Modeling the shared deep structure of information encoded in fine-scale cortical topographies

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Hyper alignment
Swaroop Guntupalli
Vicarious

Individual differences
Feilong Ma
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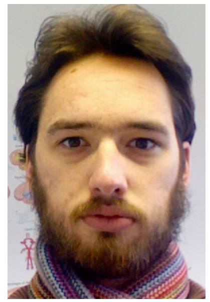
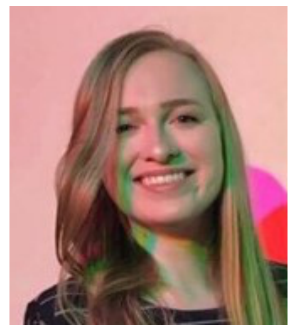
Attention
Sam Nastase
Graduate student



Action representation, computational methods
Nick Oosterhof
Emeritus



Forward encoding
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Undrgraduate student

PyMVPA
NeuroDebian

Yaroslav Halchenko
Research professor, software

Analysis of similarity structure, representation of biological classes
Andy Connolly
Asst prof, Geisel School of Medicine

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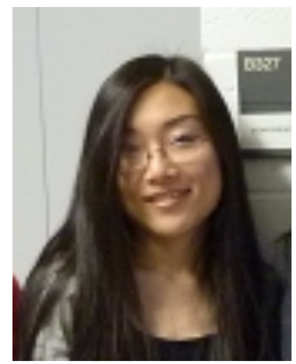


Hao Xu
Google

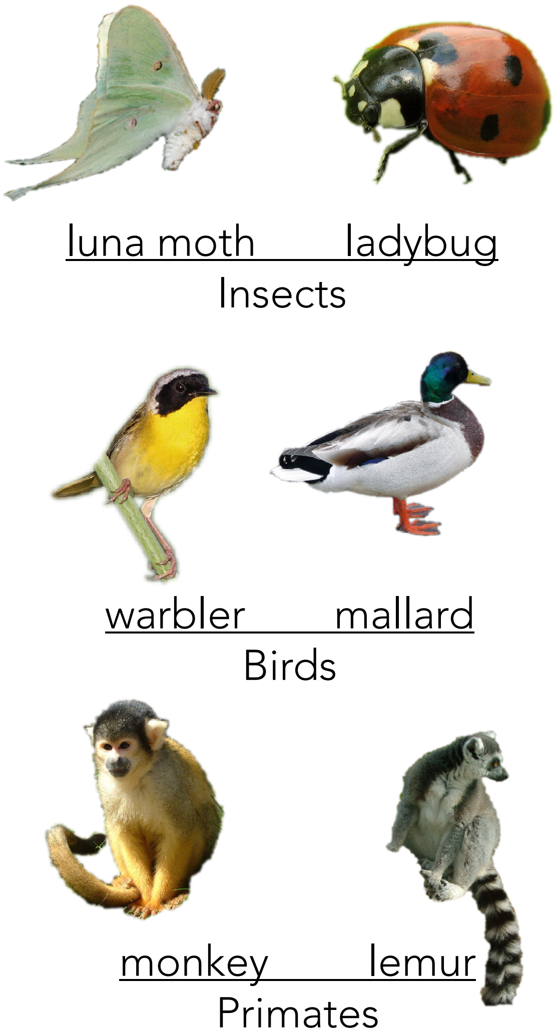
Cameron Chen
current

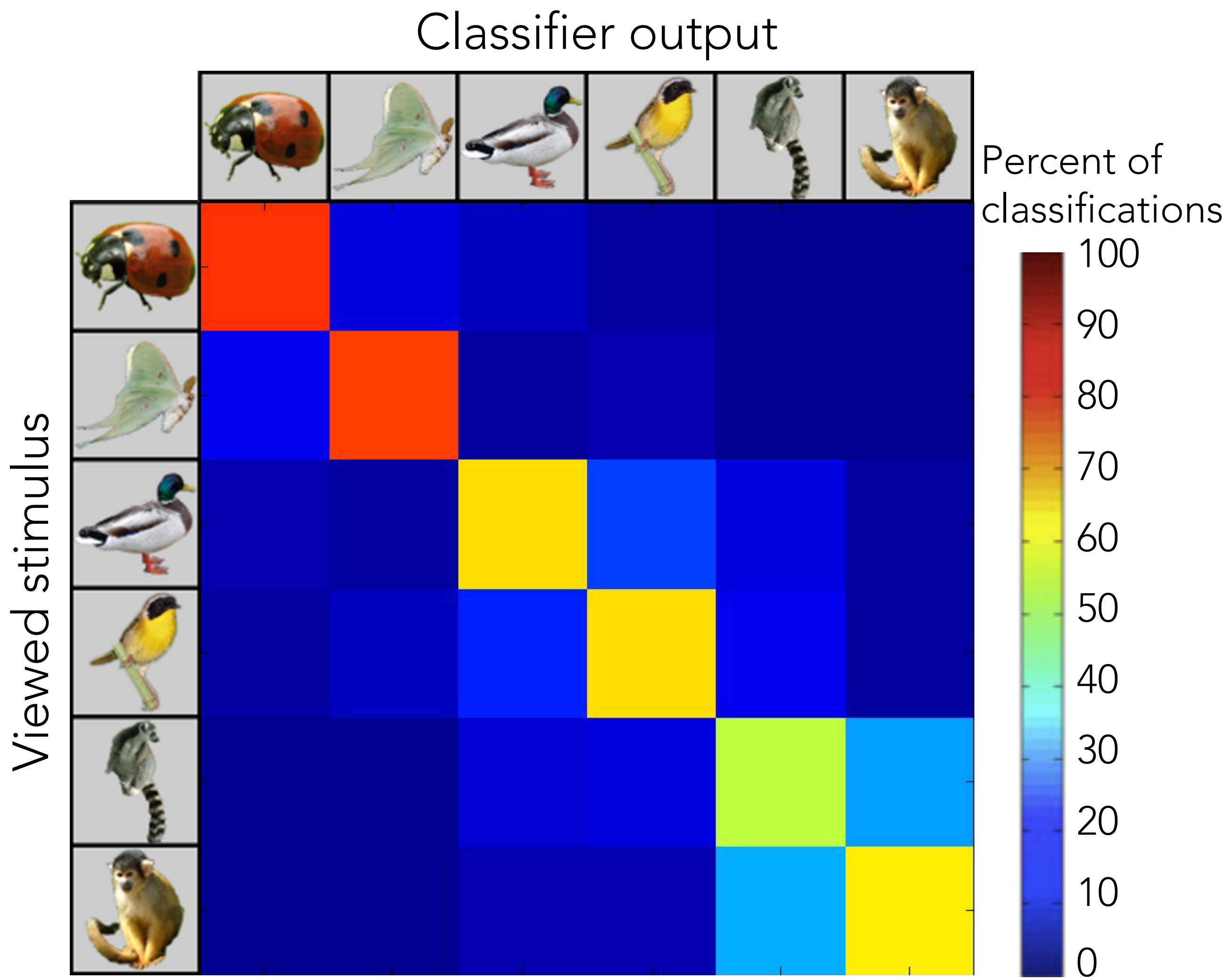
A common high-dimensional linear model of information spaces in human cortex

- Statement of the problem: capturing coarse- and fine-grained topographies in a common model
- Conceptual framework: high-dimensional representational spaces
- Deriving the common space and individual transformation matrices with hyperalignment
- Validation
- Connectivity hyperalignment
- Individual differences in fine-scale cortical functional architecture
- Conclusions

Multivariate Pattern Classification Example: Classifying responses during viewing of animal species

(VT cortex, SVM)

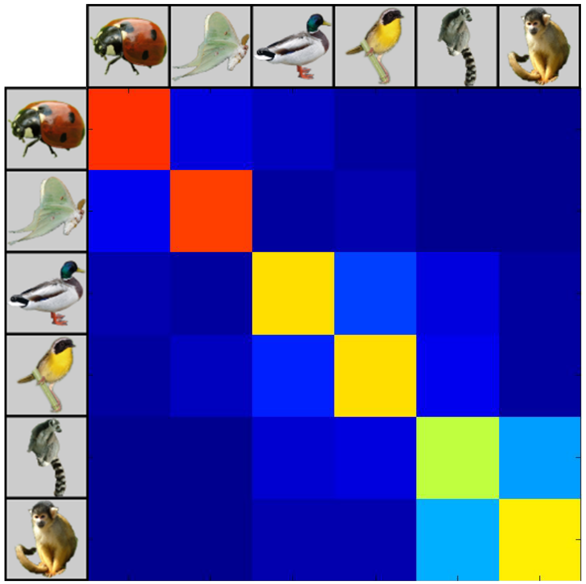




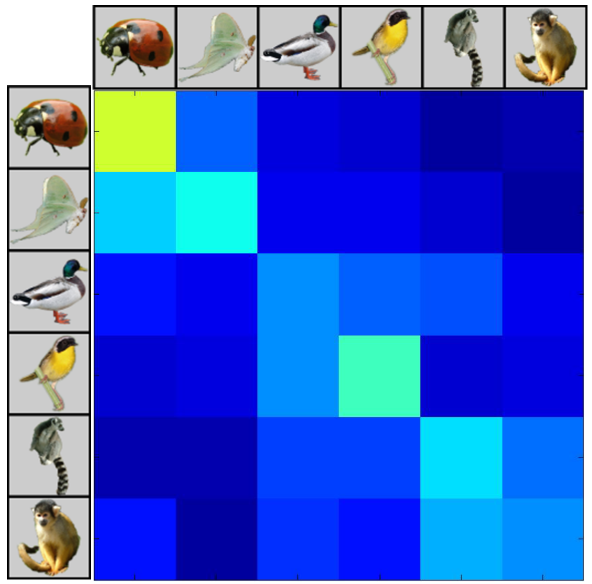
(Haxby et al. 2011; Connolly et al. 2012)

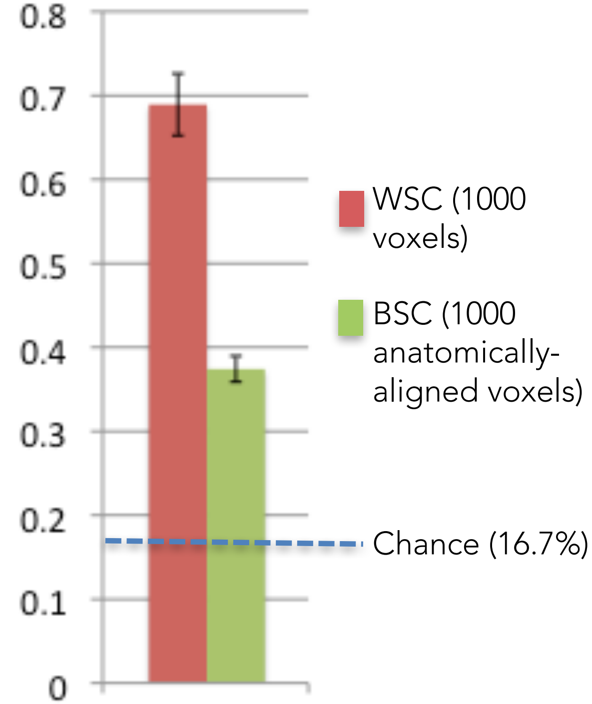
The problem:
Loss of fine-grained distinctions among representations after anatomical alignment of brains

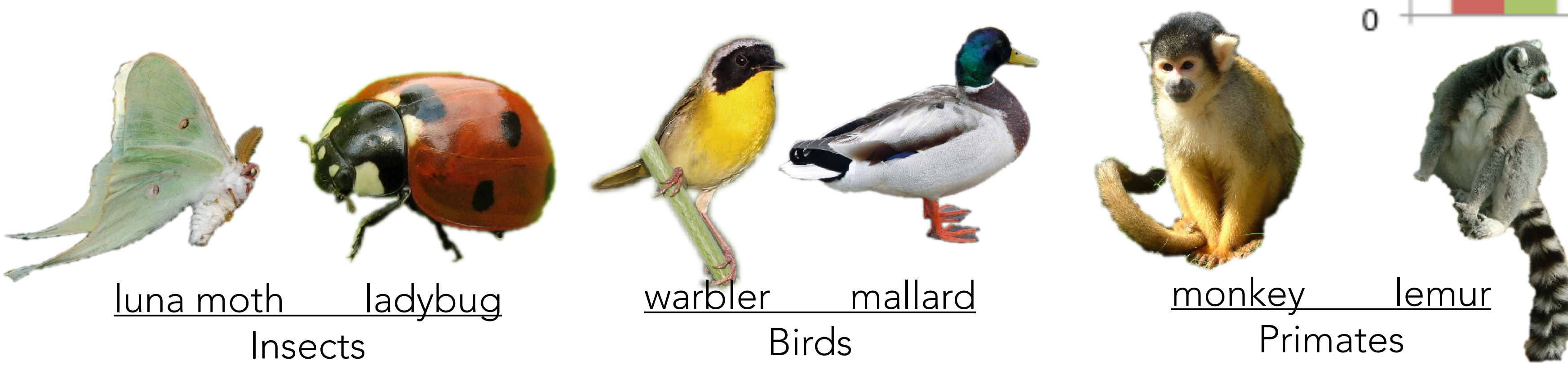
Within-subject classification
(new model for each subject)



Between-subject classification
(common model based on anatomy)



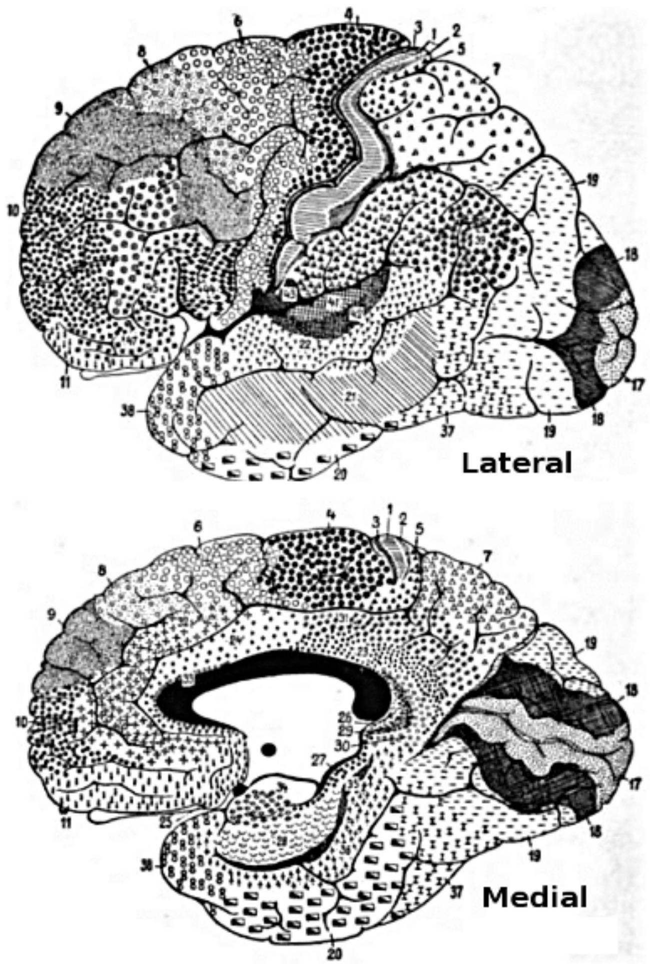




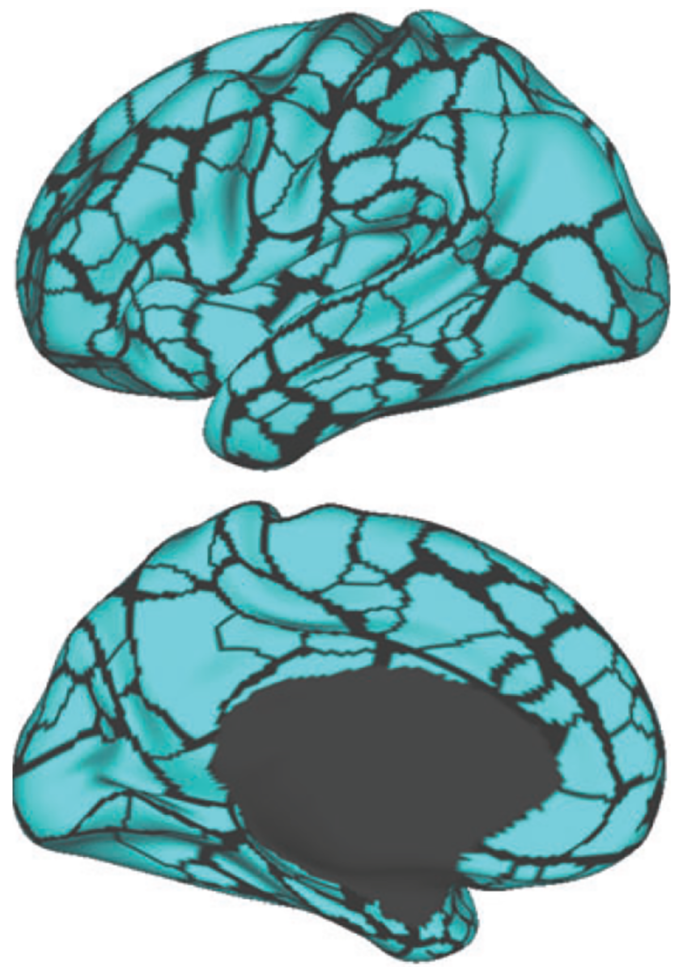
(Haxby et al. 2011; Connolly et al. 2012)

Models of cortical architecture: parcellation of cortex into areas and systems

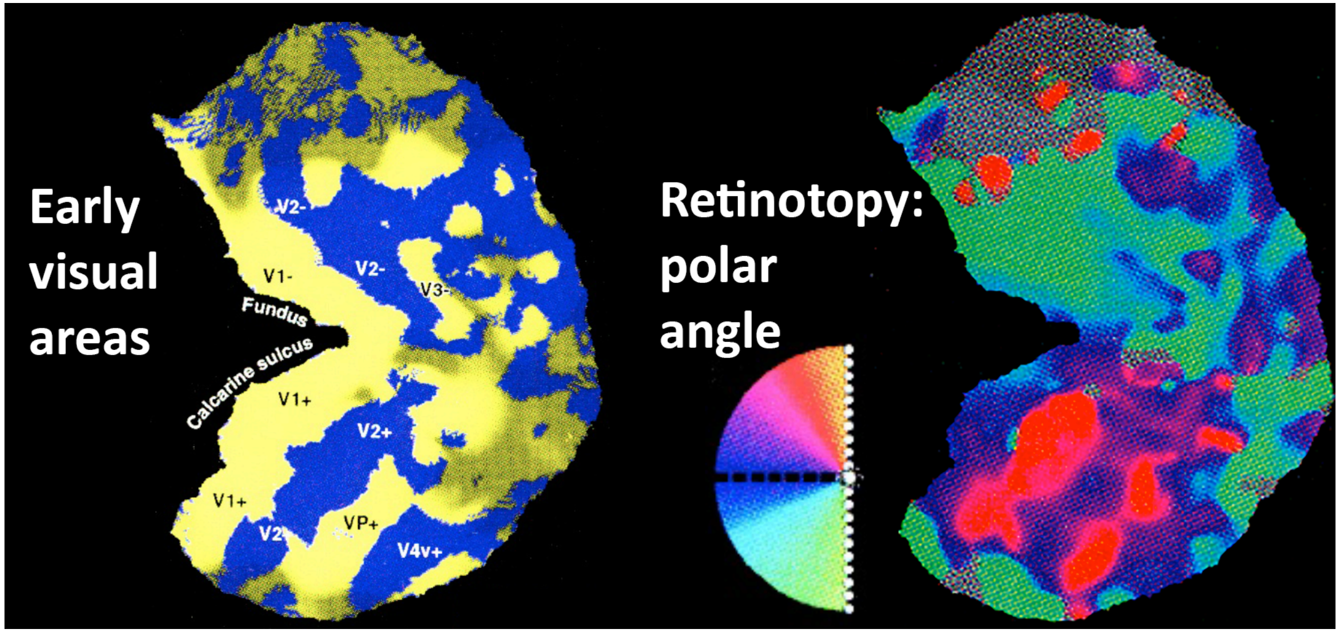
52 areas
(Brodmann, 1909)



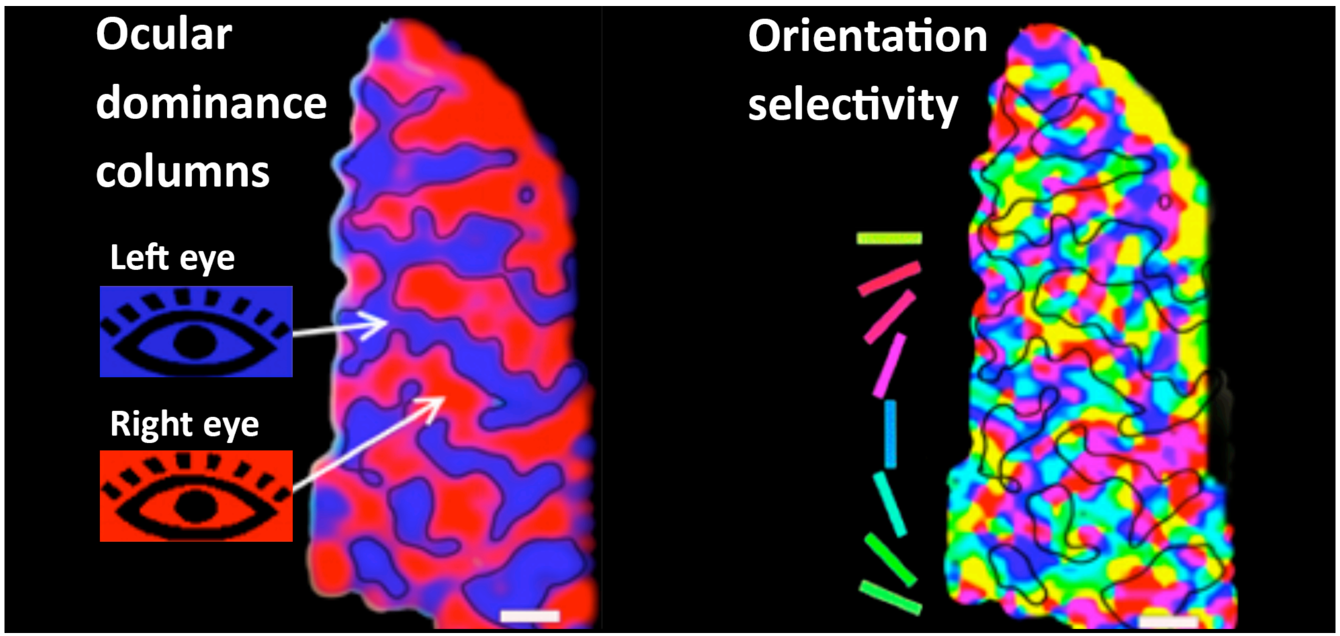
422 areas
(Gordon et al. 2014)



Known topographies of different scales in early visual cortex

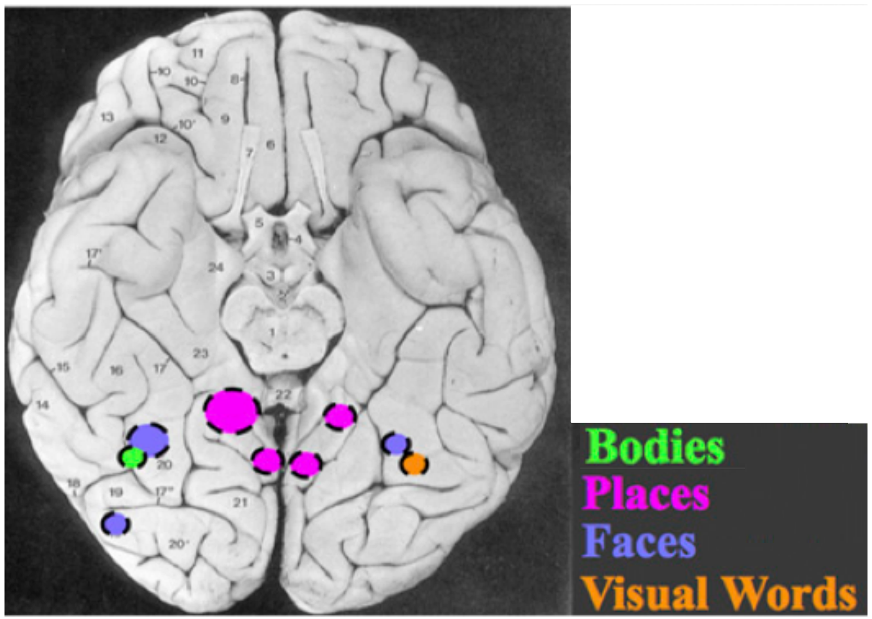


Sereno et al. 1995

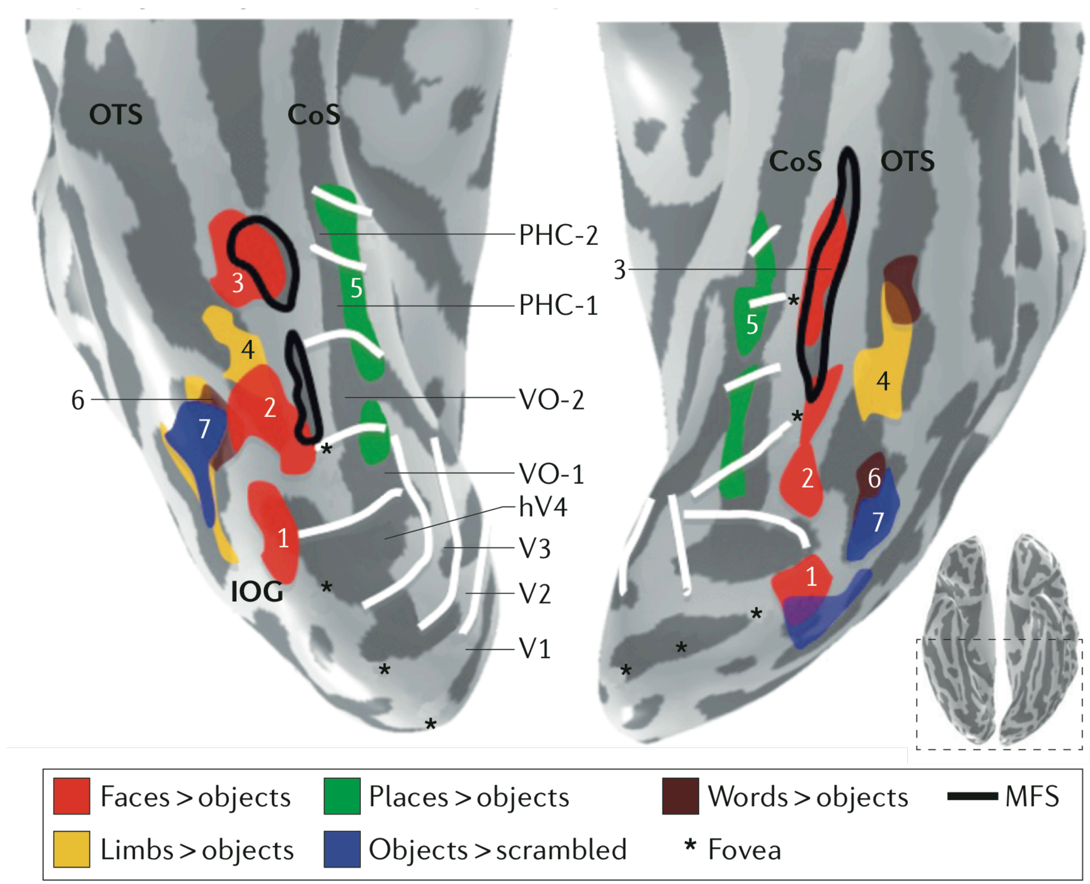


Yacoub et al. 2007, 2008

Category-selective regions in ventral temporal cortex also carry finer distinctions carried by fine-grained topographies



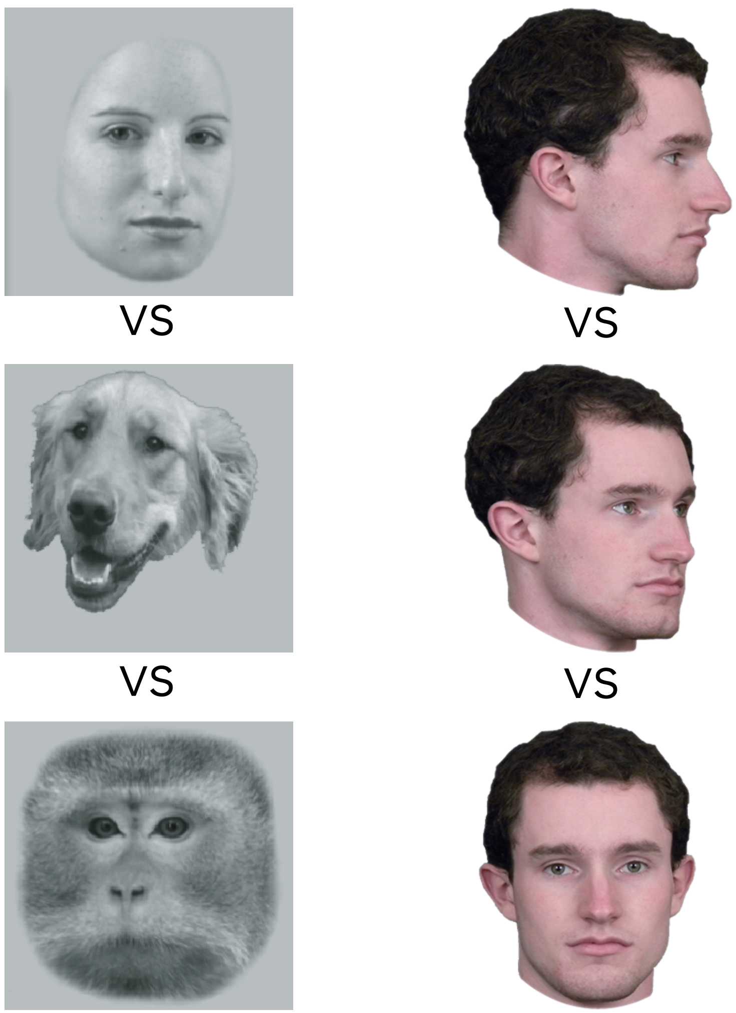
Kanwisher (2010)



Grill-Spector & Weiner (2014)

Category-selective regions in ventral temporal cortex also carry finer distinctions carried by fine-grained topographies:

Distinctions that can be decoded from response patterns in the FFA



Haxby et al. 2011; Connolly et al. 2012; Guntupalli et al. 2017

Question

- Can the information that is encoded in fine-grained topographies be modeled in a computational framework that is common across brains?
  - i.e. Is there a common deep structure for these population responses, or does each brain develop an idiosyncratic code?

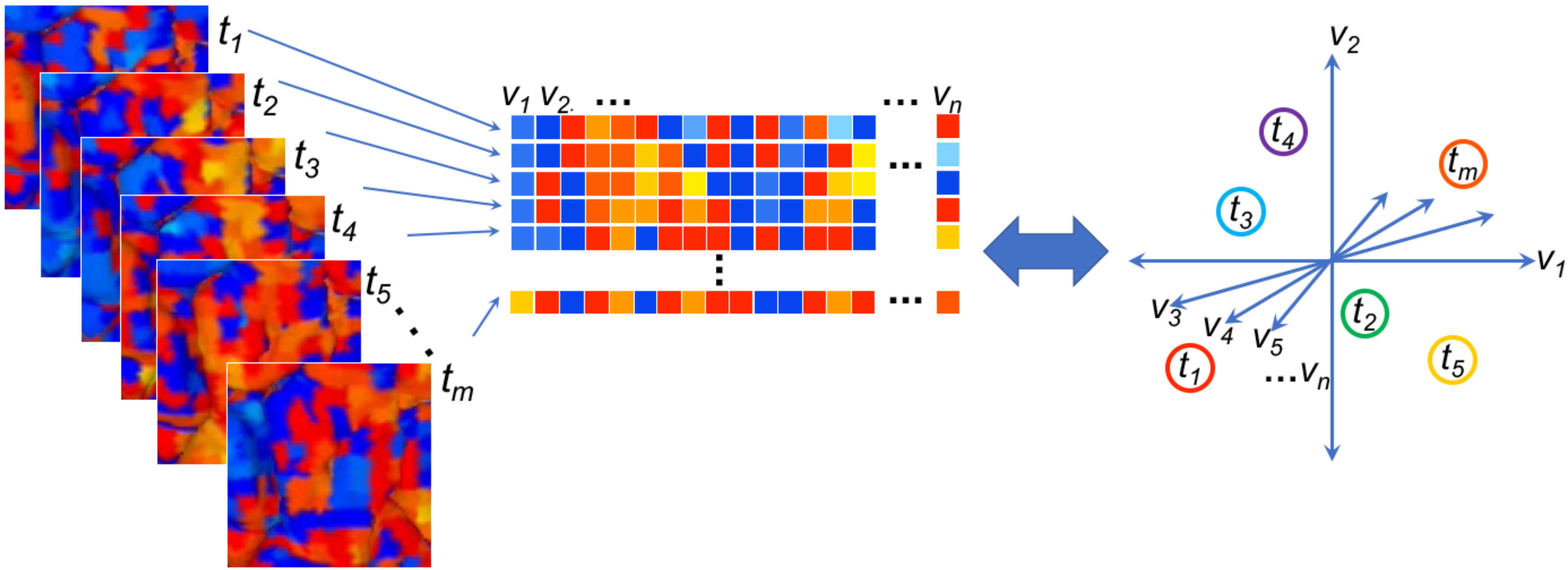
A common high-dimensional linear model of representational spaces in human cortex

- Statement of the problem: capturing fine-grained distinctions in a common model
- Conceptual framework: high-dimensional representational spaces
  - A model space based on features (dimensions) with common tuning profiles
- Deriving the common space and individual transformation matrices with hyperalignment
- Validation
- Connectivity hyperalignment
- Individual differences in fine-scale cortical functional architecture
- Conclusions

Conceptual framework:
High-dimensional information spaces

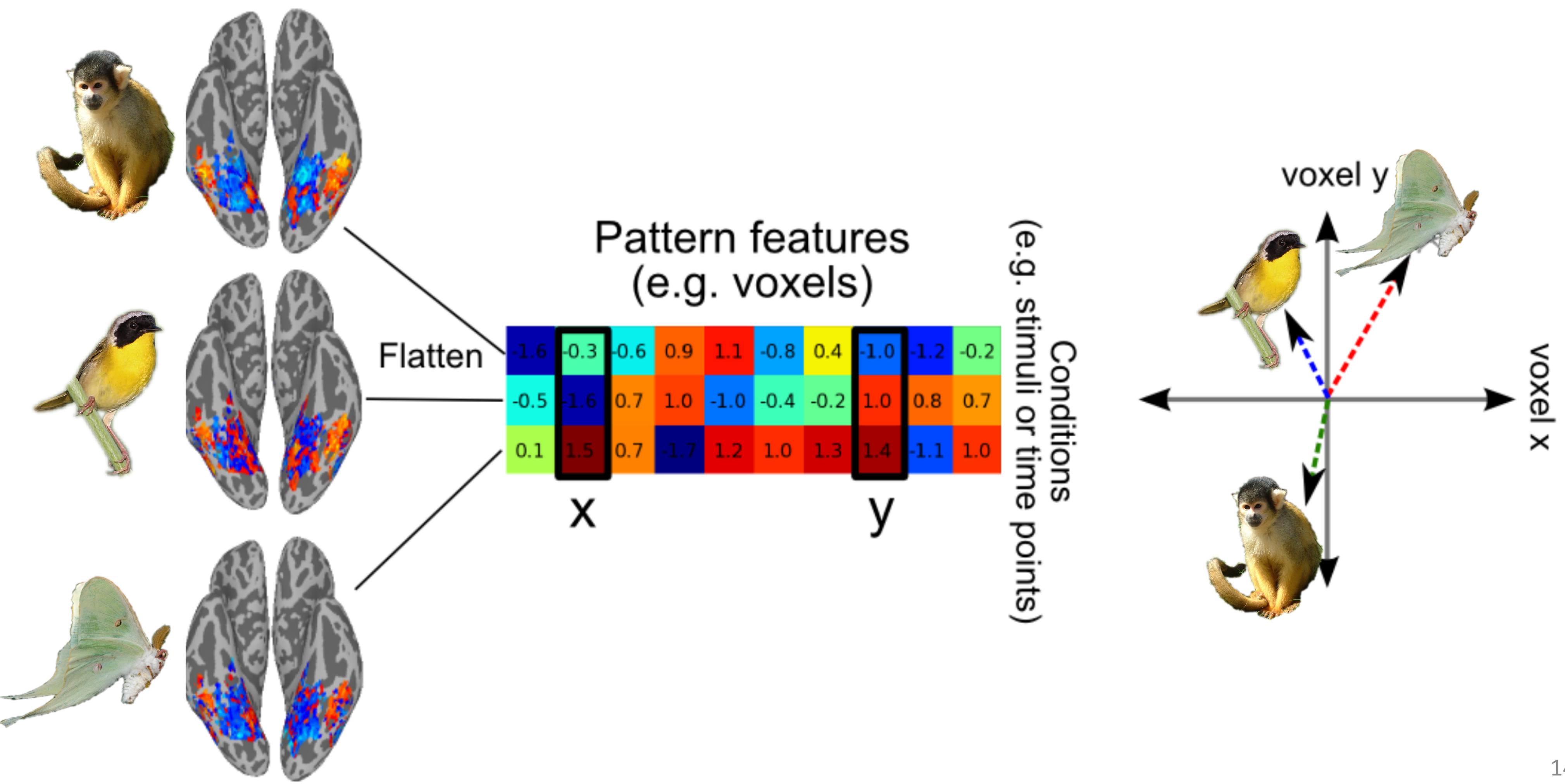
A. Cortical patterns

B. Individual data matrices and high-dimensional spaces

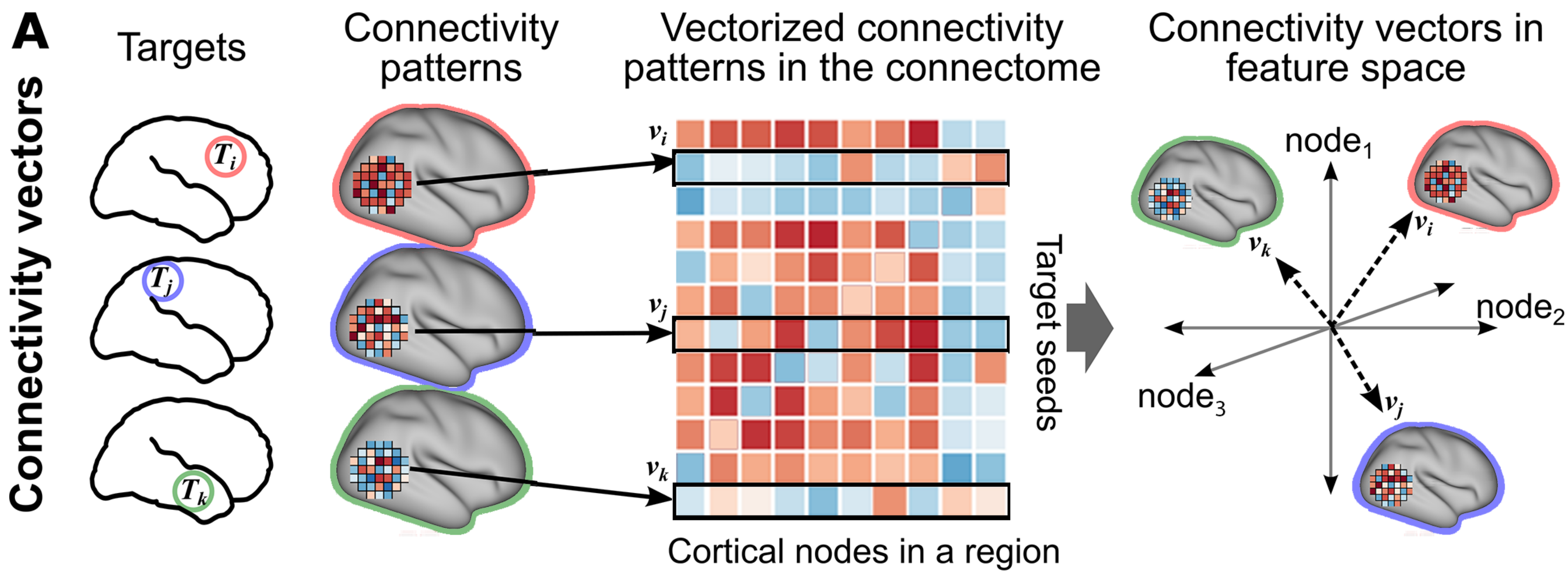


Conceptual framework: High-dimensional information spaces

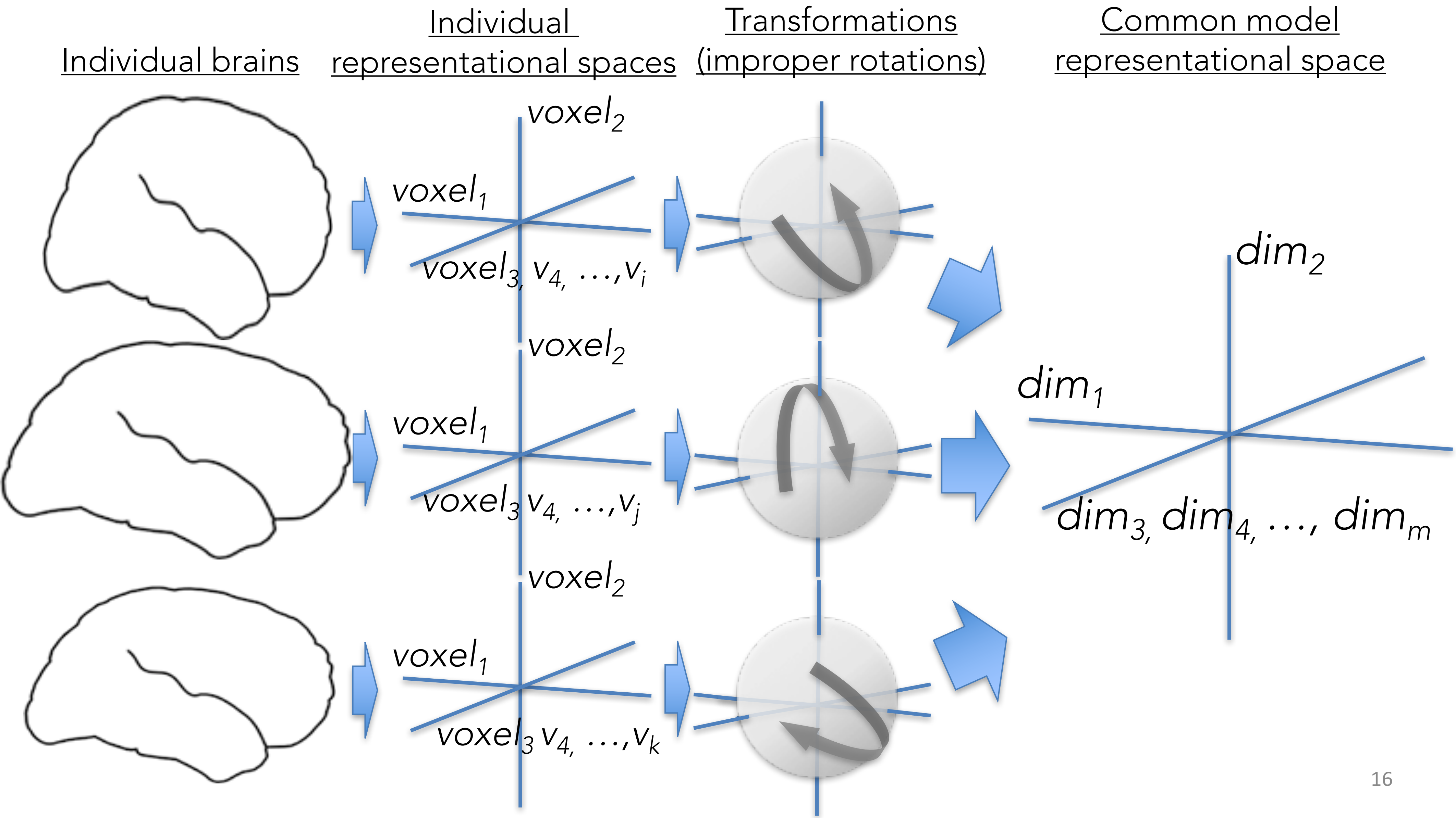
Brain activation patterns | Data matrix | Information space



Conceptual framework: High-dimensional information spaces also can accommodate connectivity and network data



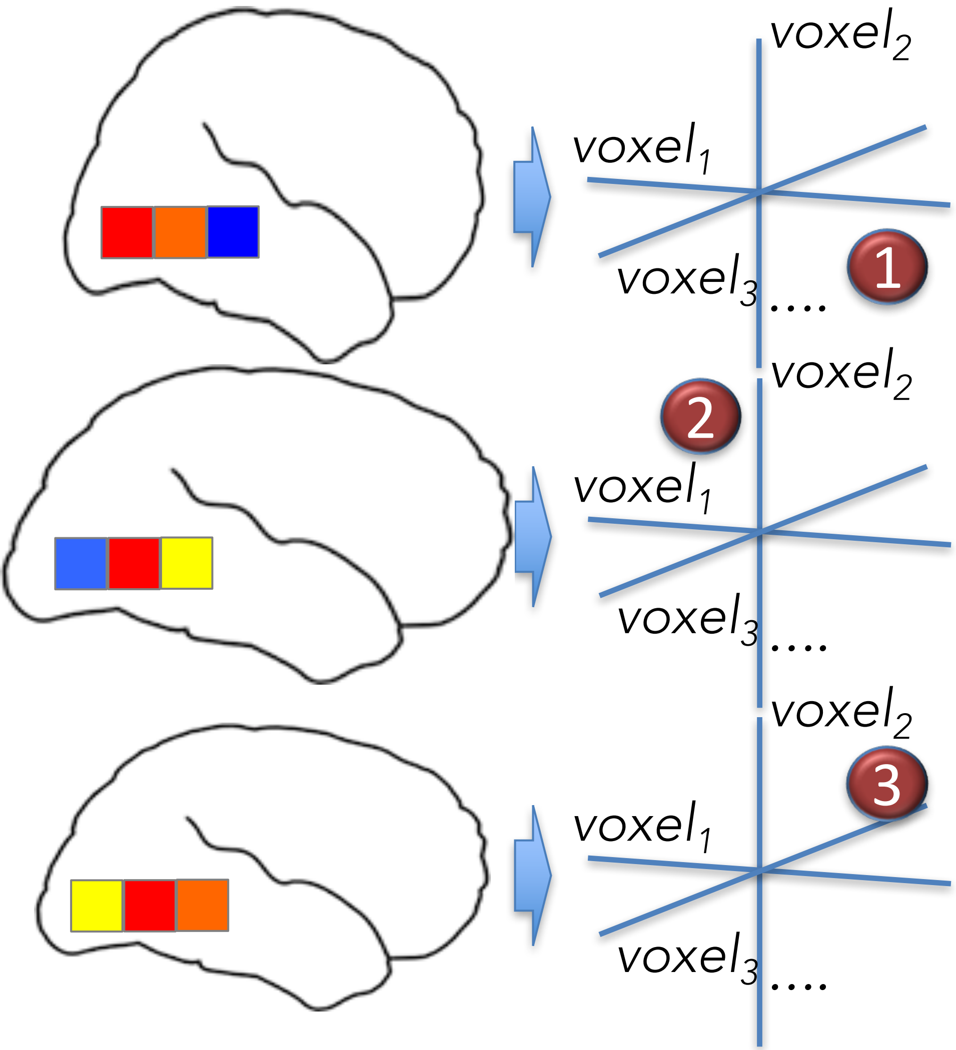
Modeling functional architecture of the human cortex: Individual representational spaces <=> common representational space



Modeling functional architecture of the human cortex: Individual representational spaces <=> common representational space

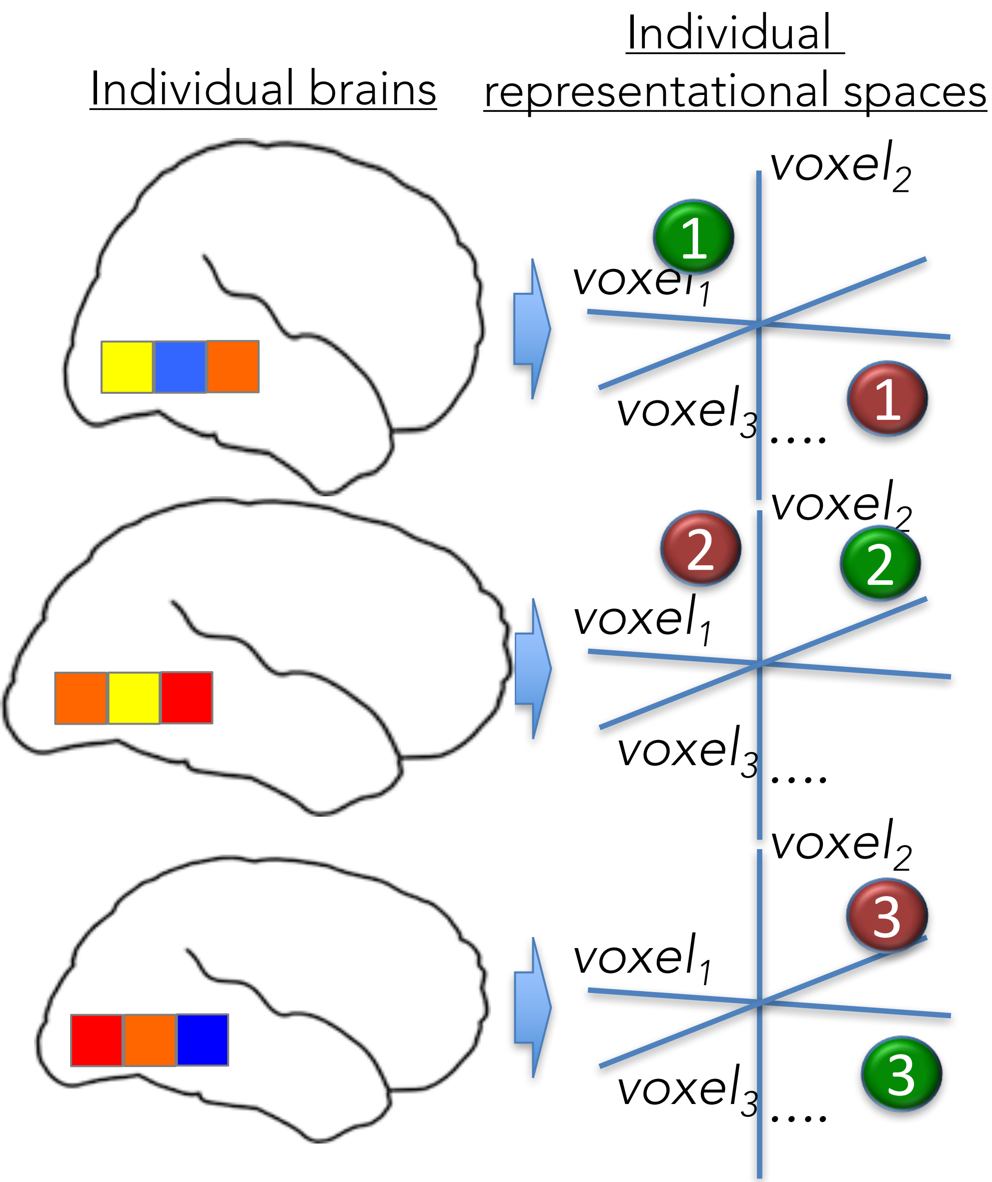
Individual brains

Individual representational spaces



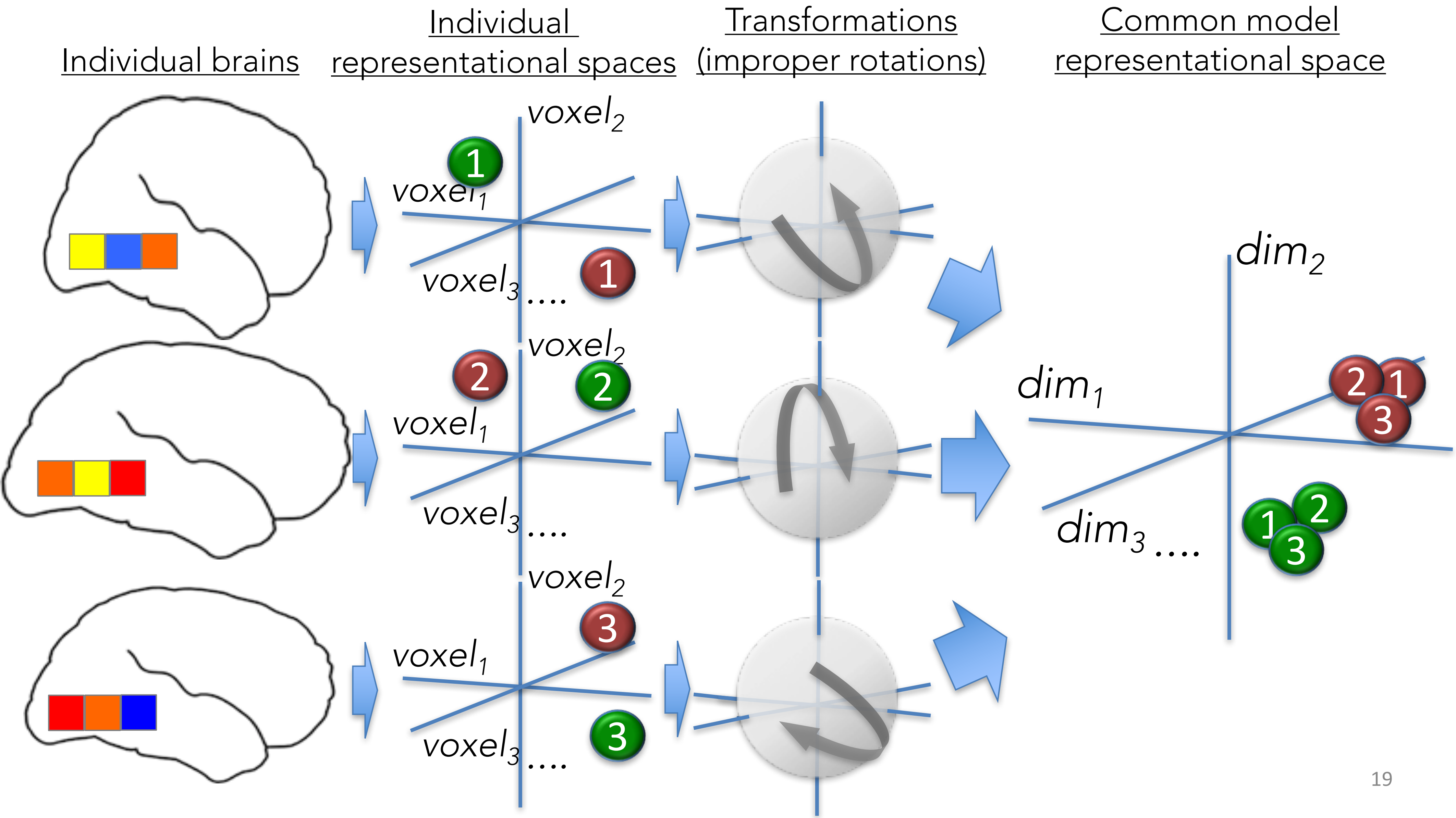
Stimulus

Modeling functional architecture of the human cortex: Individual representational spaces <=> common representational space



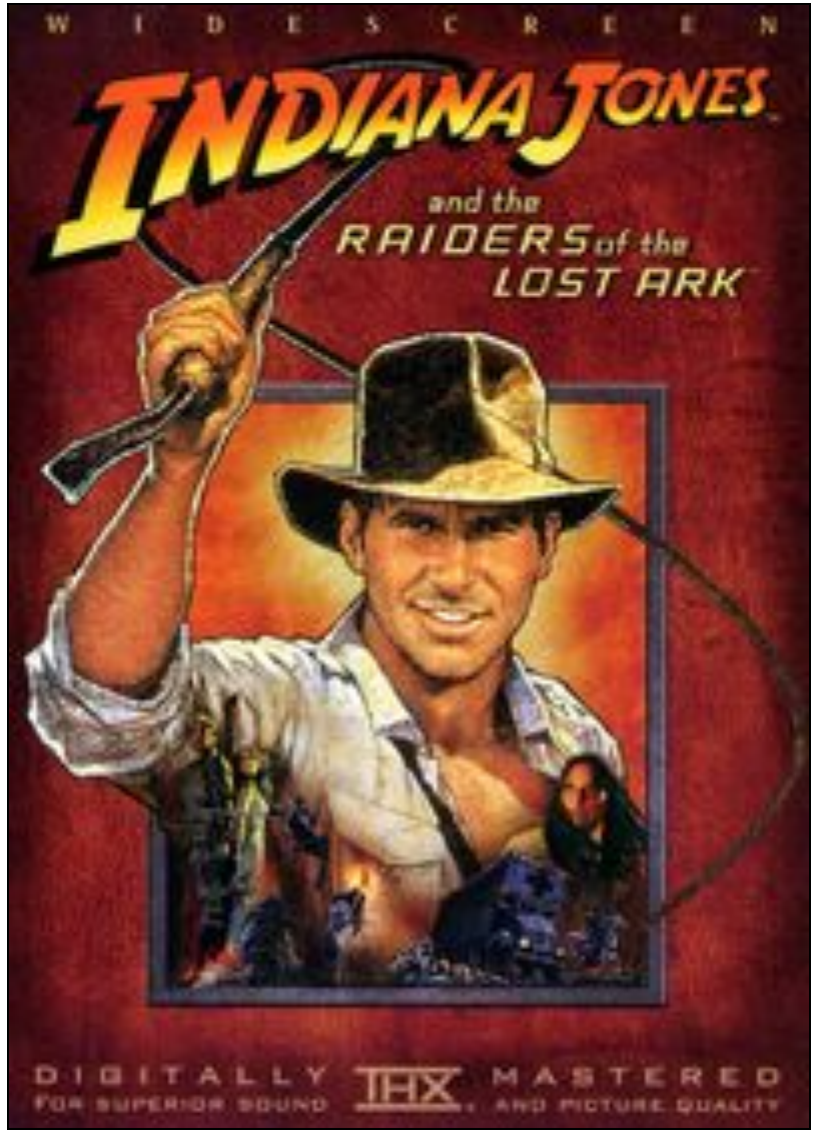
Another stimulus

Modeling functional architecture of the human cortex: Individual representational spaces <=> common representational space

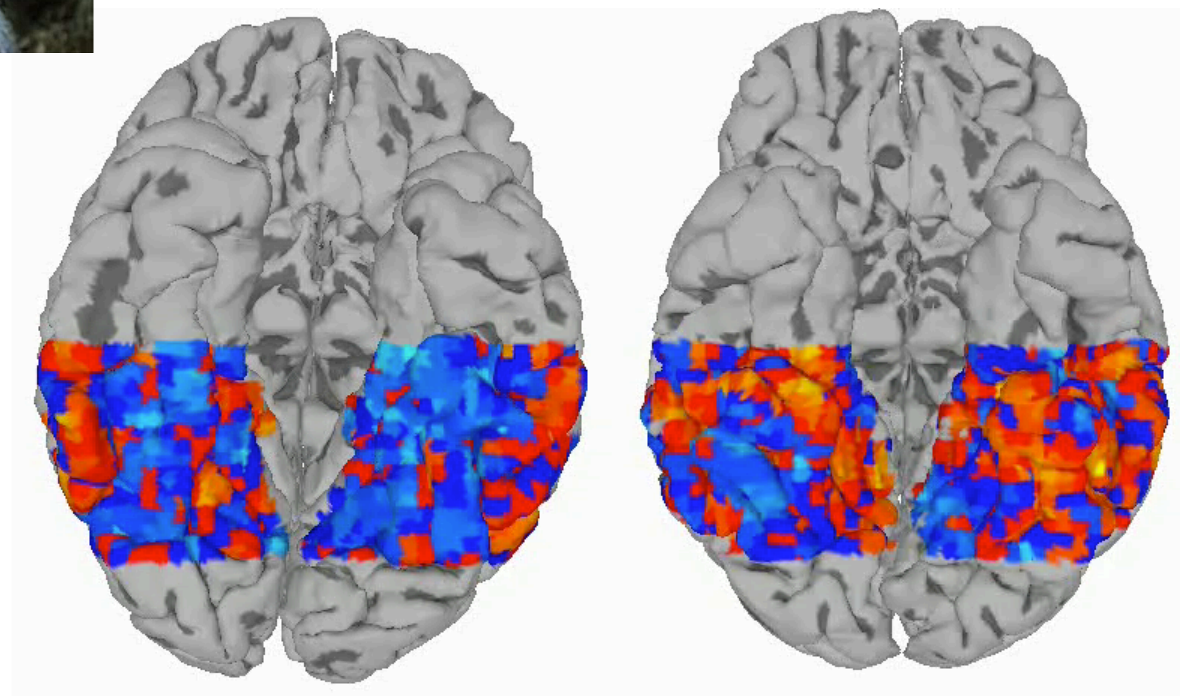


A common high-dimensional linear model of representational spaces in human cortex

- Statement of the problem: capturing fine-grained distinctions in a common model
- Conceptual framework: high-dimensional representational spaces
- Deriving the common space and individual transformation matrices with hyperalignment
  - Hyperalignment algorithm based on Procrustes transformations
  - A rich sampling of response vectors using natural stimulus
- Validation
- Connectivity hyperalignment
- Individual differences in fine-scale cortical functional architecture
- Conclusions


WIDESCREEN
INDIANA JONES
and the
RAIDERS of the
LOST ARK
DIGITALLY THX MASTERED
FOR SUPERIOR SOUND AND PICTURE QUALITY

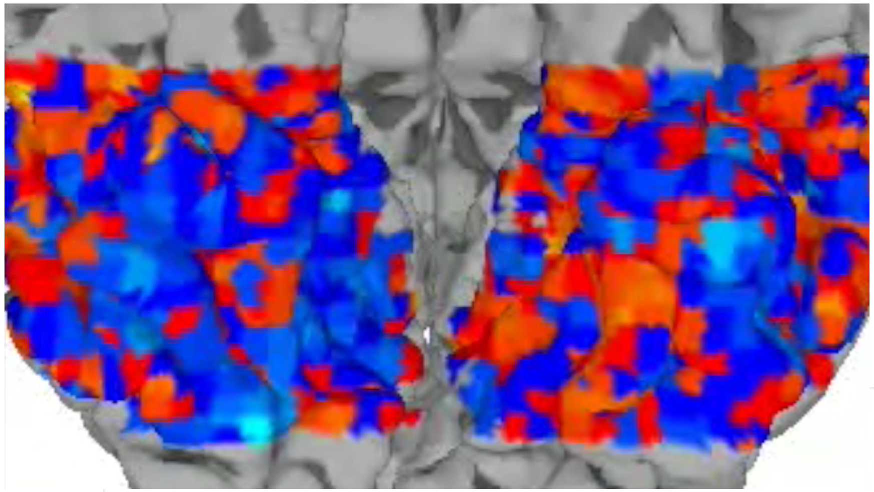
Subject 1 Subject 2

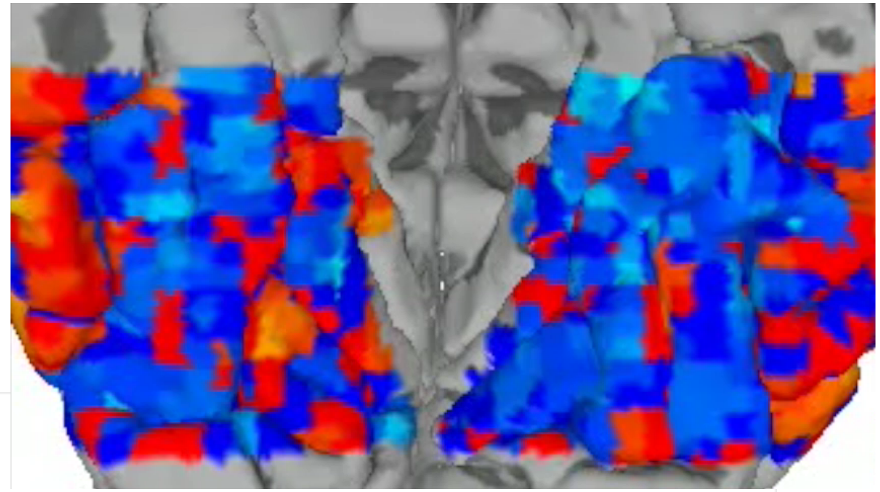


Broad sampling of a neural representational space with a movie

Subject 1 | Subject 2

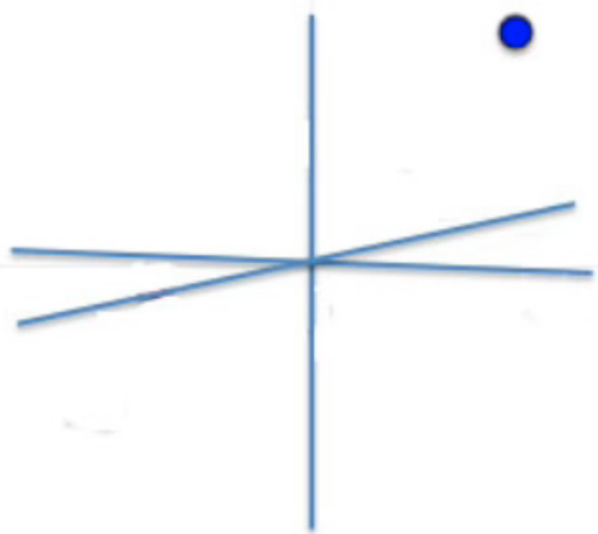
Response patterns in cortex

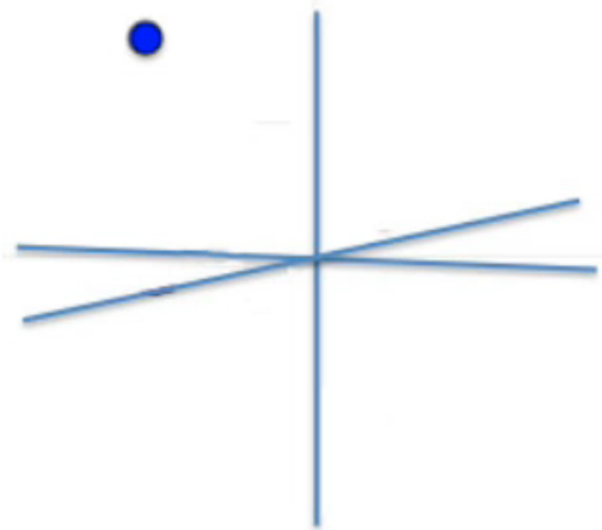




15 response pattern vectors in individual 3D representational spaces

(full exp't has >2600 vectors in >50,000D space)

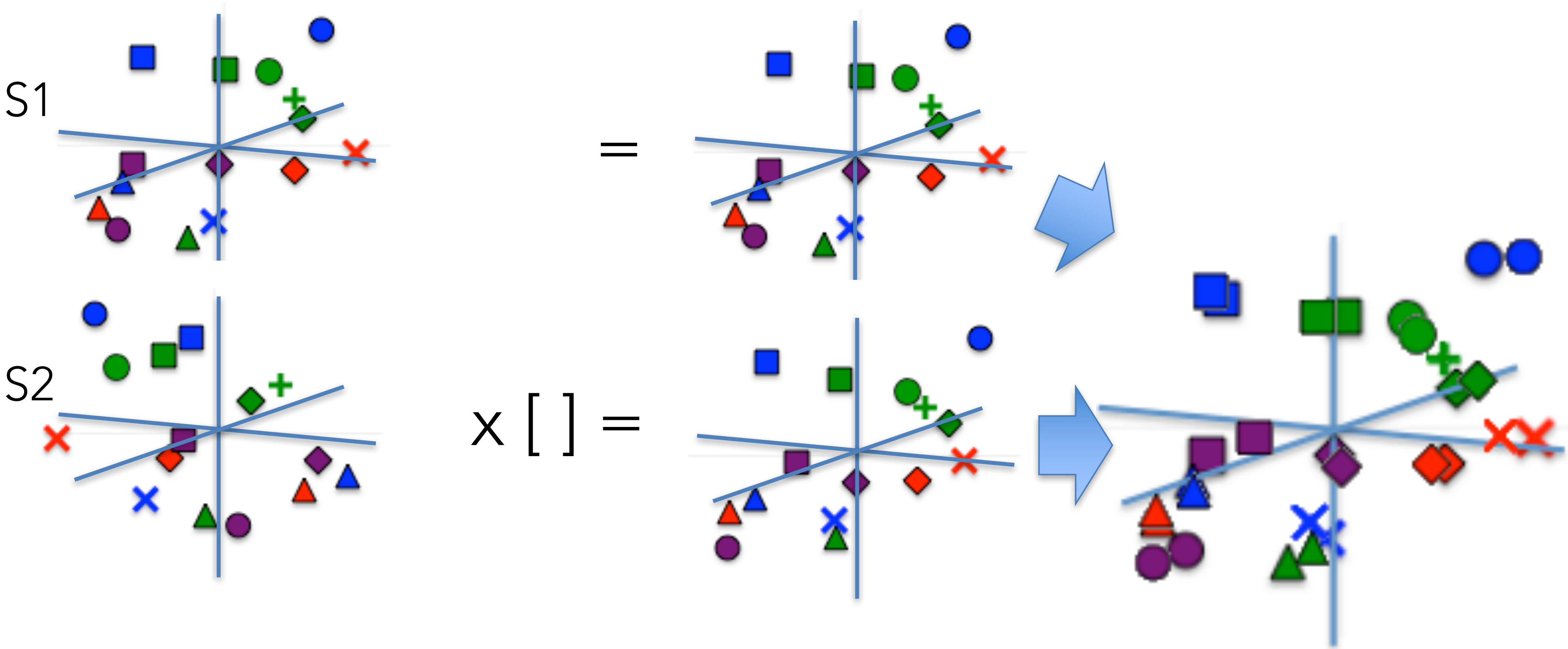




Individual representational spaces

Procrustes transformations (improper rotations)

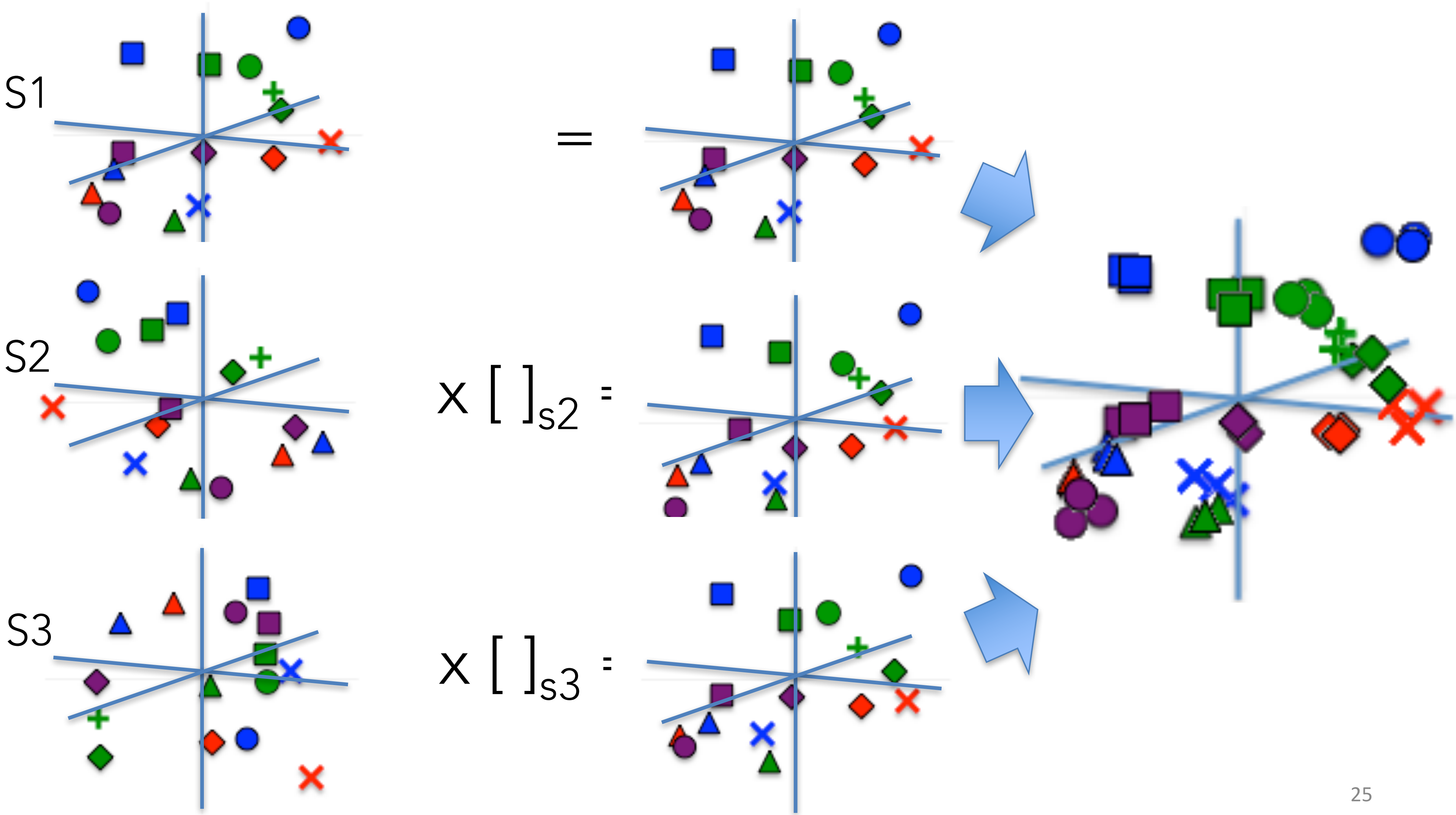
Common model representational space



Individual representational spaces

Procrustes transformations (improper rotations)

Common model representational space



Modeling representational spaces in human cortex with hyperalignment

Basic equation:

$$M_j = (1/N)\sum_{i=1}^{N}(B_{ij}R_{ij})$$

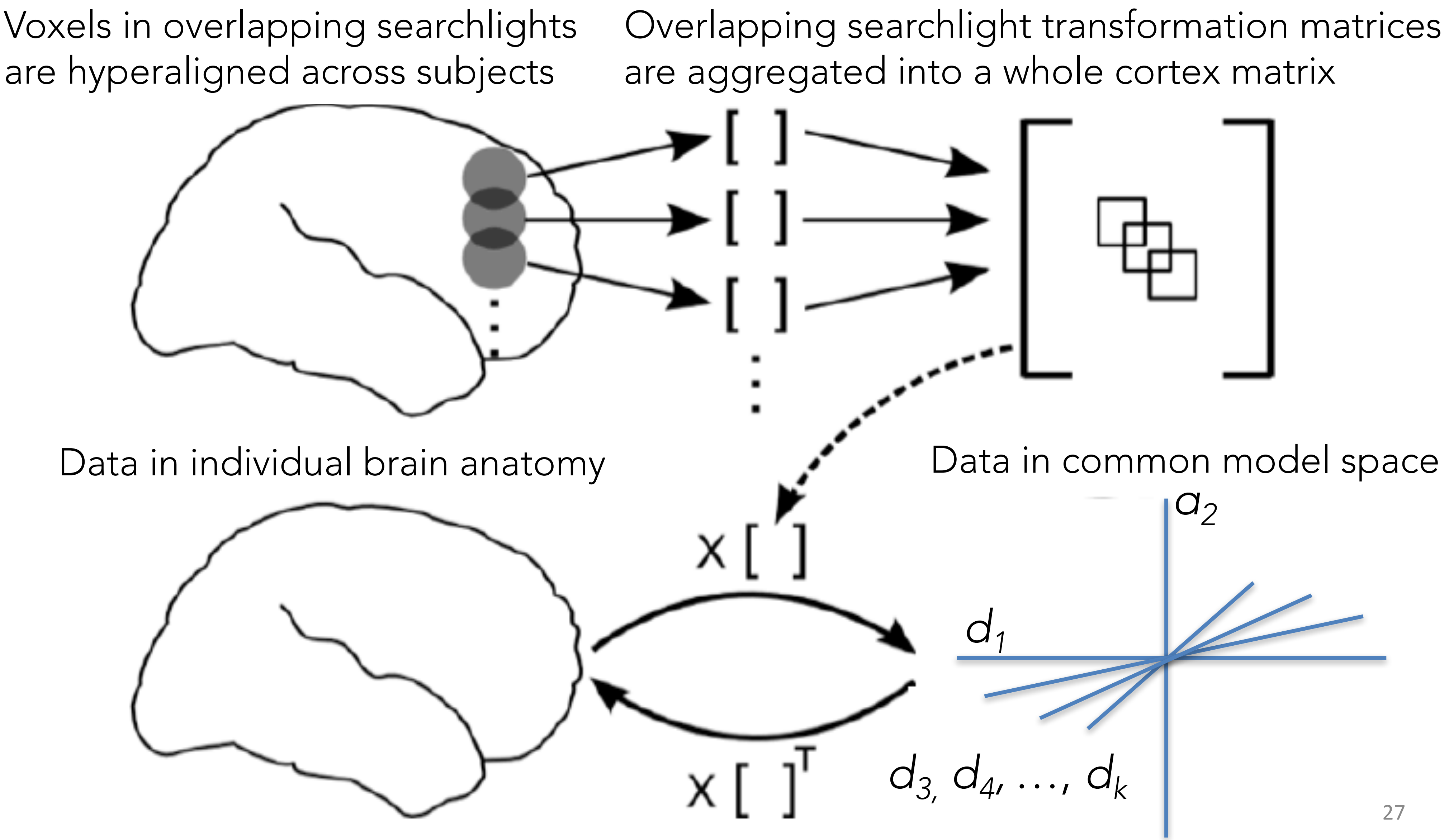
minimizing:

$$R_{ij} = argmin_R \sum_{i=1}^{N} ||B_{ij}R_{ij} - M_j||_{\mathrm{F}}$$

iteratively using:

- Procrustes transformations (Haxby et al. 2011, Guntupalli et al. 2016)
- Regularized CCA (Xu, Lorbert et al. 2012)
- Probabalistic hyperalignment (Chen et al. 2015)

Modeling representational spaces in all human cortex with searchlight hyperalignment



A common high-dimensional linear model of representational spaces in human cortex

- Statement of the problem: capturing fine-grained distinctions in a common model
- Conceptual framework: high-dimensional representational spaces
- Deriving the common space and individual transformation matrices with hyperalignment
- Validation
  - Between-subject classification of movie time segments
  - Between-subject correlations of local similarity structures
  - Estimation spatial granularity of common model features
- Connectivity hyperalignment
- Individual differences in fine-scale cortical functional architecture
- Conclusions

Data in subject brain voxel x time-points data matrix

Time-points / Voxels

B	v_1	v_2	v_3	…	v_l
t_1	$x_{1,1}$	$x_{2,1}$	$x_{3,1}$	…	$x_{l,1}$
t_2	$x_{1,2}$	$x_{2,2}$	$x_{3,2}$	…	$x_{l,2}$
t_3	$x_{1,3}$	$x_{2,3}$	$x_{3,3}$	…	$x_{l,3}$
t_4	$x_{1,4}$	$x_{2,4}$	$x_{3,4}$	…	$x_{l,4}$
…	…	…	…		…
t_j	$x_{1,j}$	$x_{2,j}$	$x_{3,j}$	…	$x_{l,j}$

Data matrix in voxel space
(*l* voxels x *j* time-points)

X

Voxels / Model dimensions

R	d_1	d_2	d_3	…	d_m
v_1	$w_{1,1}$	$w_{2,1}$	$w_{3,1}$	…	$w_{m,1}$
v_2	$w_{1,2}$	$w_{2,2}$	$w_{3,2}$	…	$w_{m,2}$
v_3	$w_{1,3}$	$w_{2,3}$	$w_{3,3}$	…	$w_{m,3}$
…	…	…	…		…
v_l	$w_{1,l}$	$w_{2,l}$	$w_{3,l}$	…	$w_{m,l,}$

Transformation matrix
(*m* dimensions x *l* voxels)

=

Time-points / Model dimensions

M	d_1	d_2	d_3	…	d_m
t_1	$y_{1,1}$	$y_{2,1}$	$y_{3,1}$	…	$y_{m,1}$
t_2	$y_{1,2}$	$y_{2,2}$	$y_{3,2}$	…	$y_{m,2}$
t_3	$y_{1,3}$	$y_{2,3}$	$y_{3,3}$	…	$y_{m,3}$
t_4	$y_{1,4}$	$y_{2,4}$	$y_{3,4}$	…	$y_{m,4}$
…	…	…	…		…
T_j	$y_{1,j}$	$y_{2,j}$	$y_{3,j}$	…	$y_{m,j}$

Data matrix in model space
(*m* dimensions x *j* time-points)

Data in subject brain voxel x time-points data matrix

B	v_1	v_2	v_3	…	v_l
t_1	$x_{1,1}$	$x_{2,1}$	$x_{3,1}$	…	$x_{l,1}$
t_2	$x_{1,2}$	$x_{2,2}$	$x_{3,2}$	…	$x_{l,2}$
t_3	$x_{1,3}$	$x_{2,3}$	$x_{3,3}$	…	$x_{l,3}$
t_4	$x_{1,4}$	$x_{2,4}$	$x_{3,4}$	…	$x_{l,4}$
…	…	…	…		…
t_j	$x_{1,j}$	$x_{2,j}$	$x_{3,j}$	…	$x_{l,j}$

Voxels (columns); Time-points (rows)

Data matrix in voxel space
(l voxels x j time-points)

Pattern of responses across voxels for one time point (t_2)

X

v_1	$w_{1,1}$	$w_{2,1}$	$w_{3,1}$	…	$w_{m,1}$
v_2	$w_{1,2}$	$w_{2,2}$	$w_{3,2}$	…	$w_{m,2}$
v_3	$w_{1,3}$	$w_{2,3}$	$w_{3,3}$	…	$w_{m,3}$
…	…	…	…		…
v_l	$w_{1,l}$	$w_{2,l}$	$w_{3,l}$	…	$w_{m,l,}$

Model dimensions (columns); Voxels (rows)

Transformation matrix
(m dimensions x l voxels)

=

					d_m
t_1	$y_{1,1}$	$y_{2,1}$	$y_{3,1}$	…	$y_{m,1}$
t_2	$y_{1,2}$	$y_{2,2}$	$y_{3,2}$	…	$y_{m,2}$
t_3	$y_{1,3}$	$y_{2,3}$	$y_{3,3}$	…	$y_{m,3}$
t_4	$y_{1,4}$	$y_{2,4}$	$y_{3,4}$	…	$y_{m,4}$
…	…	…	…		…
T_j	$y_{1,j}$	$y_{2,j}$	$y_{3,j}$	…	$y_{m,j}$

Model dimensions (columns); Time-points (rows)

Data matrix in model space
(m dimensions x j time-points)

Transforming patterns and time-series into common model space

Pattern of responses across model dimensions for one time point (t_2)

Voxels

Time-points

B	v_1	v_2	v_3	…	v_l
t_1	$x_{1,1}$	$x_{2,1}$	$x_{3,1}$	…	$x_{l,1}$
t_2	$x_{1,2}$	$x_{2,2}$	$x_{3,2}$	…	$x_{l,2}$
t_3	$x_{1,3}$	$x_{2,3}$	$x_{3,3}$	…	$x_{l,3}$
t_4	$x_{1,4}$	$x_{2,4}$	$x_{3,4}$	…	$x_{l,4}$
…	…	…	…		…
t_j	$x_{1,j}$	$x_{2,j}$	$x_{3,j}$	…	$x_{l,j}$

Data matrix in voxel space
(*l* voxels x *j* time-points)

X

Model dimensions

Voxels

R	d_1	d_2	d_3	…	d_m
v_1	$w_{1,1}$	$w_{2,1}$	$w_{3,1}$	…	$w_{m,1}$
v_2	$w_{1,2}$	$w_{2,2}$	$w_{3,2}$	…	$w_{m,2}$
v_3	$w_{1,3}$	$w_{2,3}$	$w_{3,3}$	…	$w_{m,3}$
…	…	…	…		…
v_l	$w_{1,l}$	$w_{2,l}$	$w_{3,l}$	…	$w_{m,l,}$

Transformation matrix
(*m* dimensions x *l* voxels)

=

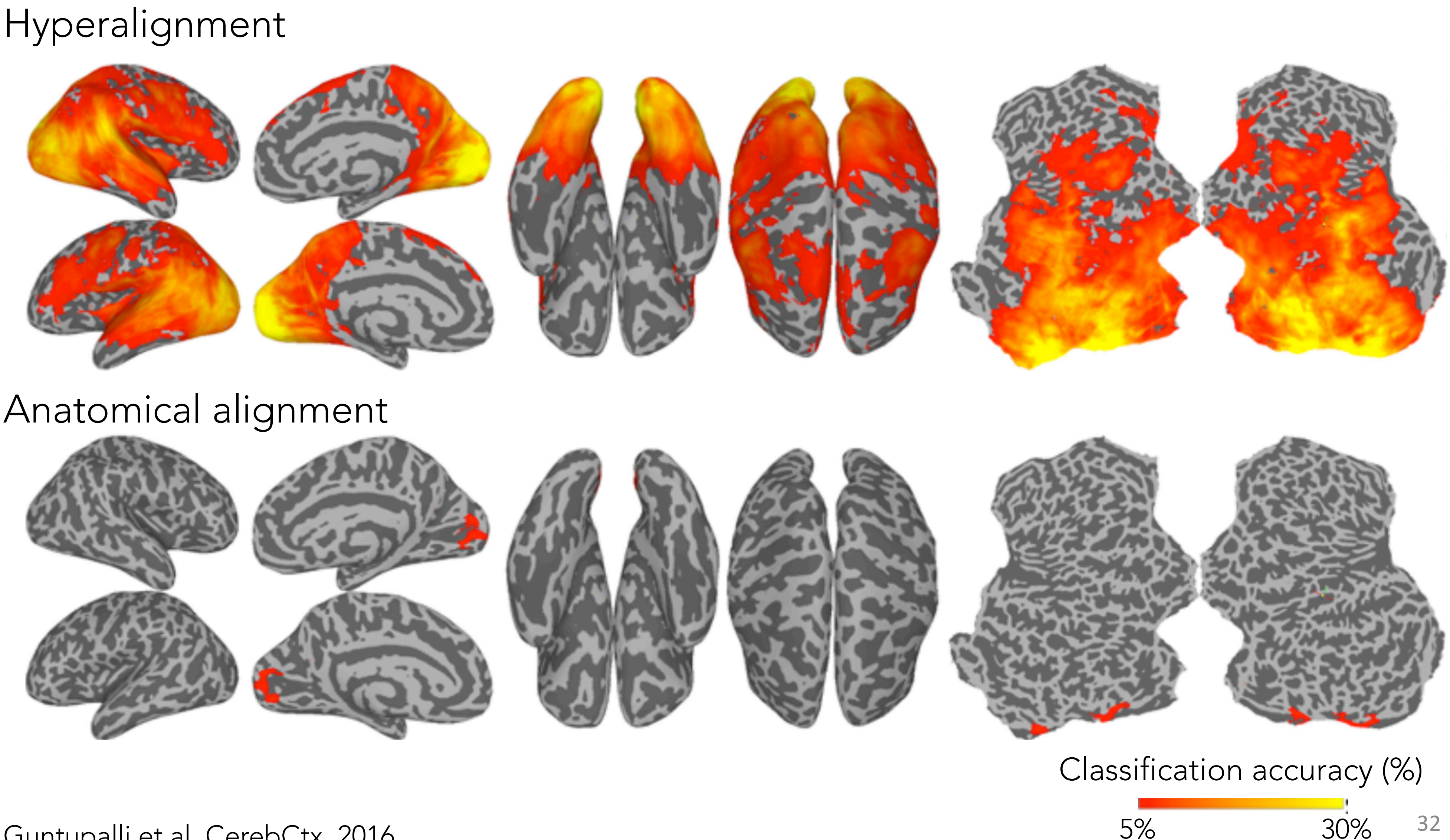
Model dimensions

Time-points

M	d_1	d_2	d_3	…	d_m
t_1	$y_{1,1}$	$y_{2,1}$	$y_{3,1}$	…	$y_{m,1}$
t_2	$y_{1,2}$	$y_{2,2}$	$y_{3,2}$	…	$y_{m,2}$
t_3	$y_{1,3}$	$y_{2,3}$	$y_{3,3}$	…	$y_{m,3}$
t_4	$y_{1,4}$	$y_{2,4}$	$y_{3,4}$	…	$y_{m,4}$
…	…	…	…		…
T_j	$y_{1,j}$	$y_{2,j}$	$y_{3,j}$	…	$y_{m,j}$

Data matrix in model space
(*m* dimensions x *j* time-points)

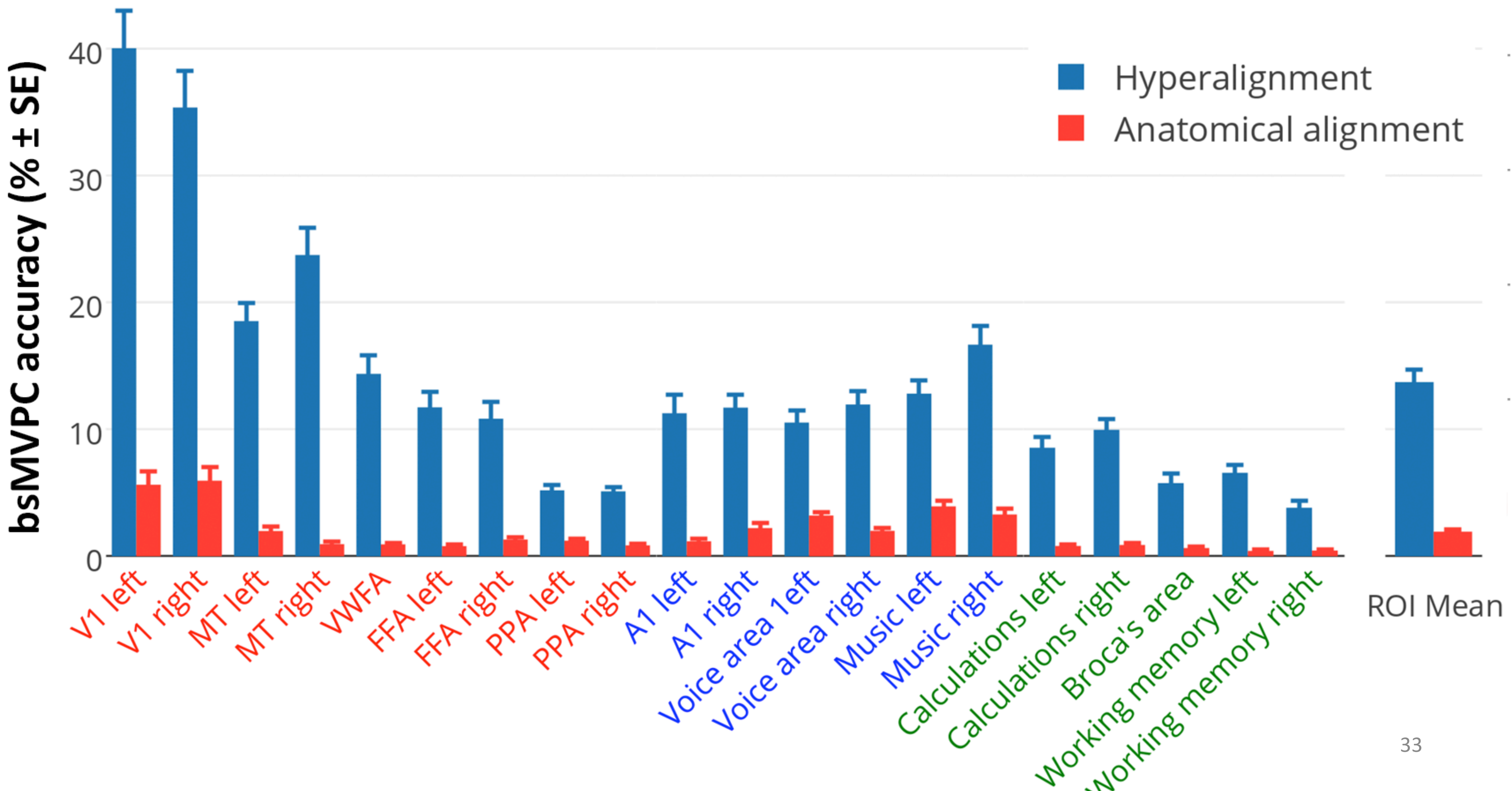
Whole-brain hyperalignment increases between-subject classification of 15 s movie time segments in occipital, temporal, parietal, and frontal cortices



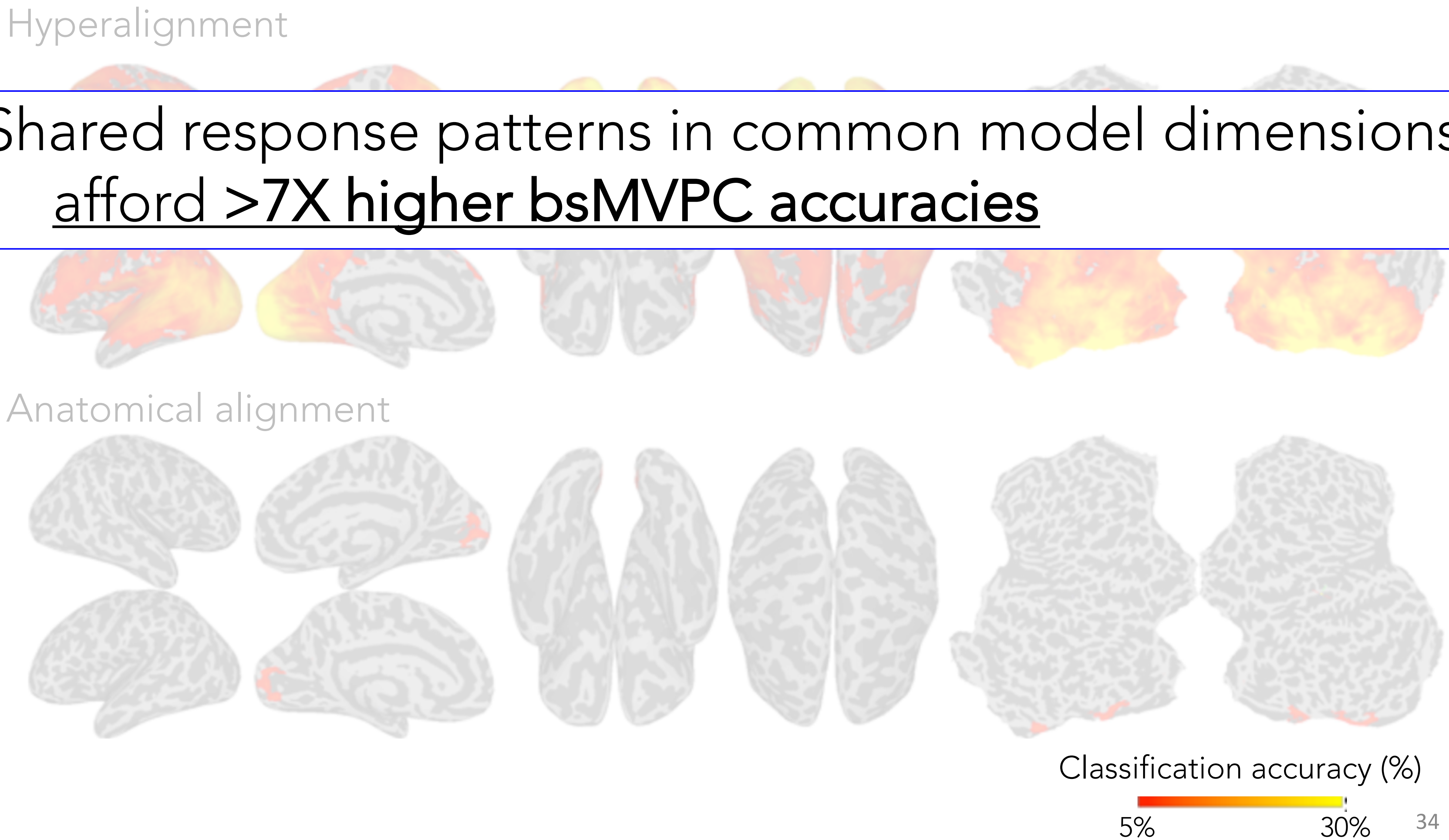
Guntupalli et al. CerebCtx, 2016

Increased bsMVPC of movie time-segments in visual, auditory, and cognitive regions of interest (ROIs)

(coordinates from NeuroSynth)

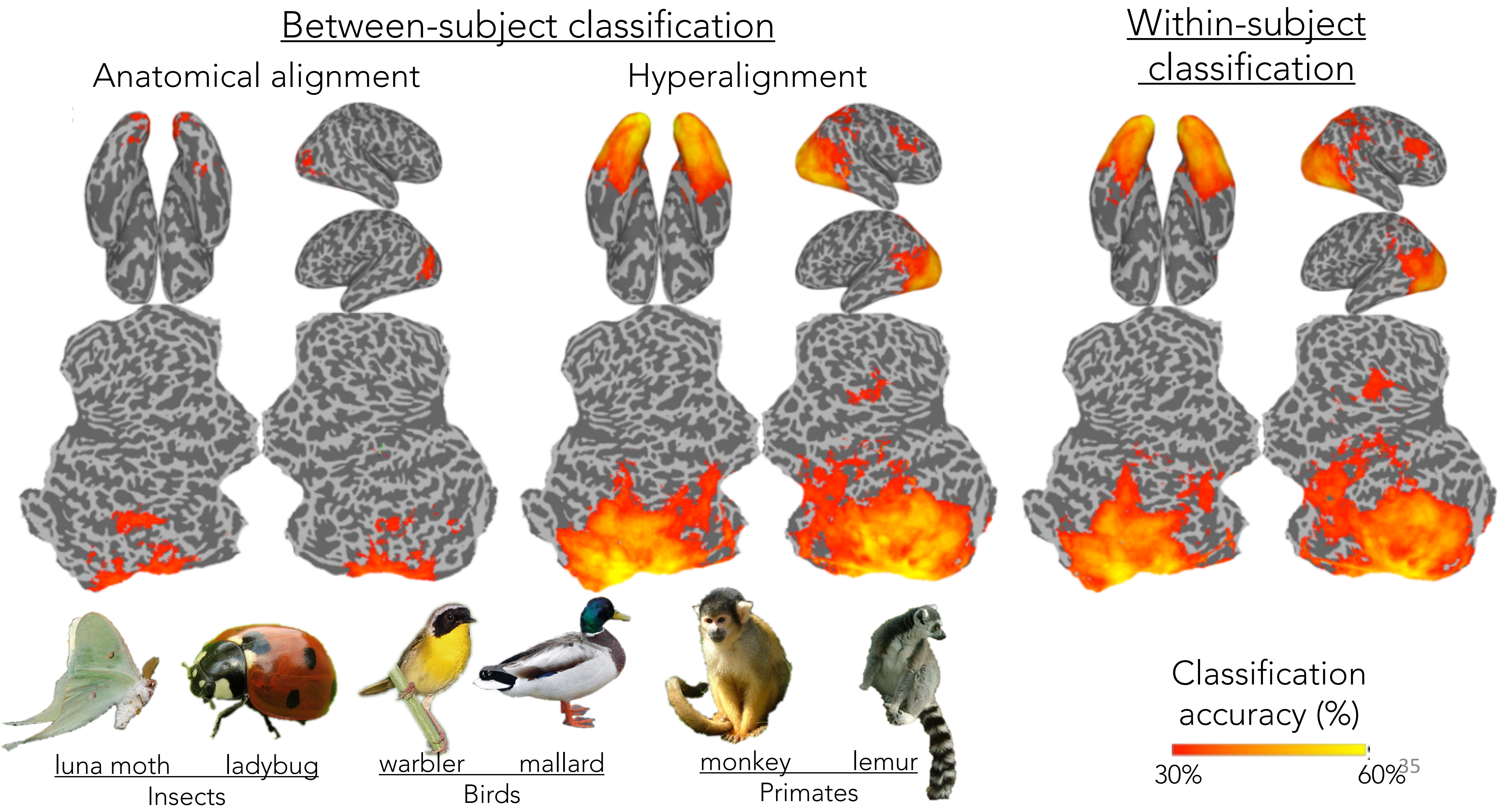


Whole-brain hyperalignment increases between-subject classification of 15 s movie time segments in occipital, temporal, parietal, and frontal cortices



Shared response patterns in common model dimensions afford **>7X higher bsMVPC accuracies**

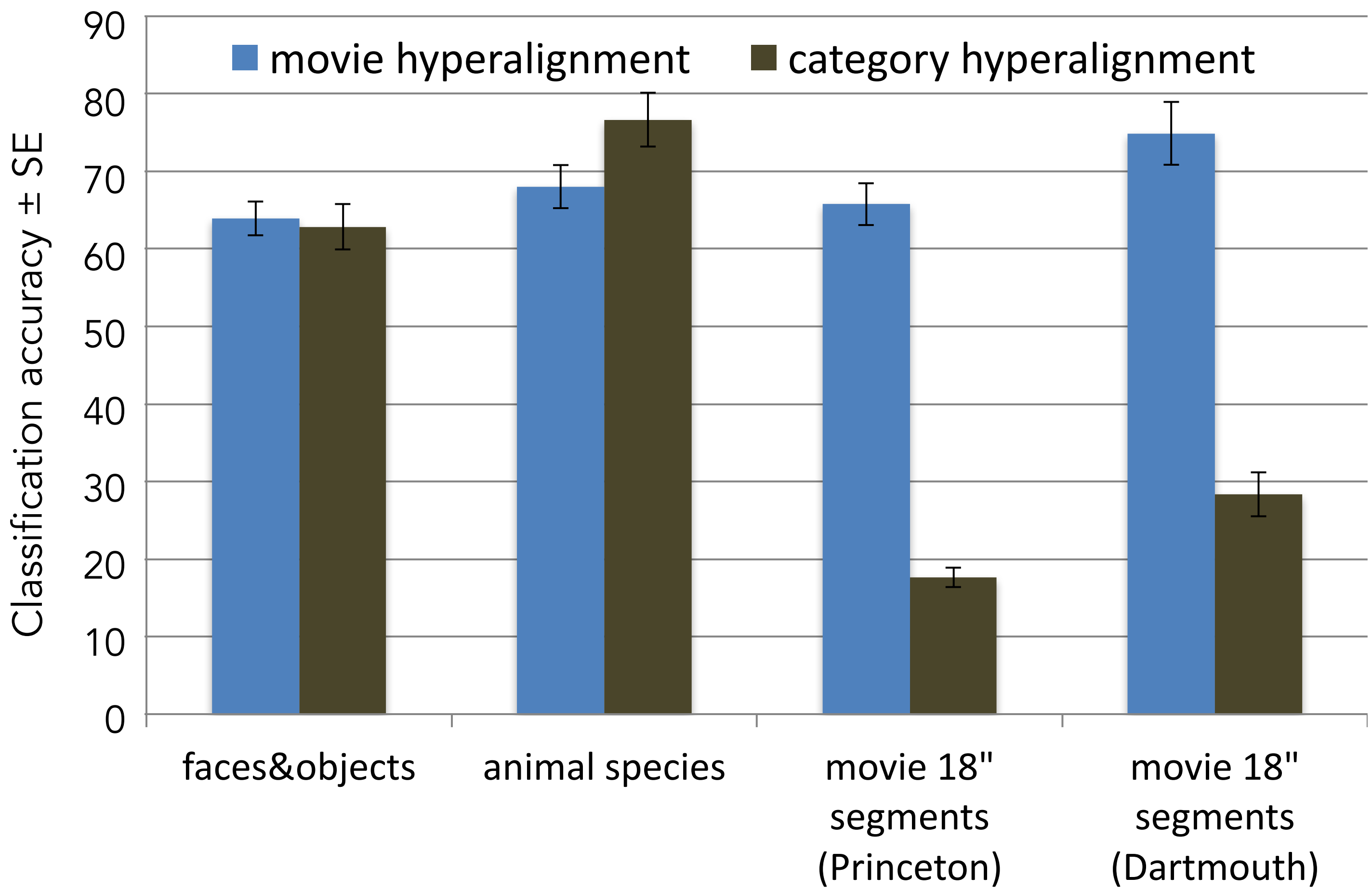
Whole-brain hyperalignment based on movie affords between-subject classification of responses in a visual category experiment (6 animal species) *at levels of accuracy that exceed within-subject classification*

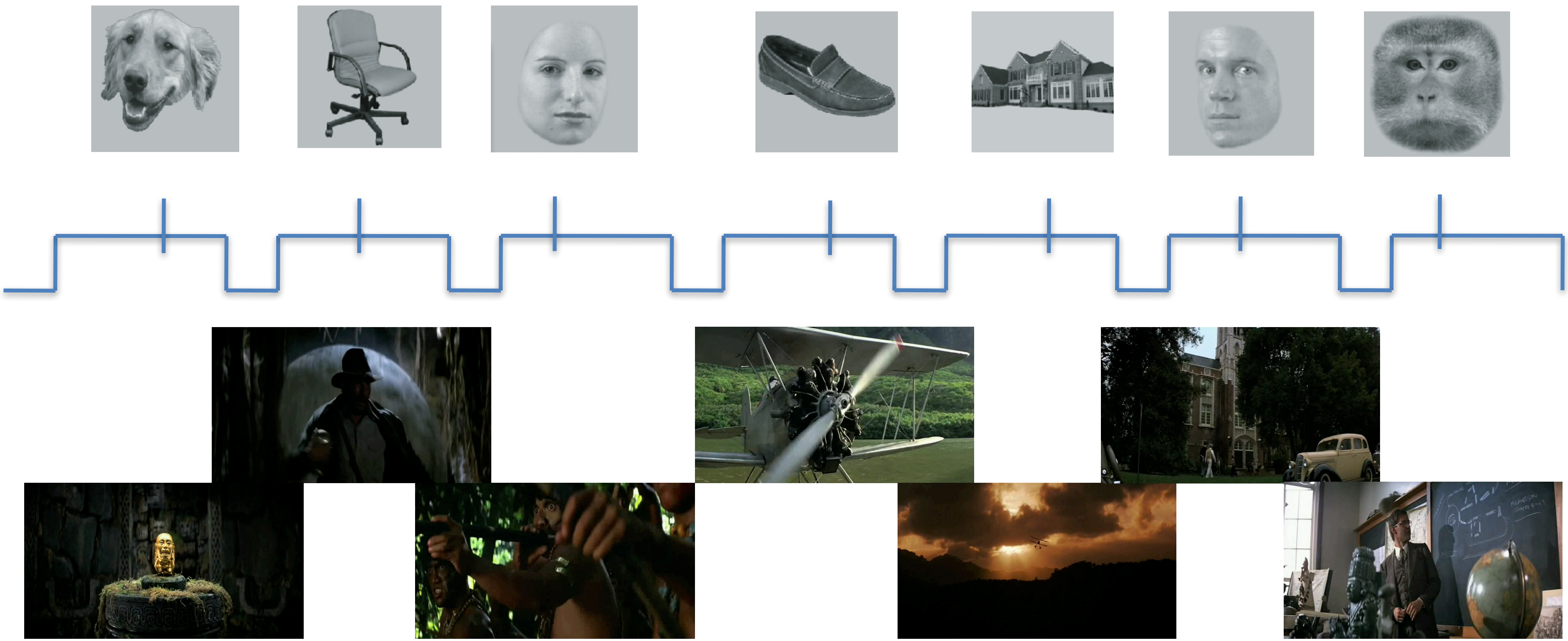


Why the movie?

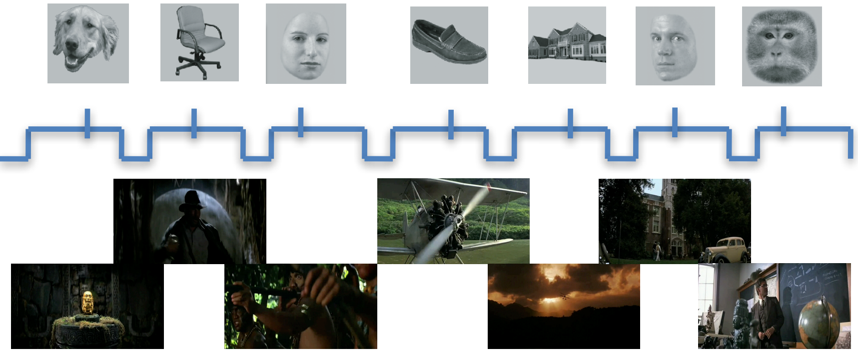
Does it add anything? *YES*

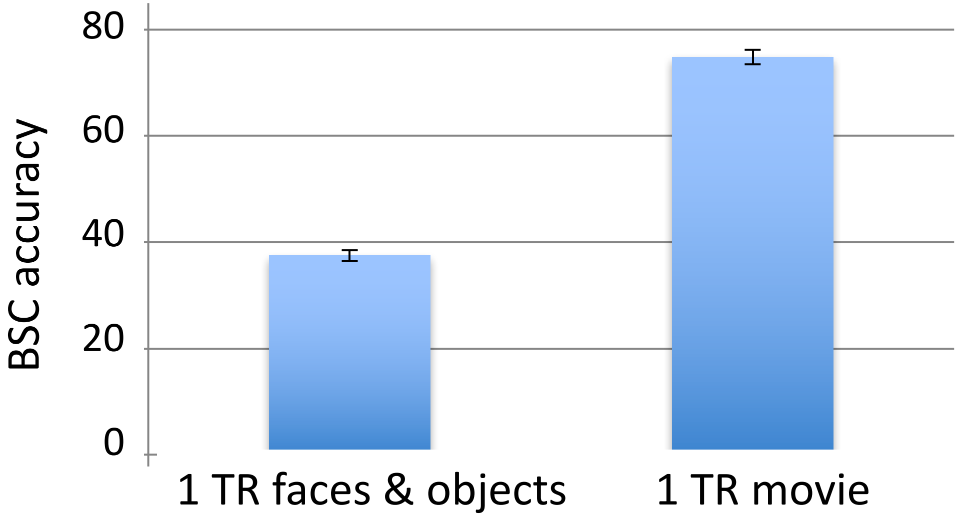
Hyperalignment based on the responses to face & object images or on the responses to animal species images works but has less general validity





Between-subject classification of single time-points from the movie vs single TRs from the faces and objects experiment





Between-subject classification of single time-points from the movie
vs single TRs from the faces and objects experiment:

<u>Movie stimuli evoke patterns of response that are more distinct</u>

Representational geometry captures information in patterns across time for the whole data set

Time-points	B	Voxels				
		v_1	v_2	v_3	…	v_l
	t_1	$x_{1,1}$	$x_{2,1}$	$x_{3,1}$	…	$x_{l,1}$
	t_2	$x_{1,2}$	$x_{2,2}$	$x_{3,2}$	…	$x_{l,2}$
	t_3	$x_{1,3}$	$x_{2,3}$	$x_{3,3}$	…	$x_{l,3}$
	t_4	$x_{1,4}$	$x_{2,4}$	$x_{3,4}$	…	$x_{l,4}$
	…	…	…	…		…
	t_j	$x_{1,j}$	$x_{2,j}$	$x_{3,j}$	…	$x_{l,j}$

Data matrix in voxel space
(*l* voxels x *j* time-points)

X

Voxels	R	Model dimensions				
		d_1	d_2	d_3	…	d_m
	v_1	$w_{1,1}$	$w_{2,1}$	$w_{3,1}$	…	$w_{m,1}$
	v_2	$w_{1,2}$	$w_{2,2}$	$w_{3,2}$	…	$w_{m,2}$
	v_3	$w_{1,3}$	$w_{2,3}$	$w_{3,3}$	…	$w_{m,3}$
	…	…	…	…		…
	v_l	$w_{1,l}$	$w_{2,l}$	$w_{3,l}$	…	$w_{m,l,}$

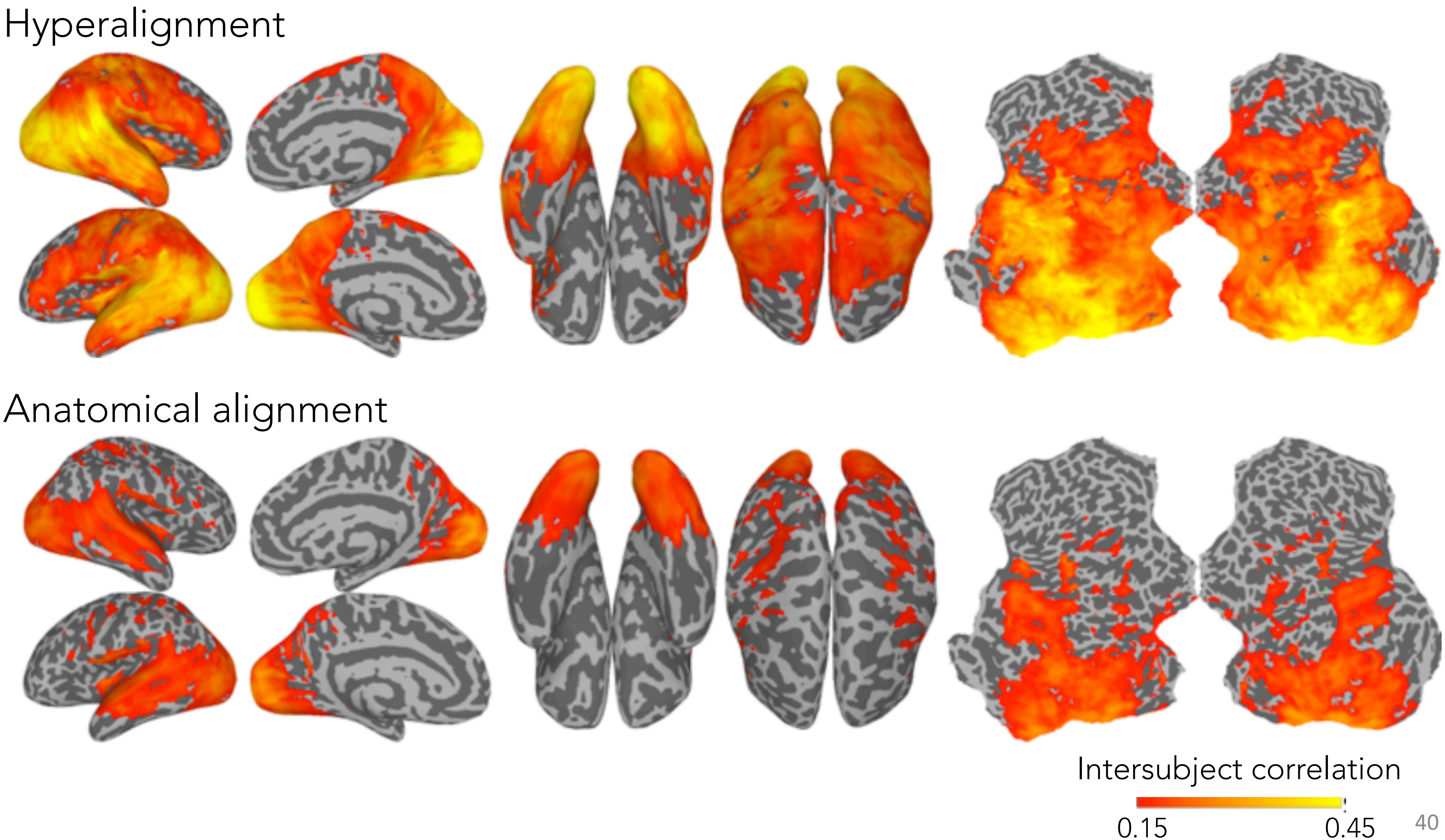
Transformation matrix
(*m* dimensions x *l* voxels)

=

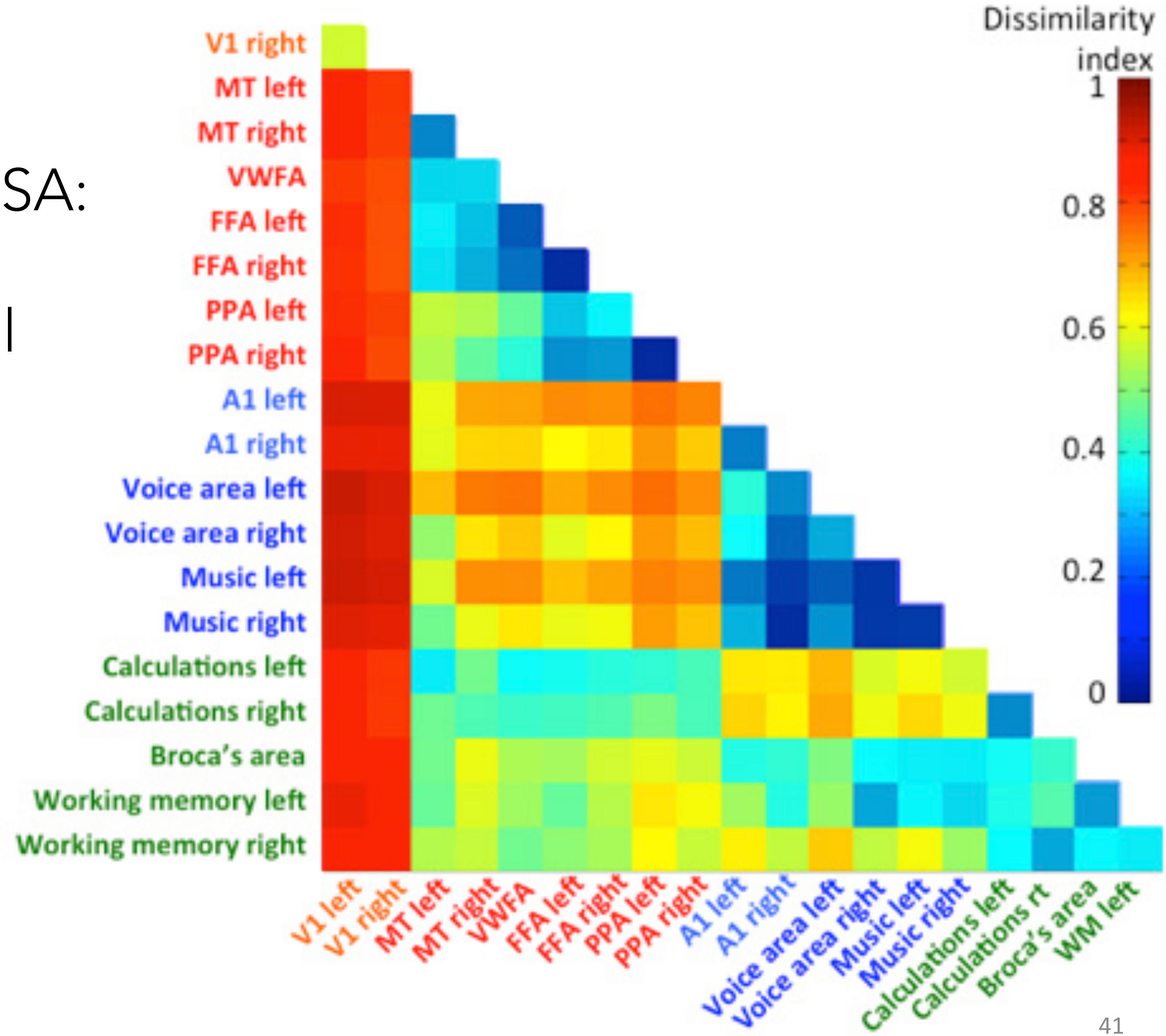
Time-points	M	Model dimensions				
		d_1	d_2	d_3	…	d_m
	t_1	$y_{1,1}$	$y_{2,1}$	$y_{3,1}$	…	$y_{m,1}$
	t_2	$y_{1,2}$	$y_{2,2}$	$y_{3,2}$	…	$y_{m,2}$
	t_3	$y_{1,3}$	$y_{2,3}$	$y_{3,3}$	…	$y_{m,3}$
	t_4	$y_{1,4}$	$y_{2,4}$	$y_{3,4}$	…	$y_{m,4}$
	…	…	…	…		…
	T_j	$y_{1,j}$	$y_{2,j}$	$y_{3,j}$	…	$y_{m,j}$

Data matrix in model space
(*m* dimensions x *j* time-points)

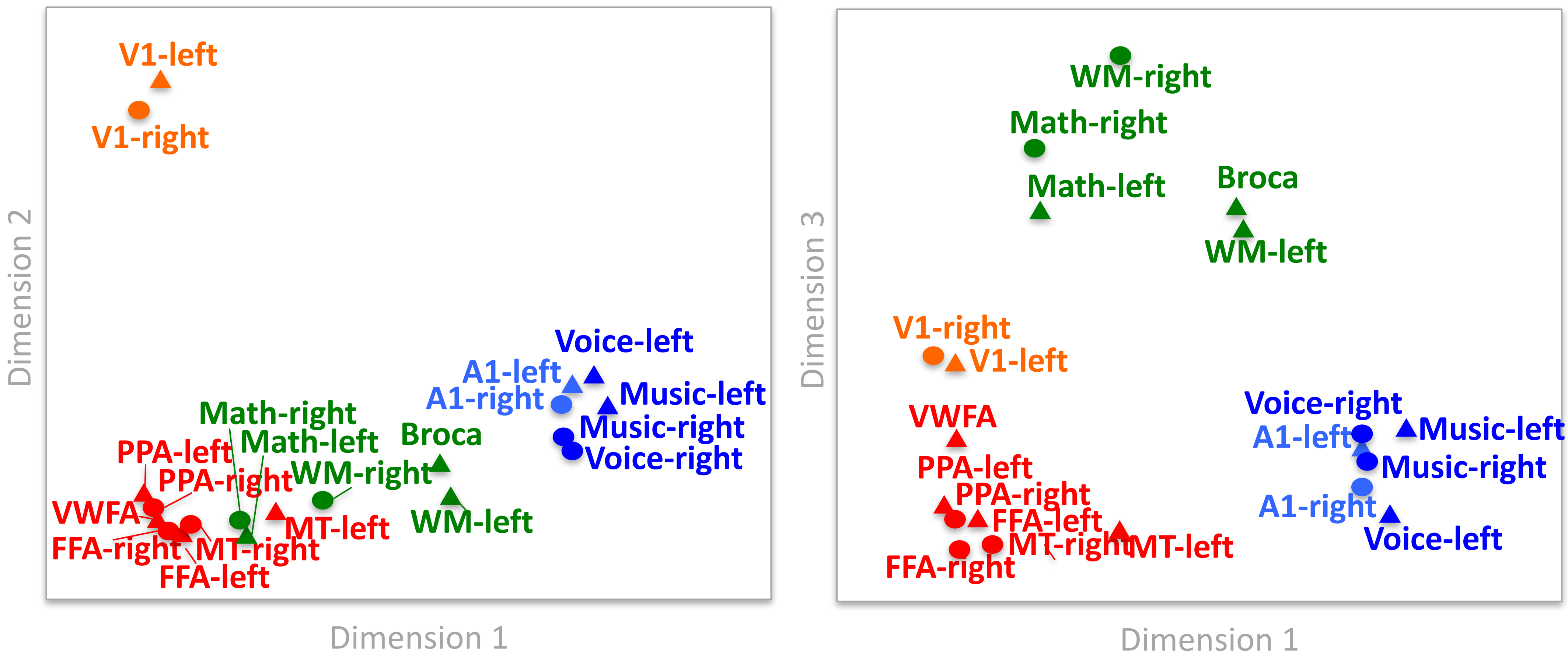
Whole-brain hyperalignment increases intersubject correlation of high-dimensional representational geometries (correlations between movie time-points)



Second-order RSA: Between-ROI representational geometry dissimilarities



Multidimensional scaling (MDS) of similarity structures in visual, auditory, and cognitive regions of interest* (ROIs)

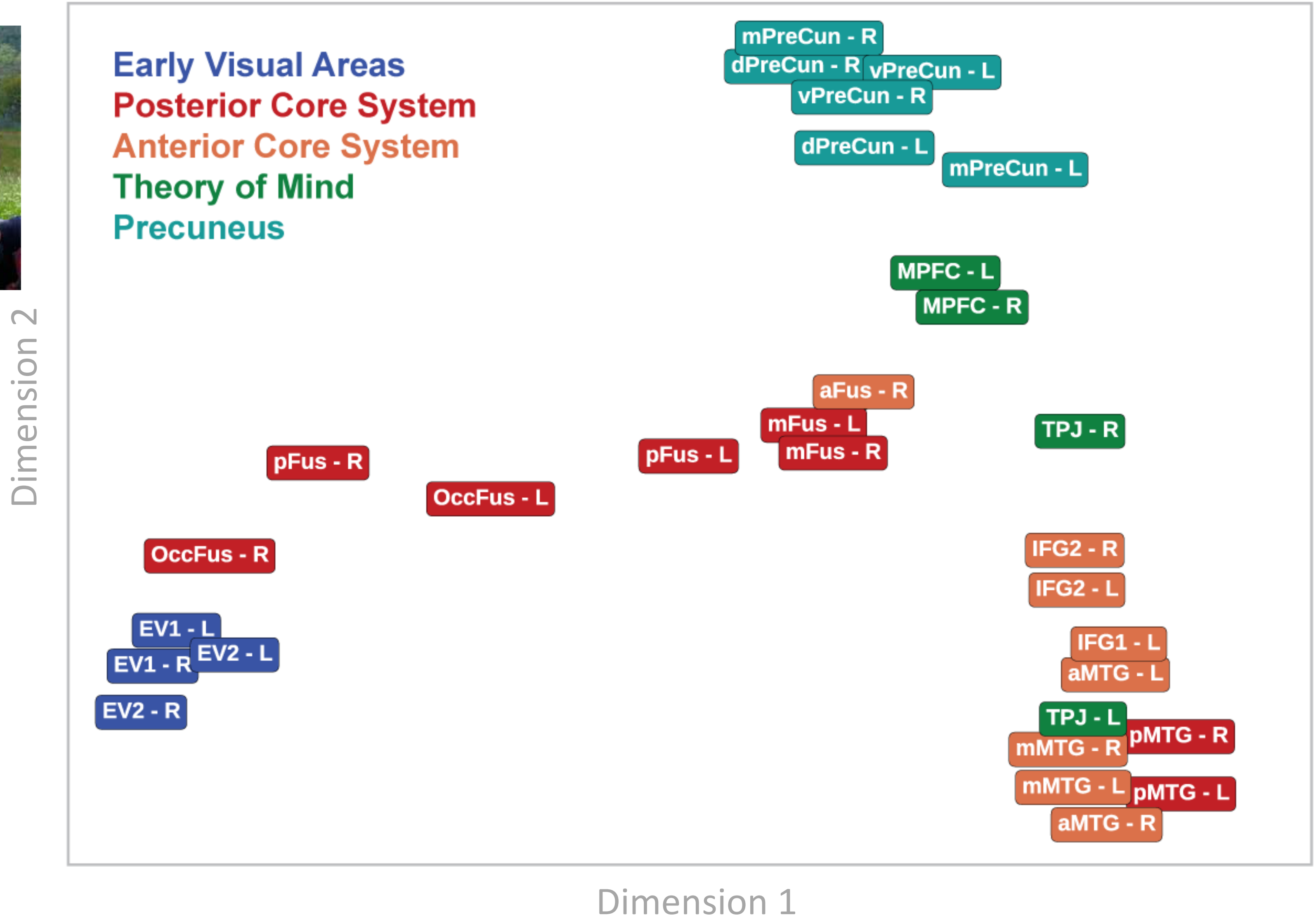


1st subspace (dimensions 1 & 2) | 2nd subspace (dimensions 1 & 3)

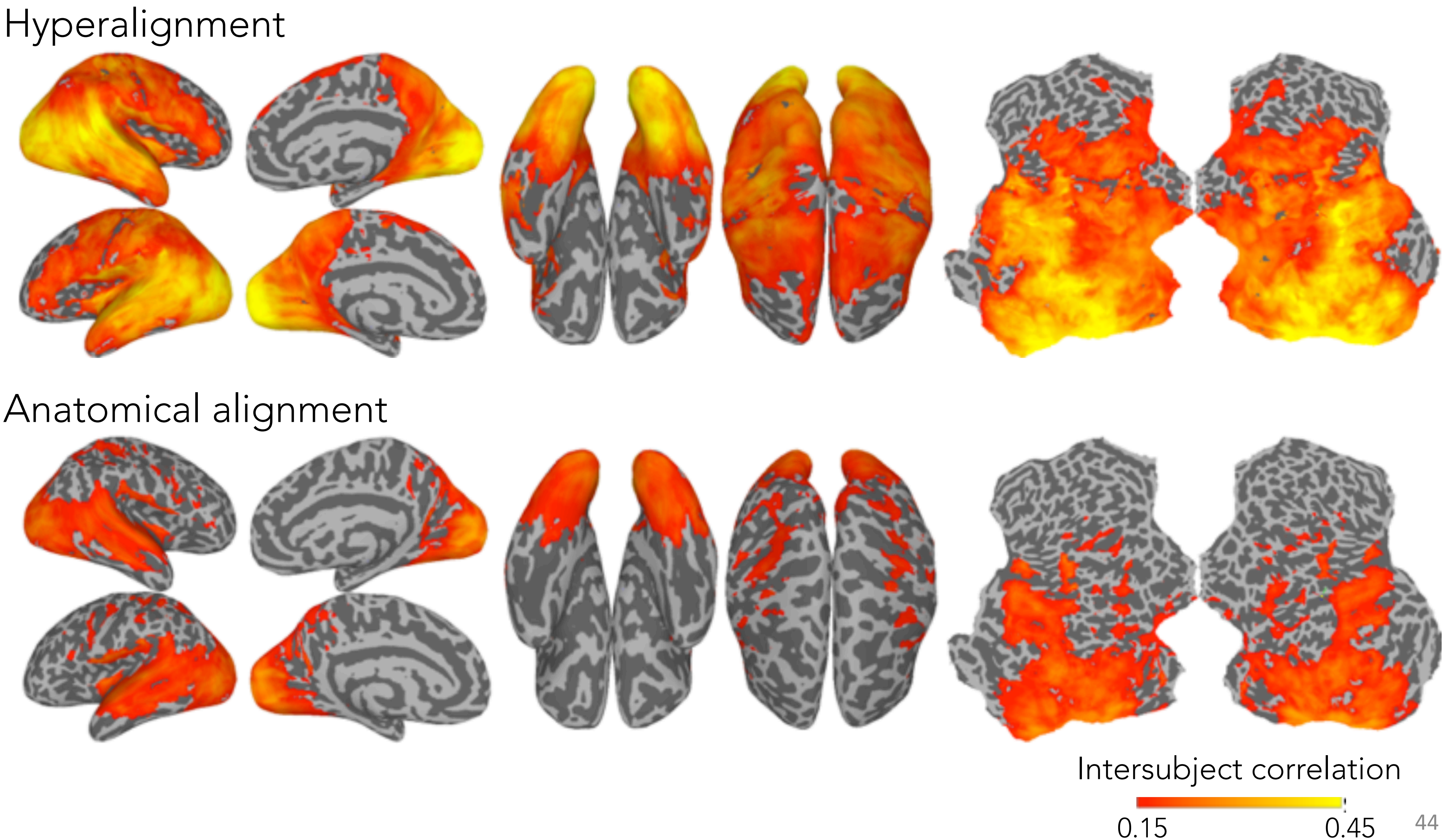
* ROI coordinates from Neurosynth

Multidimensional scaling (MDS) of regions in the face processing system

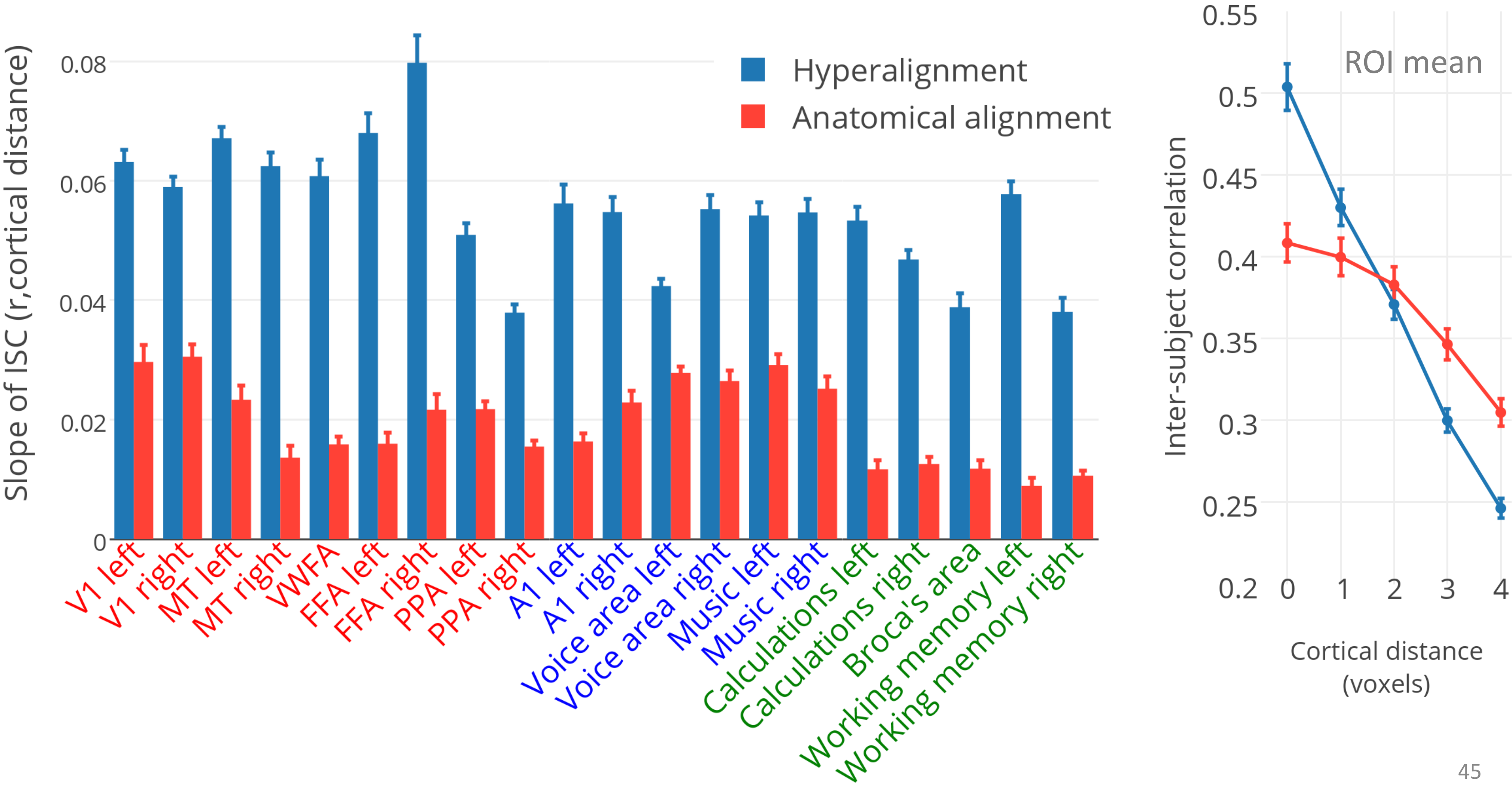
(Visconti di Oleggio Castello, Halchenko, …, Gobbini, 2017)



Whole-brain hyperalignment increases intersubject correlation of high-dimensional representational geometries *that reflect widely divergent domains of information*



Point spread function (intersubject correlations of movie time series): Fine spatial scale of alignment of local variation in response tunings



A common high-dimensional linear model of representational spaces in human cortex

- Statement of the problem: capturing coarse- and fine-grained topographies in a common model
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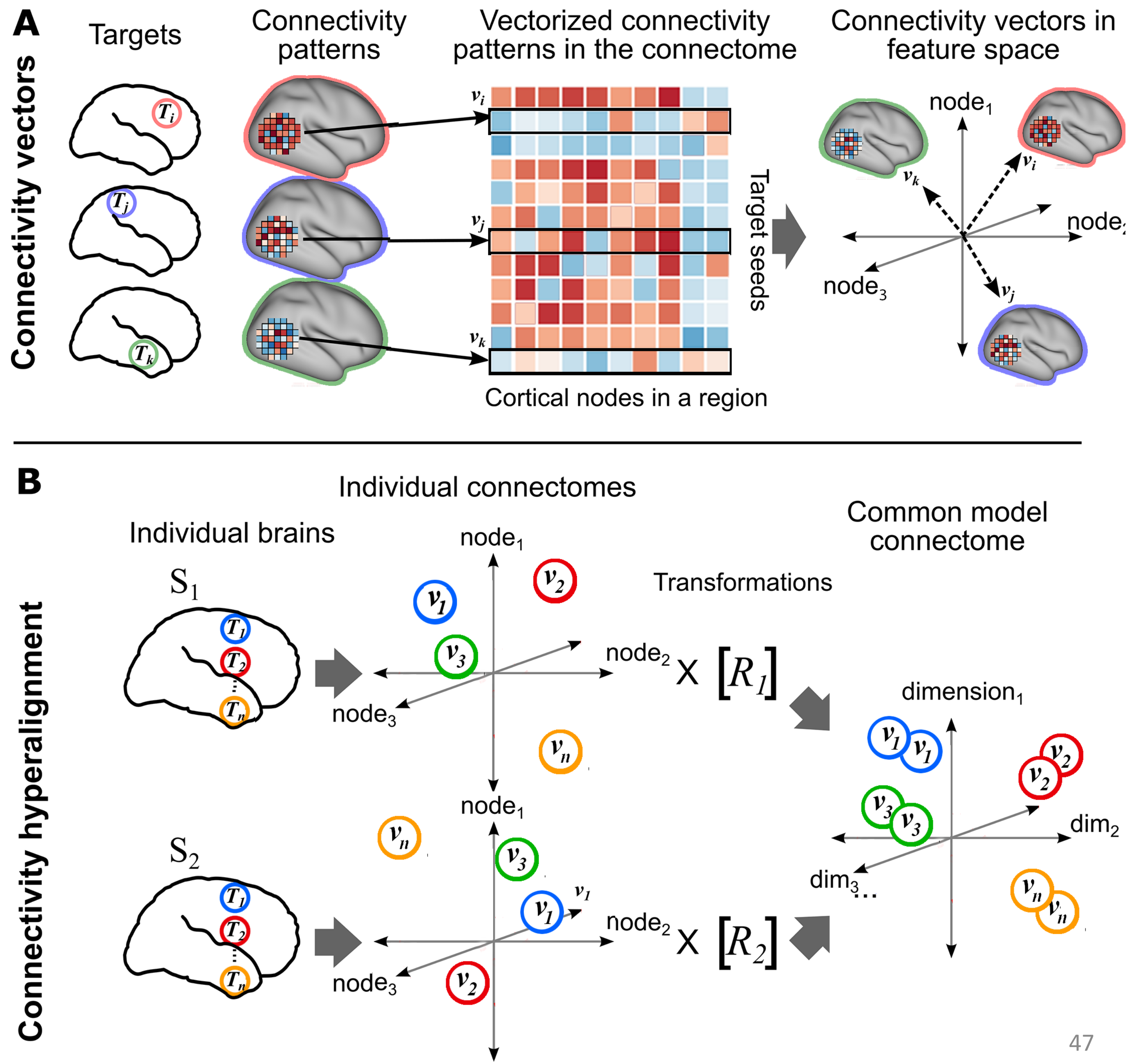
Connectivity hyperalignment



Connectivity data in subject brain voxel data (B_s)

Voxels

B	v_1	v_2	v_3	…	v_l
t_1	$x_{1,1}$	$x_{2,1}$	$x_{3,1}$	…	$x_{l,1}$
t_2	$x_{1,2}$	$x_{2,2}$	$x_{3,2}$	…	$x_{l,2}$
t_3	$x_{1,3}$	$x_{2,3}$	$x_{3,3}$	…	$x_{l,3}$
t_4	$x_{1,4}$	$x_{2,4}$	$x_{3,4}$	…	$x_{l,4}$
…	…	…	…		…
t_j	$x_{1,j}$	$x_{2,j}$	$x_{3,j}$	…	$x_{l,j}$

Connectivity targets

Pattern of connectivities to one target (t_2) across voxels

X

Model dimensions

T					
v_1	$w_{1,1}$	$w_{2,1}$	$w_{3,1}$	…	$w_{m,1}$
v_2	$w_{1,2}$	$w_{2,2}$	$w_{3,2}$	…	$w_{m,2}$
v_3	$w_{1,3}$	$w_{2,3}$	$w_{3,3}$	…	$w_{m,3}$
…	…	…	…		…
v_l	$w_{1,l}$	$w_{2,l}$	$w_{3,l}$	…	$w_{m,l}$

Voxels

=

Model dimensions

M				…	d_m
t_1	$y_{1,1}$	$y_{2,1}$	$y_{3,1}$	…	$y_{m,1}$
t_2	$y_{1,2}$	$y_{2,2}$	$y_{3,2}$	…	$y_{m,2}$
t_3	$y_{1,3}$	$y_{2,3}$	$y_{3,3}$		$y_{m,3}$
t_4	$y_{1,4}$	$y_{2,4}$	$y_{3,4}$	…	$y_{m,4}$
…	…	…	…		…
T_j	$y_{1,j}$	$y_{2,j}$	$y_{3,j}$	…	$y_{m,j}$

Connectivity targets

Data matrix in voxel space
(l voxels x j time-points)

Transformation matrix
(m dimensions x l voxels)

Data matrix in model space
(m dimensions x j time-points)

Connectivity data in subject brain voxel data (B_s)

Connectivity profile for one voxel (v_3)

Pattern of connectivities to one target (t_2) across voxels

Voxels

B	v_1	v_2	v_3	…	v_l
t_1	$x_{1,1}$	$x_{2,1}$	$x_{3,1}$	…	$x_{l,1}$
t_2	$x_{1,2}$	$x_{2,2}$	$x_{3,2}$	…	$x_{l,2}$
t_3	$x_{1,3}$	$x_{2,3}$	$x_{3,3}$	…	$x_{l,3}$
t_4	$x_{1,4}$	$x_{2,4}$	$x_{3,4}$	…	$x_{l,4}$
…	…	…	…		…
t_j	$x_{1,j}$	$x_{2,j}$	$x_{3,j}$	…	$x_{l,j}$

Connectivity targets

Data matrix in voxel space
(*l* voxels x *j* time-points)

X

Model dimensions

v_1	$w_{1,1}$	$w_{2,1}$	$w_{3,1}$	…	$w_{m,1}$
v_2	$w_{1,2}$	$w_{2,2}$	$w_{3,2}$	…	$w_{m,2}$
v_3	$w_{1,3}$	$w_{2,3}$	$w_{3,3}$	…	$w_{m,3}$
…	…	…	…		…
v_l	$w_{1,l}$	$w_{2,l}$	$w_{3,l}$	…	$w_{m,l}$

Voxels

Transformation matrix
(*m* dimensions x *l* voxels)

=

Model dimensions

					d_m
t_1	$y_{1,1}$	$y_{2,1}$	$y_{3,1}$	…	$y_{m,1}$
t_2	$y_{1,2}$	$y_{2,2}$	$y_{3,2}$	…	$y_{m,2}$
t_3	$y_{1,3}$	$y_{2,3}$	$y_{3,3}$	…	$y_{m,3}$
t_4	$y_{1,4}$	$y_{2,4}$	$y_{3,4}$	…	$y_{m,4}$
…	…	…	…		…
T_j	$y_{1,j}$	$y_{2,j}$	$y_{3,j}$	…	$y_{m,j}$

Connectivity targets

Data matrix in model space
(*m* dimensions x *j* time-points)

Deriving response tuning profiles for model space (M_s) dimensions (d_i)

Functional connectivity profile across targets for one model dimension (d_2)

Voxels (columns) / **Connectivity targets** (rows)

B	v_1	v_2	v_3	…	v_l
t_1	$x_{1,1}$	$x_{2,1}$	$x_{3,1}$	…	$x_{l,1}$
t_2	$x_{1,2}$	$x_{2,2}$	$x_{3,2}$	…	$x_{l,2}$
t_3	$x_{1,3}$	$x_{2,3}$	$x_{3,3}$	…	$x_{l,3}$
t_4	$x_{1,4}$	$x_{2,4}$	$x_{3,4}$	…	$x_{l,4}$
…	…	…	…		…
t_j	$x_{1,j}$	$x_{2,j}$	$x_{3,j}$	…	$x_{l,j}$

Data matrix in voxel space
(*l* voxels x *j* time-points)

X

Model dimensions (columns) / **Voxels** (rows)

R	d_1	d_2	d_3	…	d_m
v_1	$w_{1,1}$	$w_{2,1}$	$w_{3,1}$	…	$w_{m,1}$
v_2	$w_{1,2}$	$w_{2,2}$	$w_{3,2}$	…	$w_{m,2}$
v_3	$w_{1,3}$	$w_{2,3}$	$w_{3,3}$	…	$w_{m,3}$
…	…	…	…		…
v_l	$w_{1,l}$	$w_{2,l}$	$w_{3,l}$	…	$w_{m,l,}$

Transformation matrix
(*m* dimensions x *l* voxels)

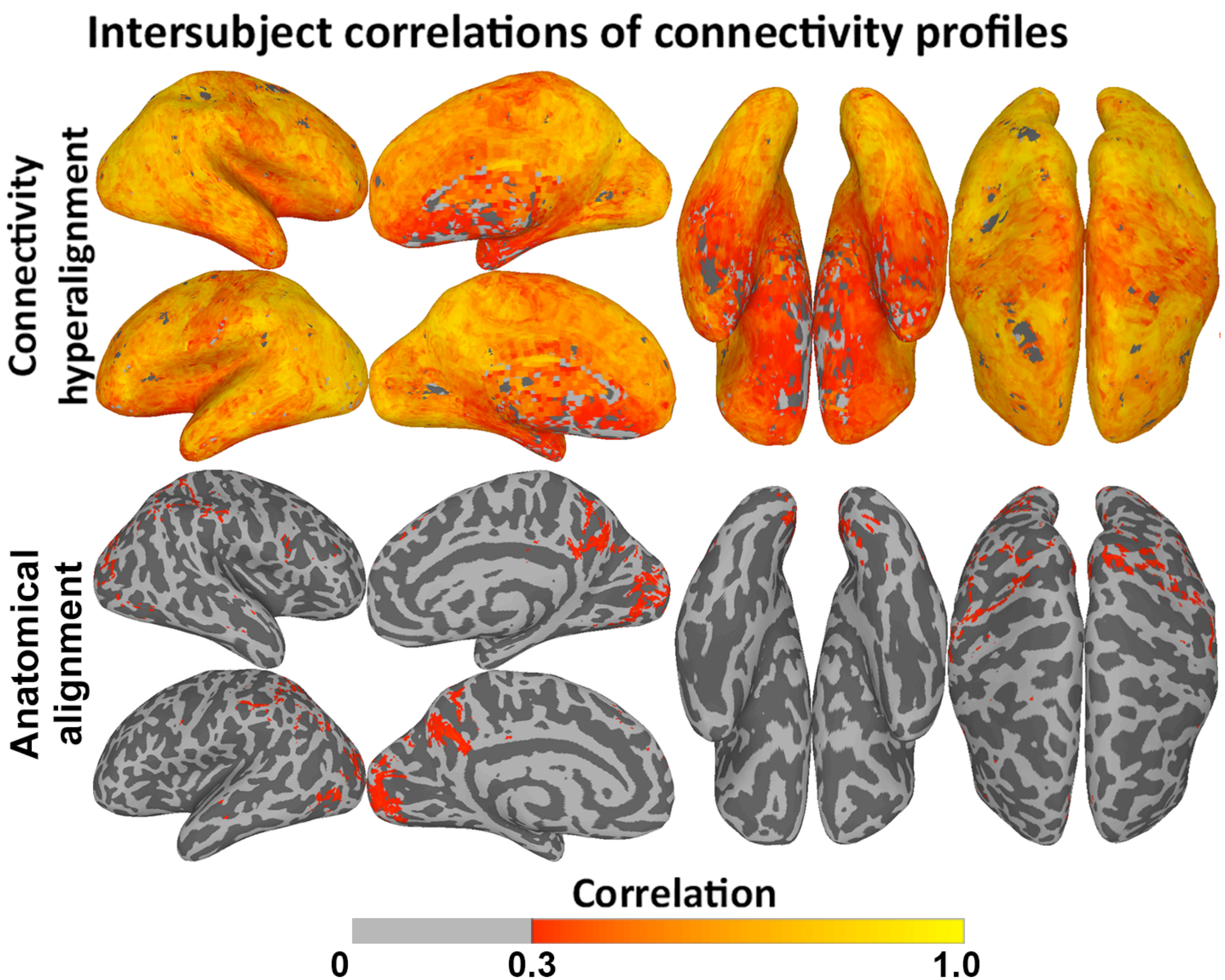
=

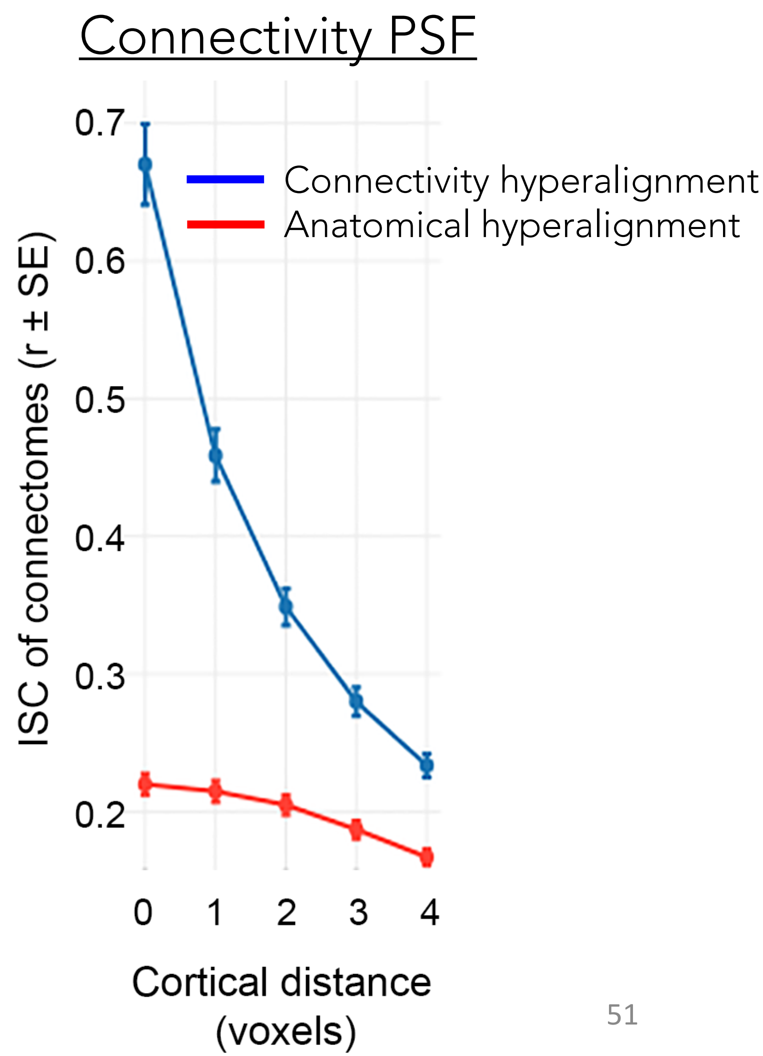
Model dimensions (columns) / **Connectivity targets** (rows)

M	d_1	d_2	d_3	…	d_m
t_1	$y_{1,1}$	$y_{2,1}$	$y_{3,1}$	…	$y_{m,1}$
t_2	$y_{1,2}$	$y_{2,2}$	$y_{3,2}$	…	$y_{m,2}$
t_3	$y_{1,3}$	$y_{2,3}$	$y_{3,3}$	…	$y_{m,3}$
t_4	$y_{1,4}$	$y_{2,4}$	$y_{3,4}$	…	$y_{m,4}$
…	…	…	…		…
T_j	$y_{1,j}$	$y_{2,j}$	$y_{3,j}$	…	$y_{m,j}$

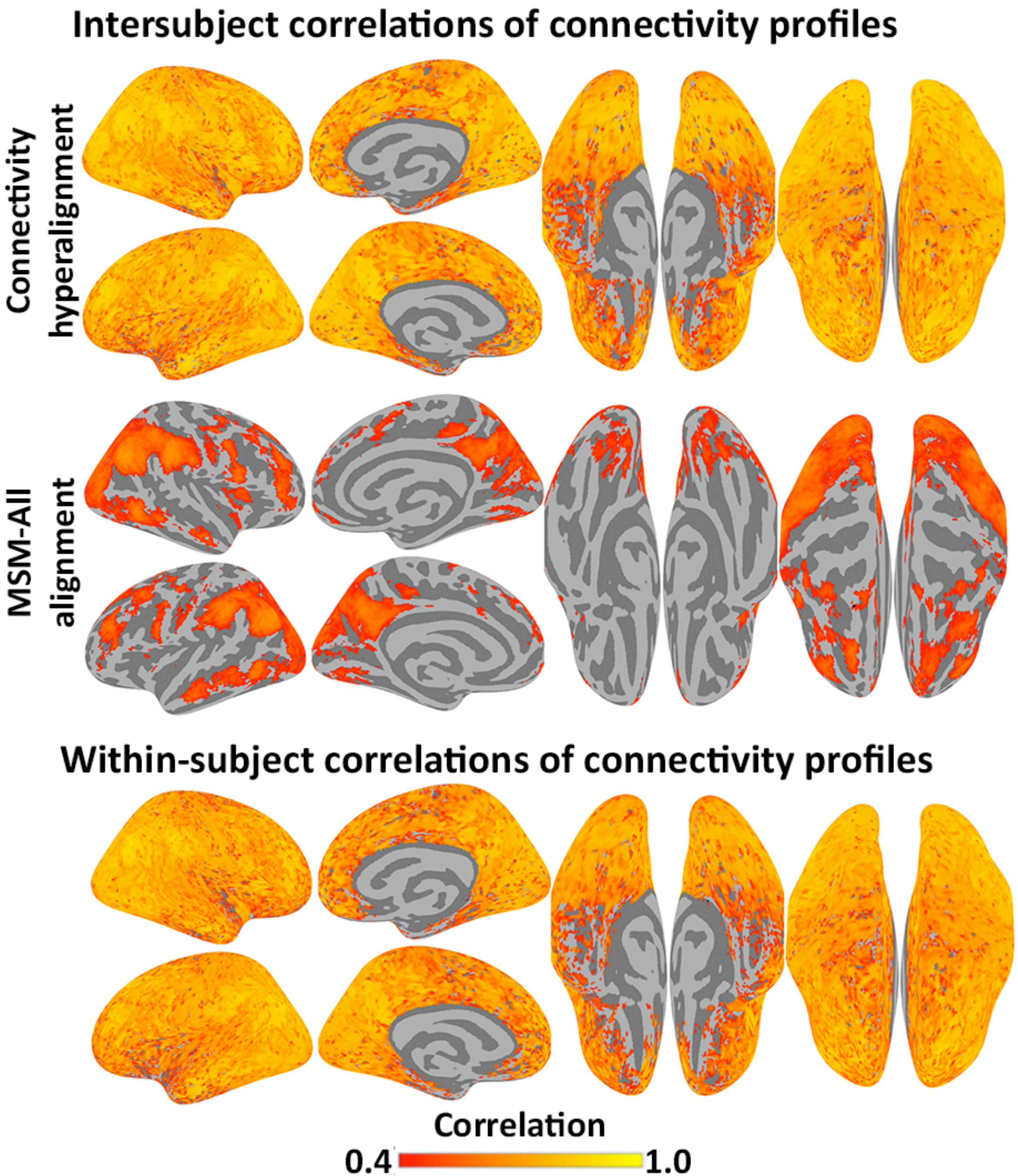
Data matrix in model space
(*m* dimensions x *j* time-points)

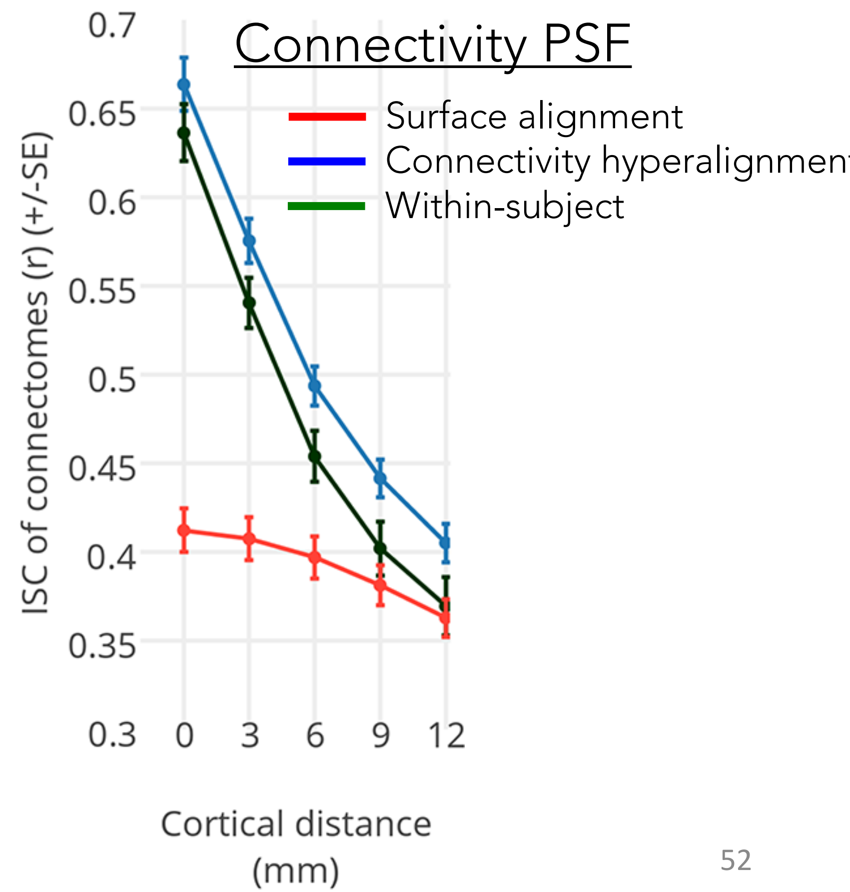
Connectivity hyperalignment of movie fMRI data increases ISC of connectivity vectors and reveals a fine-scale architecture





Connectivity hyperalignment of Human Connectome Project (HCP) resting state fMRI data (N=20) increases ISC of connectivity vectors <u>and</u> reveals a fine-scale architecture





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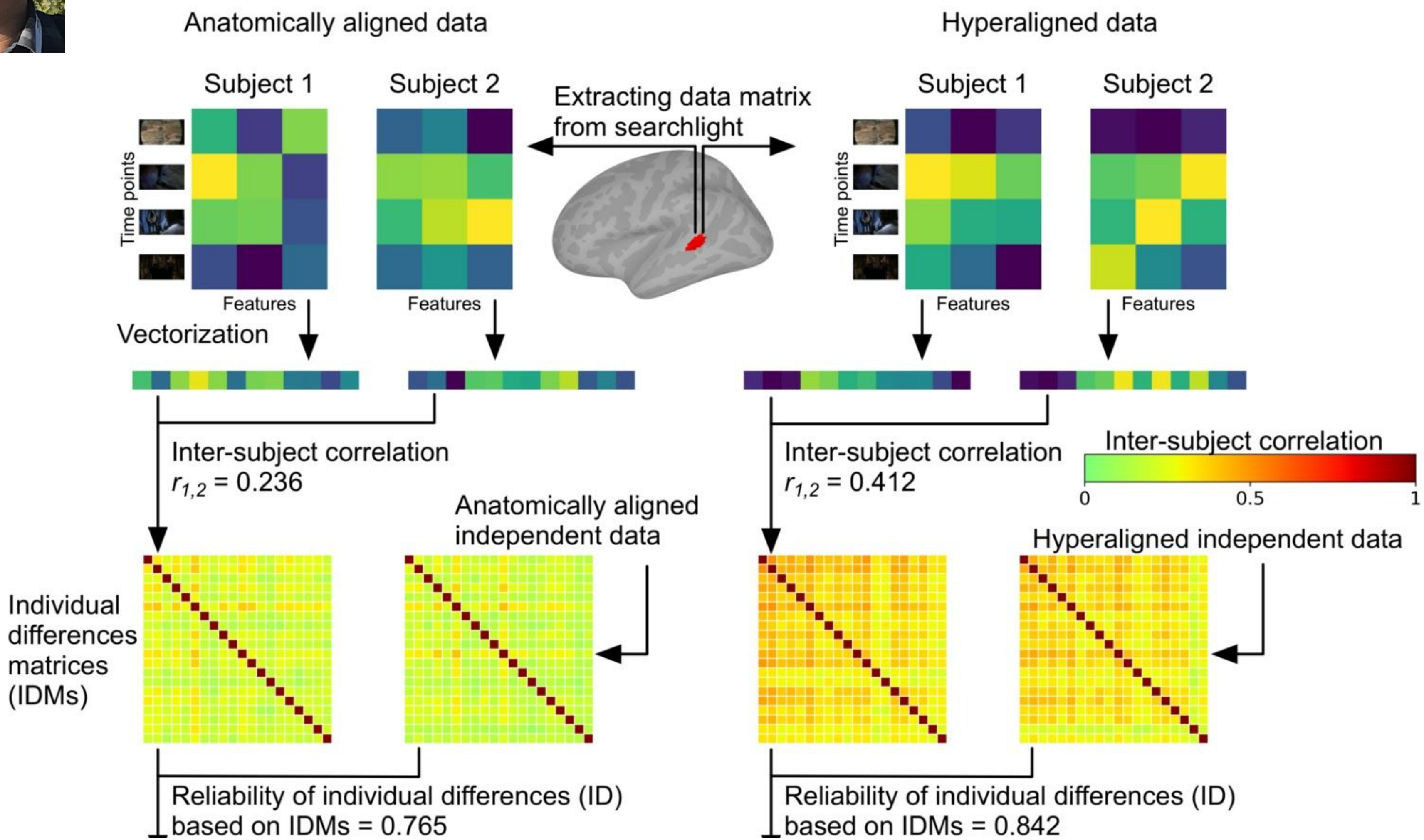
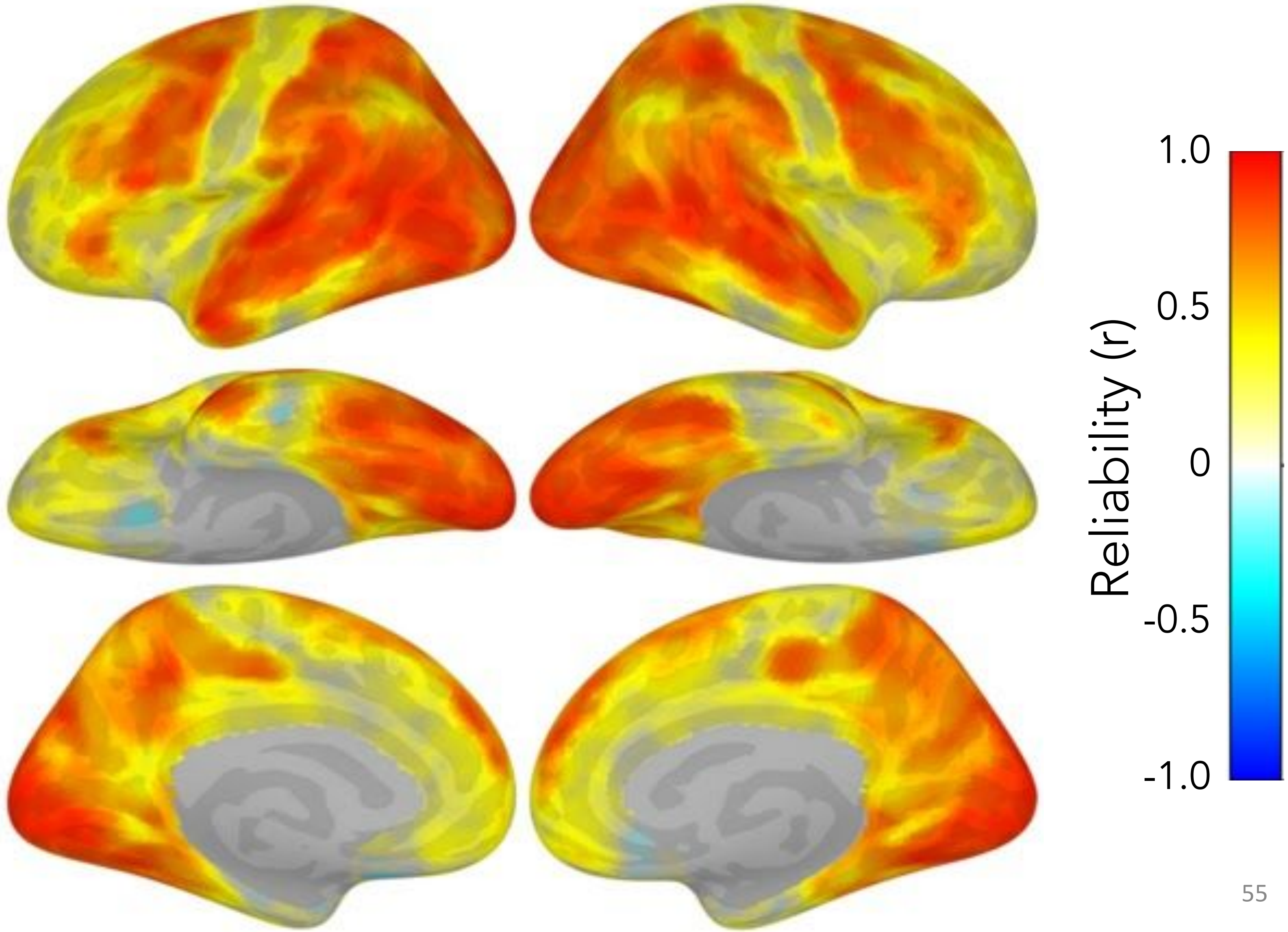
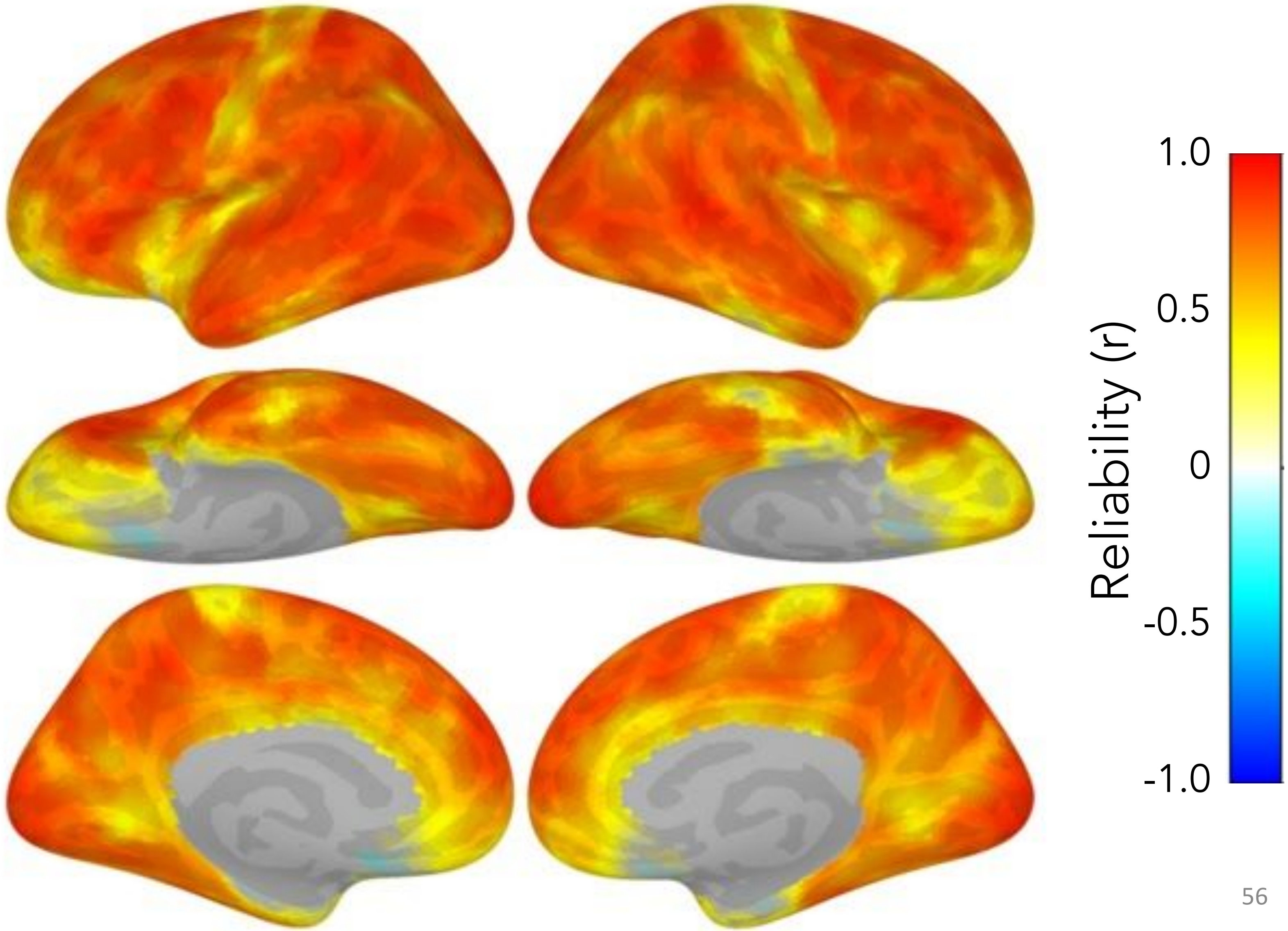
Individual differences dissimilarity matrix (IDM) (Feilong M, 2018)



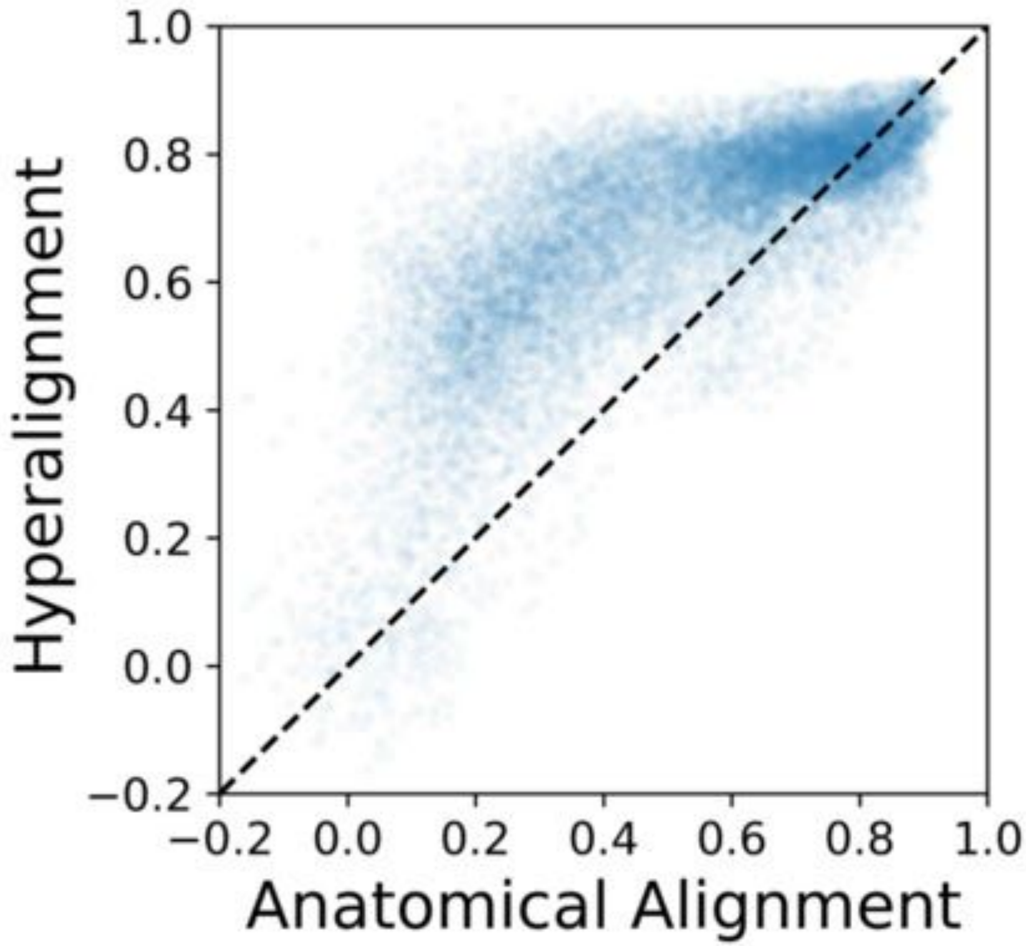
Reliability of IDMs
(anatomical alignment)



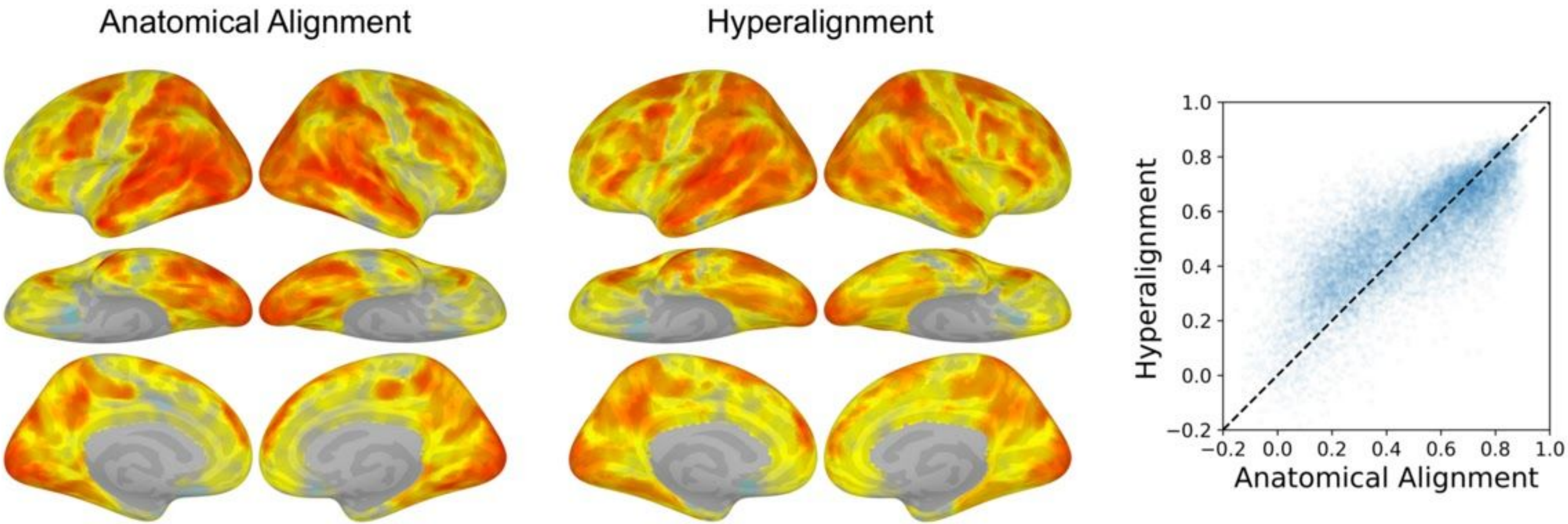
Reliability of IDMs (hyperaligned common model space)



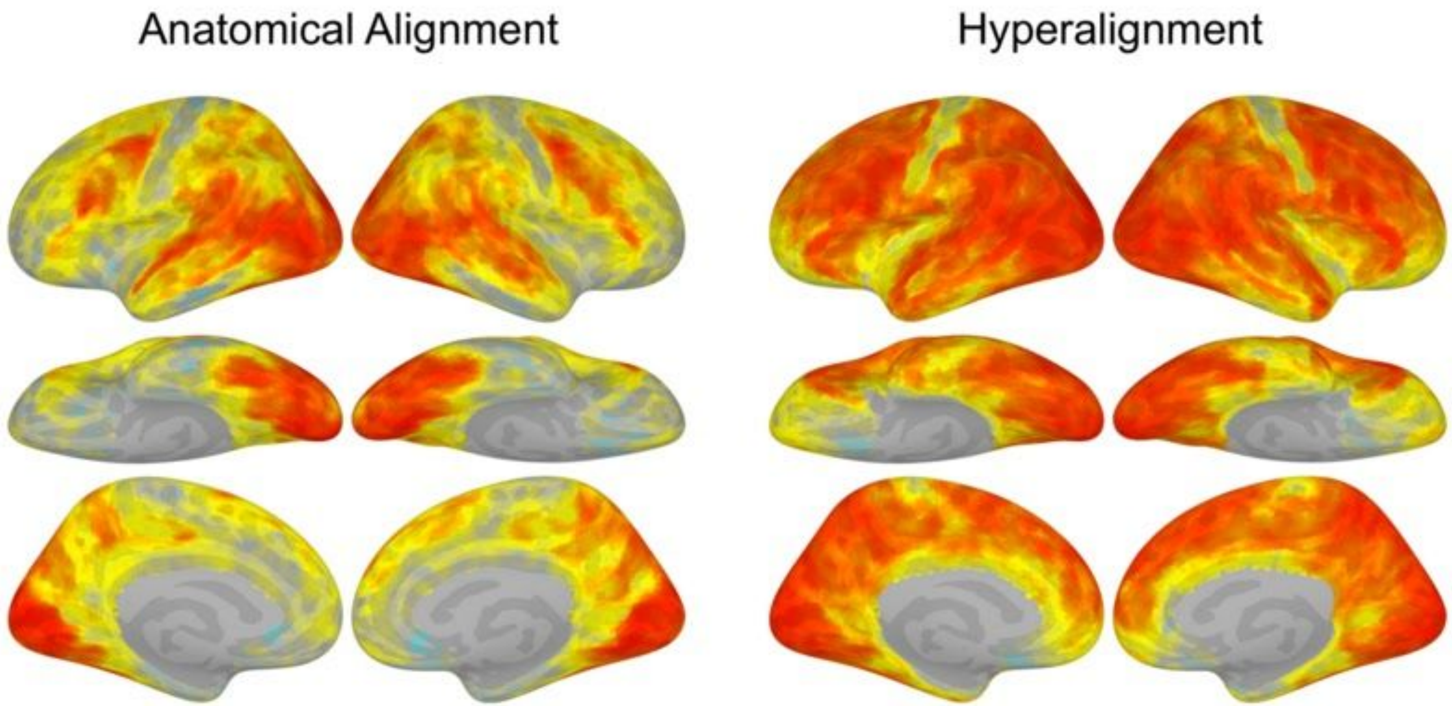
Reliability of IDMs

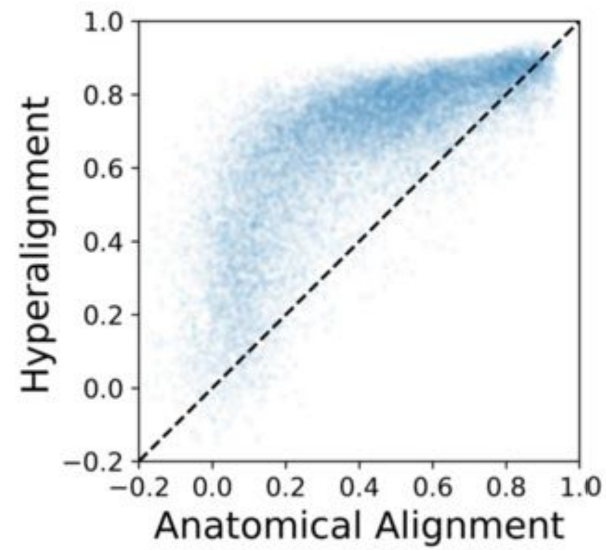


Reliability of coarse-scale IDMs
(based on searchlight mean time-series)

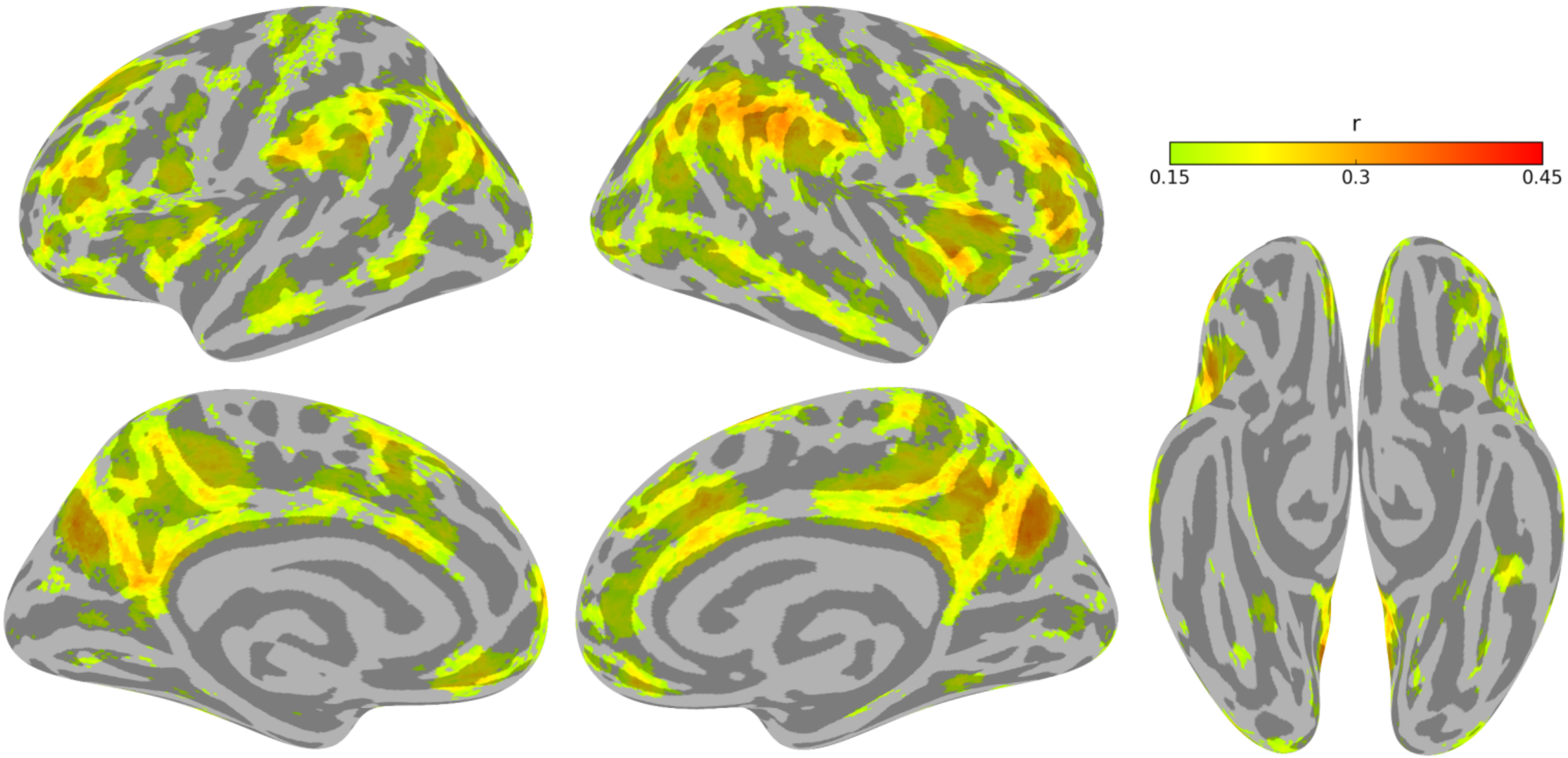


Reliability of fine-scale IDMs
(based on residual time-series after removing searchlight mean)

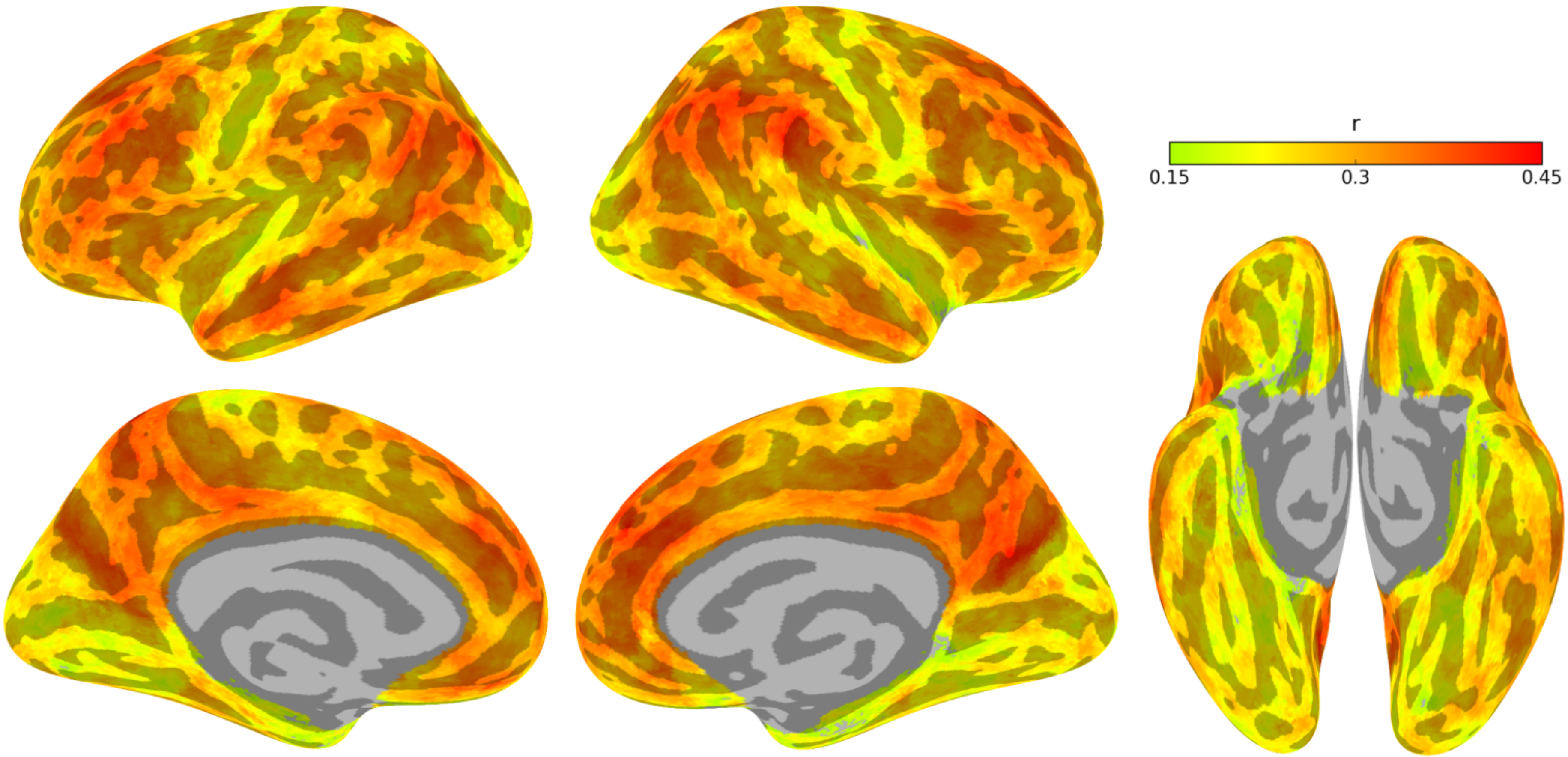




Correlation of functional connectivity IDs with verbal ability (picture vocabulary) (anatomical alignment)



Correlation of functional connectivity IDs with verbal ability (picture vocabulary) (hyperaligned data)



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Common model: Basic components

- Common, high-dimensional representational/connectivity space
- Individual transformation matrices
- Algorithm for calculating transformation matrices and deriving the common model space (hyperalignment)

Common model dimensions

- Response tuning basis functions
  - Common across brains
  - Model population responses that carry fine distinctions
  - Capture variations with a fine spatial granularity
  - Valid for diverse domains of information
- Functional connectivity vectors
  - Common across brains
  - Capture variations with a fine spatial granularity
- Topographic basis functions
  - Individual specific
  - Model individual variations in functional topography with high fidelity

Fine-scale structure in cortical functional architecture: How big a factor is it?

The common model

- affords <u>7X higher bsMVPC accuracies</u>
- greatly increases ISCs of
  - response tuning profiles
  - local representational geometries
  - connectivity profiles

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  - local representational geometries
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Fine-scale structure is the "dark matter" of cortical functional architecture

The Common Model captures the shared information that is encoded in idiosyncratic fine-scale functional topographies

- Captures common bases for the fine-grained structure of local variations in response tuning and functional connectivity profiles

- There is no canonical brain
  - Each individual brain has idiosyncratic fine-scale topographies
  - The common model finds the shared deep structure of information that is encoded in idiosyncratic topographies

Individual differences in the Common Model capture how the representation of fine-scale information varies across brains

- Hyperalignment increases reliability of individual differences by capturing variation in the deep structure of information that is not accessible in anatomically aligned data.

- Individual differences in hyperaligned data better predict cognitive differences.

- The granularity of cortical architecture that underlies cognitive differences is matched better by the scale of fine-scale topographies, than by the coarse scale of systems of functional areas.

Software for hyperalignment and data are on PyMVPA (www.pymvpa.org)

Guntupalli et al. (2016) A model of representational spaces in human cortex. *Cerebral Cortex*.

Guntupalli & Haxby (2018) Computational model of shared fine-scale structure in the human connectome. *PLoS Computational Biology.*

Feilong, Nastase, Haxby (2018) Reliable individual differences in fine-grained cortical functional architecture. *bioRxiv.*