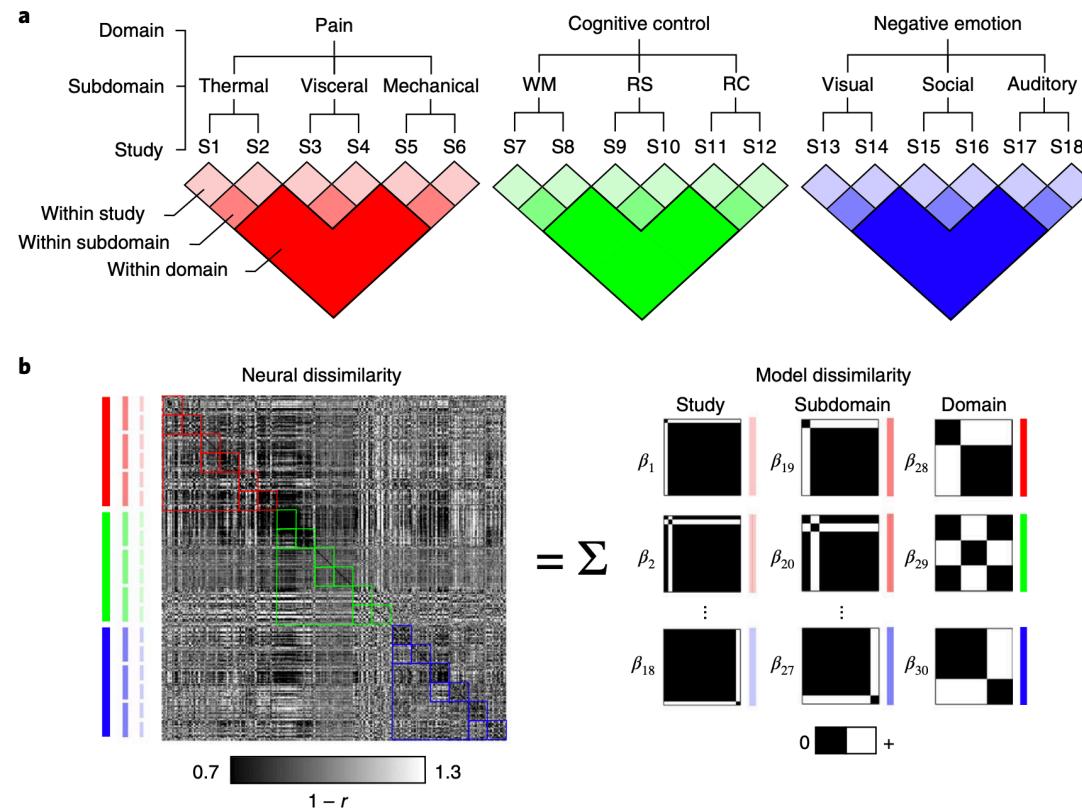


Example: 3. Searchlight RSA

We can also cluster the regions based on the RDM patterns (for each individual or for group)



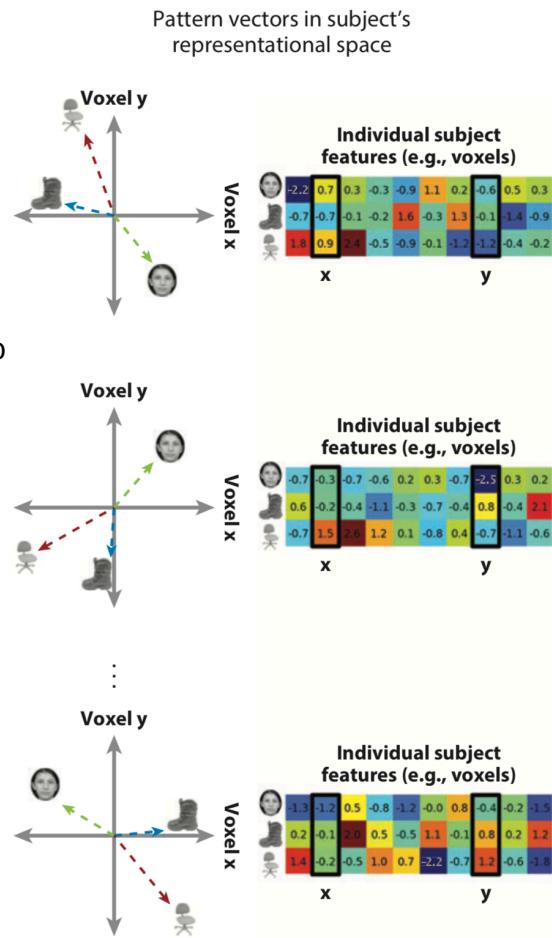
Example: 4. RSA in the GLM context



Hyper-alignment

Hyper-alignment:
aligning individual neural
representational spaces into
a common model space

**Iterative procrustean
transformation** to the
common representational
space



Hyperalignment of representational spaces

Transformation matrices
(hyperalignment parameters)

Common model dimensions

0.4	0.3	0.3	0.0	0.2	-0.1	0.4	0.3	-0.2
0.0	-0.5	0.1	-0.2	0.2	0.2	-0.2	0.5	-0.1
-0.4	0.3	0.1	-0.3	-0.2	-0.1	0.5	0.2	-0.4
-0.2	0.1	0.1	-0.3	-0.2	0.2	-0.5	-0.5	0.4
0.0	0.6	-0.4	-0.3	-0.2	0.0	0.3	0.4	0.2
-0.2	0.0	0.1	-0.2	0.5	-0.8	-0.3	0.0	0.0
-0.5	-0.2	0.6	0.1	-0.2	0.0	0.0	-0.0	0.2
0.5	0.0	0.1	-0.1	-0.6	-0.5	0.2	0.4	-0.1
-0.3	0.3	-0.6	-0.2	-0.2	0.0	-0.1	-0.0	0.1
0.0	0.1	-0.1	-0.1	0.3	0.0	0.5	-0.5	0.0

Individual subject features

0.4	-0.3	-0.6	-0.1	-0.0	-0.3	0.2	0.4	0.2
0.0	0.3	-0.1	-0.1	-0.5	-0.2	0.4	-0.4	0.0
-0.2	-0.0	0.0	-0.5	0.4	0.0	0.1	0.5	0.0
0.0	0.5	0.1	-0.6	-0.0	-0.2	0.1	-0.4	0.2
0.2	-0.2	0.4	-0.4	0.3	0.6	-0.0	0.1	-0.2
0.1	-0.4	-0.3	-0.3	-0.2	0.3	0.3	0.6	-0.2
0.4	0.1	0.1	-0.0	-0.2	0.3	0.6	0.1	0.6
0.4	-0.0	0.3	-0.1	0.5	0.2	-0.0	0.1	-0.2
0.5	0.3	-0.3	-0.2	-0.3	-0.1	0.4	0.1	0.5
0.5	0.5	0.3	-0.1	-0.4	-0.1	-0.1	0.1	0.0

Individual subject features

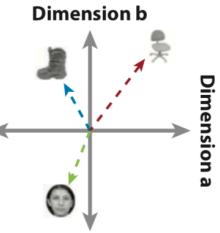
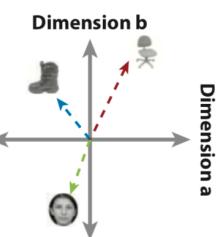
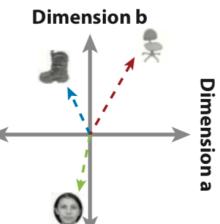
0.4	0.4	0.4	-0.5	-0.2	0.1	-0.2	0.3	0.3
0.4	0.2	0.1	0.1	0.2	0.2	0.4	-0.2	0.4
0.4	0.7	0.3	0.0	0.2	-0.1	0.1	0.3	0.4
0.3	0.1	-0.1	-0.2	-0.4	-0.4	0.2	0.3	-0.6
0.3	-0.3	0.0	0.5	-0.3	0.0	0.2	0.3	0.0
-0.1	-0.2	0.3	0.2	0.6	-0.1	0.6	-0.3	-0.0
0.5	0.2	0.6	0.1	-0.3	0.2	0.1	-0.3	0.1
-0.1	0.1	0.2	0.5	-0.1	0.1	0.5	-0.2	0.1
0.1	0.2	0.4	0.3	-0.3	-0.1	0.6	-0.3	0.3
0.3	-0.3	-0.3	0.1	-0.3	-0.0	-0.1	0.4	-0.3

Individual subject features

0.4	0.2	0.5	1.0	1.2	-0.6	0.4	-0.8	0.1
-0.4	-1.6	0.8	1.1	-0.9	-0.3	-0.1	1.2	0.9
0.1	1.6	0.8	-1.7	1.4	1.1	1.5	-0.9	1.1
0.1	1.7	0.8	-1.7	1.3	1.1	1.5	1.0	1.2
0.1	1.7	0.8	-1.7	1.3	1.1	1.5	1.0	1.2
0.1	1.7	0.8	-1.7	1.3	1.1	1.5	1.0	1.2
0.1	1.7	0.8	-1.7	1.3	1.1	1.5	1.0	1.2
0.1	1.7	0.8	-1.7	1.3	1.1	1.5	1.0	1.2
0.1	1.7	0.8	-1.7	1.3	1.1	1.5	1.0	1.2

Individual subject features

Pattern vectors in
common model space



Procrustes



From Greek mythology,

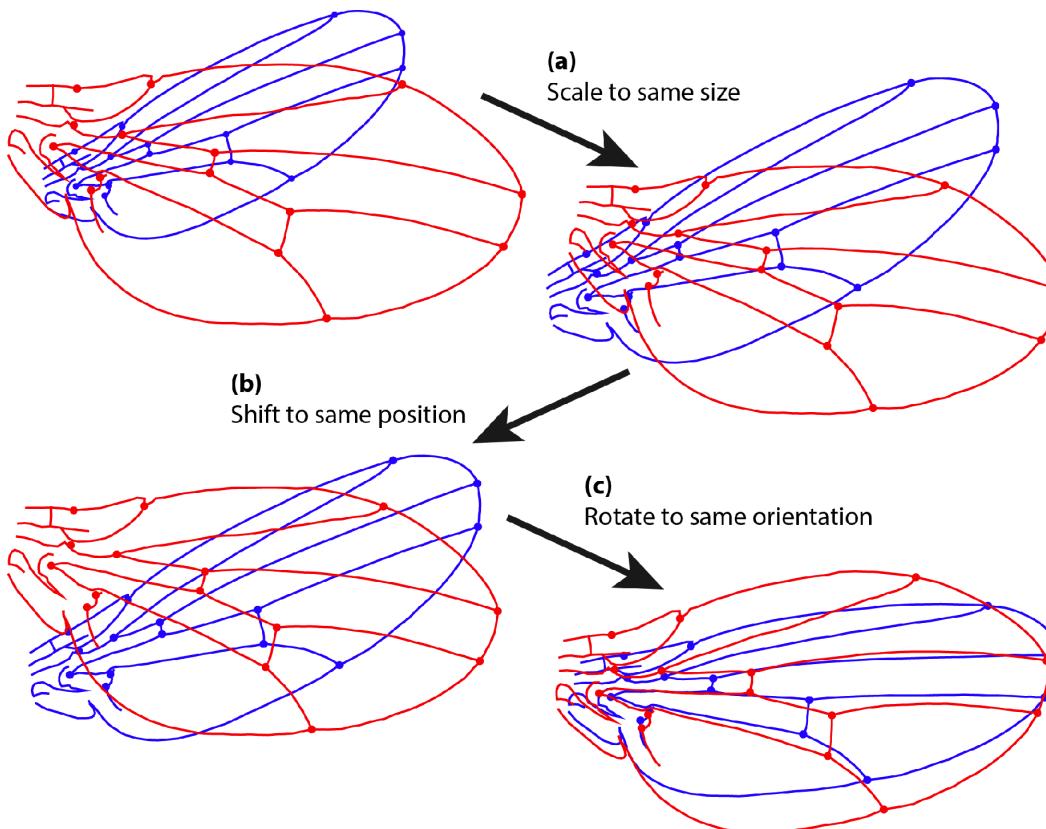
Procrustes (or “the stretcher”) was a bandit from Attica

He attached people by stretching them or cutting off their legs, so as to force them to fit the size of an iron bed

The word "Procrustean" is thus used to describe situations where different lengths or sizes or properties are fitted to an arbitrary standard.

(from Wikipedia)
<https://en.wikipedia.org/wiki/Procrustes>

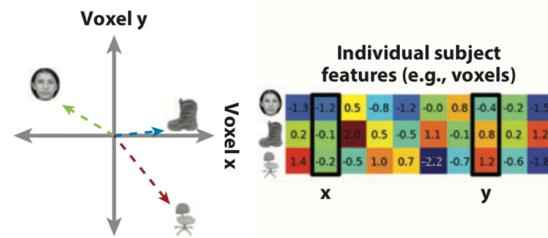
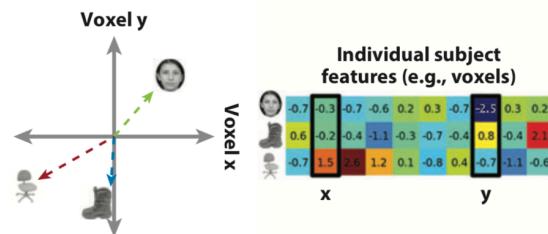
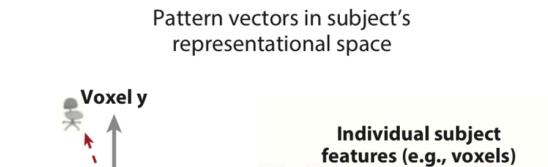
Procrustes analysis



Hyper-alignment

Hyper-alignment:
aligning individual neural
representational spaces into
a common model space

**Iterative procrustean
transformation** to the
common representational
space



Hyperalignment of representational spaces

Transformation matrices
(hyperalignment parameters)

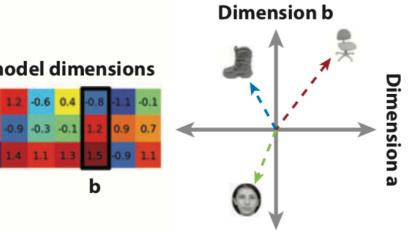
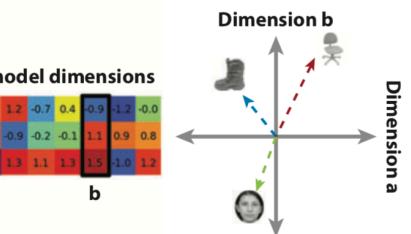
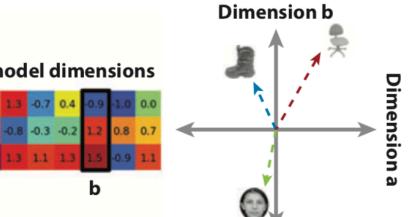
Common model dimensions

0.4 0.3 0.3 ...	0.0 0.2 -0.1 0.4 0.3 -0.2
0.0 0.5 0.1 ...	-0.2 0.2 0.2 0.2 0.5 0.1
-0.4 0.3 0.1 ...	-0.3 -0.2 -0.1 0.5 0.2 -0.2
-0.2 0.1 0.1 ...	-0.3 -0.2 0.2 0.5 -0.5 0.2
0.0 0.6 0.4 ...	0.3 -0.3 0.0 0.3 0.4 0.2
-0.2 0.0 0.1 ...	-0.2 0.5 -0.8 -0.3 0.0 0.0
-0.5 -0.2 0.6 ...	0.1 -0.2 0.0 0.0 0.0 0.2
0.5 0.0 0.1 ...	0.1 -0.6 -0.5 0.2 0.4 -0.1
-0.3 0.3 -0.6 ...	-0.2 -0.2 0.0 -0.1 -0.0 -0.1
0.0 0.1 -0.1 ...	0.3 0.0 0.5 -0.5 0.6 -0.1

0.4 -0.3 -0.6 ...	-0.1 -0.0 -0.3 0.2 0.4 0.2 0.2
0.0 0.3 -0.1 ...	-0.5 -0.2 0.0 0.5 0.4 0.0 0.0
0.2 -0.0 0.0 ...	0.0 0.5 0.1 -0.6 -0.0 -0.2 0.1
0.2 -0.2 0.4 ...	0.2 0.2 0.4 -0.3 0.6 -0.0 0.1
0.1 -0.4 -0.3 ...	0.1 -0.2 0.3 0.2 0.3 0.0 -0.2
0.4 0.1 0.1 ...	0.4 0.1 0.0 -0.2 0.3 0.0 0.1
0.4 -0.0 0.3 ...	0.4 0.0 0.3 -0.1 0.2 0.0 0.1
0.5 0.3 -0.3 ...	0.5 0.3 -0.2 0.3 -0.1 0.4 0.1 0.0
0.5 0.5 0.3 ...	0.1 -0.4 -0.1 0.4 -0.1 -0.1 0.1 0.0

0.4 0.4 0.4 ...	-0.5 -0.2 0.1 -0.2 0.3 0.3 0.0
0.4 0.2 0.1 ...	0.2 0.2 0.4 0.2 0.4 0.2 0.5
0.4 0.7 0.3 ...	0.0 0.2 0.1 0.0 0.1 0.1 0.4
0.3 0.1 -0.1 ...	0.2 -0.1 0.2 -0.4 -0.4 0.2 0.3
0.3 -0.3 0.0 ...	0.3 0.0 0.5 -0.3 0.0 0.2 0.3
0.3 0.2 0.3 ...	0.0 0.2 0.3 0.2 0.6 -0.1 0.6
-0.1 -0.2 0.3 ...	0.6 -0.1 0.2 0.6 -0.1 0.6 -0.3
0.5 0.2 0.6 ...	0.1 0.2 0.1 0.3 0.2 0.1 -0.3
-0.1 0.1 0.2 ...	0.5 0.1 0.2 0.5 -0.1 0.1 0.5
0.1 0.2 0.4 ...	0.1 0.2 0.4 0.3 -0.3 0.1 0.6
0.3 -0.3 -0.3 ...	0.4 -0.3 -0.3 0.1 -0.3 0.4 0.6

Pattern vectors in
common model space



Thank you for your attention

Hope our representations about “RSA” to be well-aligned

Any questions?