

A common model of representational spaces in human cortex:  
capturing common fine-scale architecture  
PRNI 2016

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Cognitive  
Neuroscience  
*at Dartmouth*

CiMeC

# Haxby Lab



Hyperalignment  
Swaroop Guntupalli  
Post-doctoral fellow



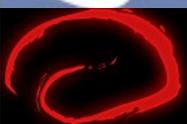
Attention  
Sam Nastase  
Graduate student



Action representation, computational methods  
Nick Oosterhof  
Post-doctoral fellow



Person perception  
Dylan Wagner  
Asst prof, Ohio State



NeuroDebian

Yaroslav Halchenko  
Research professor, software



Analysis of similarity structure,  
representation of biological classes  
Andy Connolly  
Research professor, ECoG

With help from



Peter Ramadge  
Electrical Engineering  
Princeton University

and EE grad students, past and present



Mert Rory Sabuncu  
now at MGH



Bryan Conroy  
Philips Research



Alex Lorbert  
Superfish, Israel



Hao Xu  
Google

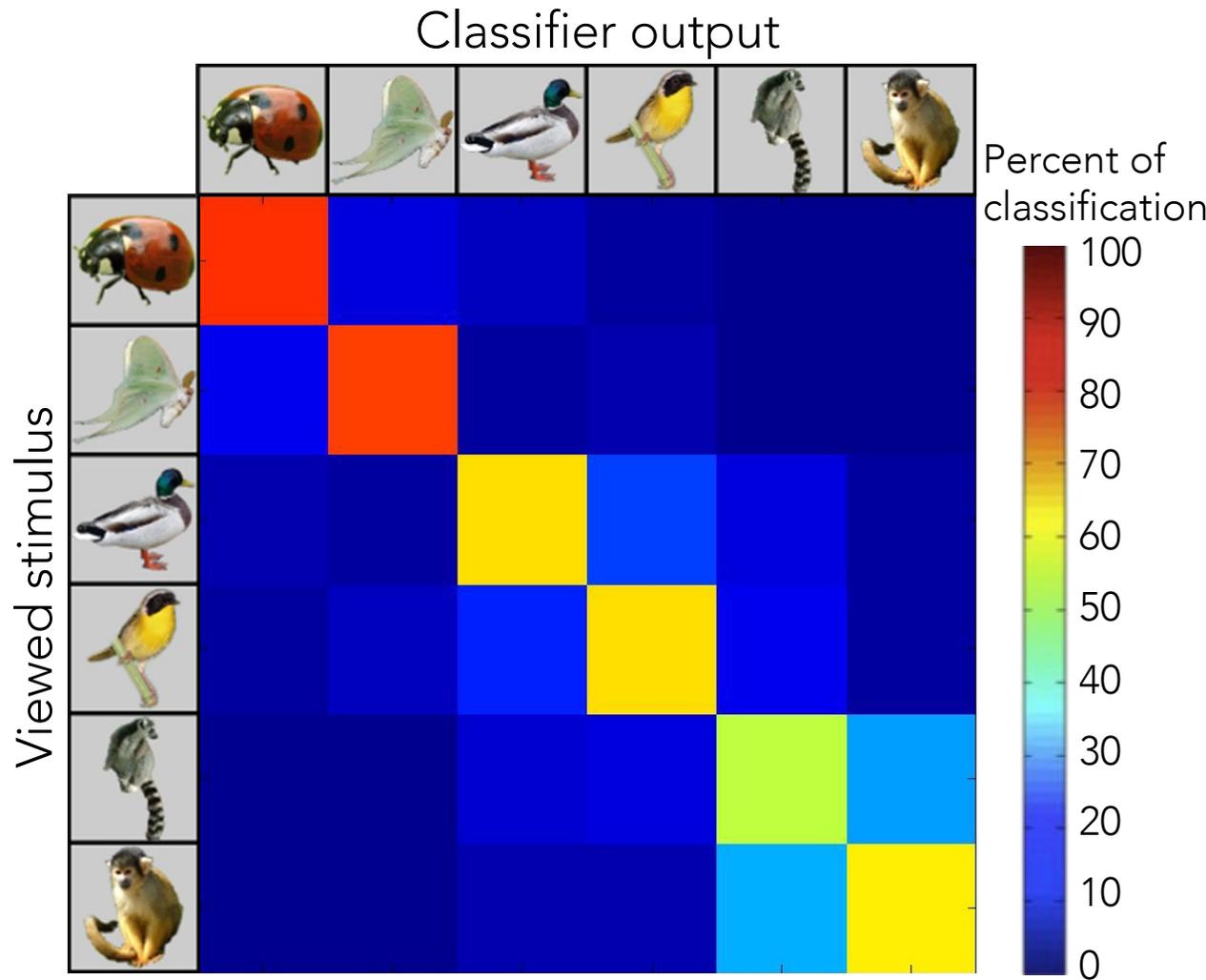
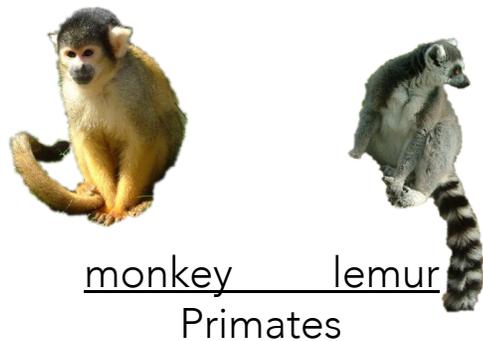
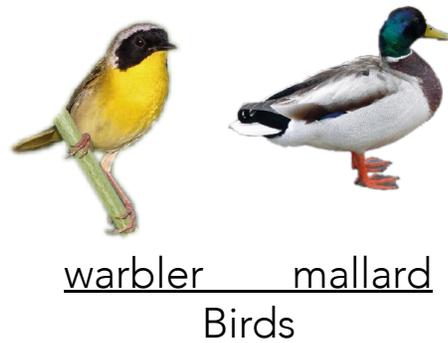
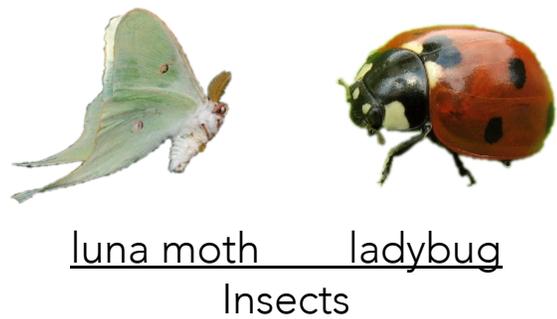


Cameron Chen  
current

# 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
- Conceptual framework: high-dimensional representational spaces
- Deriving the common space and individual transformation matrices with hyperalignment
- Validation
- Conclusions

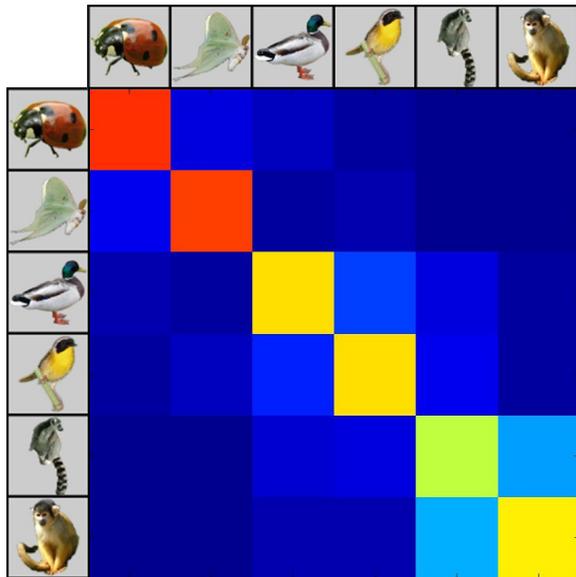
# Multivariate Pattern Classification Example: Classifying responses during viewing of animal species (VT cortex, SVM)



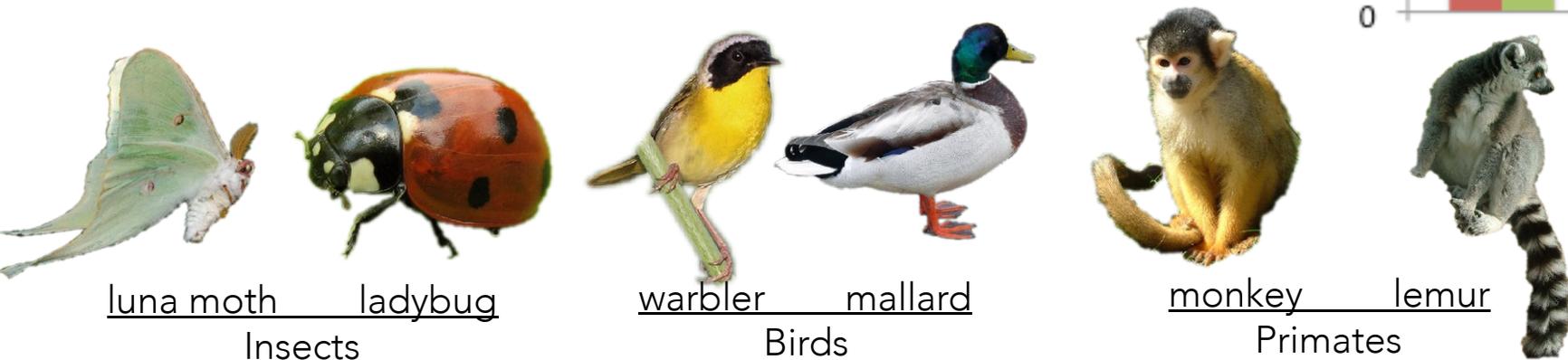
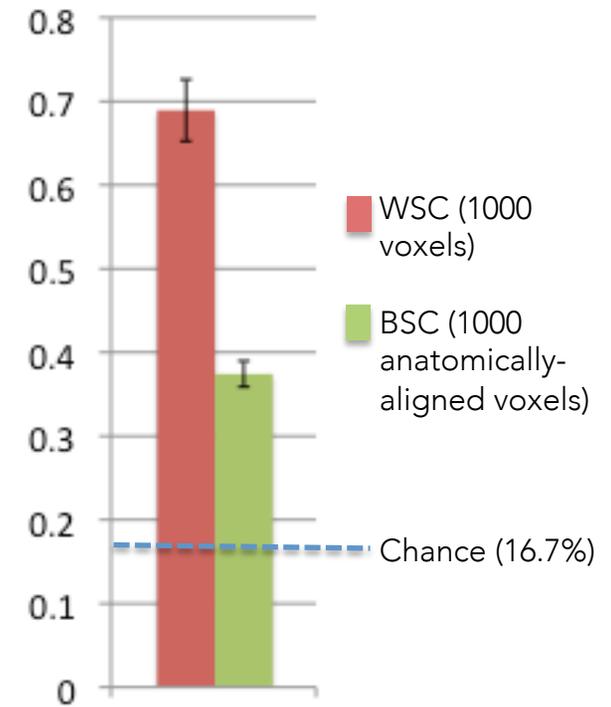
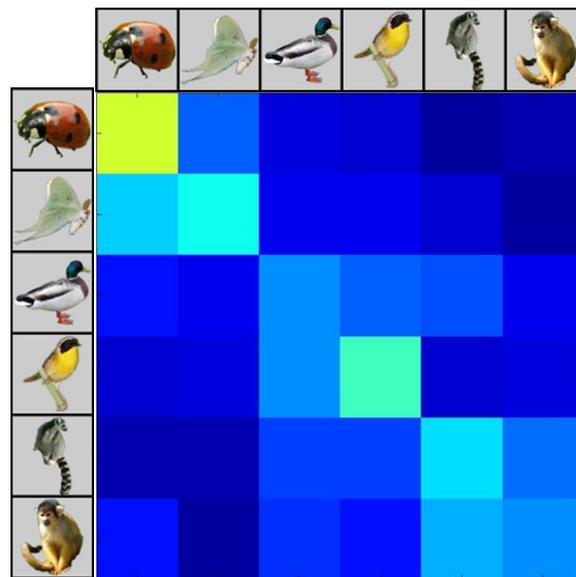
(Haxby et al. 2011; Connolly et al. 2012)

# 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)



Insects

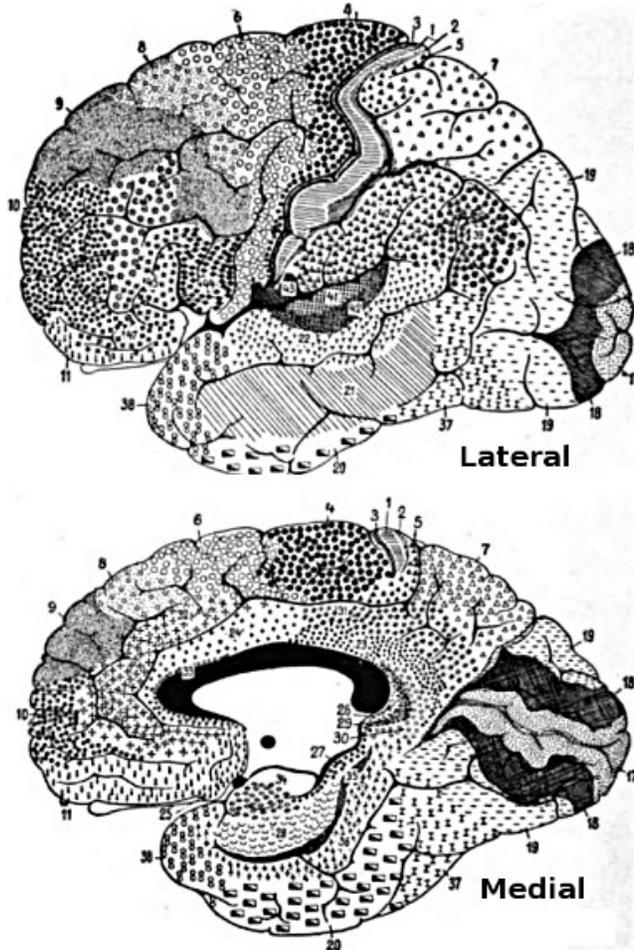
Birds

Primates

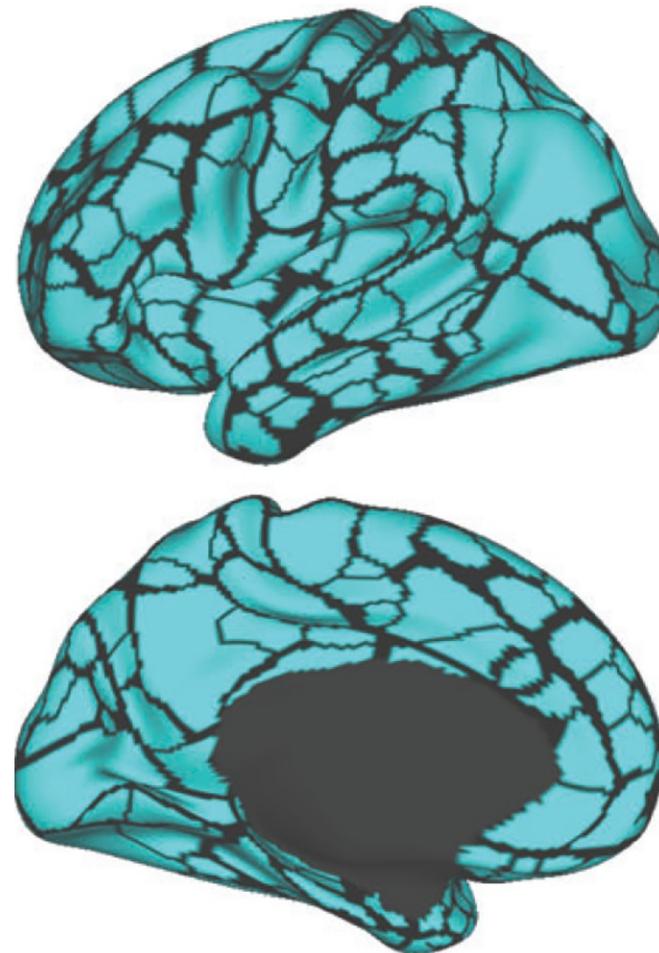
(Haxby et al. 2011; Connolly et al. 2012)

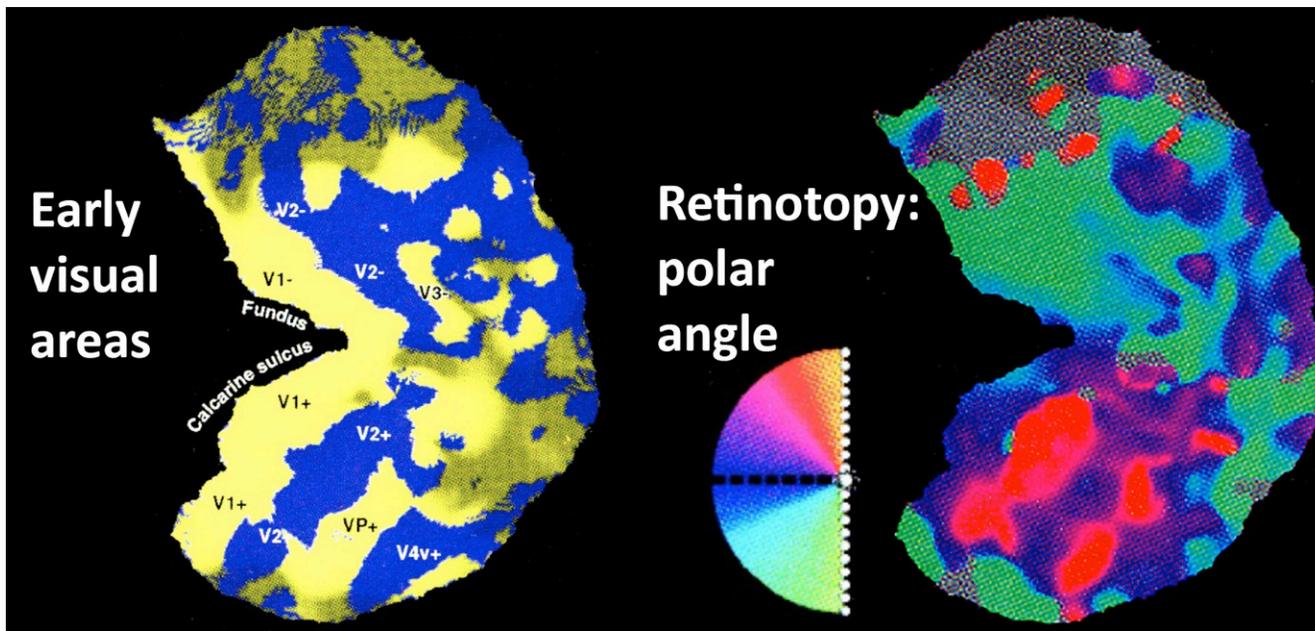
# Models of cortical architecture: parcellation of cortex into areas and systems

52 areas  
(Brodmann, 1909)



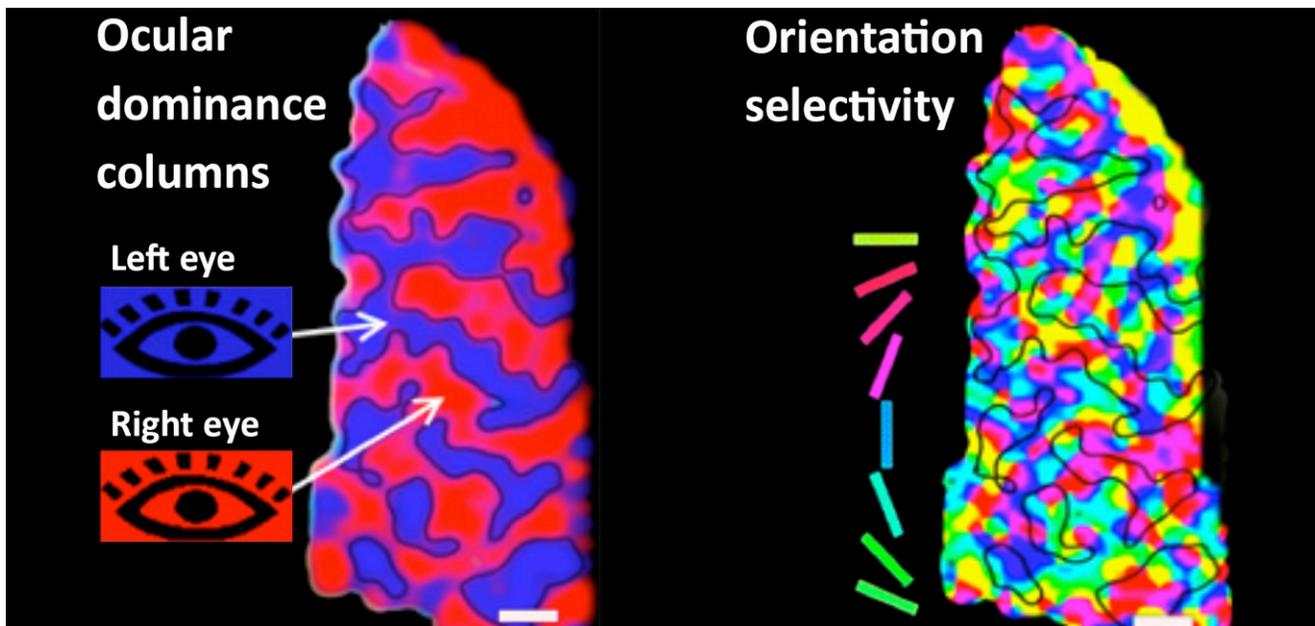
422 areas  
(Gordon et al. 2014)





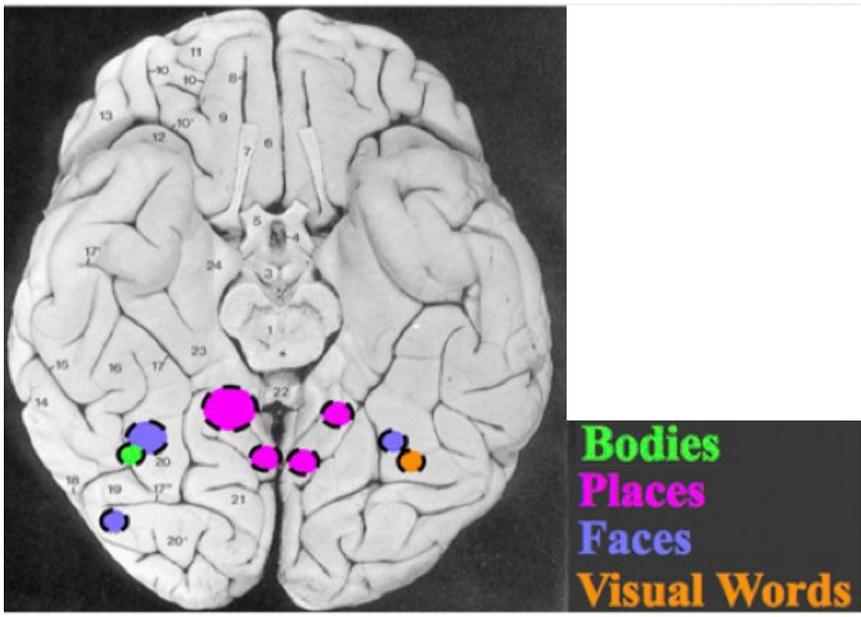
Known topographies of different scales in early visual cortex

Sereno et al. 1995

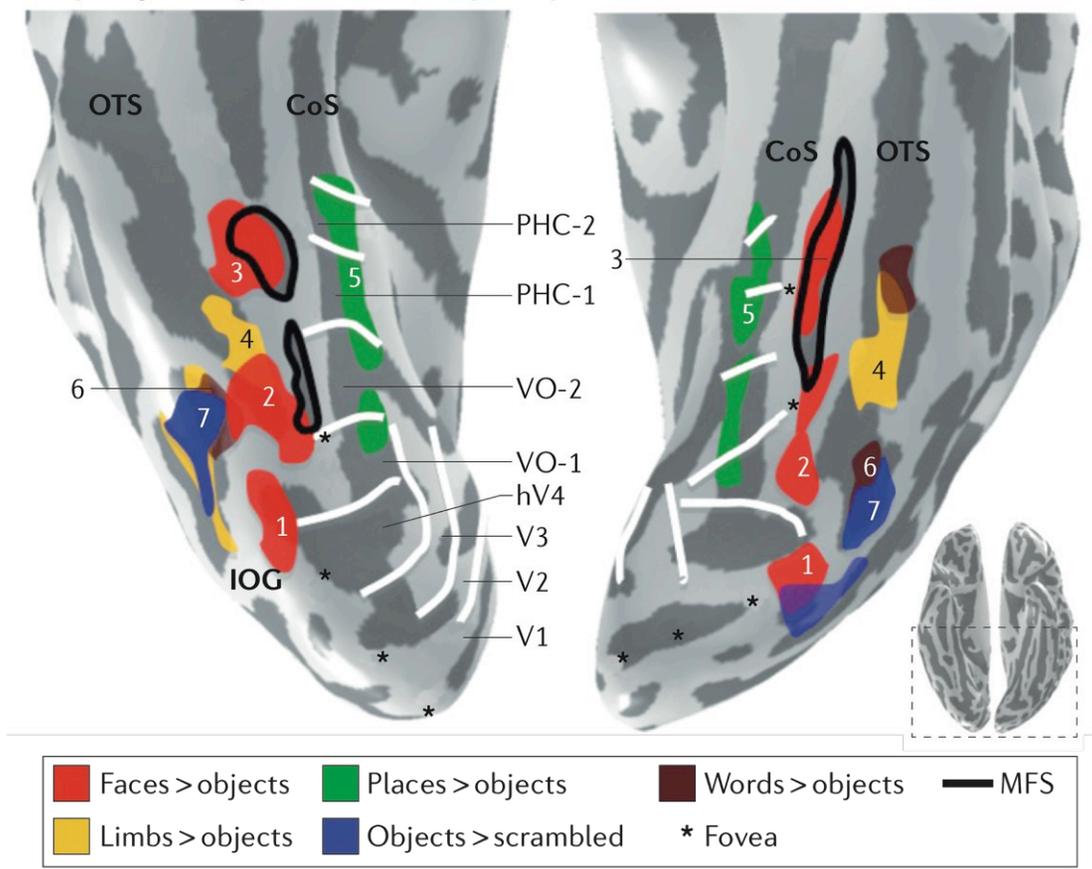


Yacoub et al. 2007, 2008

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

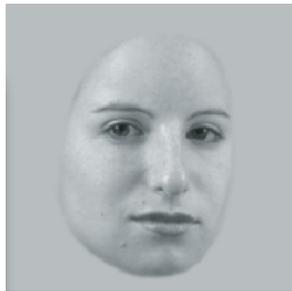


Kanwisher (2010)



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



VS



VS



VS



VS



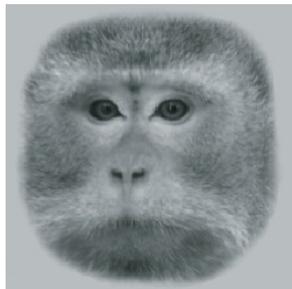
VS



VS



VS



## Question

- Can the fine-grained topographies that carry fine distinctions be modeled in a computational framework that is common across brains?
  - i.e. Is there a common basis – shared principles and features - for these population responses, or does each brain develop an idiosyncratic code?

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

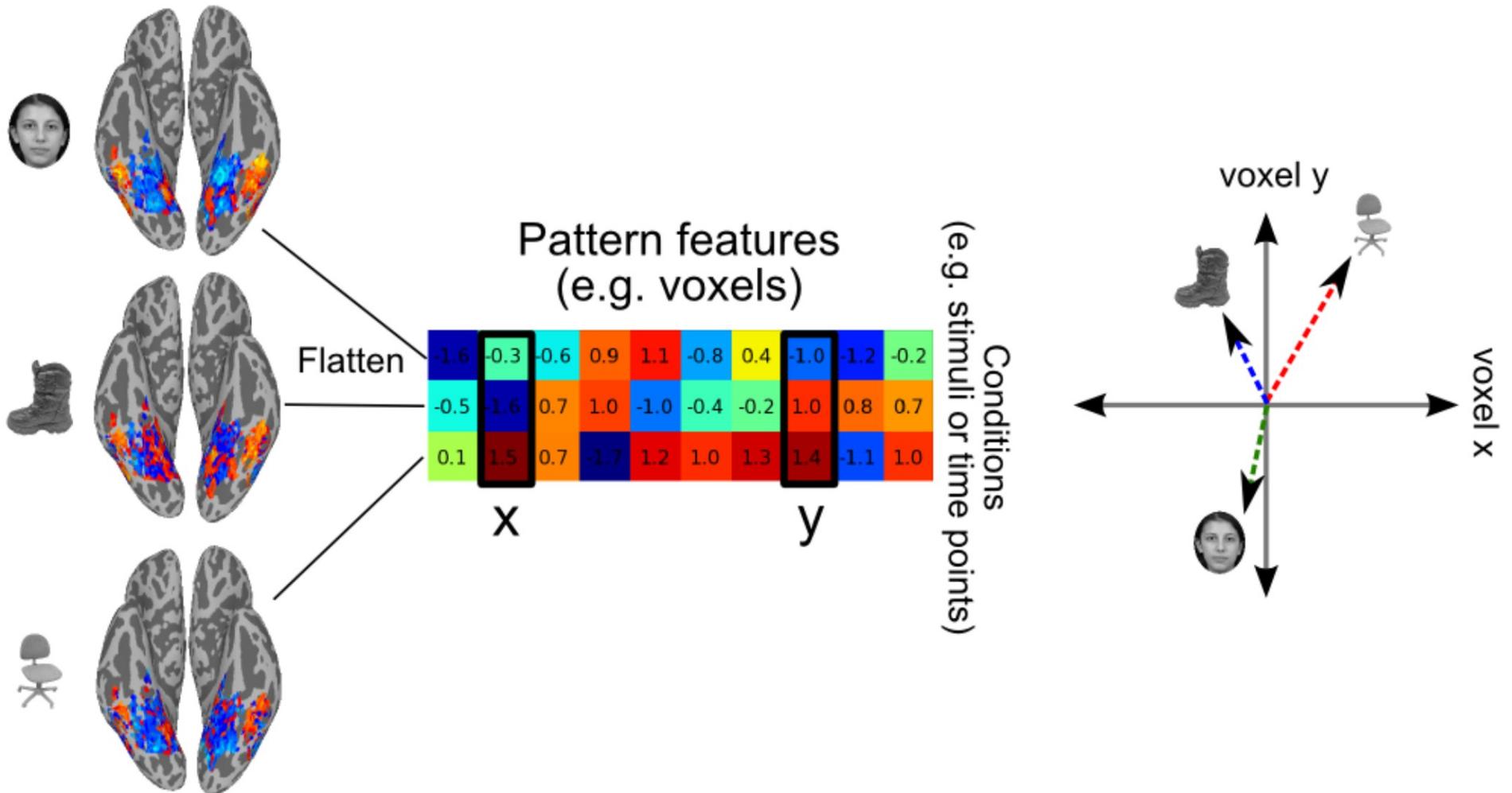
- Statement of the problem: capturing fine-grained distinctions in a common model
- Conceptual framework: high-dimensional representational spaces
  - A model space based on features (dimensions) with common tuning profiles
- Deriving the common space and individual transformation matrices with hyperalignment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

# Conceptual framework: High-dimensional representational spaces

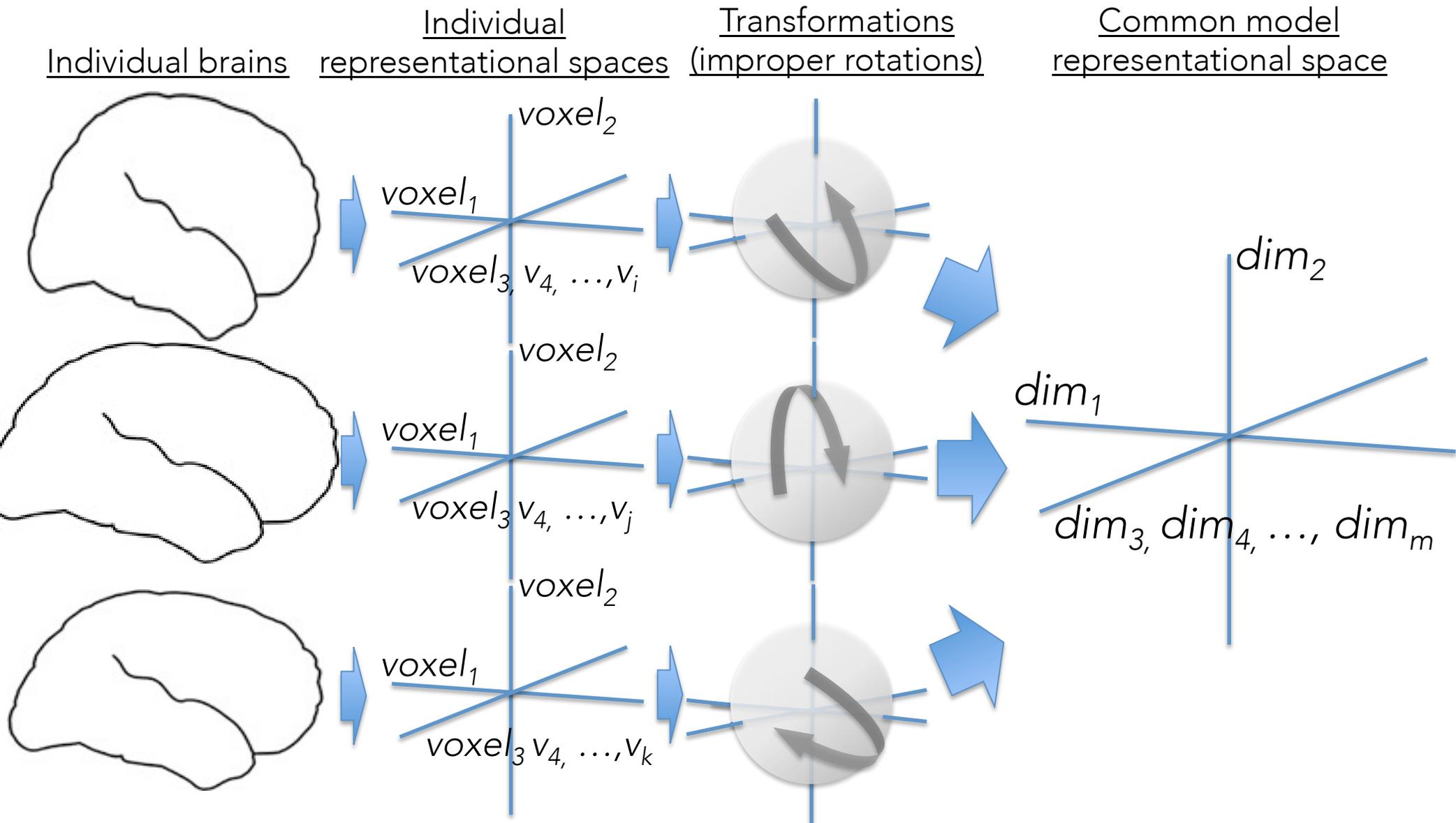
Brain activation patterns

Data matrix

Representational space (2 voxels)

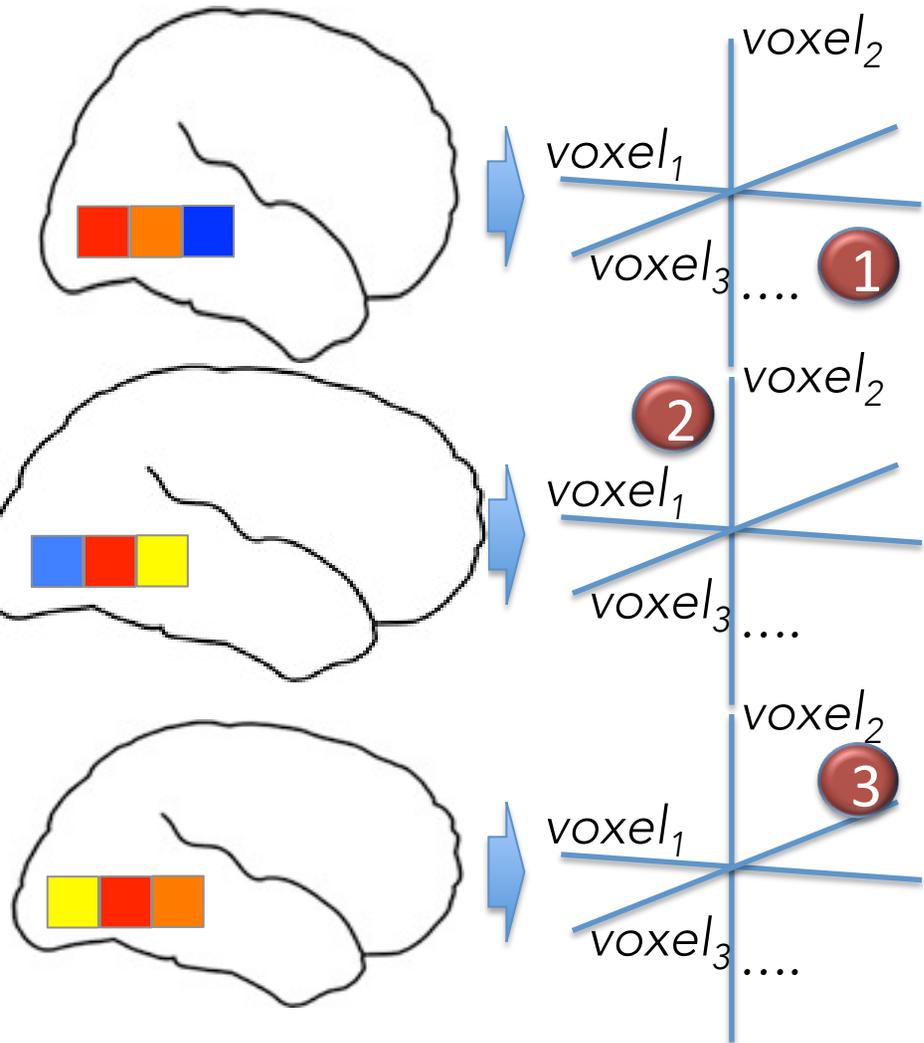


# Modeling functional architecture of the human cortex: Individual representational spaces $\Leftrightarrow$ common representational space



# Modeling functional architecture of the human cortex: Individual representational spaces $\Leftrightarrow$ common representational space

Individual brains      Individual representational spaces

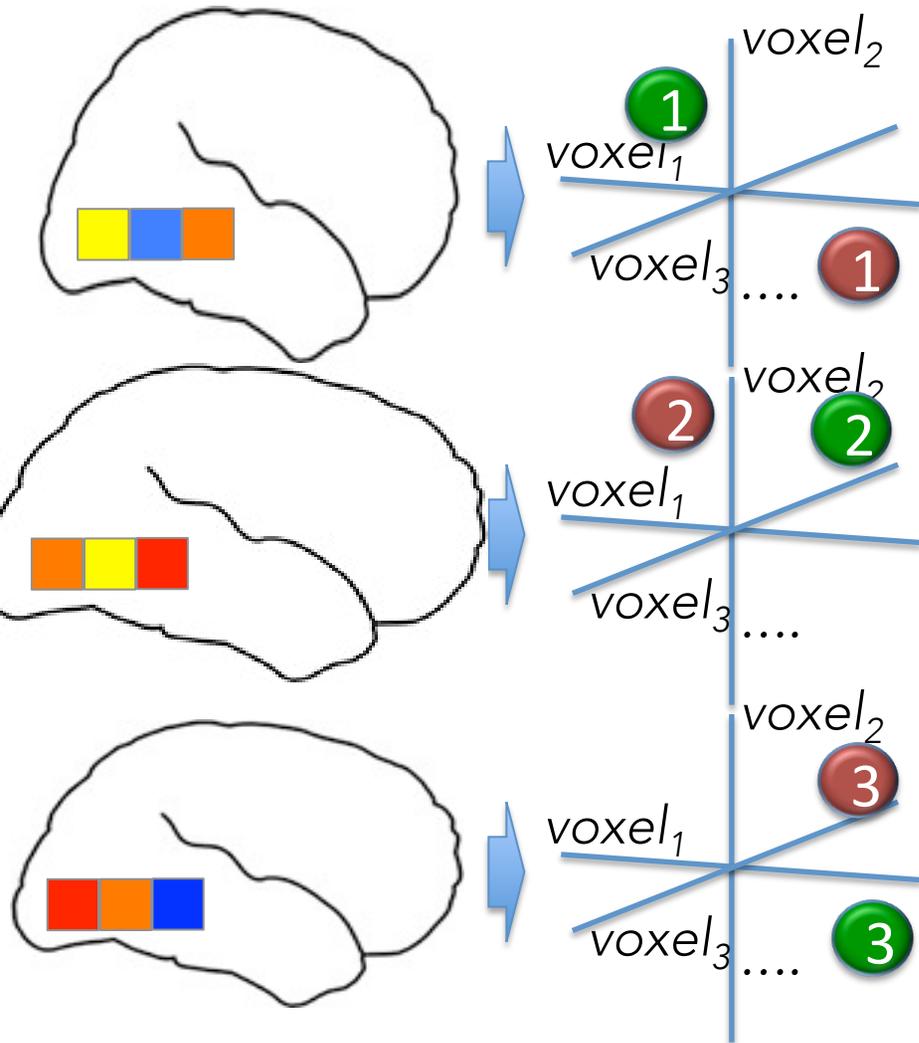


Stimulus



# Modeling functional architecture of the human cortex: Individual representational spaces $\Leftrightarrow$ common representational space

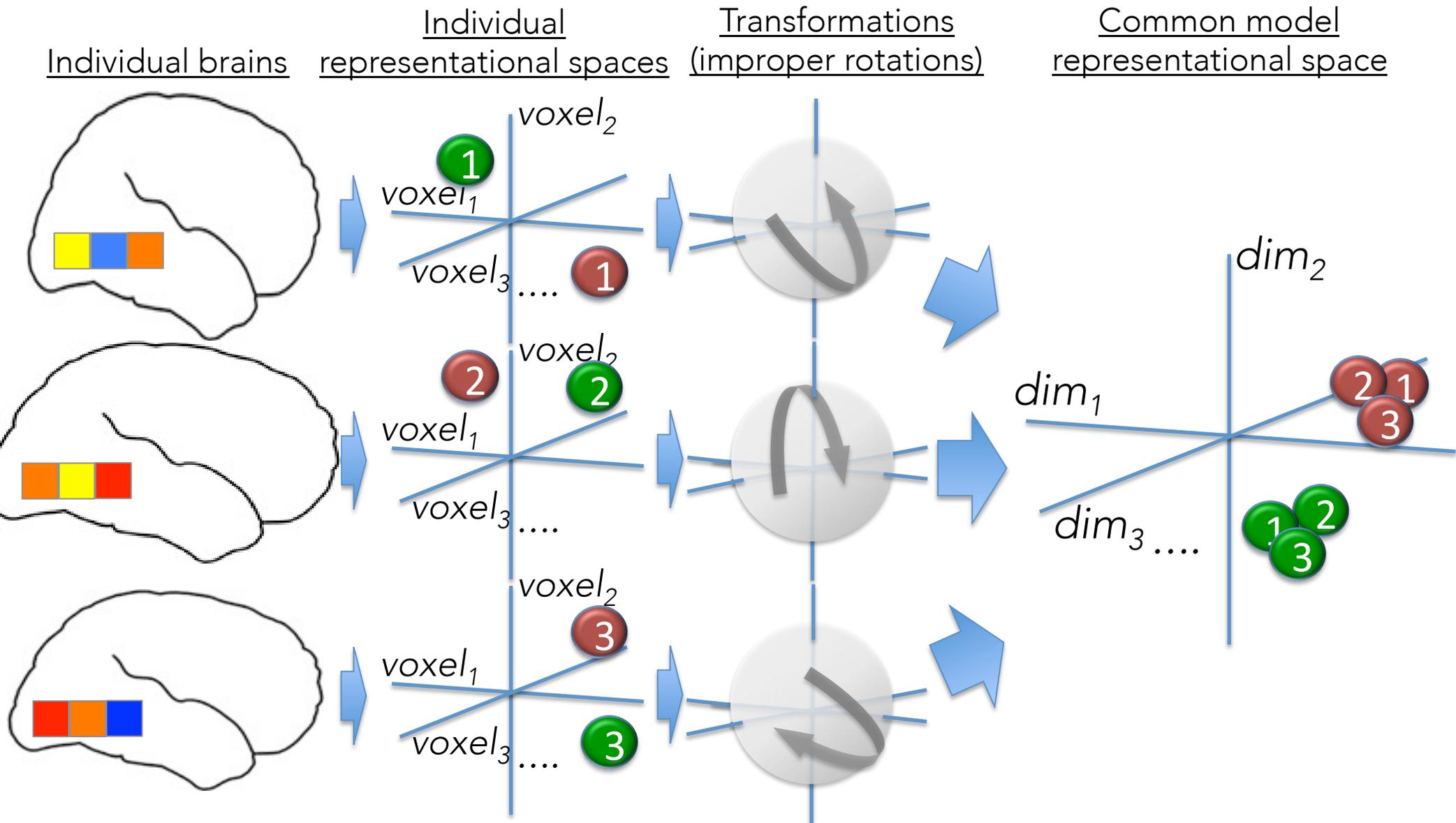
Individual brains      Individual representational spaces



Another stimulus



# Modeling functional architecture of the human cortex: Individual representational spaces $\Leftrightarrow$ 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
- Conclusions

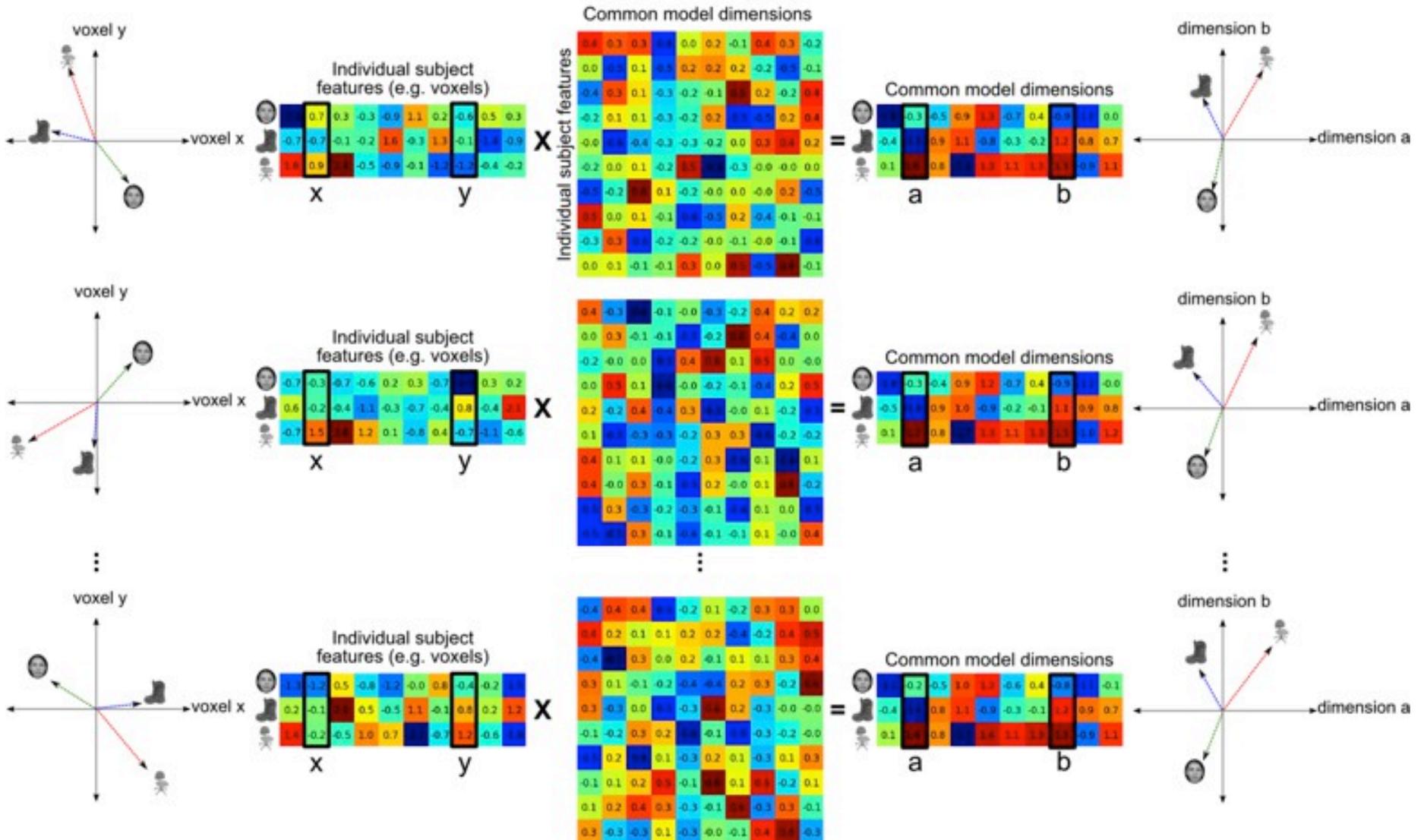
# Matrix math:

Individual transformation matrices rotate individual brain spaces into common model space coordinates

Individual brain spaces

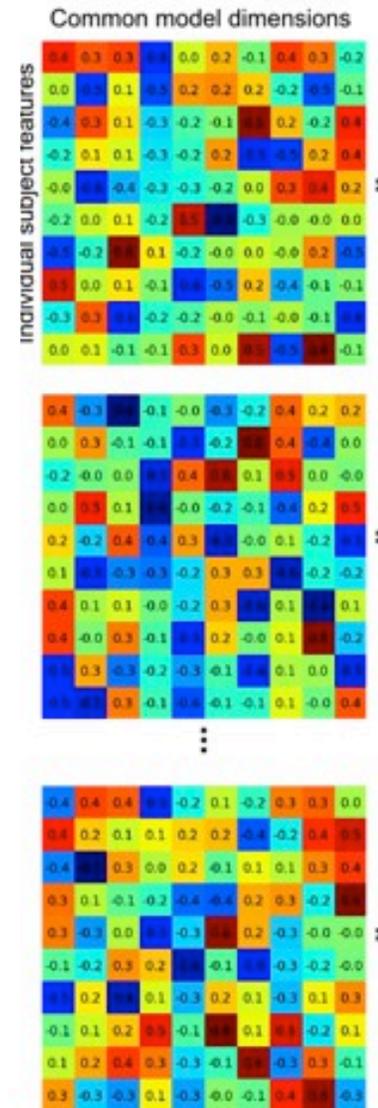
Transformation matrices

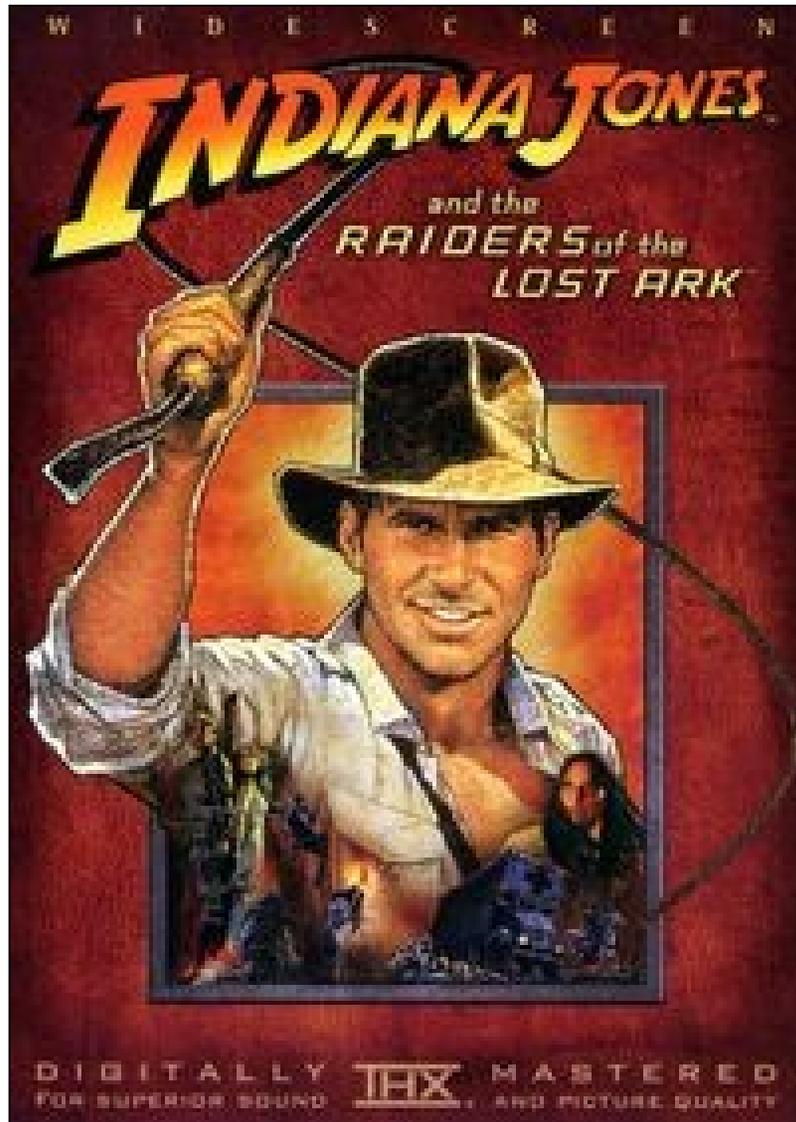
Common model space



Individual transformation matrices are the key to building the common model: How can the parameters be derived?

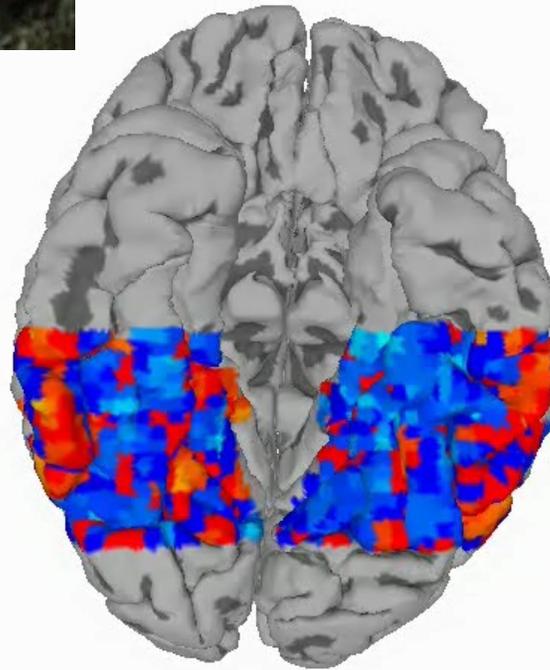
Transformation matrices



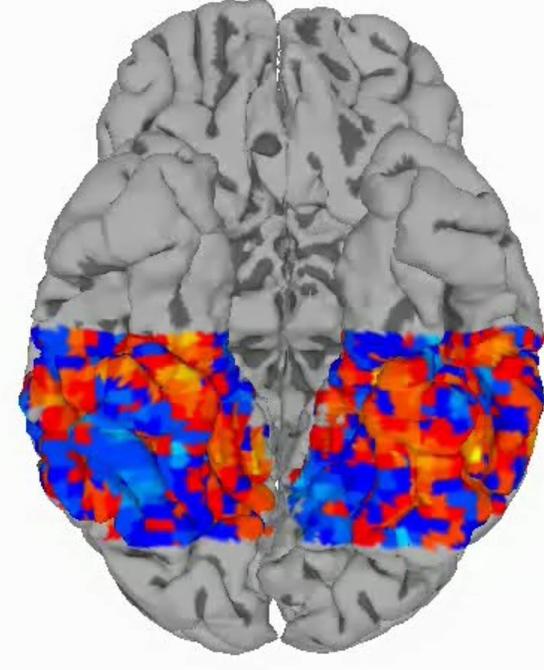




Subject 1



Subject 2

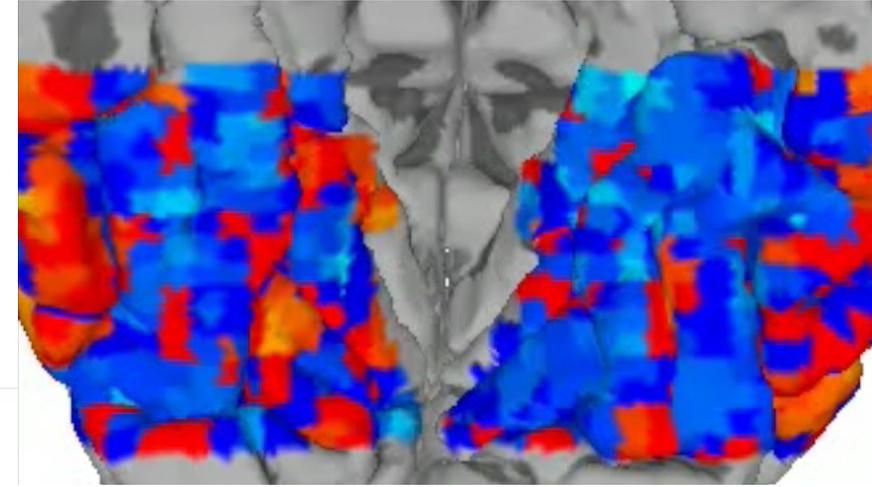
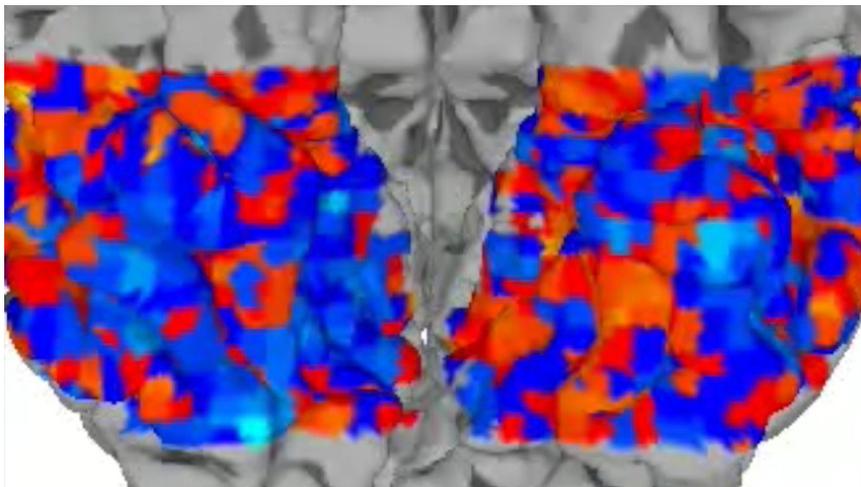


# Broad sampling of a neural representational space with a movie

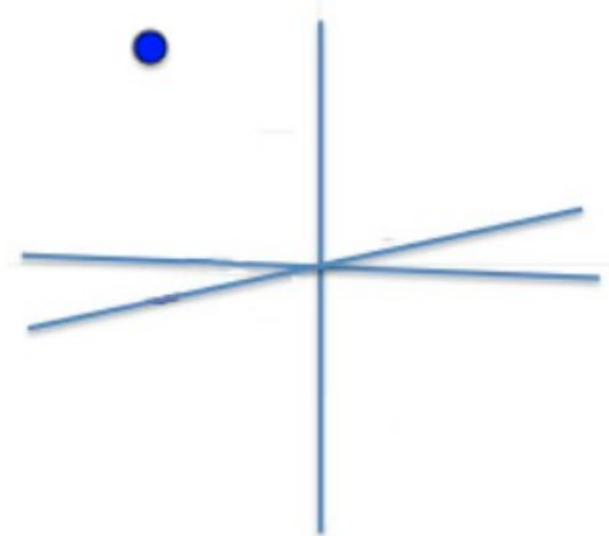
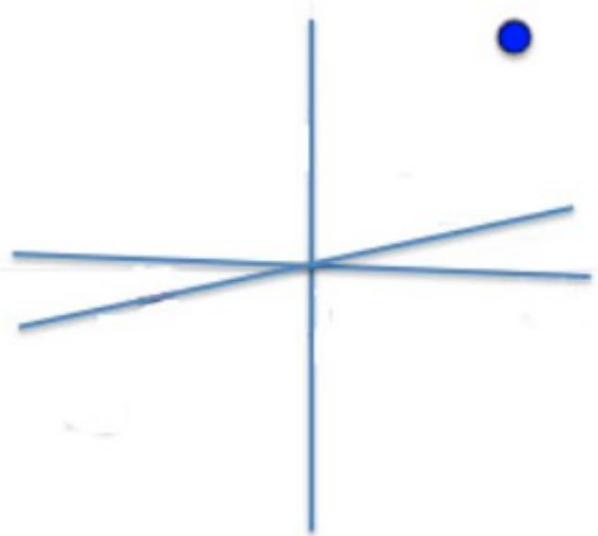
Subject 1

Subject 2

Response patterns in cortex



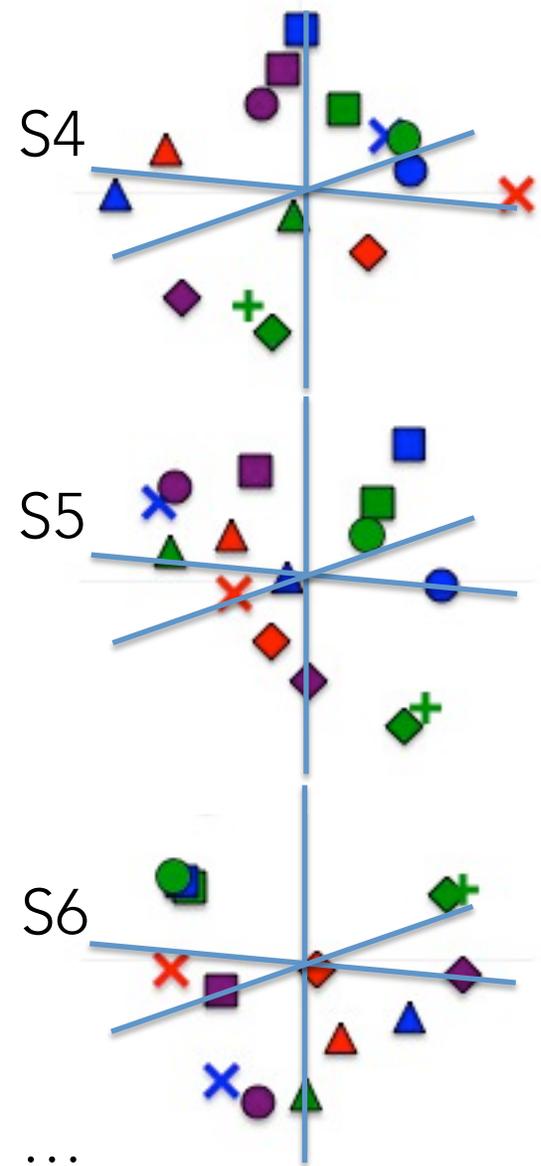
15 response pattern vectors in individual 3D representational spaces  
(full exp't has >2600 vectors in >50,000D space)



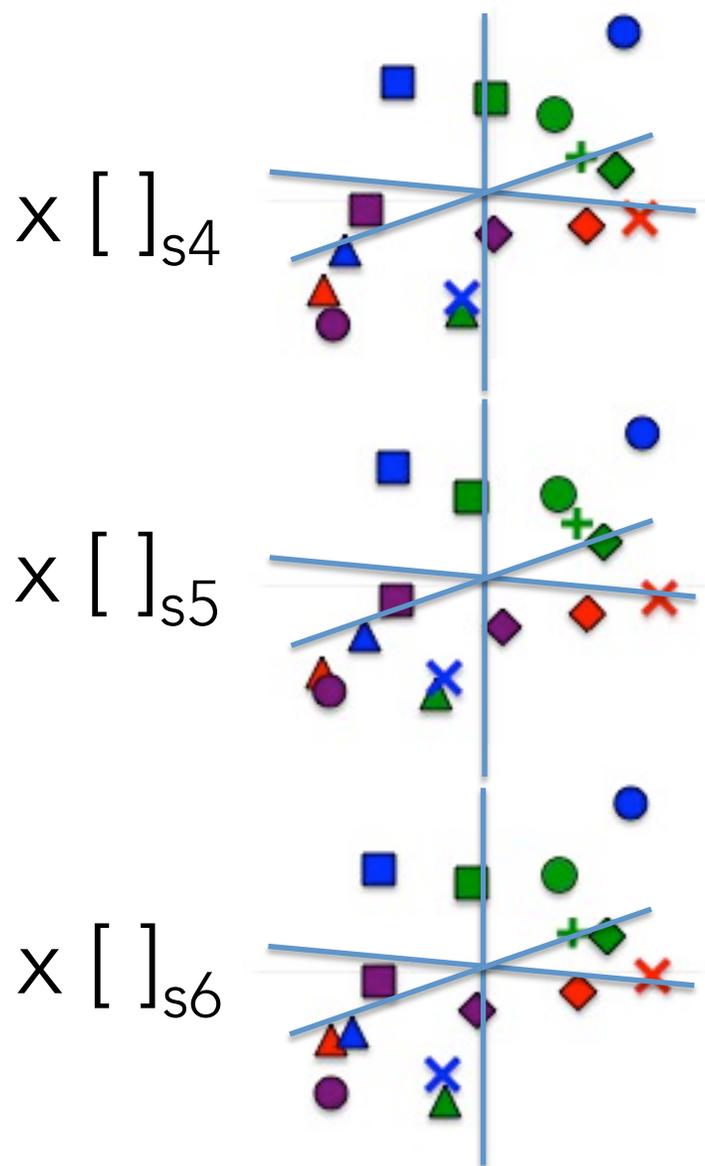




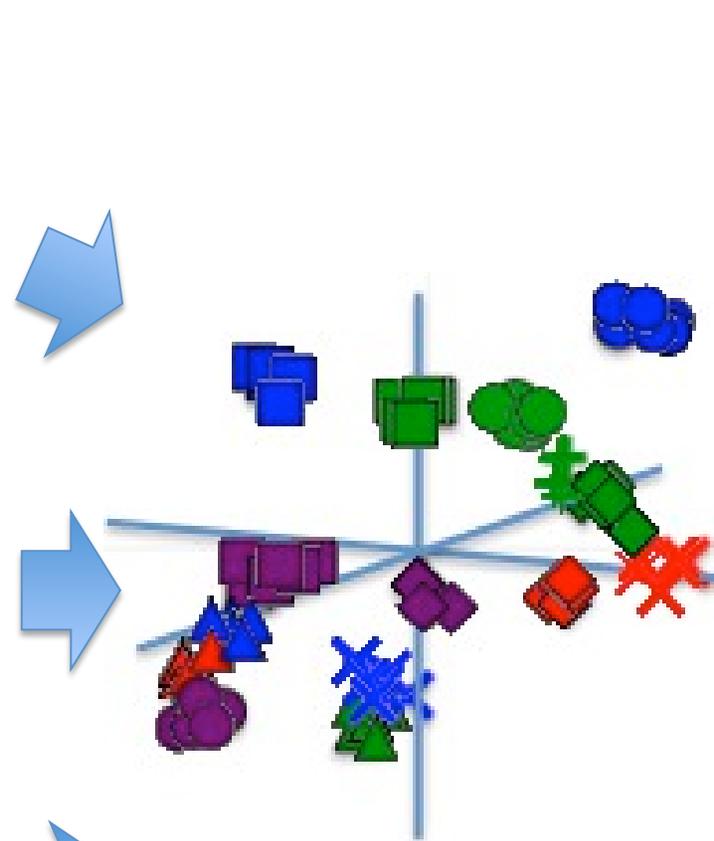
Individual  
representational spaces



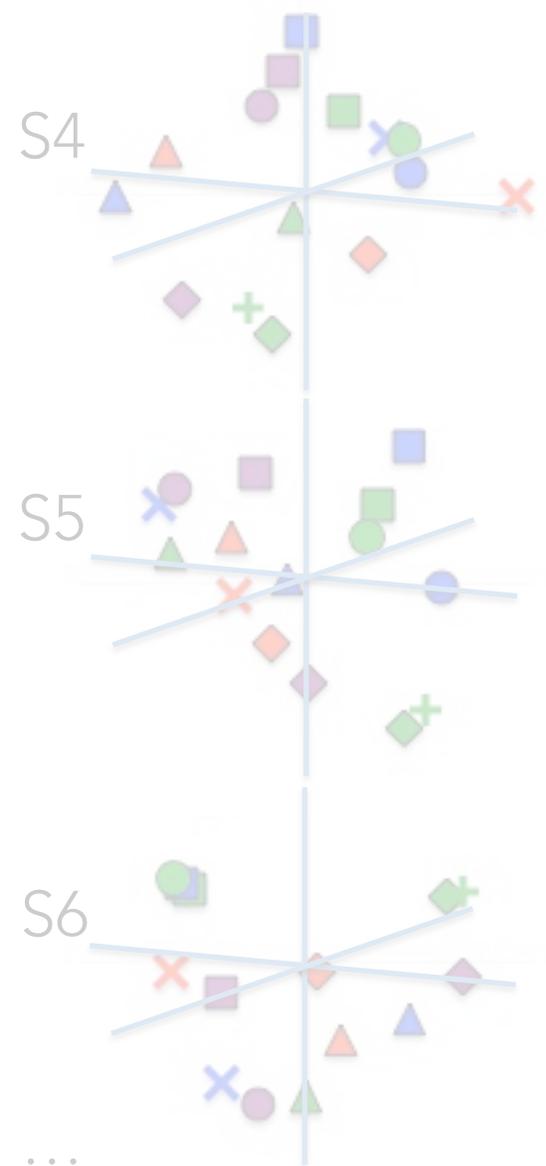
Procrustes transformations  
(improper rotations)



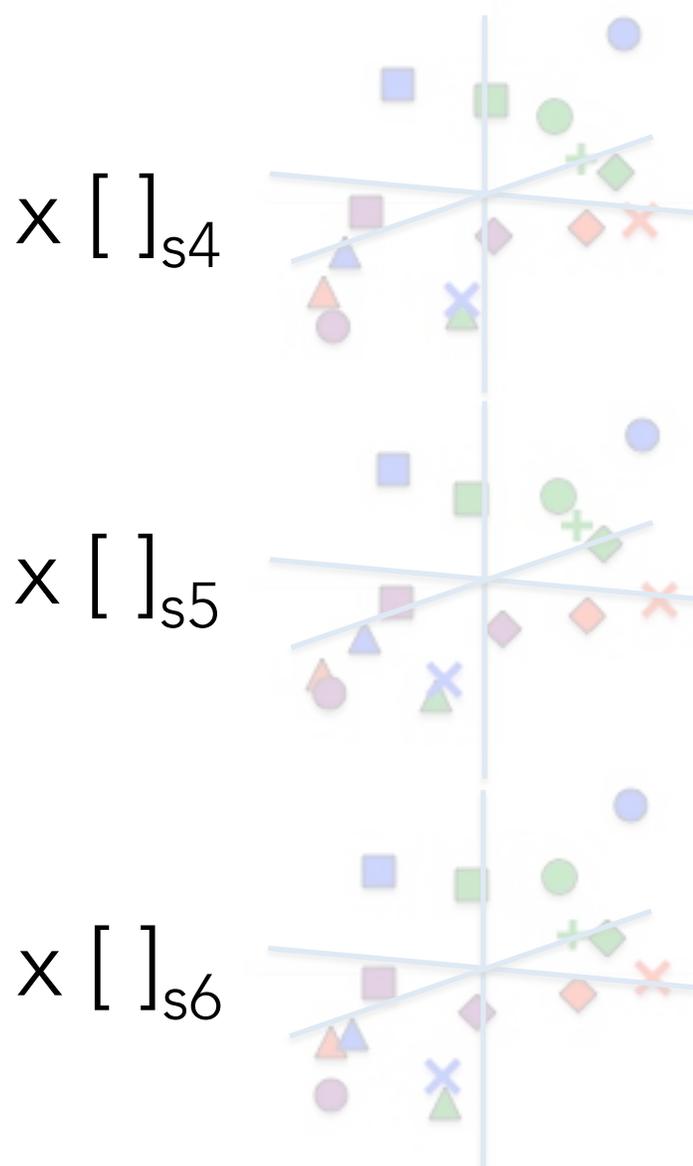
Common model  
representational space



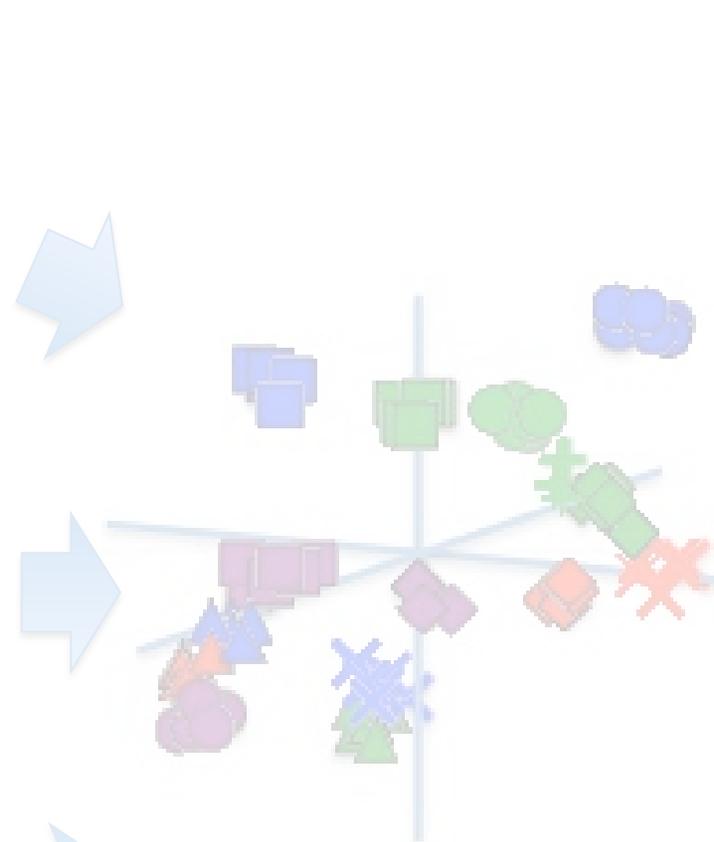
Individual  
representational spaces



Procrustes transformations  
(improper rotations)



Common model  
representational space

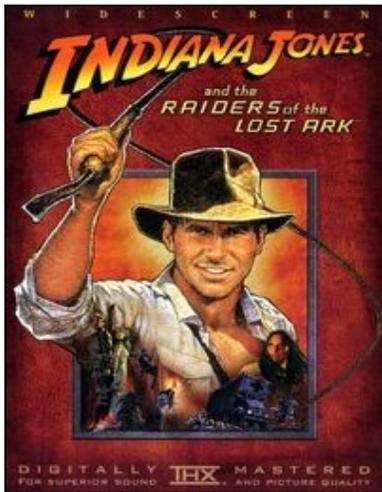


## Movie data in Brain Space

## Subject-specific Transformation Matrix

## Movie data in Model Space

		<u>Voxels</u>											<u>Model dimensions</u>															
		$v_1$	$v_2$	$v_3$	...	$v_i$							$d_1$	$d_2$	$d_3$	...	$d_k$							$d_1$	$d_2$	$d_3$	...	$d_k$
<u>Time-points</u>	$t_1$	$x_{1,1}$	$x_{2,1}$	$x_{3,1}$	...	$x_{i,1}$	X	$v_1$	$w_{1,1}$	$w_{2,1}$	$w_{3,1}$	...	$w_{k,1}$	=	<u>Time-points</u>	$t_1$	$y_{1,1}$	$y_{2,1}$	$y_{3,1}$	...	$y_{k,1}$							
	$t_2$	$x_{1,2}$	$x_{2,2}$	$x_{3,2}$	...	$x_{i,2}$		$v_2$	$w_{1,2}$	$w_{2,2}$	$w_{3,2}$	...	$w_{k,2}$			$t_2$	$y_{1,2}$	$y_{2,2}$	$y_{3,2}$	...	$y_{k,2}$							
	$t_3$	$x_{1,3}$	$x_{2,3}$	$x_{3,3}$	...	$x_{i,3}$		$v_3$	$w_{1,3}$	$w_{2,3}$	$w_{3,3}$	...	$w_{k,3}$			$t_3$	$y_{1,3}$	$y_{2,3}$	$y_{3,3}$	...	$y_{k,3}$							
	$t_4$	$x_{1,4}$	$x_{2,4}$	$x_{3,4}$	...	$x_{i,4}$		...	...	...	...	...	...			$t_4$	$y_{1,4}$	$y_{2,4}$	$y_{3,4}$	...	$y_{k,4}$							
	...	...	...	...	...	...		$v_i$	$w_{1,i}$	$w_{2,i}$	$w_{3,i}$	...	$w_{k,i}$			...	...	...	...	...	...							
	$t_j$	$x_{1,j}$	$x_{2,j}$	$x_{3,j}$	...	$x_{i,j}$											$t_j$	$y_{j,i}$	$y_{j,i}$	$y_{j,i}$	...	$y_{j,k}$						



Subject-specific  
Transformation Matrix

		<u>Model dimensions</u>				
		$d_1$	$d_2$	$d_3$	...	$d_k$
<u>Voxels</u>	$v_1$	$w_{1,1}$	$w_{2,1}$	$w_{3,1}$	...	$w_{k,1}$
	$v_2$	$w_{1,2}$	$w_{2,2}$	$w_{3,2}$	...	$w_{k,2}$
	$v_3$	$w_{1,3}$	$w_{2,3}$	$w_{3,3}$	...	$w_{k,3}$
	...	...	...	...		...
	$v_i$	$w_{1,i}$	$w_{2,i}$	$w_{3,i}$	...	$w_{k,i}$

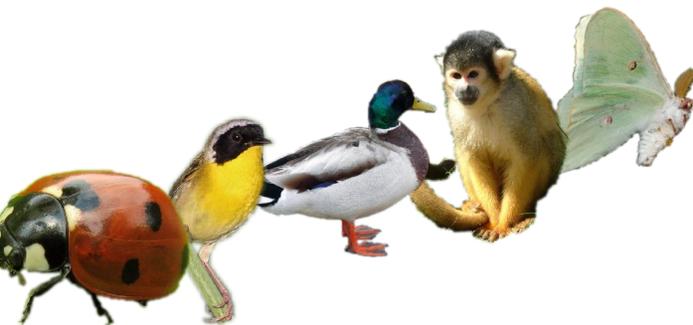
The key that unlocks an individual's neural code

Experiment 2 data in Brain Space

Subject-specific Transformation Matrix

Experiment 2 data in Model Space

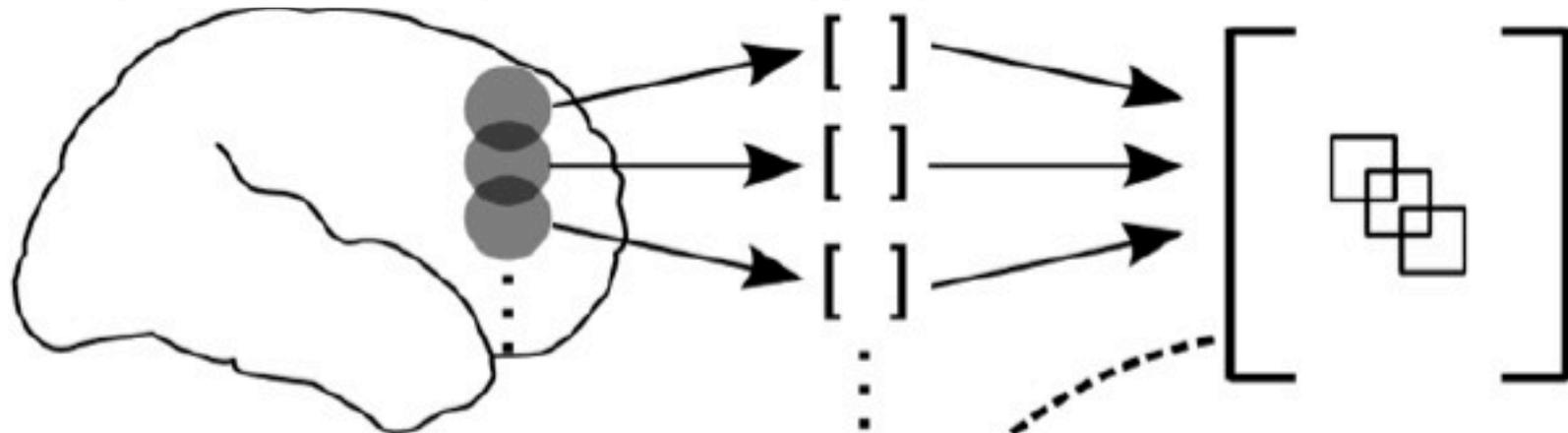
		<u>Voxels</u>					<u>Model dimensions</u>								<u>Model dimensions</u>						
		$v_1$	$v_2$	$v_3$	...	$v_i$									$d_1$	$d_2$	$d_3$	...	$d_k$		
<u>Stimuli</u>	$S_1$	$X_{1,1}$	$X_{2,1}$	$X_{3,1}$	...	$X_{i,1}$	<u>Voxels</u>	$v_1$	$w_{1,1}$	$w_{2,1}$	$w_{3,1}$	...	$w_{k,1}$	=	<u>Stimuli</u>	$S_1$	$y_{1,1}$	$y_{2,1}$	$y_{3,1}$	...	$y_{k,1}$
	$S_2$	$X_{1,2}$	$X_{2,2}$	$X_{3,2}$	...	$X_{i,2}$		$v_2$	$w_{1,2}$	$w_{2,2}$	$w_{3,2}$	...	$w_{k,2}$			$S_2$	$y_{1,2}$	$y_{2,2}$	$y_{3,2}$	...	$y_{k,2}$
	$S_3$	$X_{1,3}$	$X_{2,3}$	$X_{3,3}$	...	$X_{i,3}$		$v_3$	$w_{1,3}$	$w_{2,3}$	$w_{3,3}$	...	$w_{k,3}$			$S_3$	$y_{1,3}$	$y_{2,3}$	$y_{3,3}$	...	$y_{k,3}$
	$S_4$	$X_{1,4}$	$X_{2,4}$	$X_{3,4}$	...	$X_{i,4}$		...	...	...	...	...	...			$S_4$	$y_{1,4}$	$y_{2,4}$	$y_{3,4}$	...	$y_{k,4}$
	...	...	...	...	...	...		$v_i$	$w_{1,i}$	$w_{2,i}$	$w_{3,i}$	...	$w_{k,i}$			...	...	...	...	...	...
	$S_m$	$X_{1,m}$	$X_{2,m}$	$X_{3,m}$	...	$X_{i,m}$											$S_m$	$y_{1,m}$	$y_{2,m}$	$y_{3,m}$	...



# Modeling representational spaces in all human cortex with searchlight hyperalignment

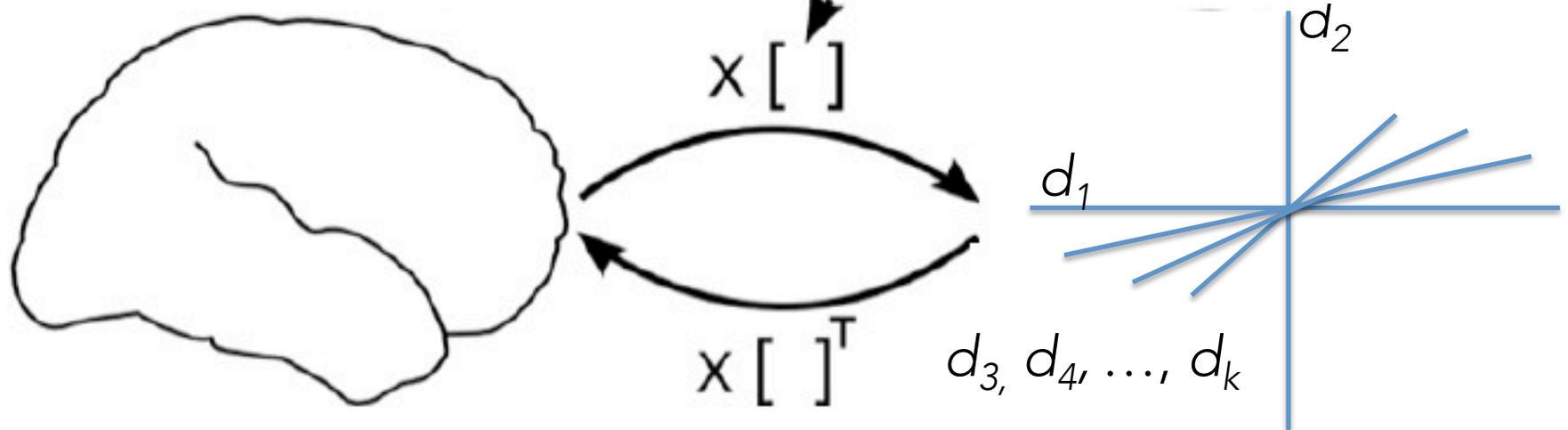
Voxels in overlapping searchlights are hyperaligned across subjects

Overlapping searchlight transformation matrices are aggregated into a whole cortex matrix



Data in individual brain anatomy

Data in common model 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
- Validation
  - Between-subject classification of movie time segments
  - Between-subject correlations of local similarity structures
  - Estimation spatial granularity of common model features
  - Applying transformation matrices to data from an unrelated experiment
  - Modeling individual variation in coarse features of functional topography
- Conclusions

Movie data in  
Brain Space

Subject-specific  
Transformation Matrix

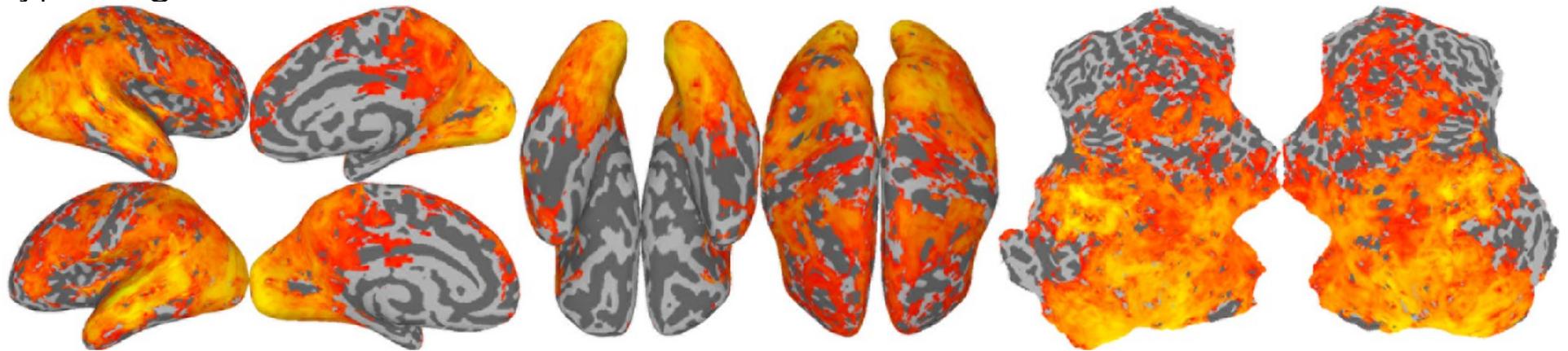
Movie data in  
Model Space

		<u>Voxels</u>							<u>Model dimensions</u>							<u>Model dimensions</u>					
		$v_1$	$v_2$	$v_3$	...	$v_i$			$d_1$	$d_2$	$d_3$	...	$d_k$			$d_1$	$d_2$	$d_3$	...	$d_k$	
<u>Time-points</u>	$t_1$	$x_{1,1}$	$x_{2,1}$	$x_{3,1}$	...	$x_{i,1}$	X	$v_1$	$w_{1,1}$	$w_{2,1}$	$w_{3,1}$	...	$w_{k,1}$	=	$t_1$	$y_{1,1}$	$y_{2,1}$	$y_{3,1}$	...	$y_{k,1}$	
	$t_2$	$x_{1,2}$	$x_{2,2}$	$x_{3,2}$	...	$x_{i,2}$		$v_2$	$w_{1,2}$	$w_{2,2}$	$w_{3,2}$	...	$w_{k,2}$		$t_2$	$y_{1,2}$	$y_{2,2}$	$y_{3,2}$	...	$y_{k,2}$	
	$t_3$	$x_{1,3}$	$x_{2,3}$	$x_{3,3}$	...	$x_{i,3}$		$v_3$	$w_{1,3}$	$w_{2,3}$	$w_{3,3}$	...	$w_{k,3}$		$t_3$	$y_{1,3}$	$y_{2,3}$	$y_{3,3}$	...	$y_{k,3}$	
	$t_4$	$x_{1,4}$	$x_{2,4}$	$x_{3,4}$	...	$x_{i,4}$		...	...	...	...	...	...		$t_4$	$y_{1,4}$	$y_{2,4}$	$y_{3,4}$	...	$y_{k,4}$	
	...	...	...	...	...	...		$v_i$	$w_{1,i}$	$w_{2,i}$	$w_{3,i}$	...	$w_{k,i}$		...	...	...	...	...	...	...
	$t_j$	$x_{1,j}$	$x_{2,j}$	$x_{3,j}$	...	$x_{i,j}$										$t_j$	$y_{1,j}$	$y_{2,j}$	$y_{3,j}$	...	$y_{k,j}$

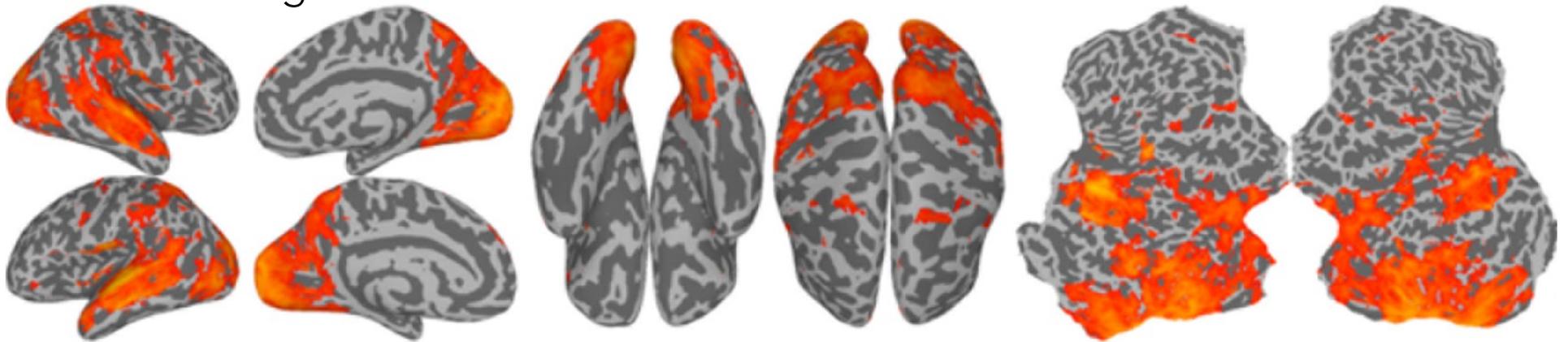
Model dimensions have common response tuning functions

Whole-brain hyperalignment increases intersubject correlations of time-series responses to movies in occipital, temporal, parietal and frontal cortices

Hyperalignment



Anatomical alignment



Intersubject correlation ( $r$ )

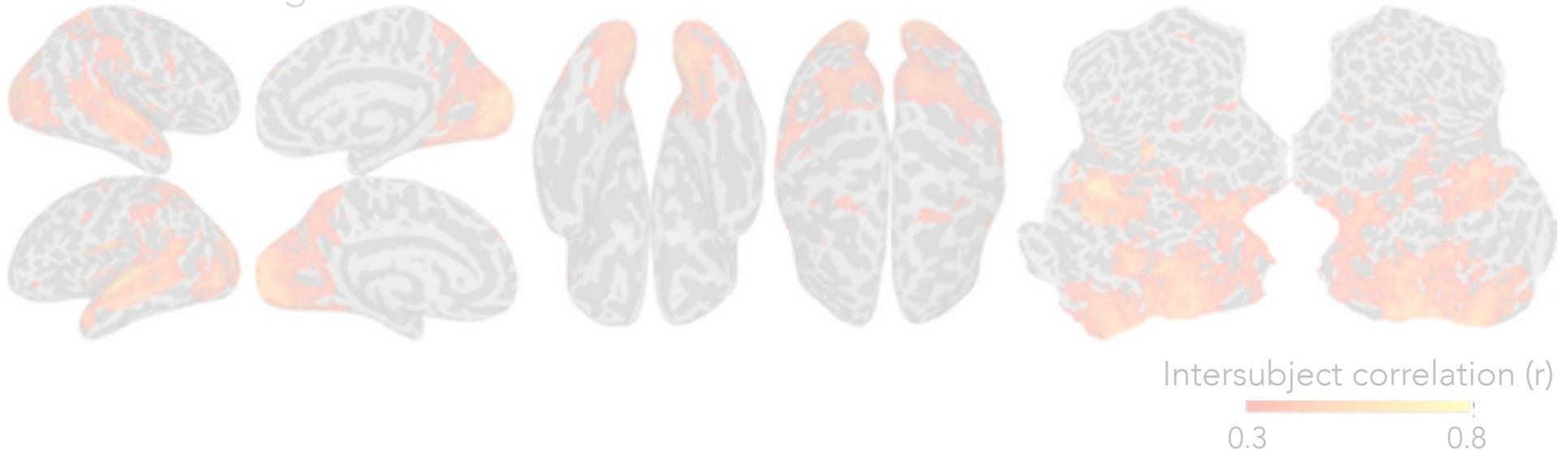


Whole-brain hyperalignment increases intersubject correlations of time-series responses to movies in occipital, temporal, parietal and frontal cortices

Hyperalignment

The tuning profiles of common model dimensions account for >4X more variance

Anatomical alignment



Movie data in  
Brain Space

Subject-specific  
Transformation Matrix

Movie data in  
Model Space

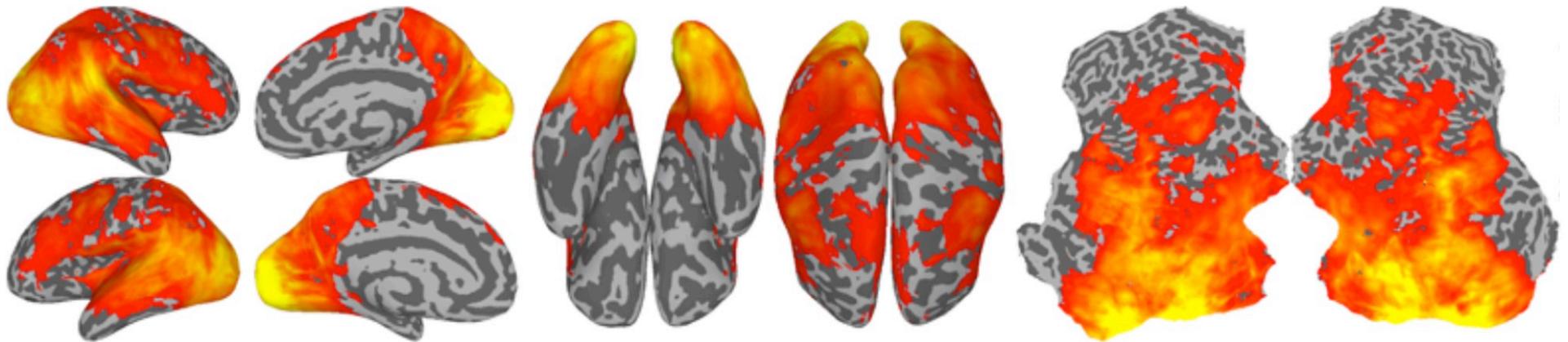
		<u>Voxels</u>							<u>Model dimensions</u>							<u>Model dimensions</u>					
		$v_1$	$v_2$	$v_3$	...	$v_i$			$d_1$	$d_2$	$d_3$	...	$d_k$			$d_1$	$d_2$	$d_3$	...	$d_k$	
<u>Time-points</u>	$t_1$	$x_{1,1}$	$x_{2,1}$	$x_{3,1}$	...	$x_{i,1}$	X	$v_1$	$w_{1,1}$	$w_{2,1}$	$w_{3,1}$	...	$w_{k,1}$	=	$t_1$	$y_{1,1}$	$y_{2,1}$	$y_{3,1}$	...	$y_{k,1}$	
	$t_2$	$x_{1,2}$	$x_{2,2}$	$x_{3,2}$	...	$x_{i,2}$		$v_2$	$w_{1,2}$	$w_{2,2}$	$w_{3,2}$	...	$w_{k,2}$		$t_2$	$y_{1,2}$	$y_{2,2}$	$y_{3,2}$	...	$y_{k,2}$	
	$t_3$	$x_{1,3}$	$x_{2,3}$	$x_{3,3}$	...	$x_{i,3}$		$v_3$	$w_{1,3}$	$w_{2,3}$	$w_{3,3}$	...	$w_{k,3}$		$t_3$	$y_{1,3}$	$y_{2,3}$	$y_{3,3}$	...	$y_{k,3}$	
	$t_4$	$x_{1,4}$	$x_{2,4}$	$x_{3,4}$	...	$x_{i,4}$		...	...	...	...	...	...		$t_4$	$y_{1,4}$	$y_{2,4}$	$y_{3,4}$	...	$y_{k,4}$	
	...	...	...	...	...	...		$v_i$	$w_{1,i}$	$w_{2,i}$	$w_{3,i}$	...	$w_{k,i}$		...	...	...	...	...	...	...
	$t_j$	$x_{1,j}$	$x_{2,j}$	$x_{3,j}$	...	$x_{i,j}$										$t_j$	$y_{1,j}$	$y_{2,j}$	$y_{3,j}$	...	$y_{k,j}$

In common model space patterns of response are more similar across brains, affording

- ☐ between-subject multivariate pattern classification (bsMVPC)
- ☐ higher inter-subject correlation of representational geometry

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

Hyperalignment



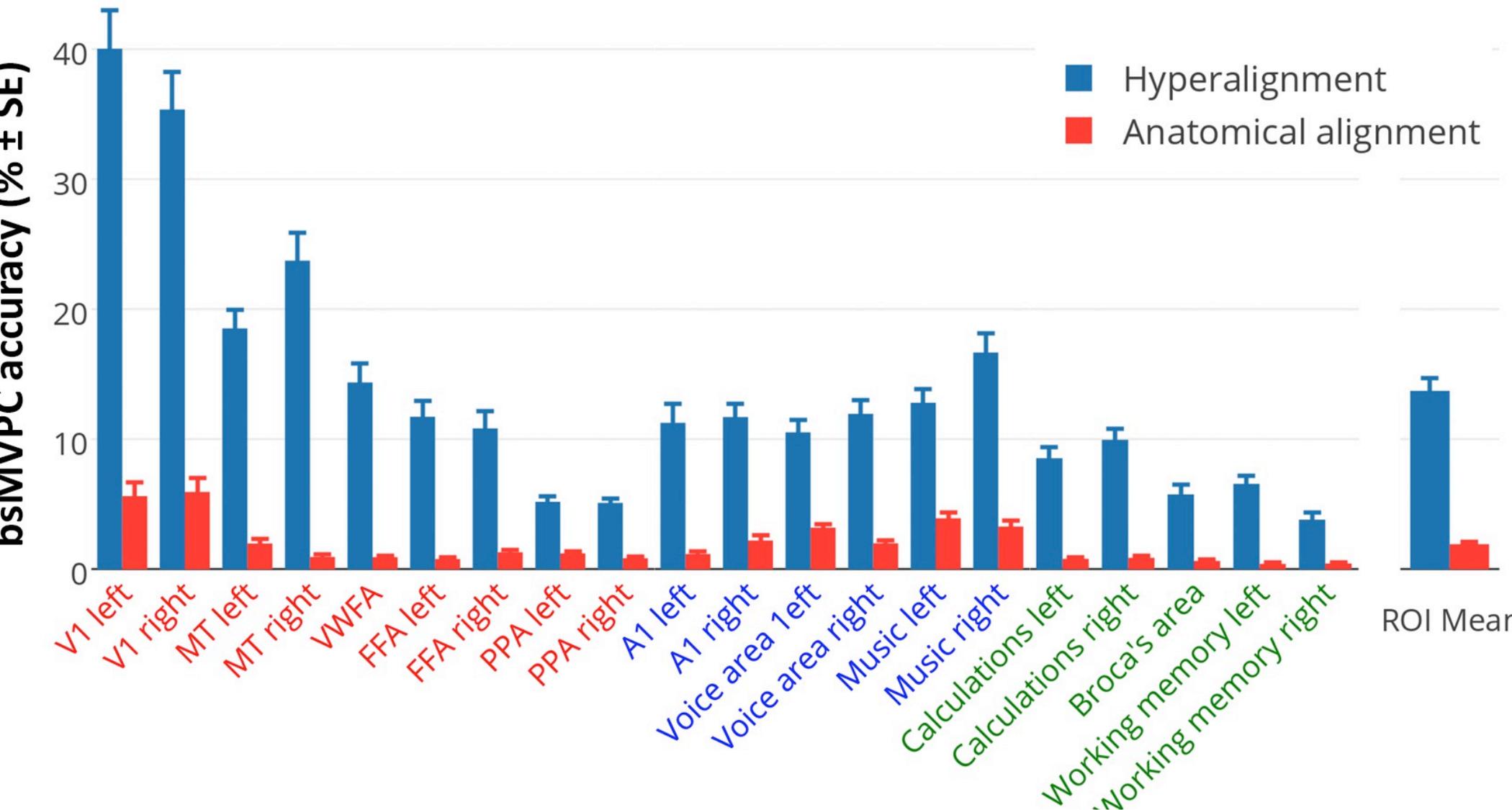
Anatomical alignment



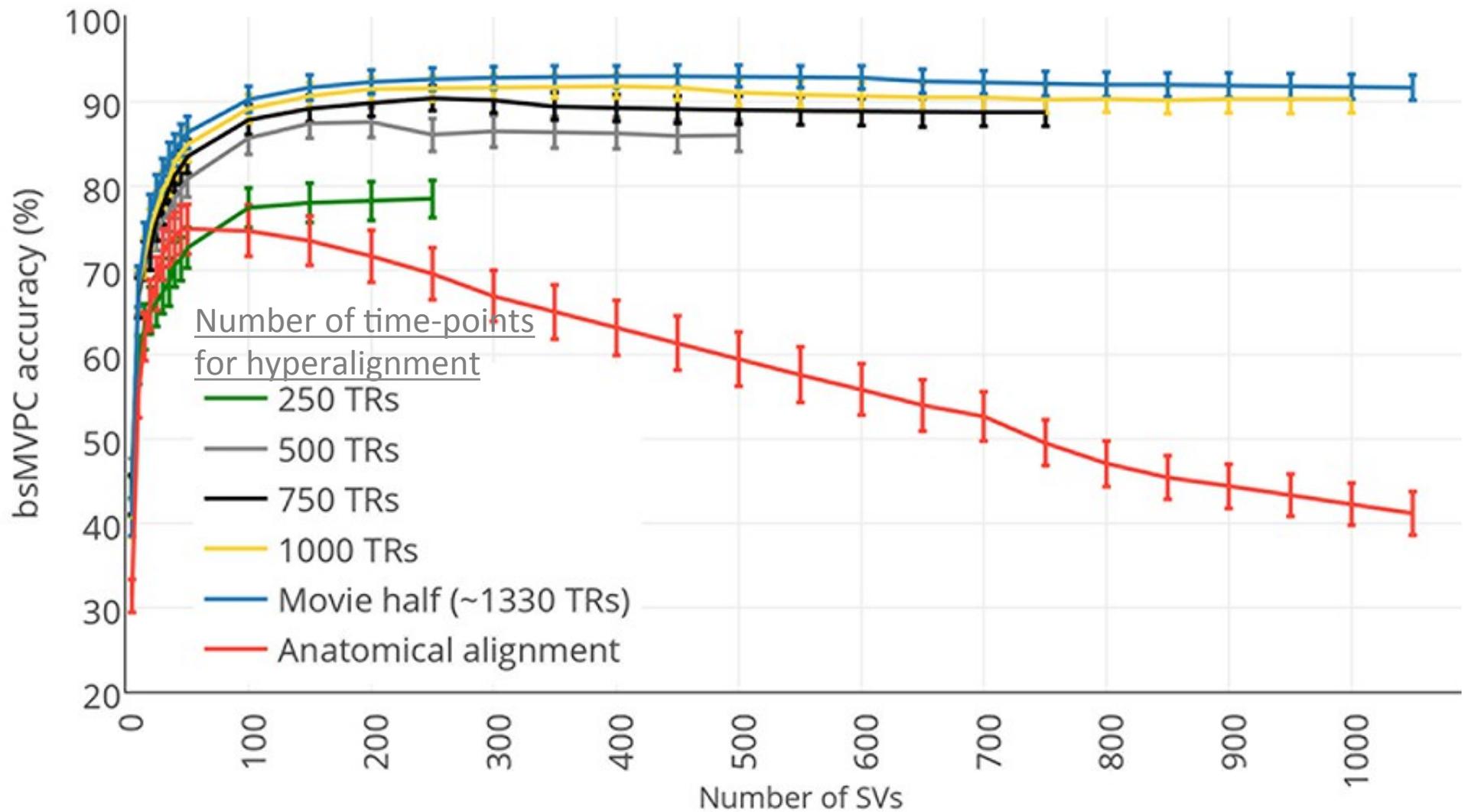
Classification accuracy (%)



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

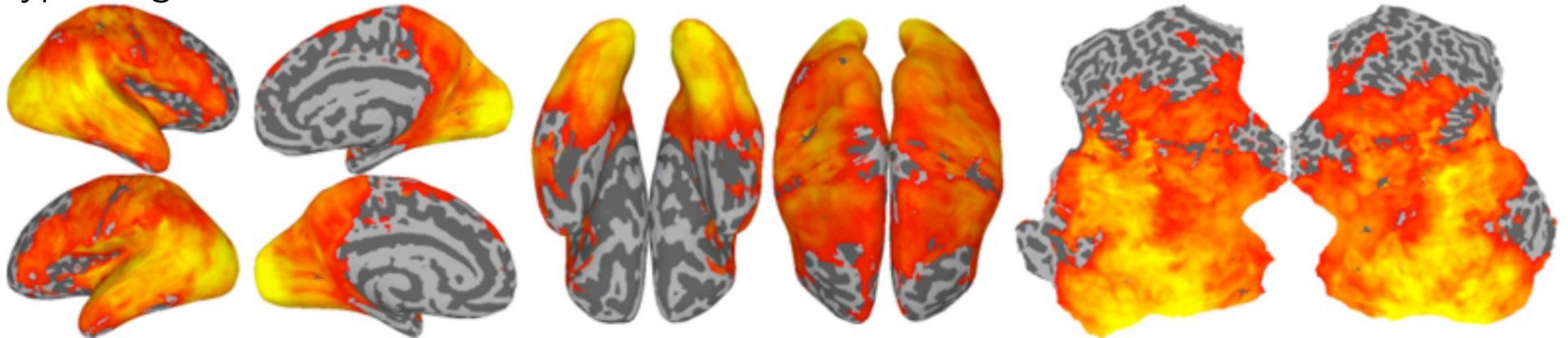


Whole-brain hyperalignment increases between-subject classification of 15 s movie time segments for the whole brain (after SVD dimensionality reduction)

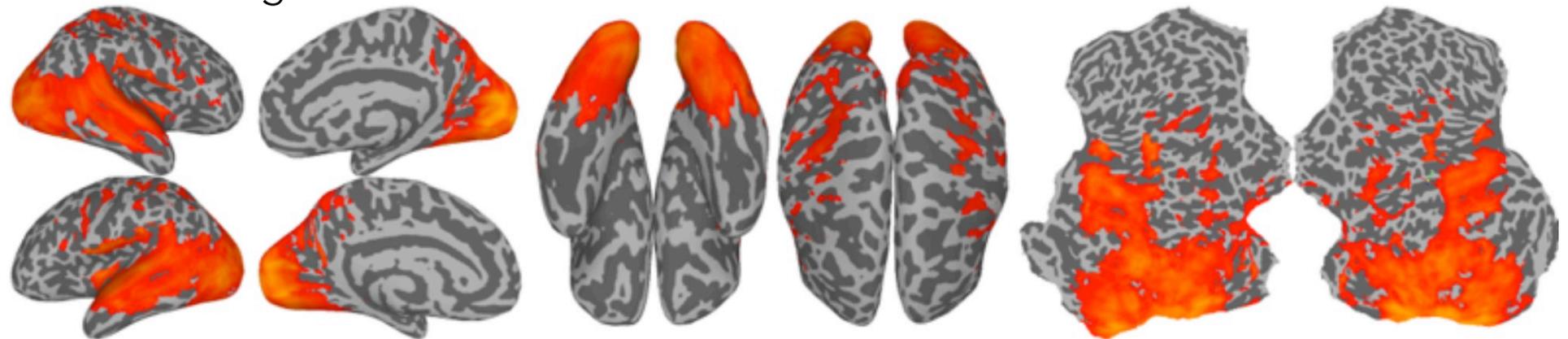


Whole-brain hyperalignment increases intersubject correlation of high-dimensional representational geometries (correlations between movie time-points)

Hyperalignment



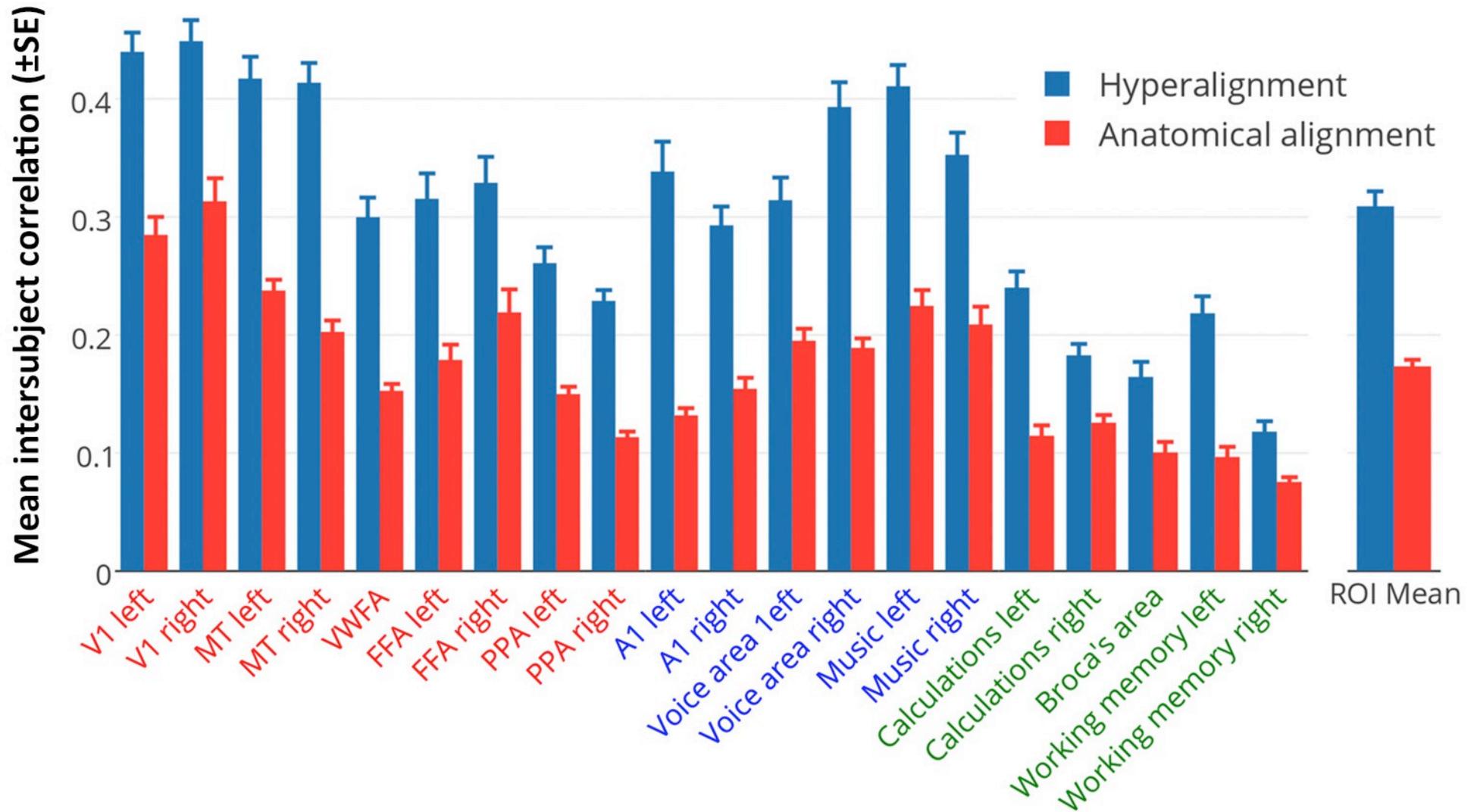
Anatomical alignment



Intersubject correlation

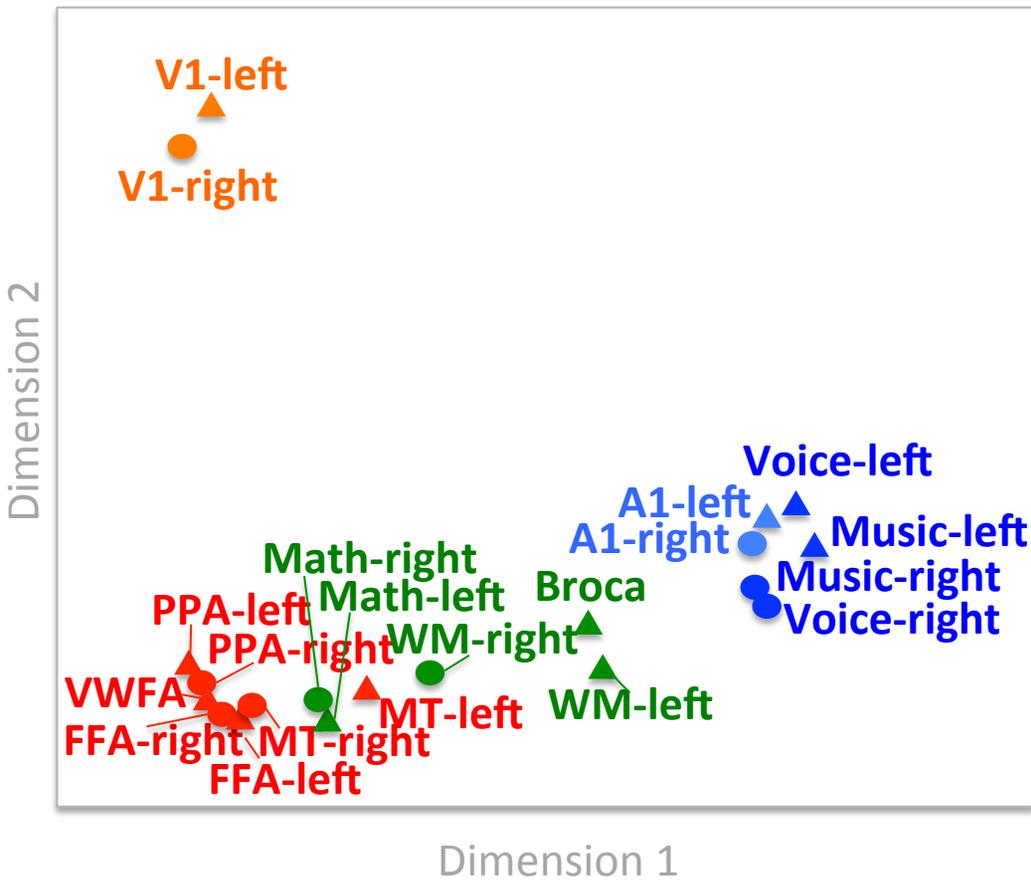


Increased intersubject correlations of representational geometries in **visual**, **auditory**, and **cognitive** regions of interest (ROIs)

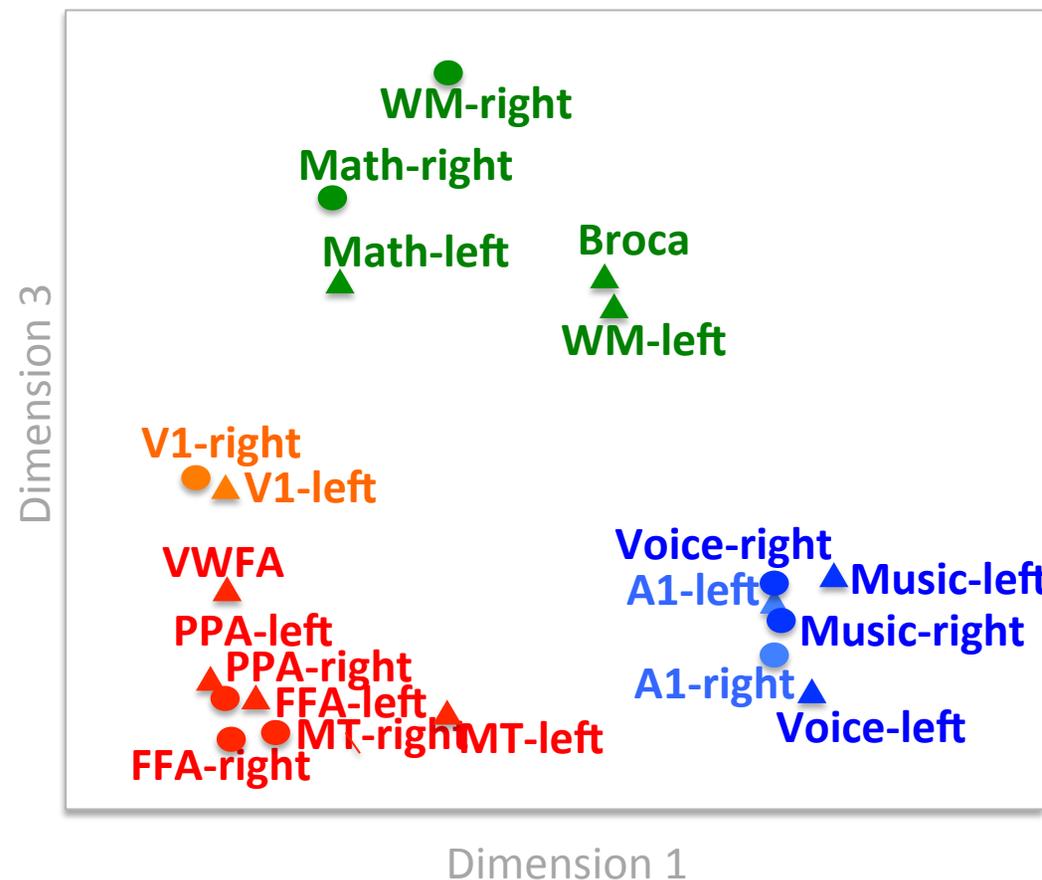




# Multidimensional scaling (MDS) of similarity structures in **visual**, **auditory**, and **cognitive** regions of interest\* (ROIs)



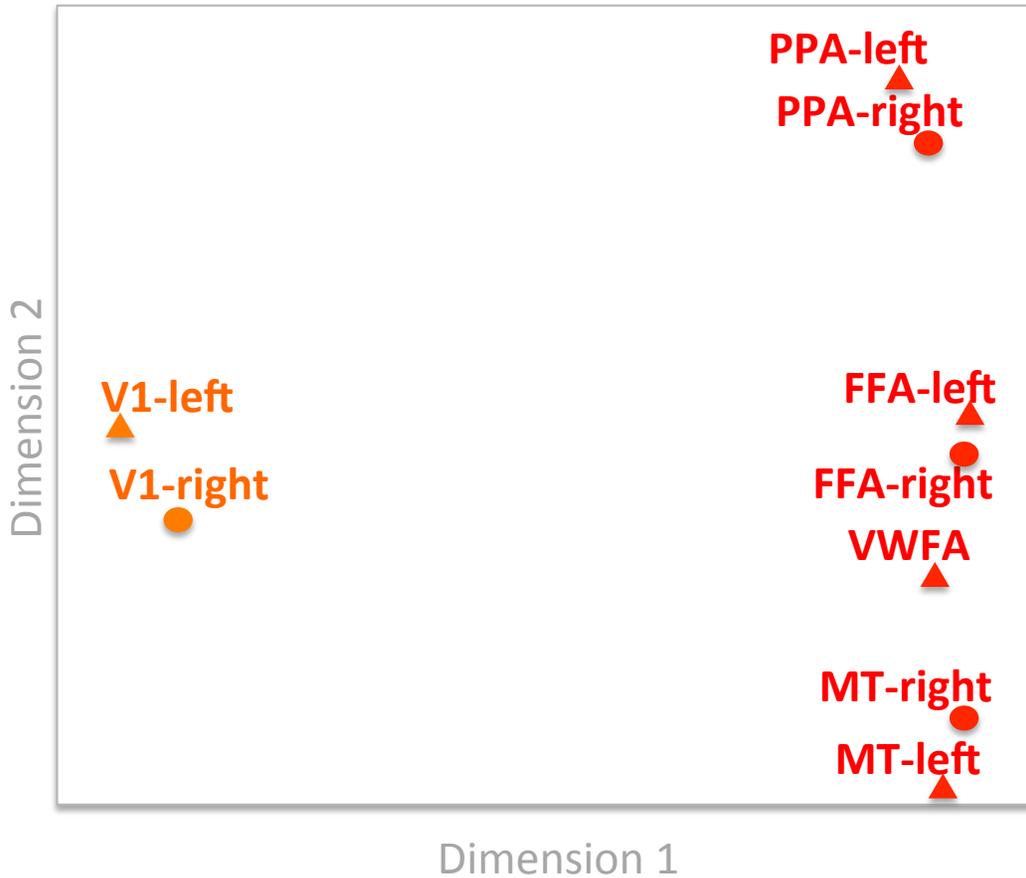
1<sup>st</sup> subspace (dimensions 1 & 2)



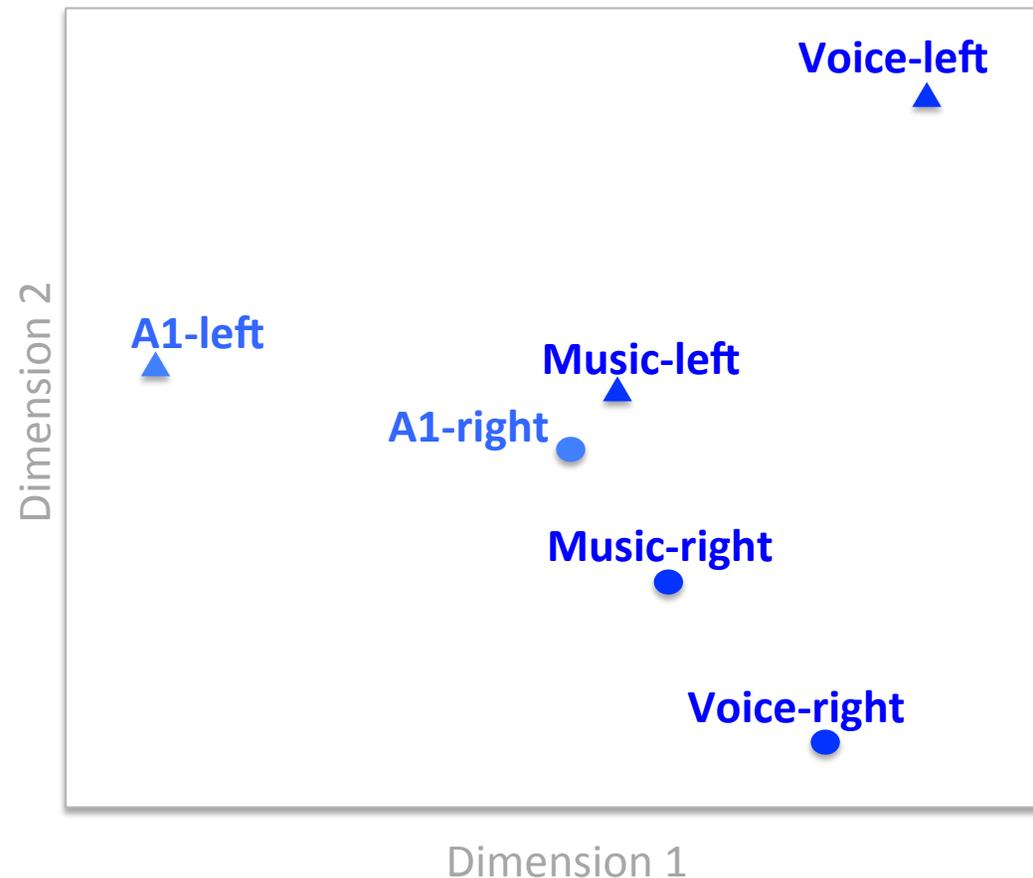
2<sup>nd</sup> subspace (dimensions 1 & 3)

\* ROI coordinates from Neurosynth

Multidimensional scaling (MDS) fit separately to  
**visual** and **auditory** ROIs



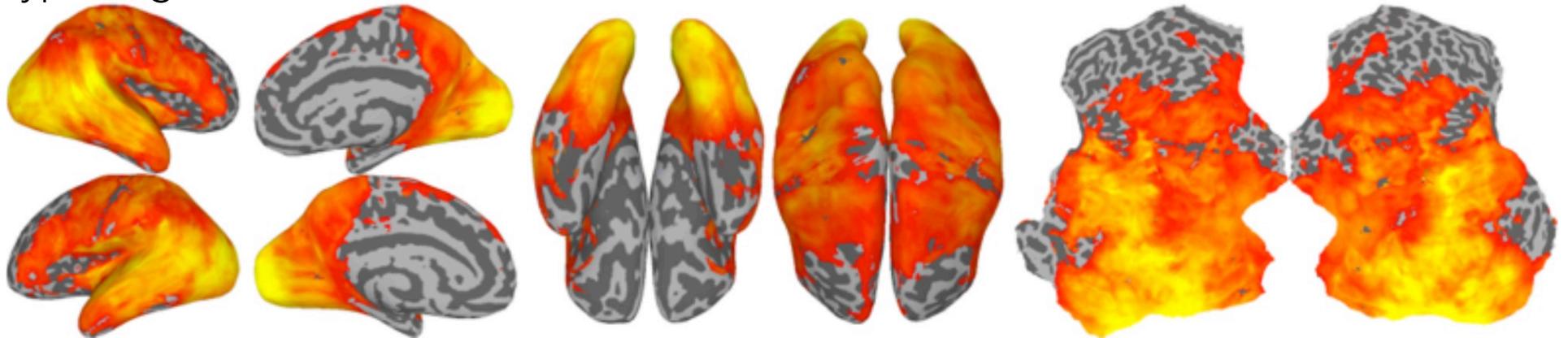
MDS of visual regions only



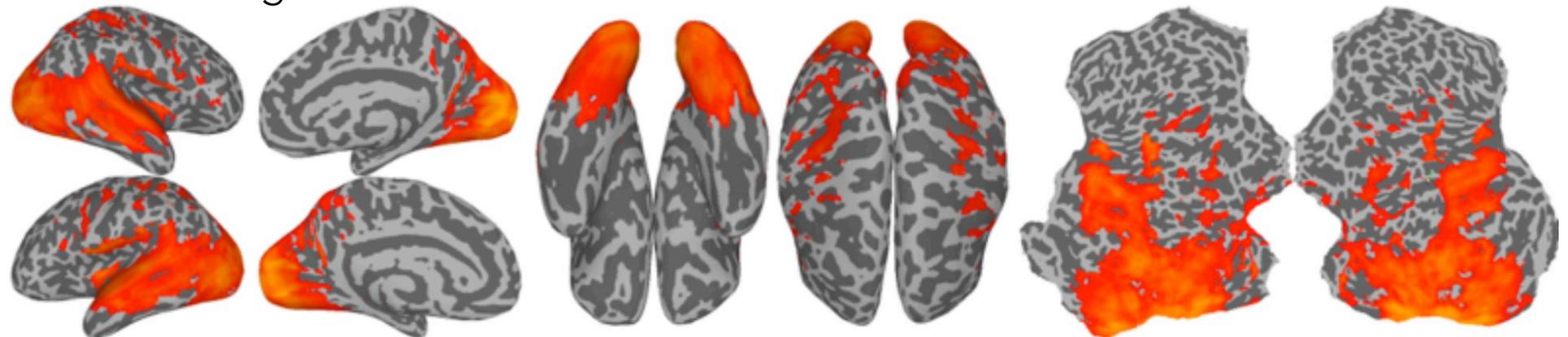
MDS of auditory regions only

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

Hyperalignment



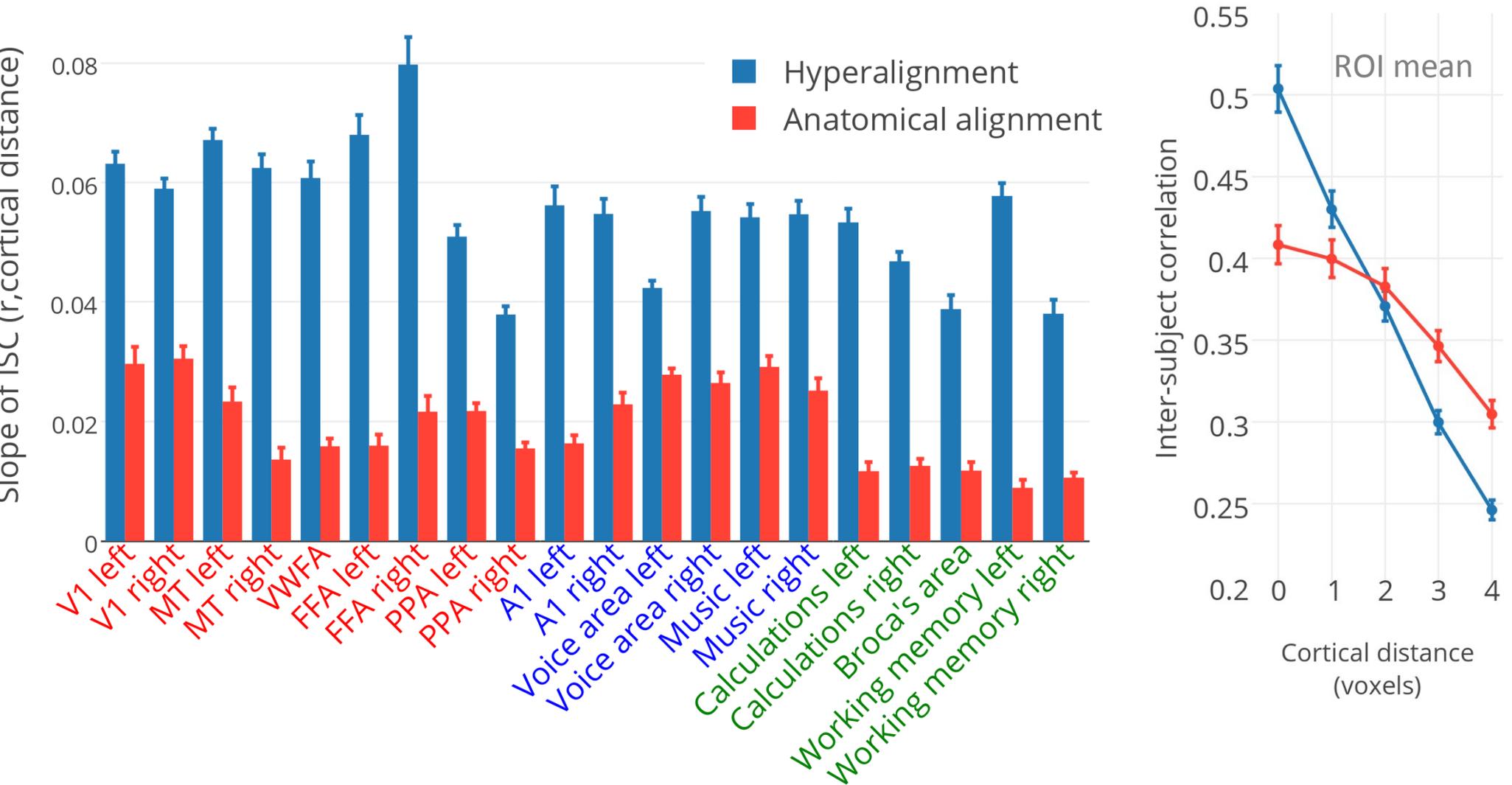
Anatomical alignment



Intersubject correlation



# Point spread function (intersubject correlations of movie time series): Fine spatial scale of alignment of function



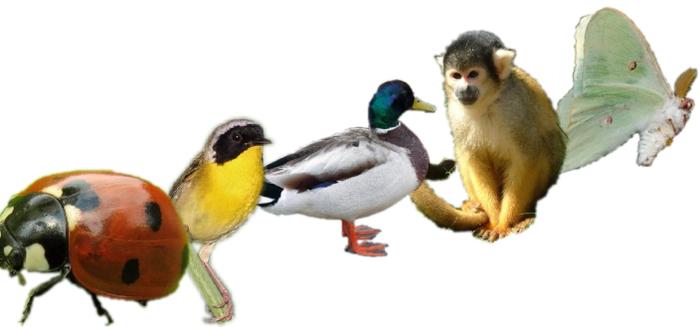
Experiment 2 data in Brain Space

Subject-specific Transformation Matrix

Experiment 2 data in Model Space

		<u>Voxels</u>					<u>Model dimensions</u>													
		$V_1$	$V_2$	$V_3$	...	$V_i$														
<u>Stimuli</u>	$S_1$	$X_{1,1}$	$X_{2,1}$	$X_{3,1}$	...	$X_{i,1}$	<u>Voxels</u>	$V_1$	$X_{1,1}$	$X_{2,1}$	$X_{3,1}$	...	$X_{k,1}$	<u>Stimuli</u>	$S_1$	$y_{1,1}$	$y_{2,1}$	$y_{3,1}$	...	$y_{k,1}$
	$S_2$	$X_{1,2}$	$X_{2,2}$	$X_{3,2}$	...	$X_{i,2}$		$V_2$	$X_{1,2}$	$X_{2,2}$	$X_{3,2}$	...	$X_{k,2}$		$S_2$	$y_{1,2}$	$y_{2,2}$	$y_{3,2}$	...	$y_{k,2}$
	$S_3$	$X_{1,3}$	$X_{2,3}$	$X_{3,3}$	...	$X_{i,3}$		$V_3$	$X_{1,3}$	$X_{2,3}$	$X_{3,3}$	...	$X_{k,3}$		$S_3$	$y_{1,3}$	$y_{2,3}$	$y_{3,3}$	...	$y_{k,3}$
	$S_4$	$X_{1,4}$	$X_{2,4}$	$X_{3,4}$	...	$X_{i,4}$		...	...	...	...	...	...		$S_4$	$y_{1,4}$	$y_{2,4}$	$y_{3,4}$	...	$y_{k,4}$
	...	...	...	...	...	...		$V_i$	$X_{1,i}$	$X_{2,i}$	$X_{3,i}$	...	$X_{i,k}$		...	...	...	...	...	...
	$S_m$	$X_{1,m}$	$X_{2,m}$	$X_{3,m}$	...	$X_{i,m}$										$S_m$	$y_{1,m}$	$y_{2,m}$	$y_{3,m}$	...

$\times$        $=$



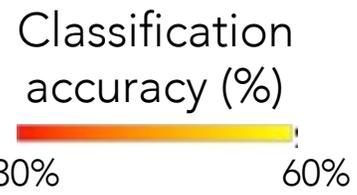
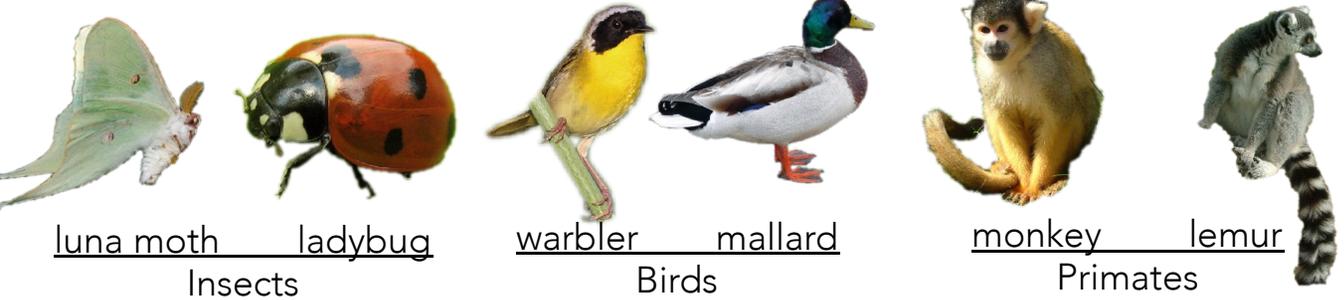
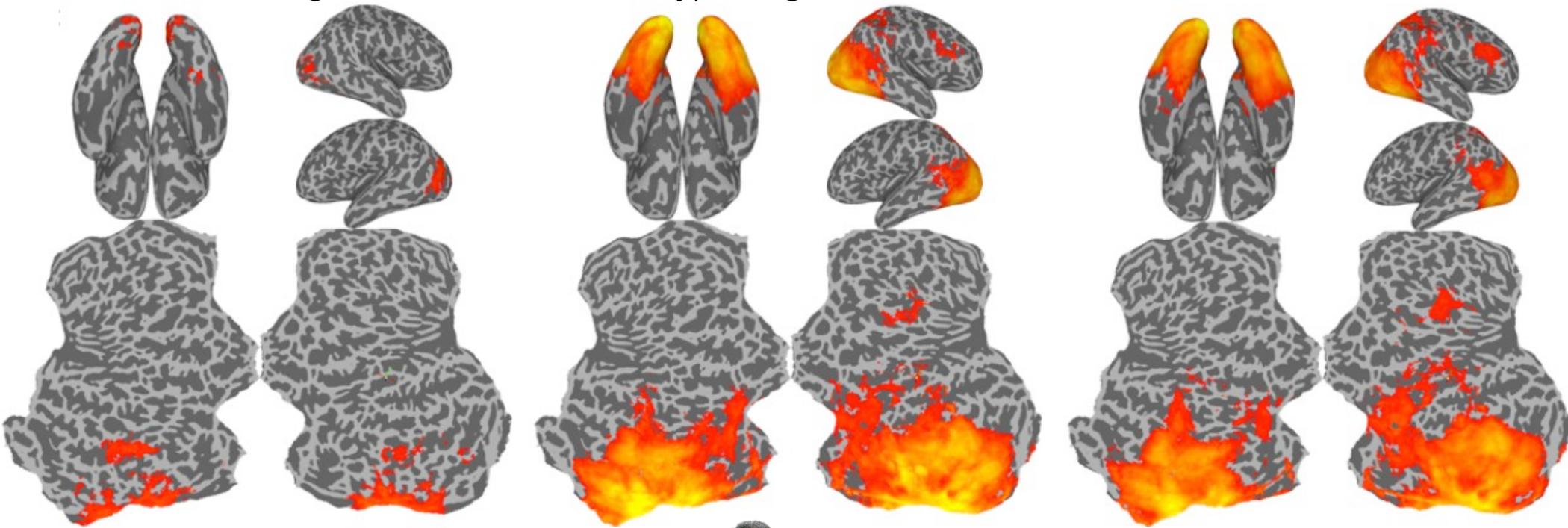
Whole-brain hyperalignment based on movie affords between-subject classification of responses in a visual category experiment (6 animal species) *at levels of accuracy that exceed within-subject classification*

Between-subject classification

Within-subject classification

Anatomical alignment

Hyperalignment





*Raiders of the Lost Ark*

*Life on Earth*

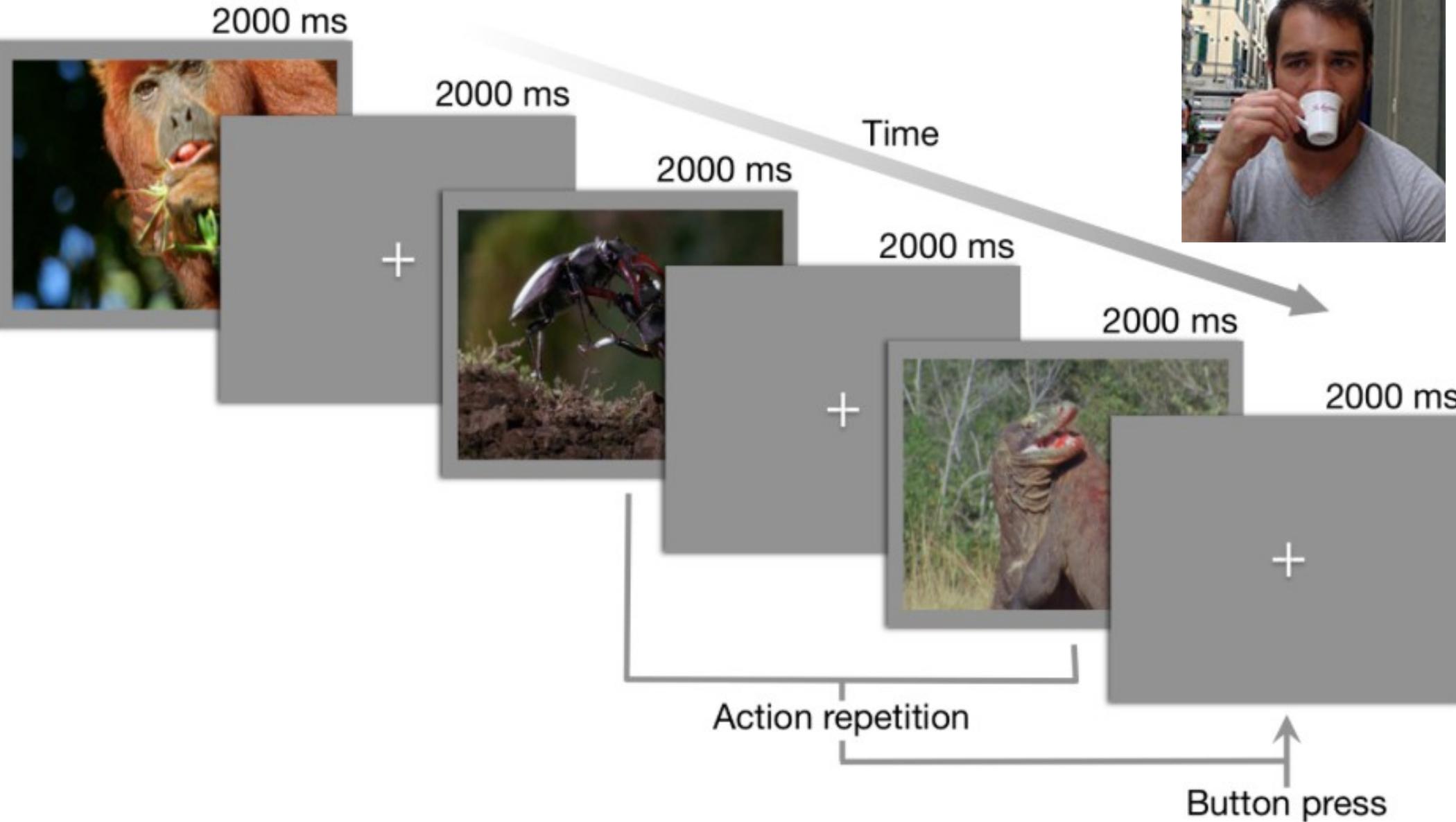


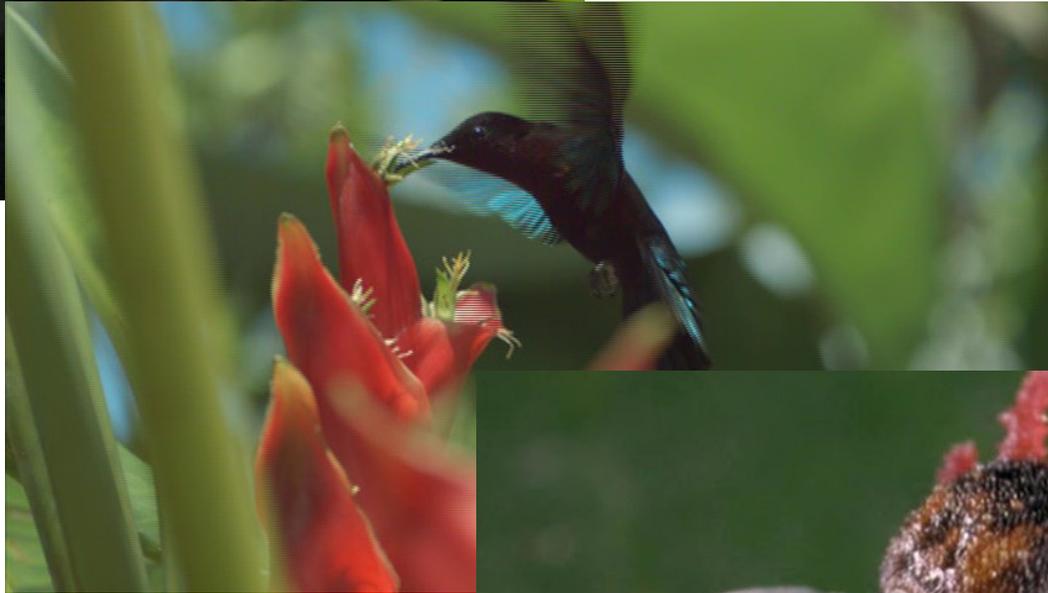
Hyperalignment parameters are estimated from responses recorded during movie viewing



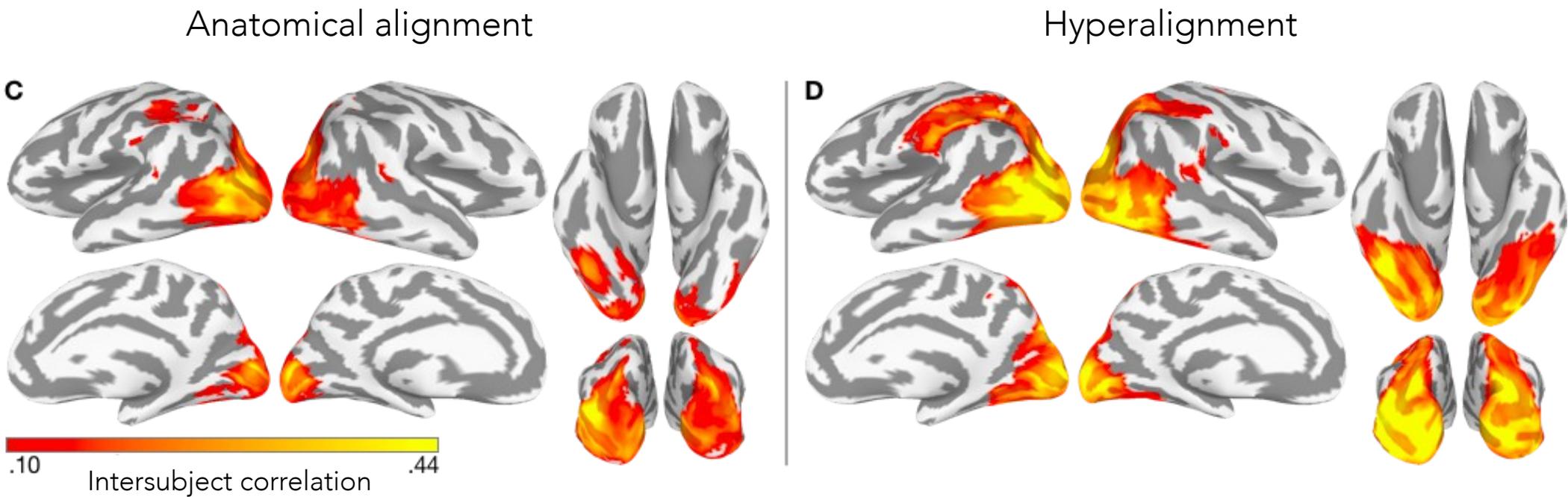
*The Wire*

Study of the effect of attention on the geometry of representations of animal taxa and animal behaviors  
(Nastase et al., bioRxiv, 2016; under review)

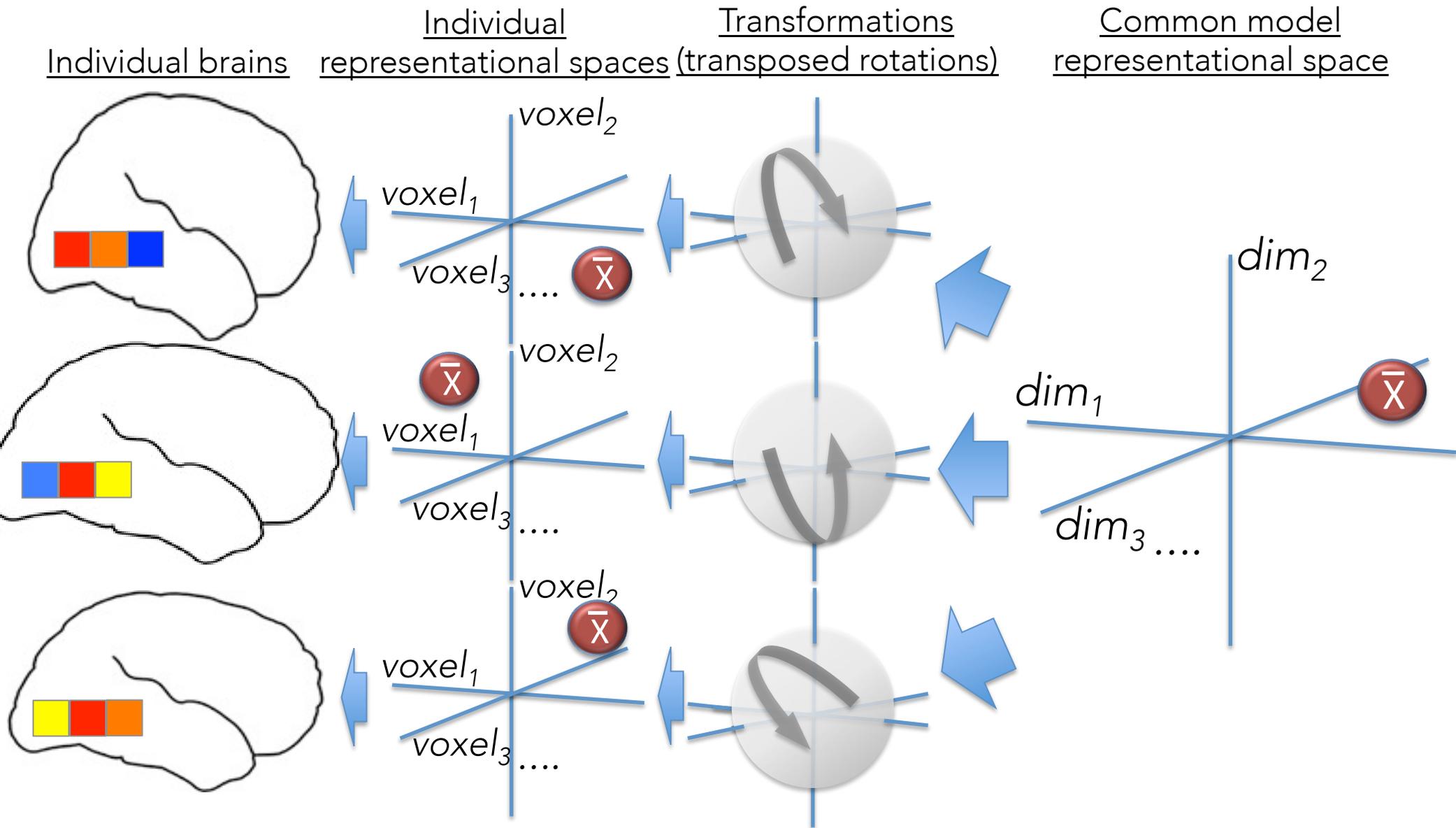




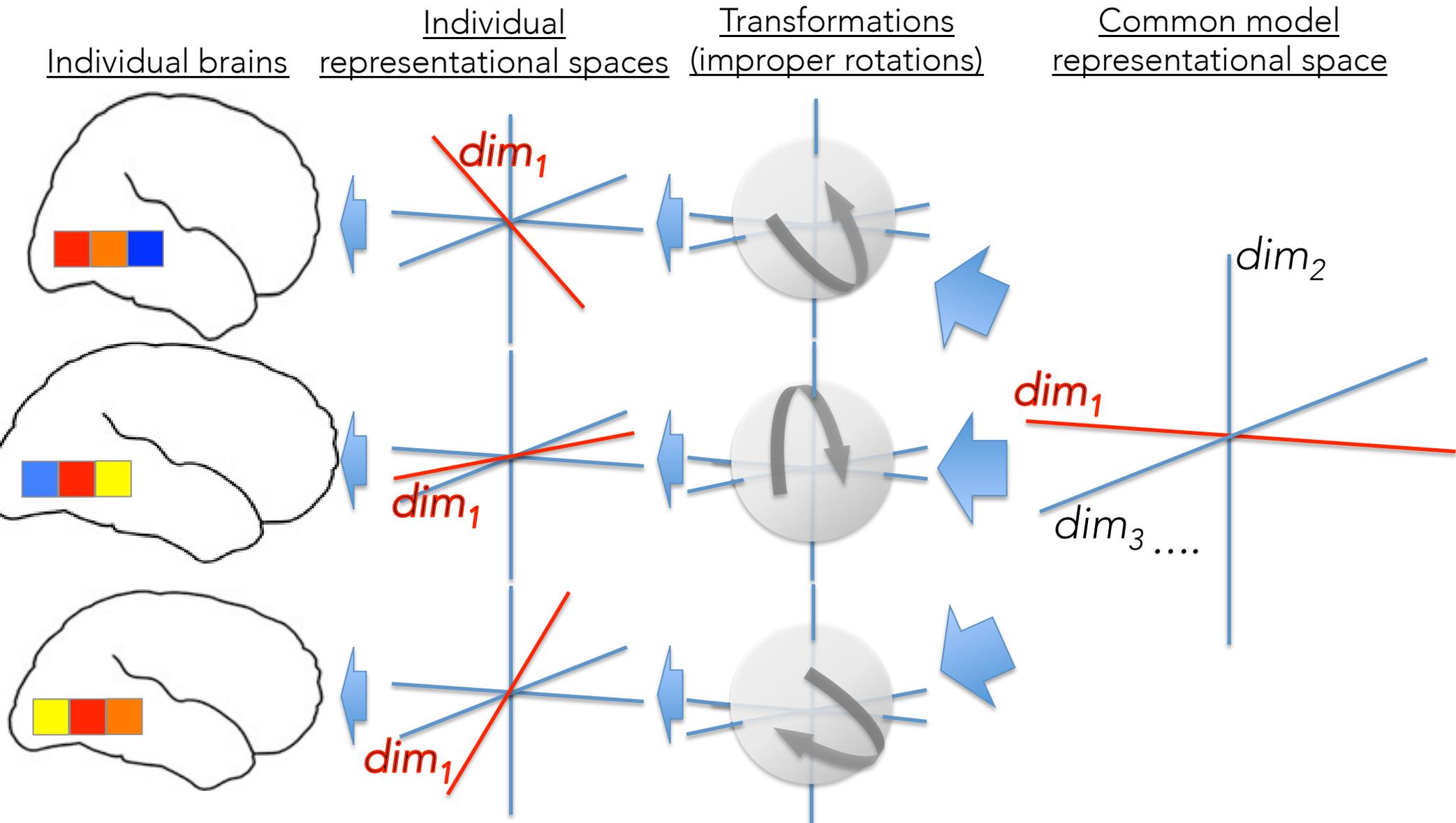
Higher inter-subject correlation of representational geometries for animal behaviors and taxa after hyperalignment  
(Nastase et al., bioRxiv, 2016; under review)



# Projecting group data from common model space into individual subject's anatomy



# Modeling functional architecture of the human cortex: common model dimensions $\neq$ voxels



Movie data in  
Brain Space

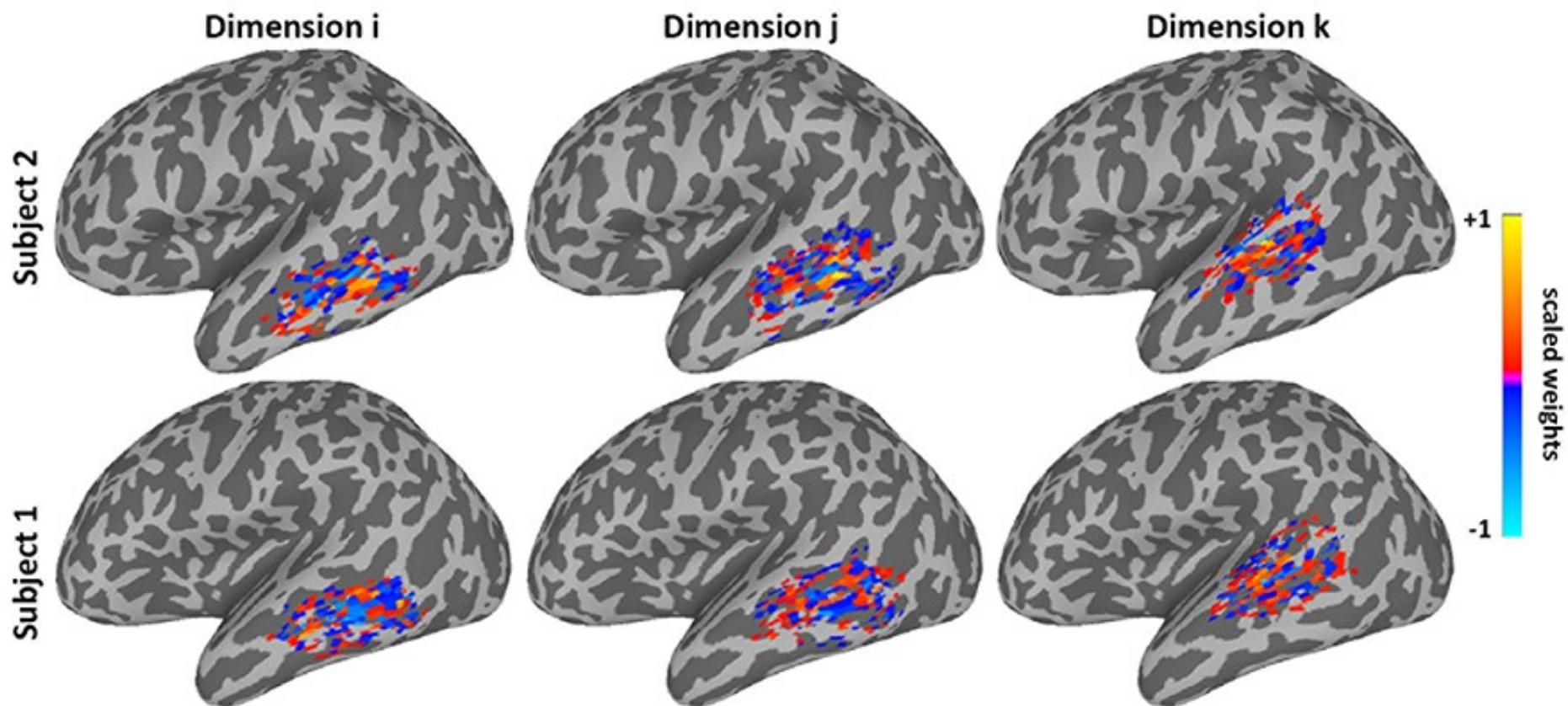
Subject-specific  
Transformation Matrix

Movie data in  
Model Space

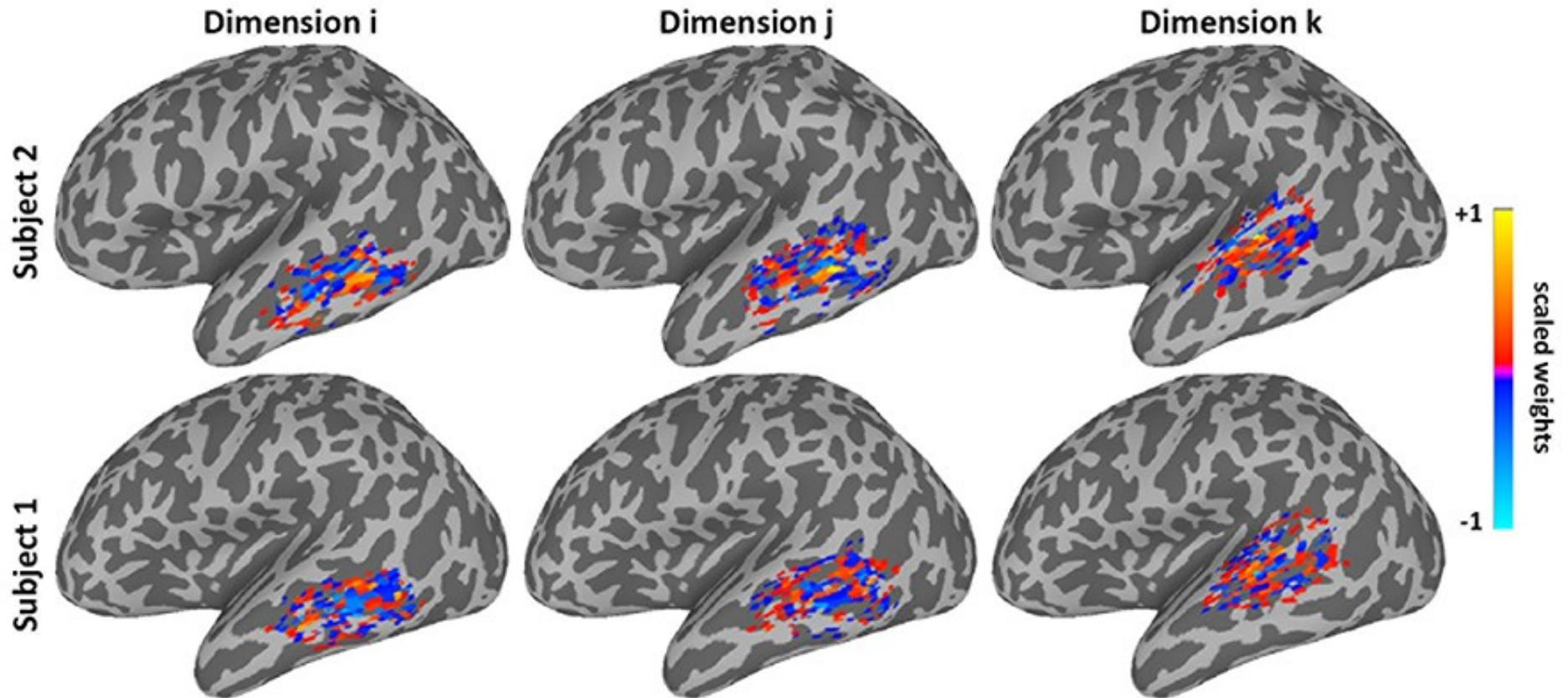
		<u>Voxels</u>											<u>Model dimensions</u>															
		$v_1$	$v_2$	$v_3$	...	$v_i$							$d_1$	$d_2$	$d_3$	...	$d_k$							$d_1$	$d_2$	$d_3$	...	$d_k$
<u>Time-points</u>	$t_1$	$x_{1,1}$	$x_{2,1}$	$x_{3,1}$	...	$x_{i,1}$	X	$v_1$	$w_{1,1}$	$w_{2,1}$	$w_{3,1}$	...	$w_{k,1}$	=	<u>Time-points</u>	$t_1$	$y_{1,1}$	$y_{2,1}$	$y_{3,1}$	...	$y_{k,1}$							
	$t_2$	$x_{1,2}$	$x_{2,2}$	$x_{3,2}$	...	$x_{i,2}$		$v_2$	$w_{1,2}$	$w_{2,2}$	$w_{3,2}$	...	$w_{k,2}$			$t_2$	$y_{1,2}$	$y_{2,2}$	$y_{3,2}$	...	$y_{k,2}$							
	$t_3$	$x_{1,3}$	$x_{2,3}$	$x_{3,3}$	...	$x_{i,3}$		$v_3$	$w_{1,3}$	$w_{2,3}$	$w_{3,3}$	...	$w_{k,3}$			$t_3$	$y_{1,3}$	$y_{2,3}$	$y_{3,3}$	...	$y_{k,3}$							
	$t_4$	$x_{1,4}$	$x_{2,4}$	$x_{3,4}$	...	$x_{i,4}$		...	...	...	...	...	...			$t_4$	$y_{1,4}$	$y_{2,4}$	$y_{3,4}$	...	$y_{k,4}$							
	...	...	...	...	...	...		$v_i$	$w_{1,i}$	$w_{2,i}$	$w_{3,i}$	...	$w_{k,i}$			...	...	...	...	...	...							
	$t_j$	$x_{1,j}$	$x_{2,j}$	$x_{3,j}$	...	$x_{i,j}$											$t_j$	$y_{1,j}$	$y_{2,j}$	$y_{3,j}$	...	$y_{k,j}$						

Model dimensions have individual-specific topographic basis functions

# Topographies of weights for three model dimensions in two subjects

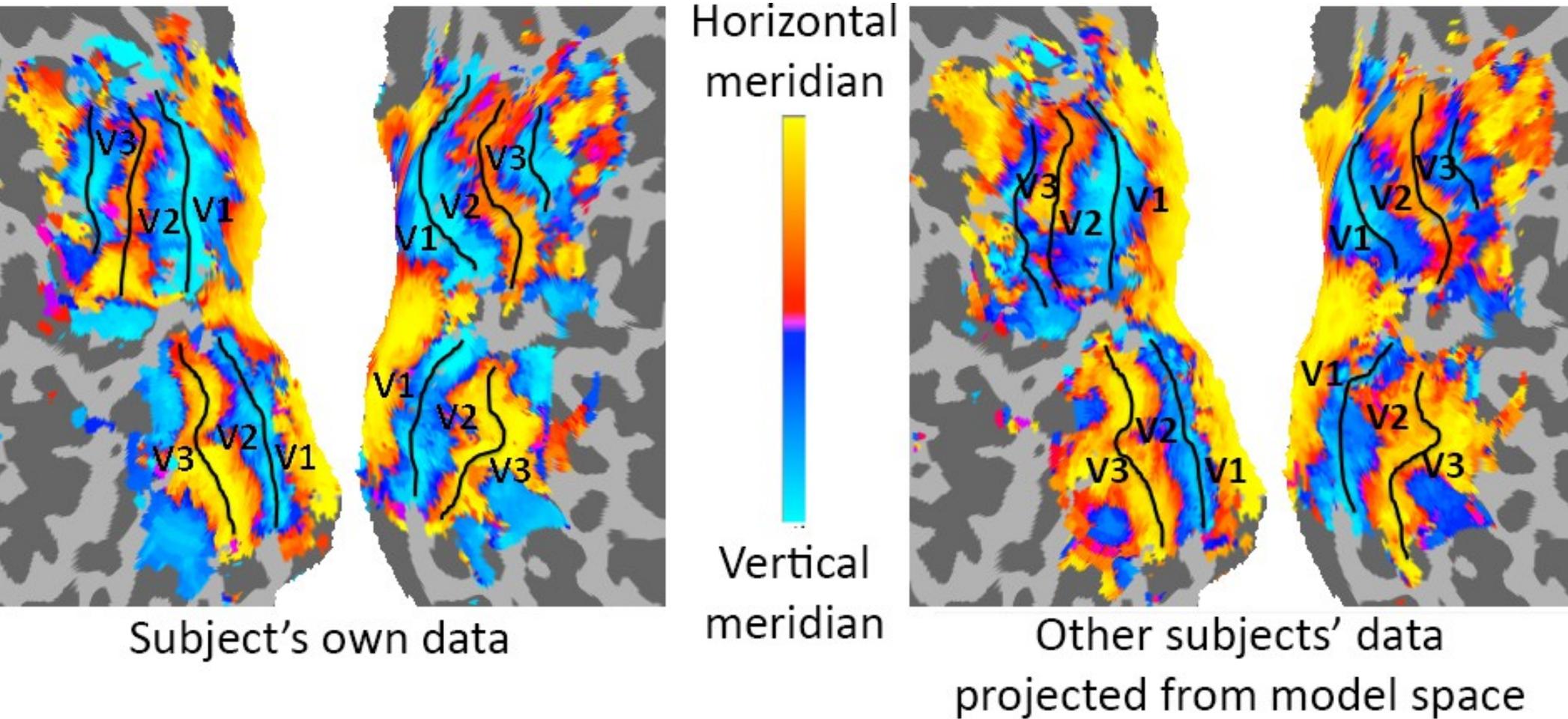


Topographies for response patterns can be modeled in different brains with these individual-specific topographic basis functions using the same weights for for all subjects



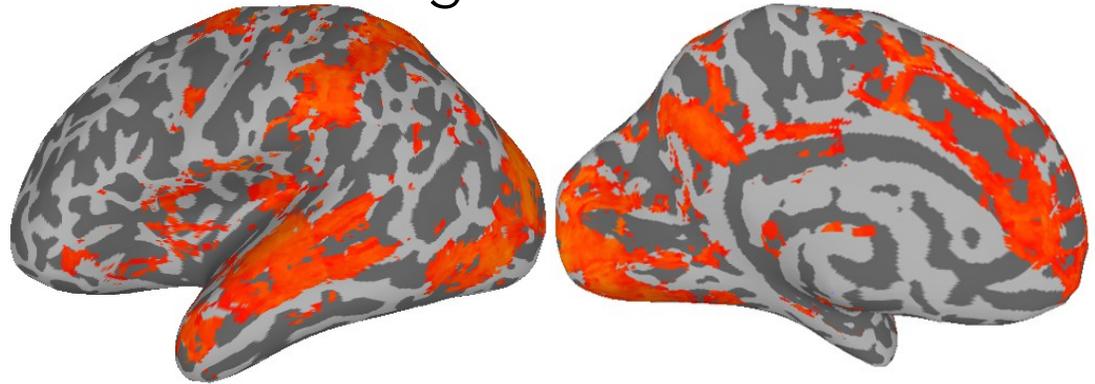
$$\sum \beta_1 * T_{1Sx} \dots + \beta_i * T_{iSx} \dots + \beta_j * T_{jSx} \dots + \beta_k * T_{kSx} \dots$$

Mapping retinotopy by projecting other subjects' polar angle maps into a different subject's occipital topography



Brain connectivity patterns are better aligned in the common model space

Anatomical alignment

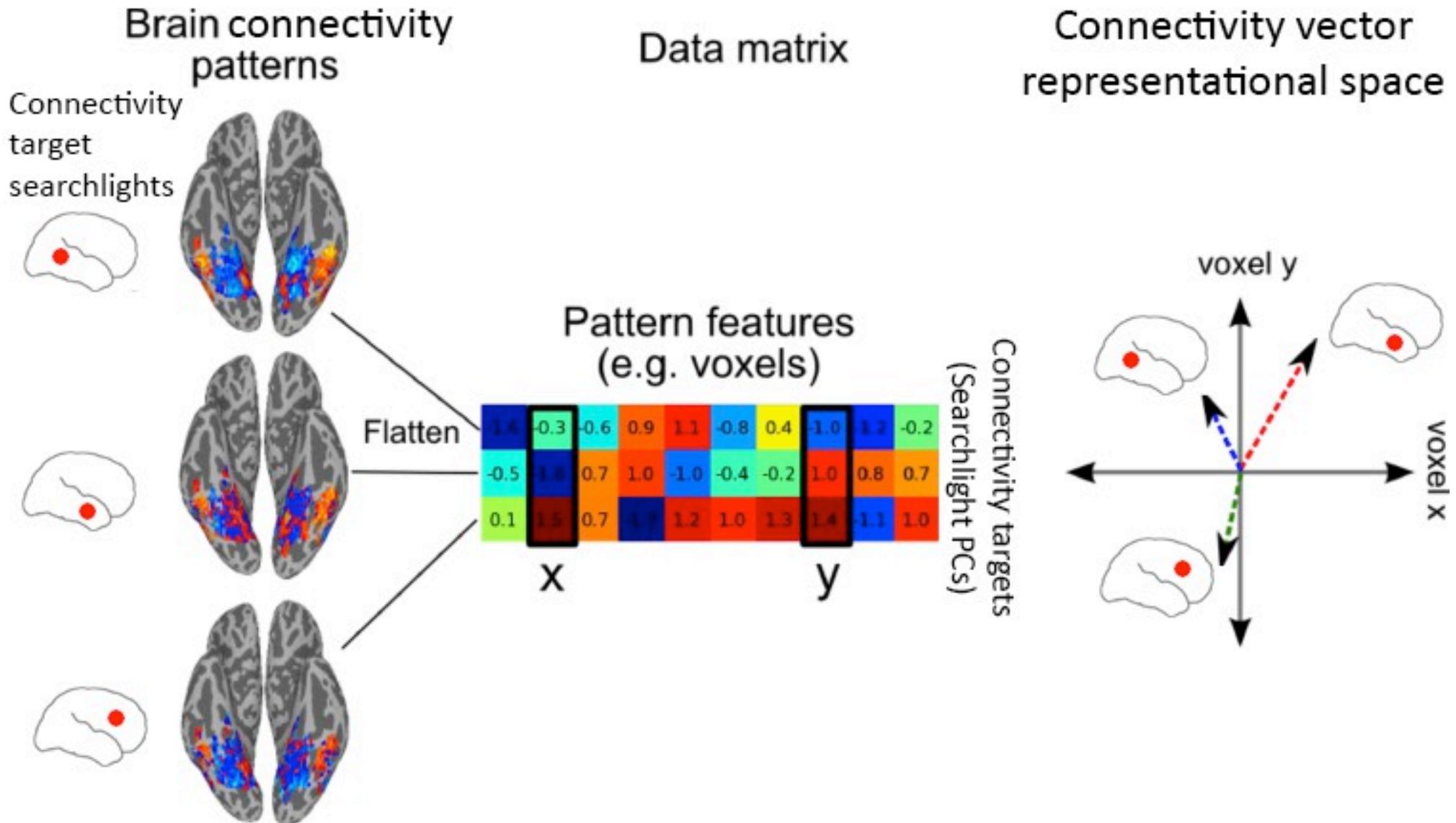


Hyperalignment



Inter-subject correlation of connectivity vectors

# Connectivity hyperalignment

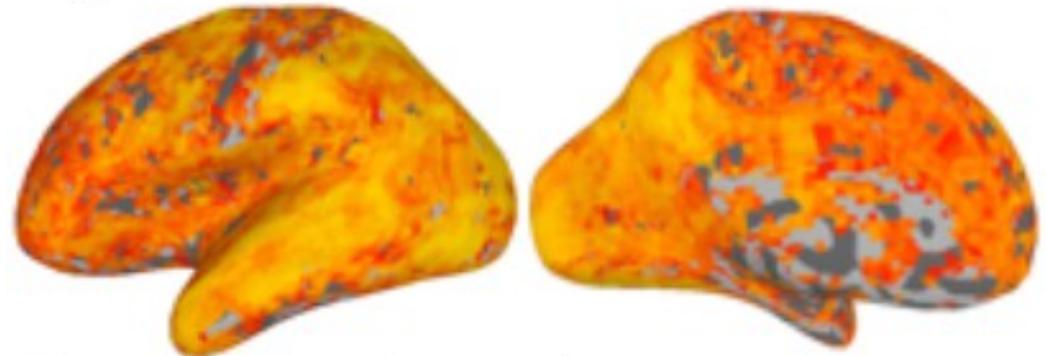


Brain connectivity patterns are better aligned in the common model space

Anatomical alignment



Hyperalignment



Connectivity hyperalignment

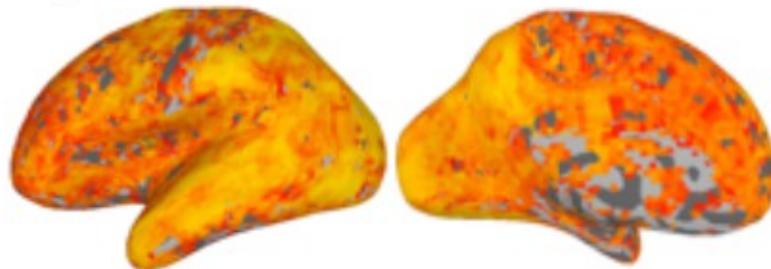


Brain connectivity patterns are better aligned in the  
common model space  
and have a surprisingly fine-scale granularity (PSF)

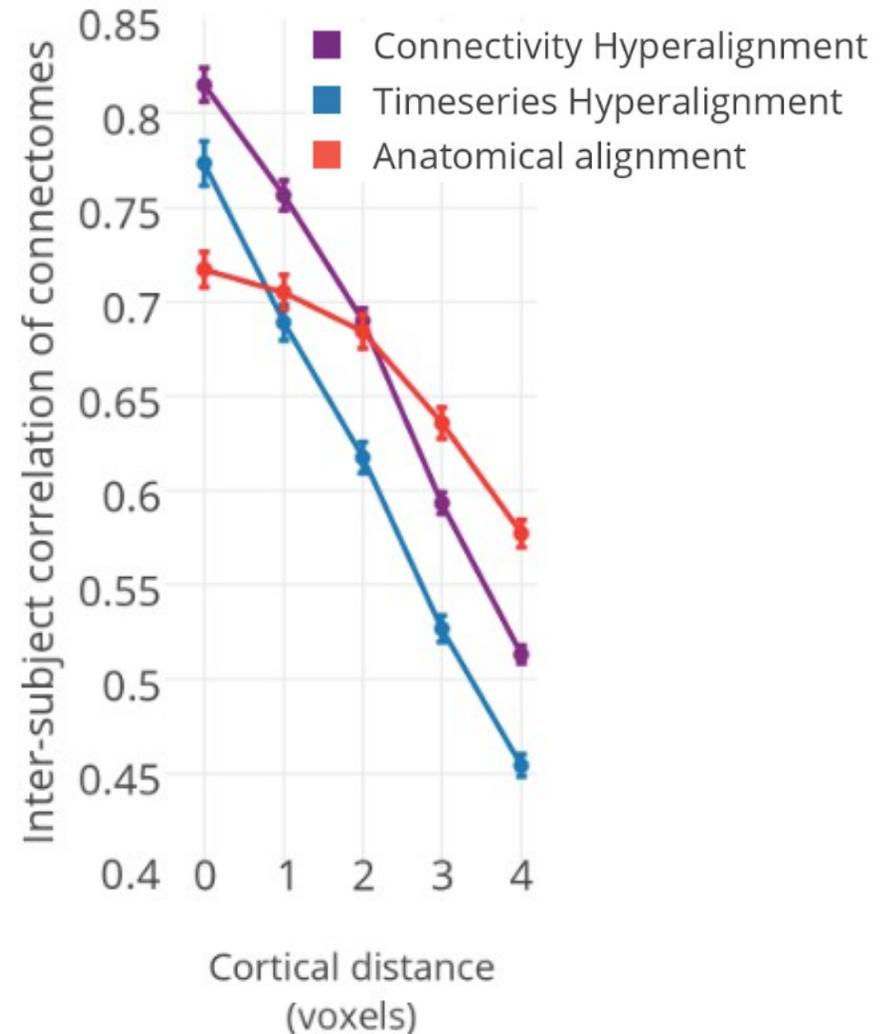
Anatomical alignment



Hyperalignment

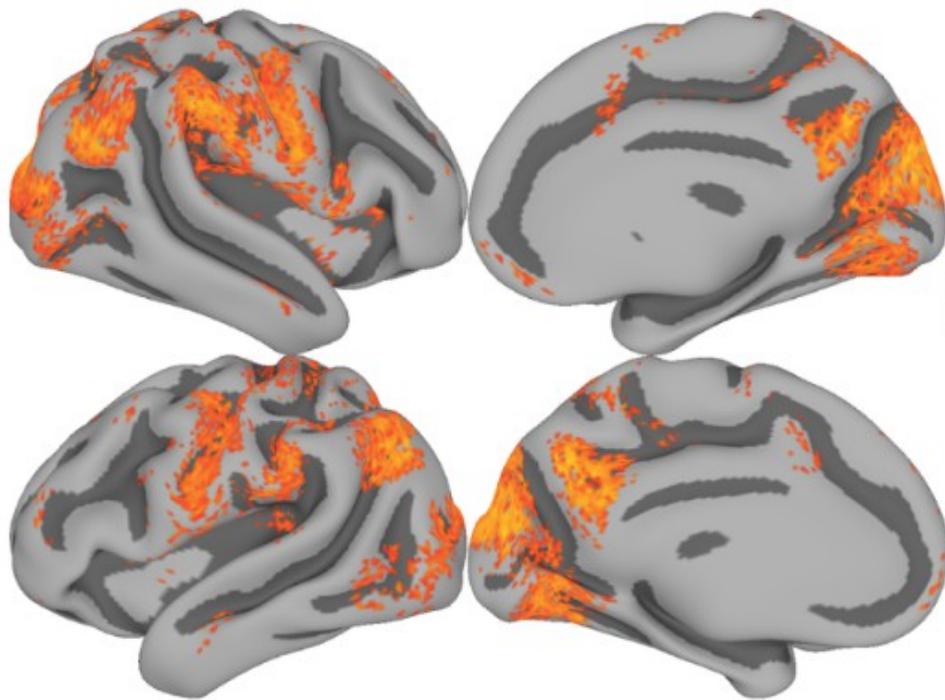


Connectivity hyperalignment

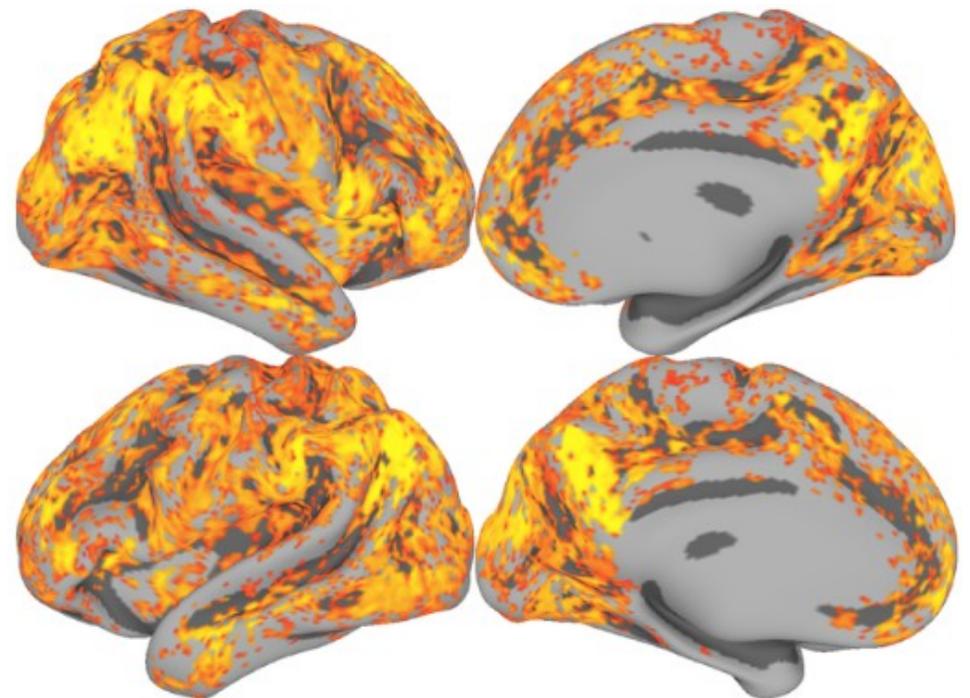


# Connectivity hyperalignment of Human Connectome Project (HCP) resting state fMRI data (n=20) increases ISC of connectivity vectors

Sulcal alignment



Connectivity hyperalignment

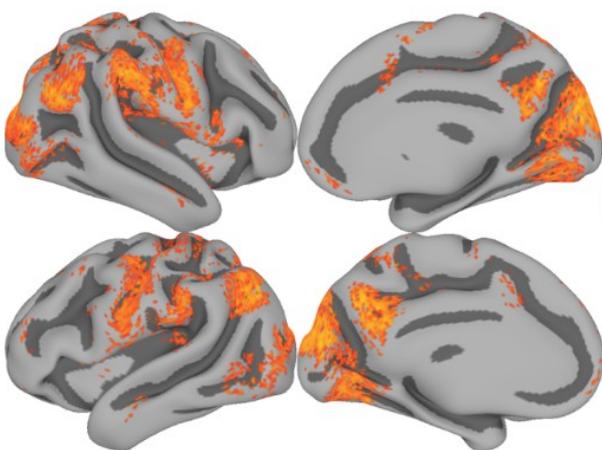


Correlation

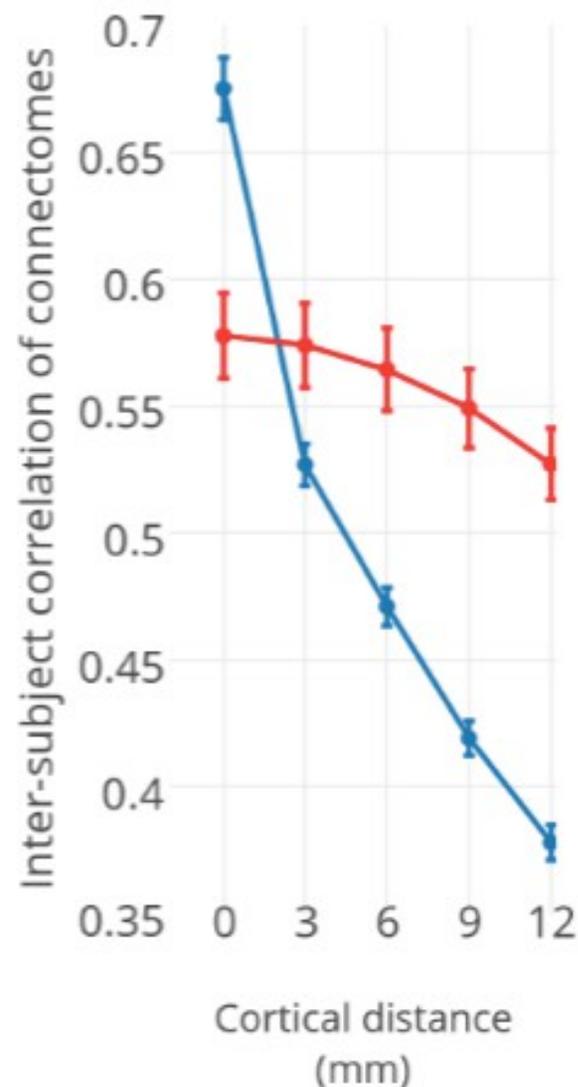
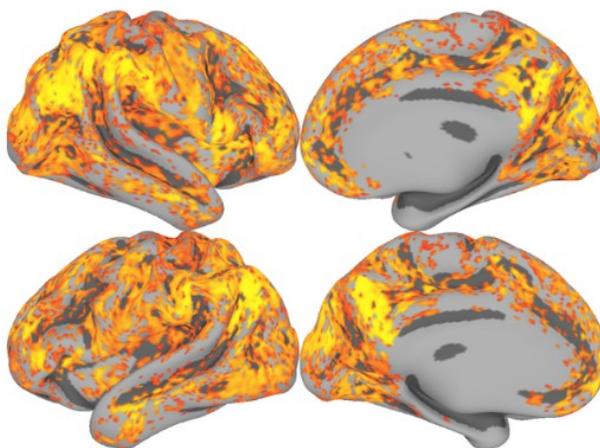


# Connectivity hyperalignment of Human Connectome Project (HCP) resting state fMRI data (N=20) increases ISC of connectivity vectors and reveals a fine-scale architecture

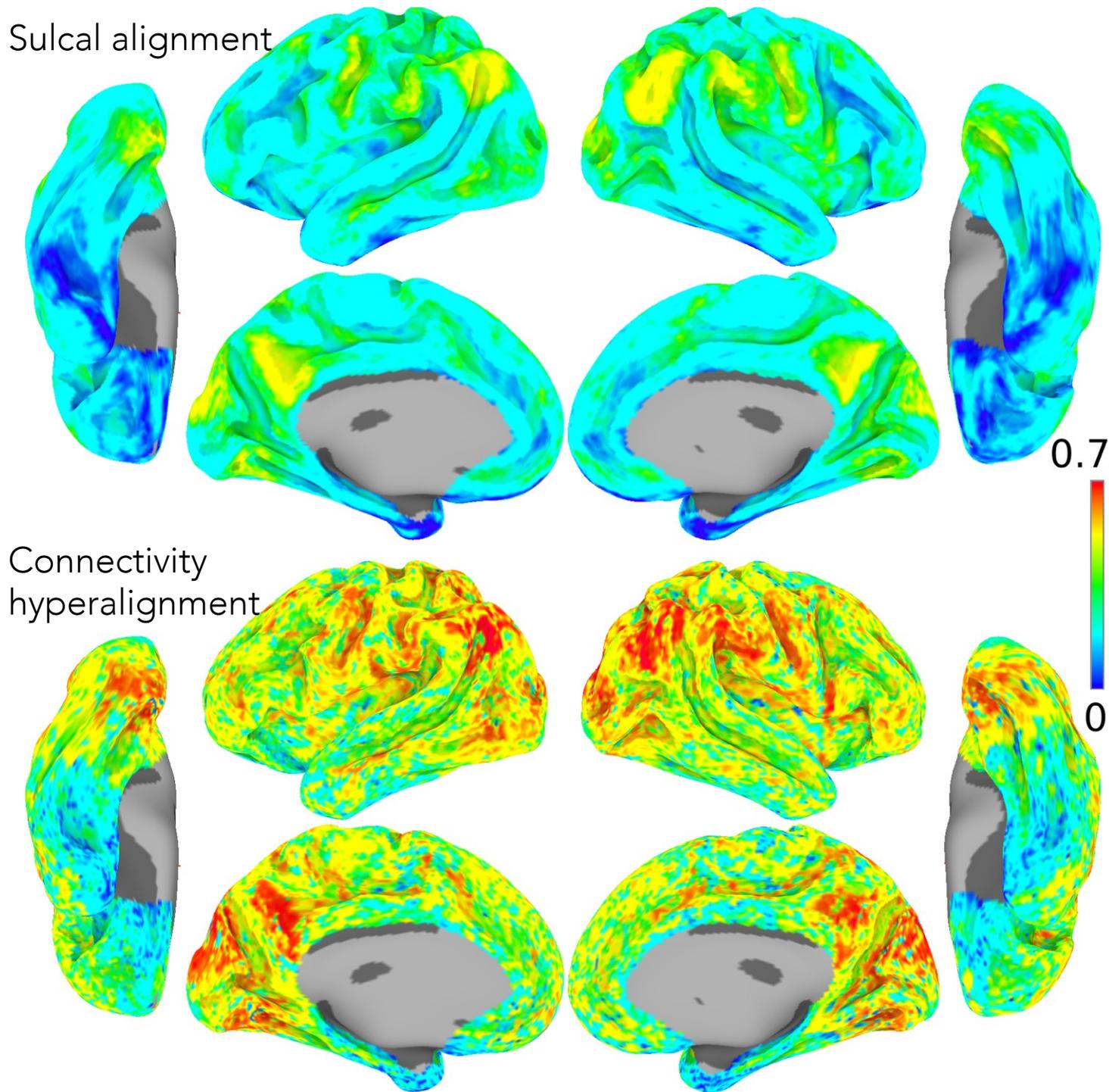
Sulcal alignment



Connectivity hyperalignment

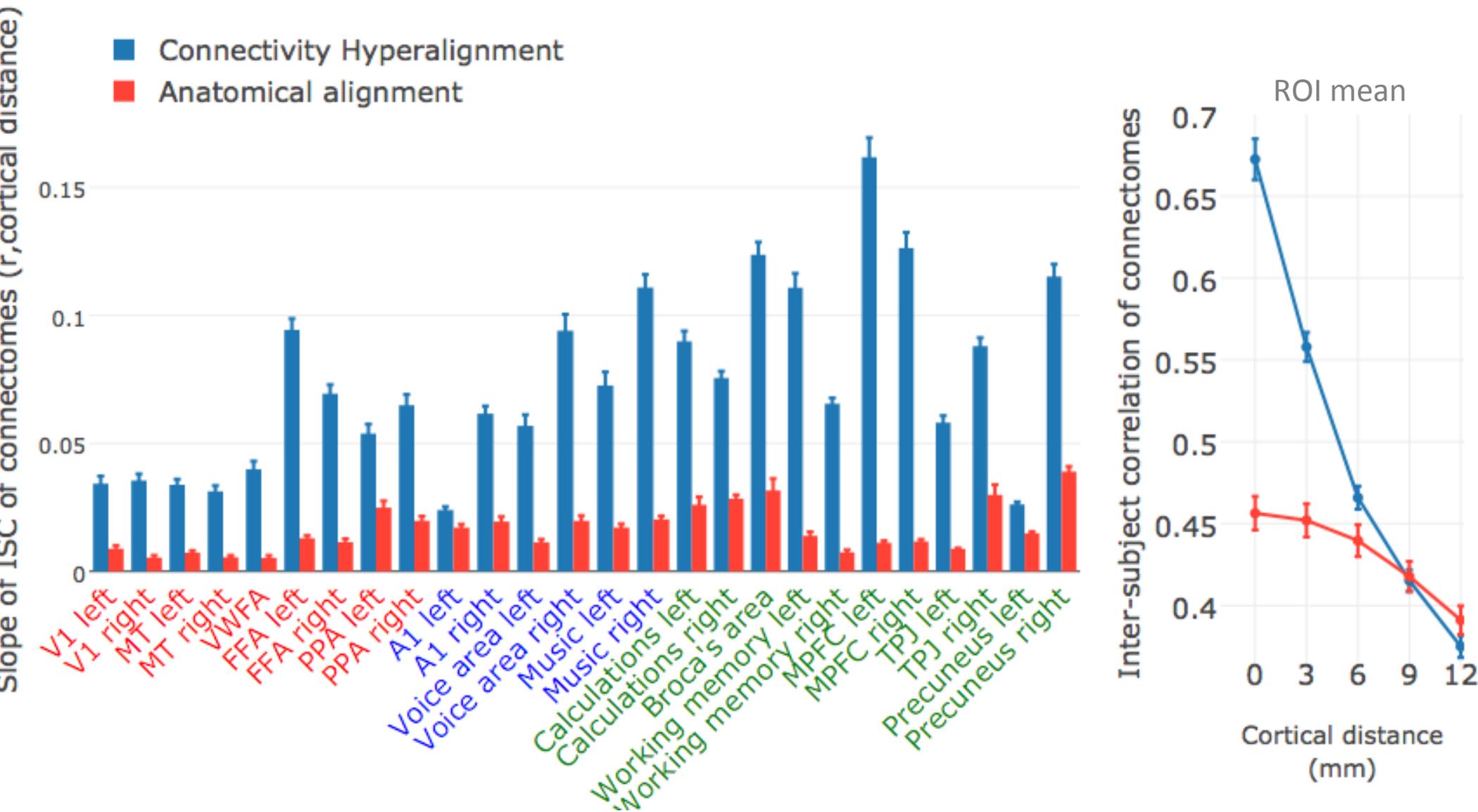


Connectivity  
hyperalignment  
of Human  
Connectome  
Project (HCP)  
resting state fMRI  
data increases  
ISC of  
connectivity  
vectors



Do variations in connectivity profiles also have a fine spatial scale? YES

Point spread function (intersubject correlations of connectivity vectors, HCP data)



# 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
- Conceptual framework: high-dimensional representational spaces
- Deriving the common space and individual transformation matrices with hyperalignment
- Validation
- **Conclusions**

## Common model: Basic components

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

# 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

The Common Model accounts for the fine-grained structure of cortical architecture and coarse-grained areal topography

- Captures common bases for the fine-grained structure of local variations in response tuning and functional connectivity profiles
- Preserves and models individual variation of coarse-grained areal topography

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

The common model

- accounts for 4X more variance
- affords 7X higher bsMVPC accuracies

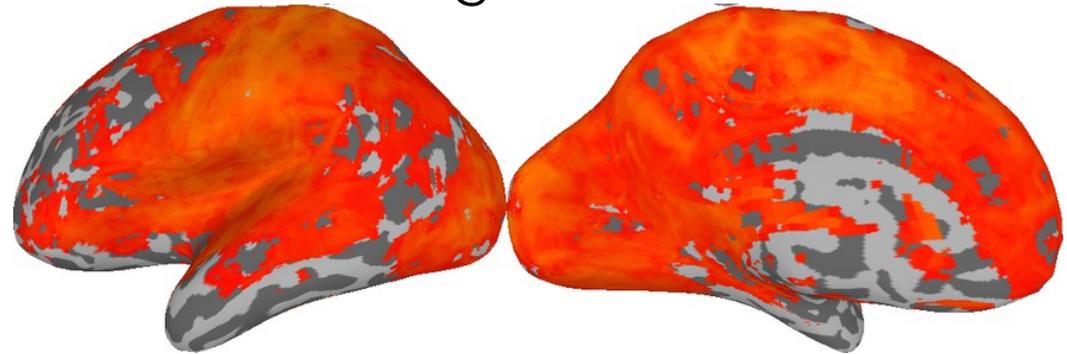
Software for hyperalignment and data are on PyMVPA  
([www.pymvpa.org](http://www.pymvpa.org))



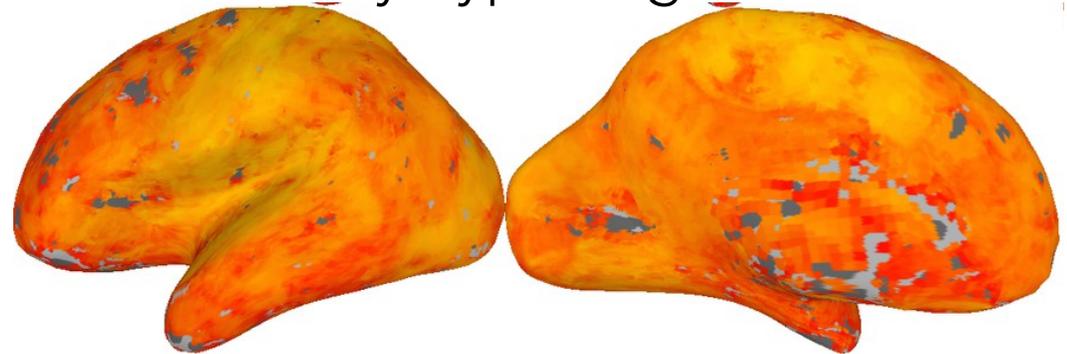
Guntupalli et al. (2016) A model of representational spaces in human cortex.  
*Cerebral Cortex*, epub ahead of print, open access.

Connectivity  
hyperalignment  
of resting state  
fMRI increases  
ISC of  
connectivity  
vectors

Anatomical alignment

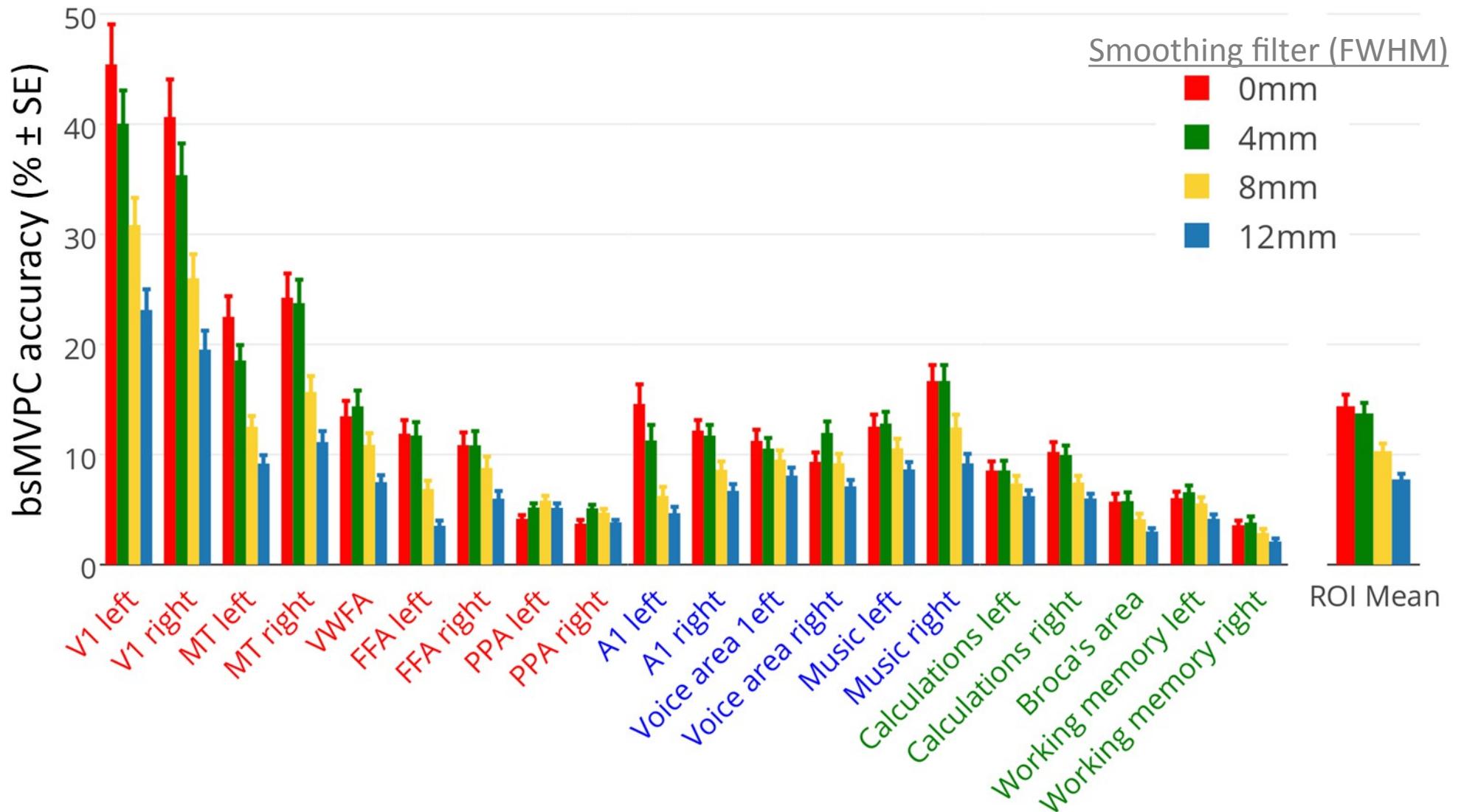


Connectivity hyperalignment



# Smoothing reduces bsMVPC accuracies

In all **visual**, **auditory**, and **cognitive** regions of interest (ROIs)





*Raiders of the Lost Ark*

*Life on Earth*

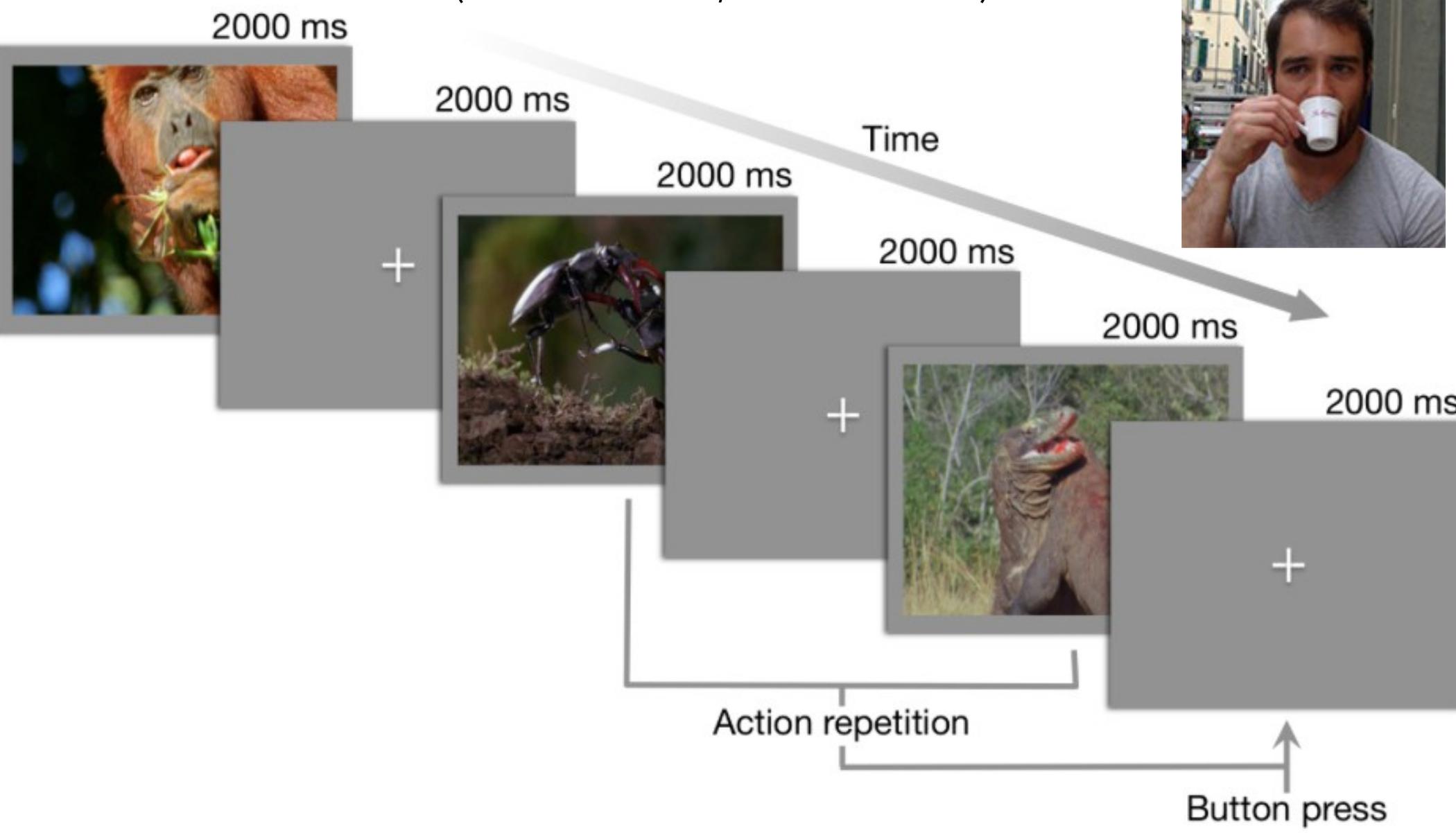


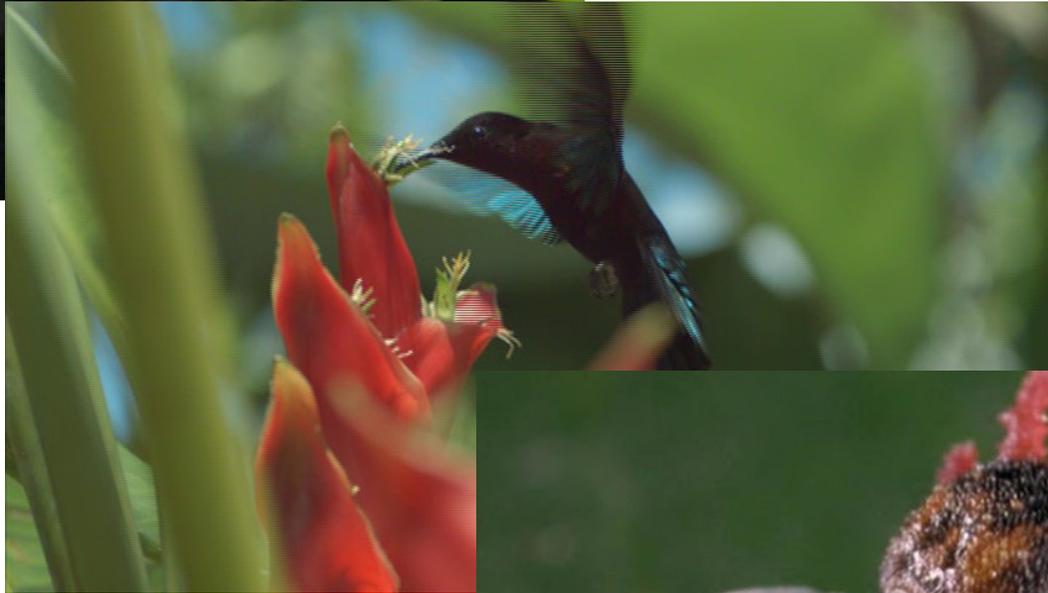
Hyperalignment parameters are estimated from responses recorded during movie viewing



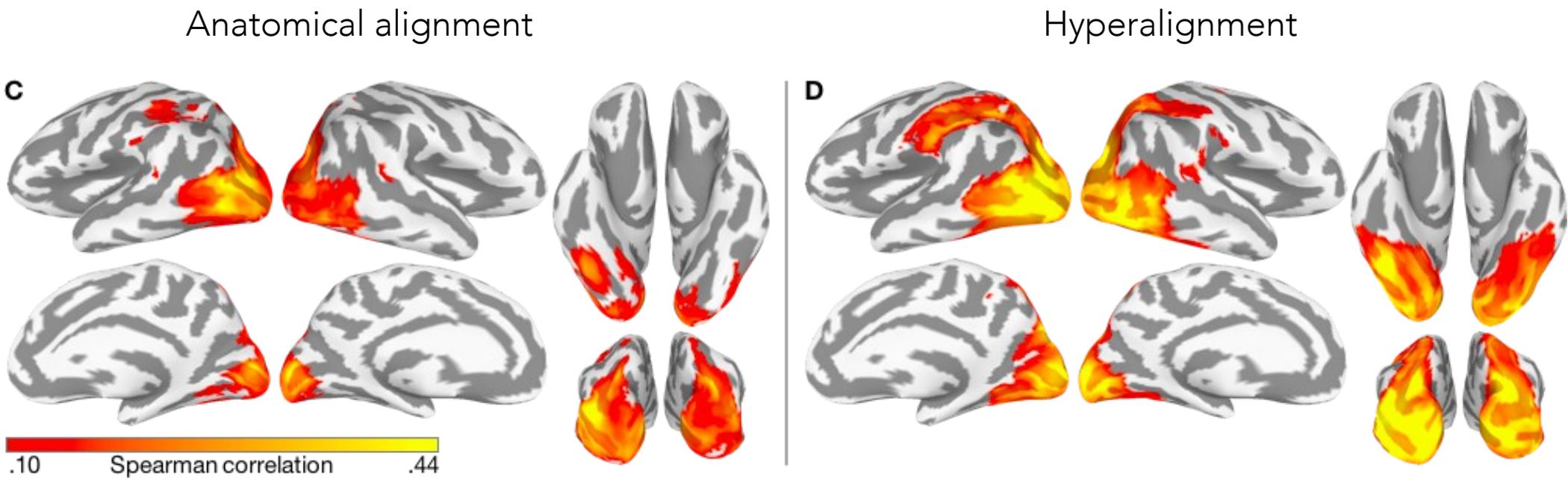
*The Wire*

Study of the effect of attention on the geometry of representations of animal taxa and animal behaviors (Nastase et al., under review)

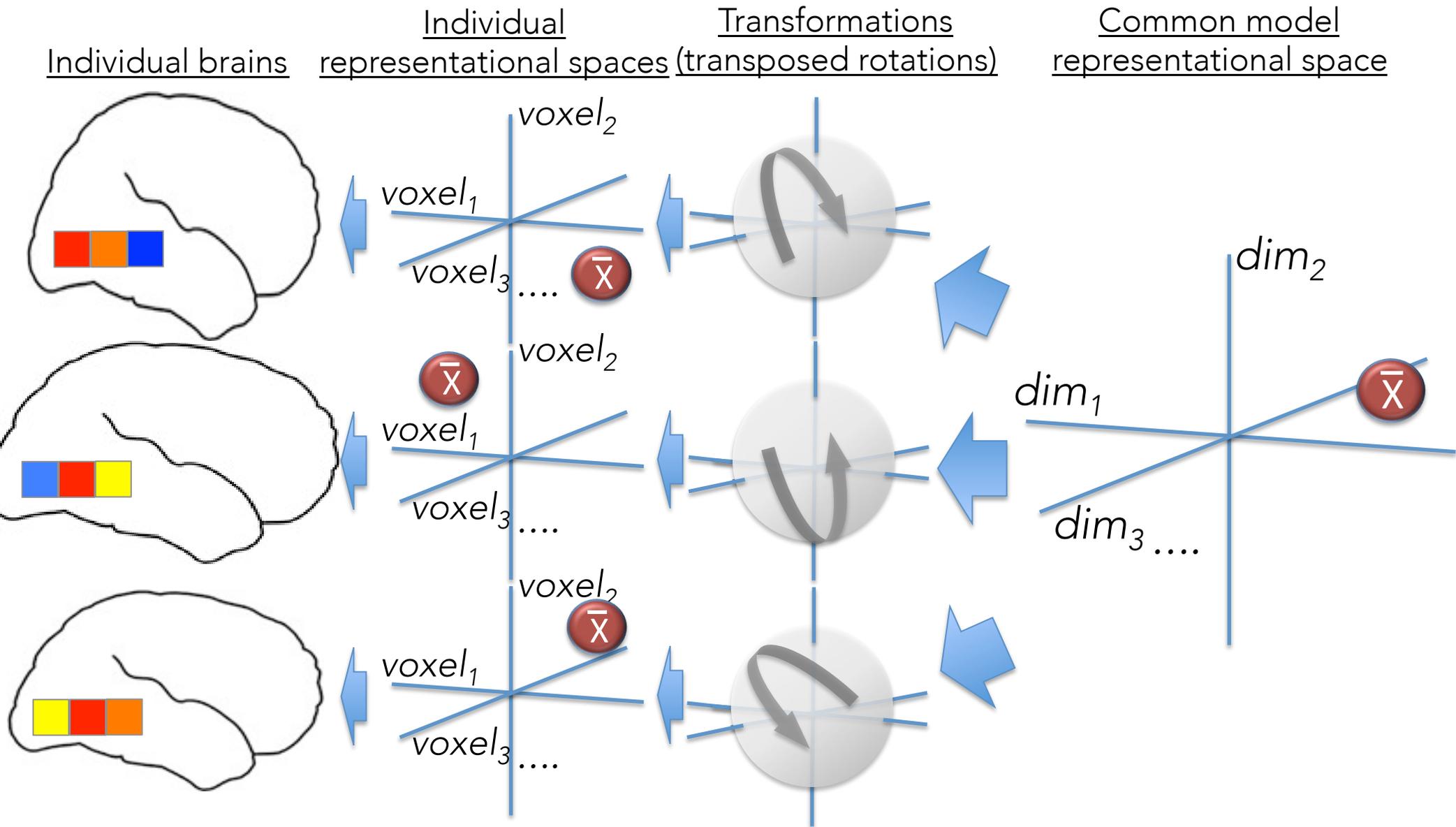




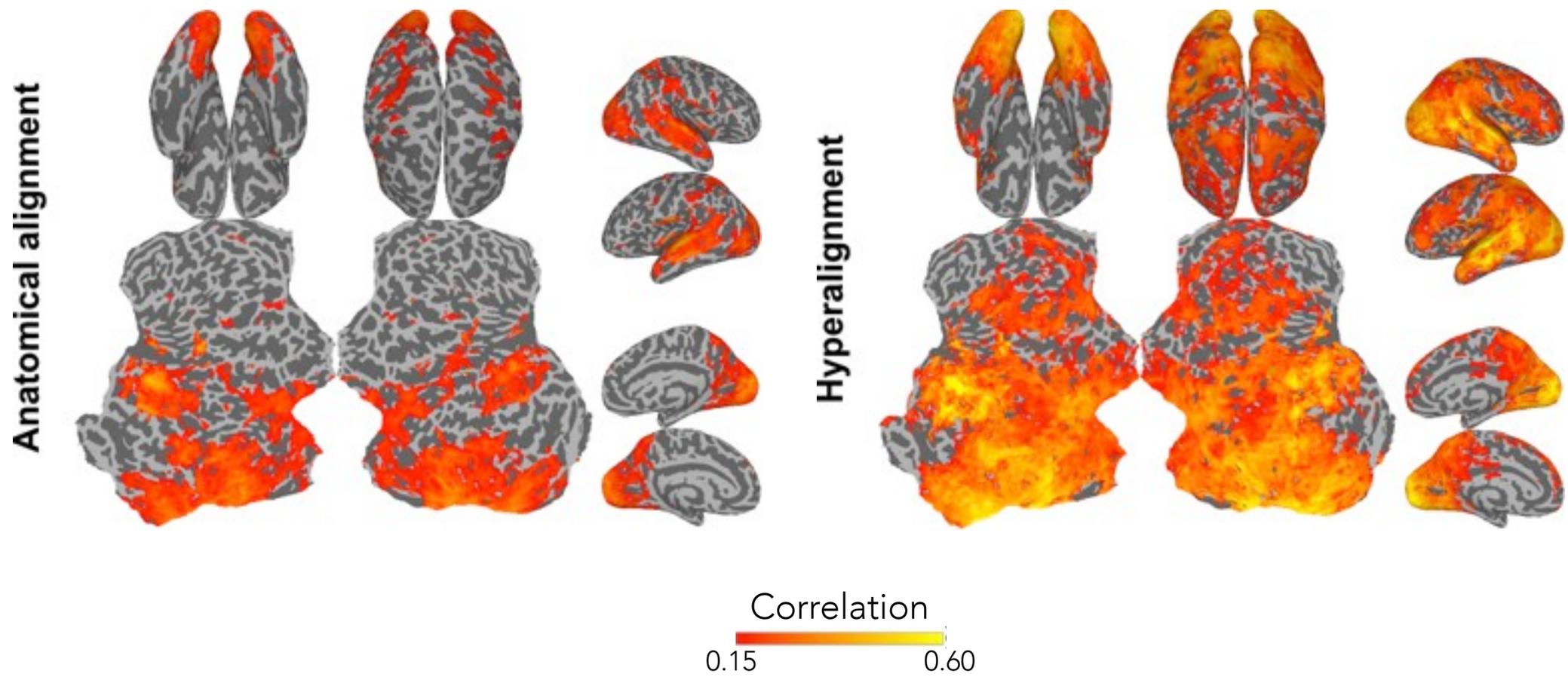
Higher inter-subject correlation of representational geometries for animal behaviors and taxa after hyperalignment  
(Nastase et al., bioRxiv, 2016; under review)



# Modeling functional architecture of the human cortex: Individual representational spaces $\Leftrightarrow$ common representational space



Whole-brain hyperalignment increases between-subject correlations of time-series in occipital, temporal, parietal, and frontal cortices





# HyperCortex

## Proposal for a new functional brain atlas

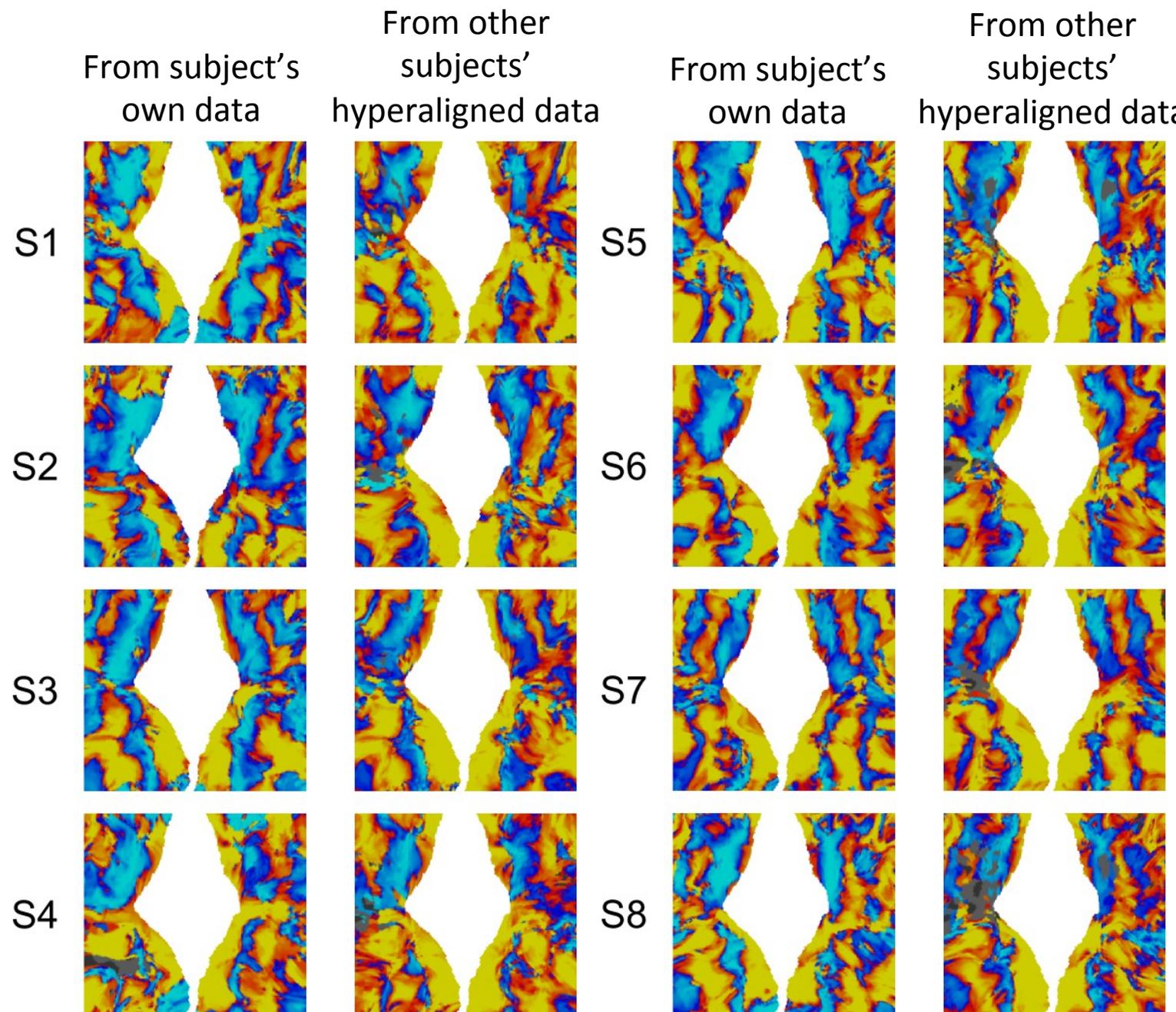
based on a high-dimensional common representational space

- Brain responses can be analyzed as pattern vectors with response basis functions that are shared across brains.
- Captures and preserves fine-scale topographies and models variability across individual brains.
- Data can be shared, interpreted, and subjected to meta-analysis in a computational structure that captures fine-scale patterns of activity that encode fine distinctions.

# Concluding comments

- Extensibility and caveats
  - Vectors can be based on other functional indices (e.g. connectivity)
  - General validity can be increased with better stimulus and task paradigms (e.g. motor execution and music)
  - Model can incorporate other modalities (e.g. MEG, ECoG)
  - Hyperalignment may be improved with better algorithm (e.g. probabilistic hyperalignment, Chen et al. submitted)

Mapping retinotopy from other subjects' hyperaligned polar angle maps



# Concluding comments

- Extensibility
  - Vectors can be based on other functional indices (e.g. connectivity)
  - Model can incorporate other modalities (e.g. MEG, ECoG)
- Caveats

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  - Hyperalignment may be improved with better algorithm (e.g. probabilistic hyperalignment, Chen et al. in prep)

## Concluding comments

- Basis for a new kind of functional brain atlas
  - Report results as vectors in common model space rather than as anatomical coordinates
  - Afford comparison and interpretation of results at a far more fine-grained level
  - Allow arbitrarily large, multi-subject data sets for MVPA
- Extensibility
- Caveats

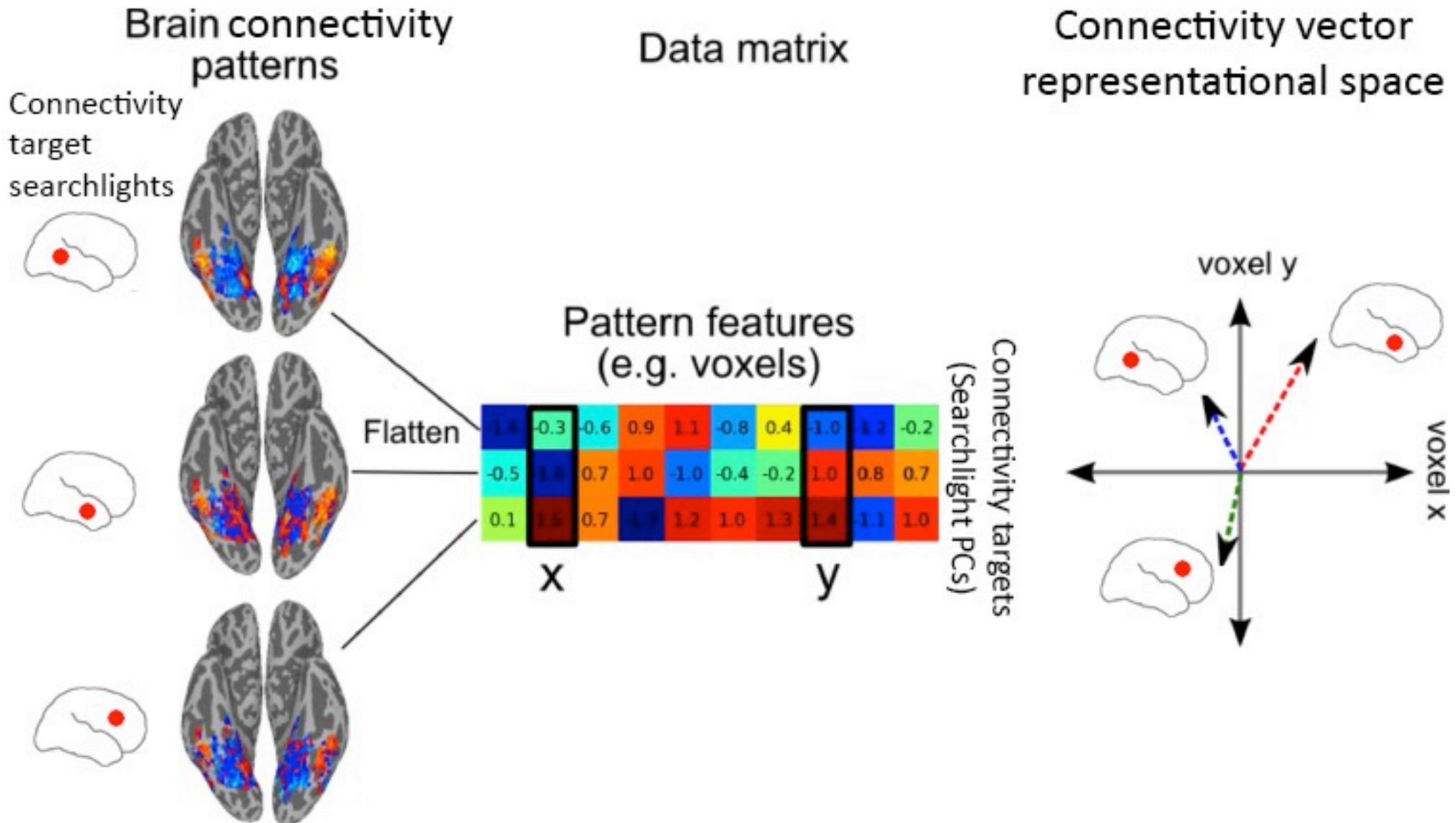
# HyperCortex

## Proposal for a new functional brain atlas

based on a high-dimensional common representational space

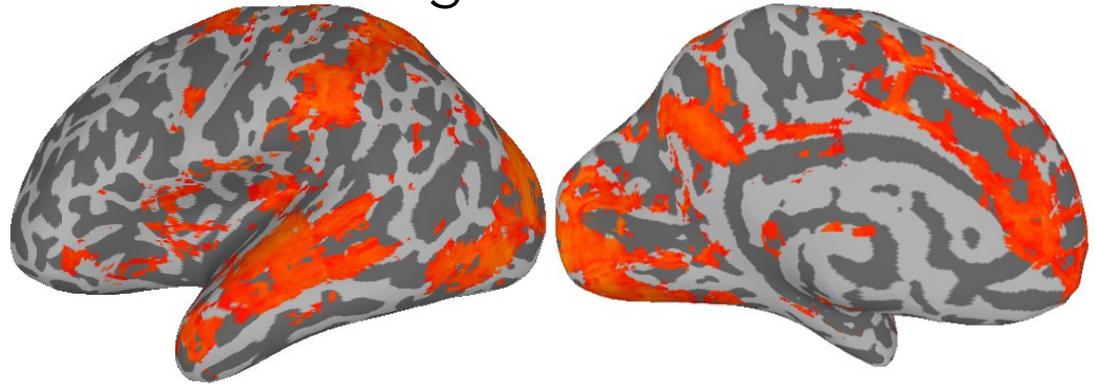
- Model dimensions have response tuning functions that are highly similar across brains.
- Brain responses are captured as pattern vectors, reflecting population codes with response basis functions that are shared across brains.
- Fine-scale topographies are preserved and can be recreated in each individual brain.
- Data can be shared, interpreted, and subjected to meta-analysis in a computational structure that captures fine-scale patterns of activity that encode fine distinctions.

# Connectivity hyperalignment

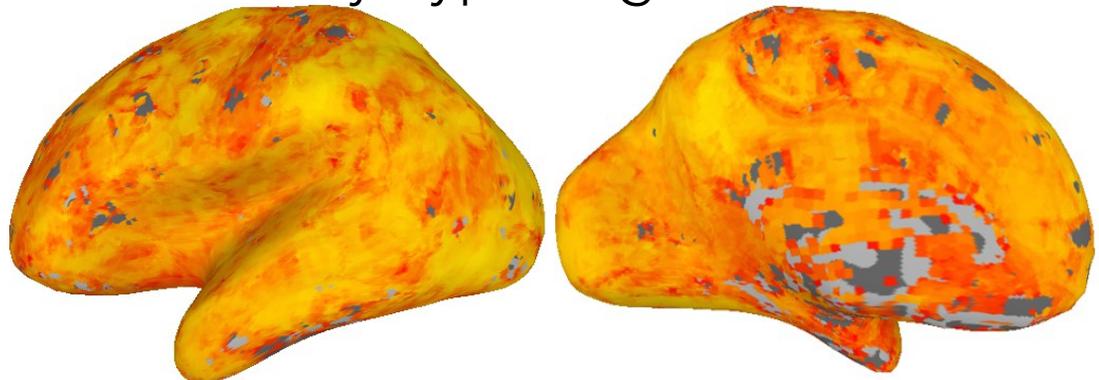


Intersubject  
correlations of  
connectivity  
vectors

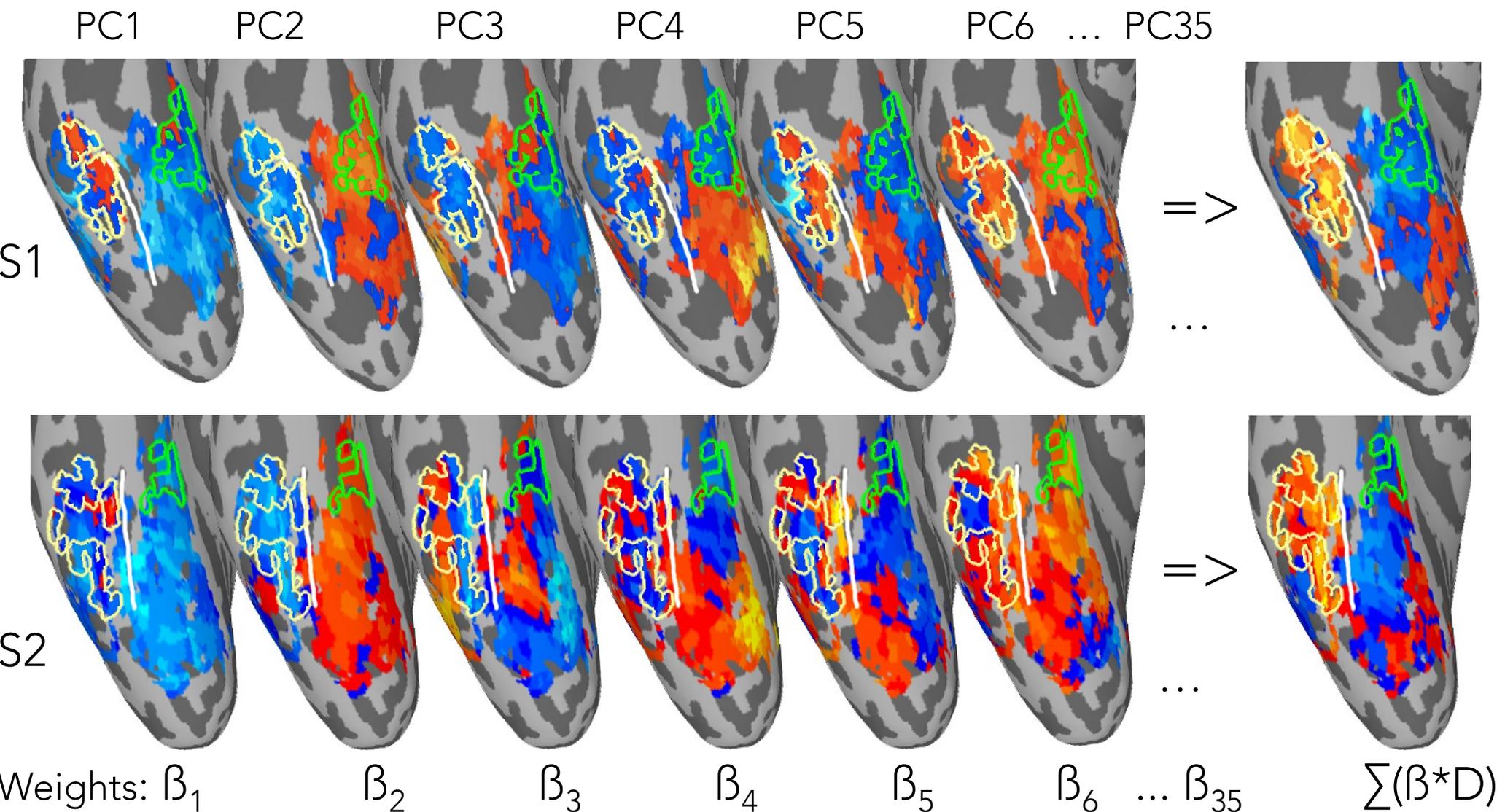
Anatomical alignment



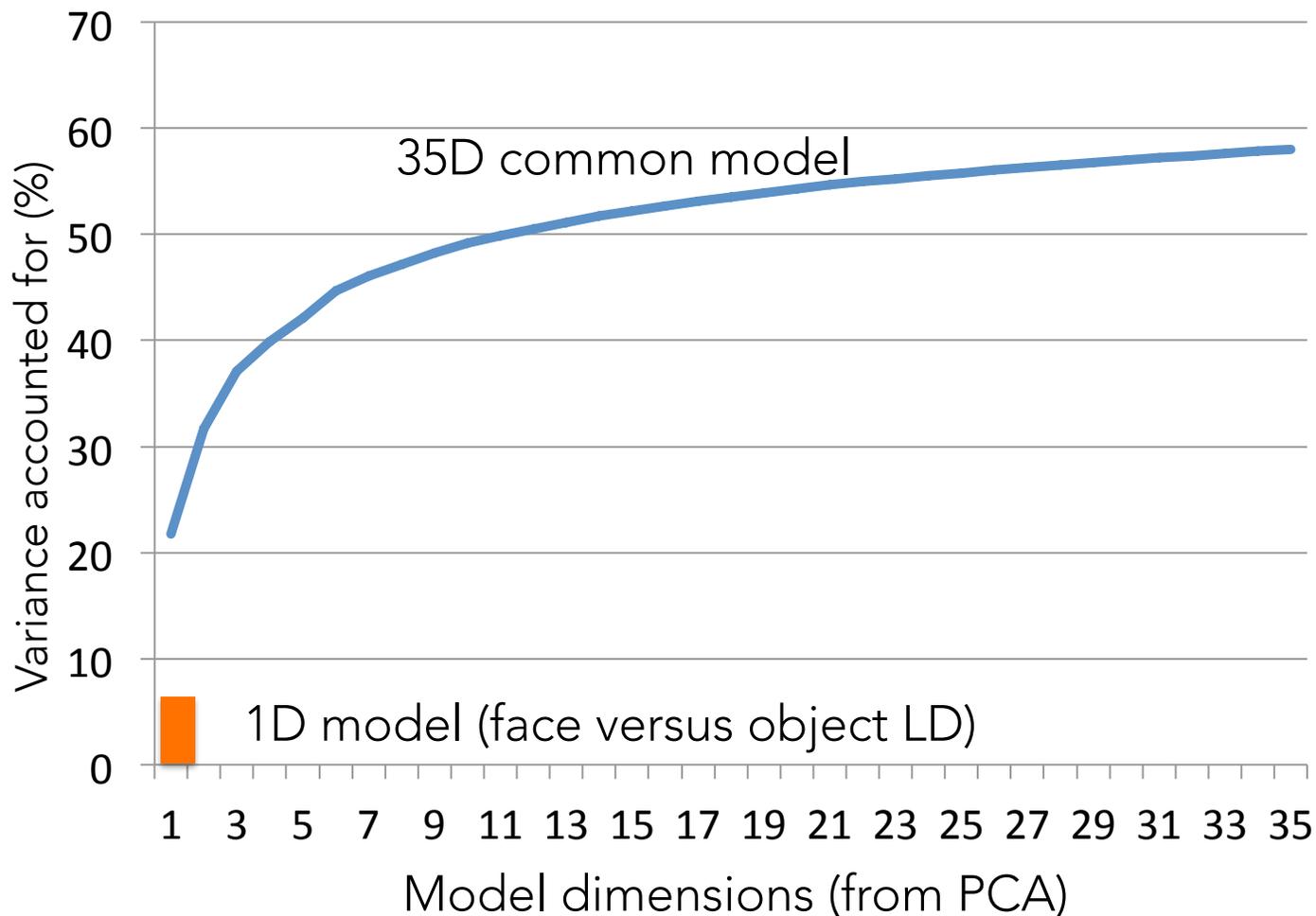
Connectivity hyperalignment



The topographic basis functions for PCs individually show little correspondence to category-selective face and place areas or the domain-specific divisions for animate and inanimate stimuli

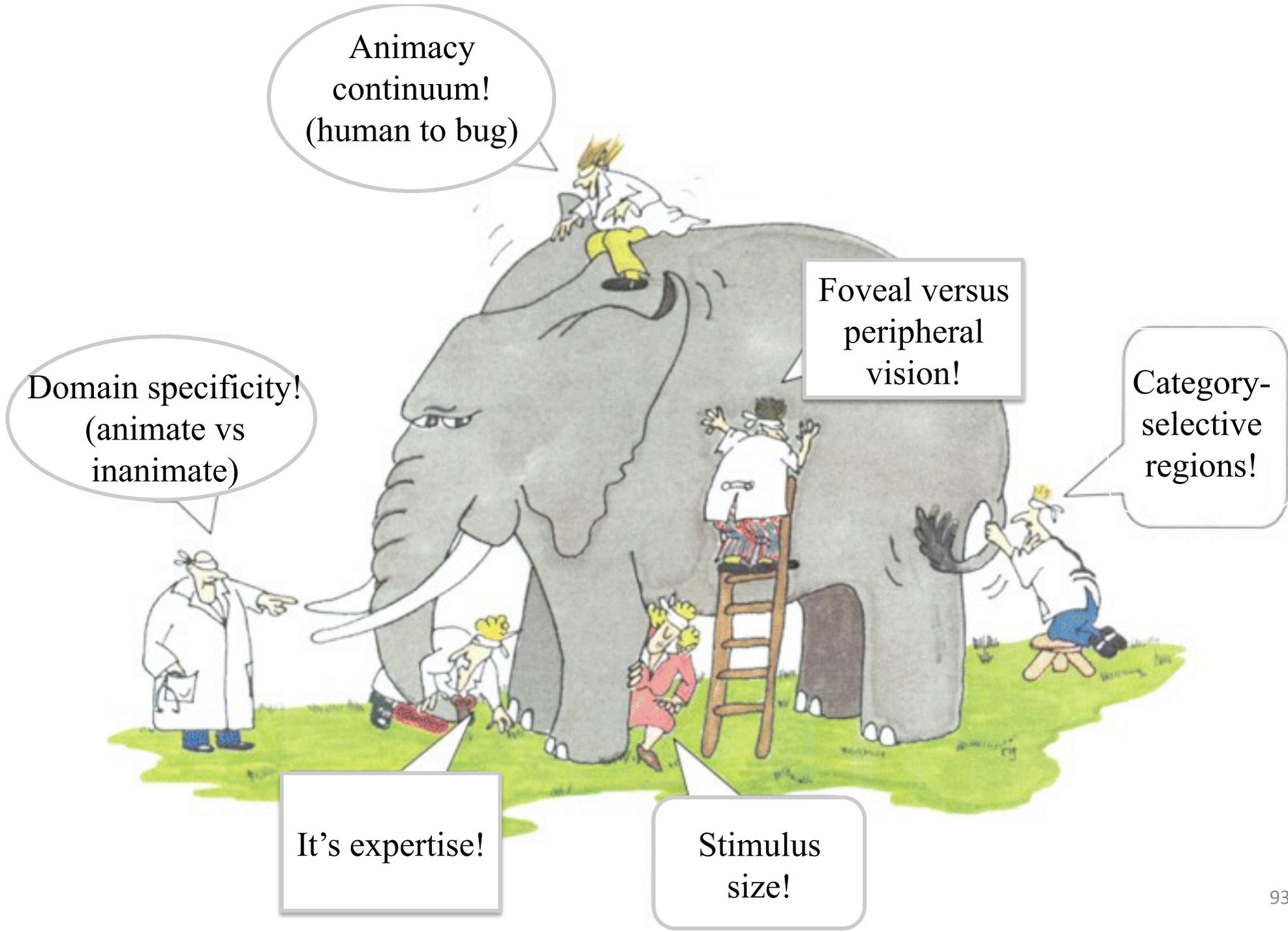


# Single dimensions (simple contrasts) are inadequate for modeling the functional architecture of cortex



The face vs object LD accounts for only 7% of movie response variance in VT cortex

- <20% of VAF by top 3 model dimensions
- <13% of VAF by 35 model dimensions



Animacy continuum!  
(human to bug)

Domain specificity!  
(animate vs inanimate)

Foveal versus peripheral vision!

Category-selective regions!

It's expertise!

Stimulus size!

Can a high-dimensional common model of human cortex be leveraged to build a new type of functional brain atlas?

Brain atlases are an essential tool for functional neuroimaging research

- Provide a common basis for reporting results
- Allow comparisons across studies affording
  - Replication testing
  - Interpretation
  - Meta-analysis
- More generally, afford accrual of knowledge about the functional organization of the human brain

## Functional Brain Atlas: Current State of the Art

Results are reported in tables with anatomical x,y,z coordinates

**Table 1. Group-Average Activation for the Biological Motion Display**

Region	Talairach Coordinates			Mean T	mm <sup>3</sup>
	X	Y	Z		
R. ITS	44	-69	-7	4.63	2101
R. ITS	52	-51	3	4.49	920
R. STS	57	-41	21	4.17	112
R. Fusiform	36	-39	-19	4.72	748
R. Fusiform	34	-68	-18	4.32	174
R. Post. Occipital	14	-96	-4	4.43	151
L. ITS	-42	-70	-4	4.59	2544
L. Supramarginal	-56	-39	25	4.37	388

from Peelen & Downing, Neuron, 2006

# Functional Brain Atlas: Current State of the Art

Results are aggregated across studies based on x,y,z coordinates

Table 1. Group-Average Activation for the Biological Motion Display

Region	Talairach Coordinates			Mean T	mm <sup>3</sup>
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body
Neurosynth.org

An automated meta-analysis of 376 studies

Maps
Studies
Help

y = -70

x = +50

z-score: 7.89 What's here?

x:  y:  z:

# Functional Brain Atlas: Current State of the Art

The function of a locus is described as a “word-cloud”

Table 1. Group-Average Activation for the Biological Motion Display

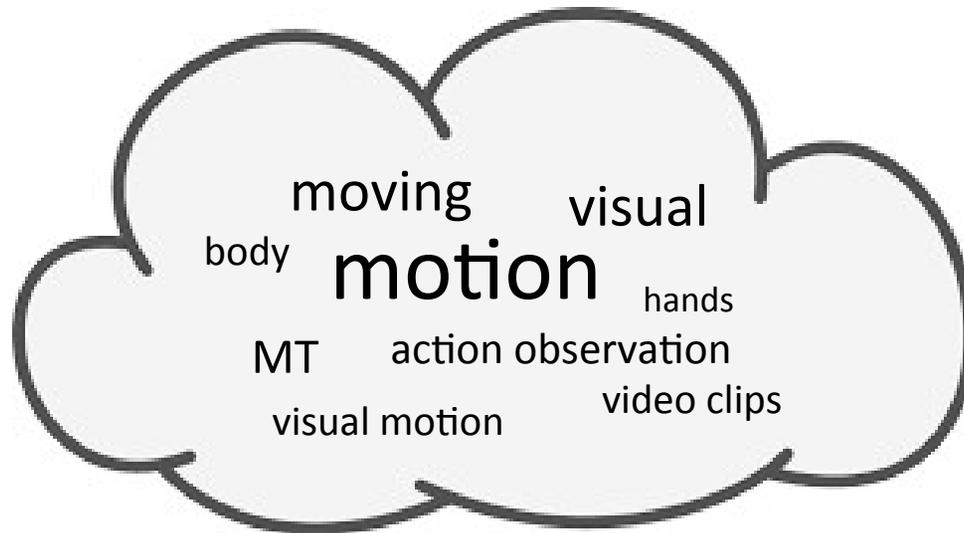
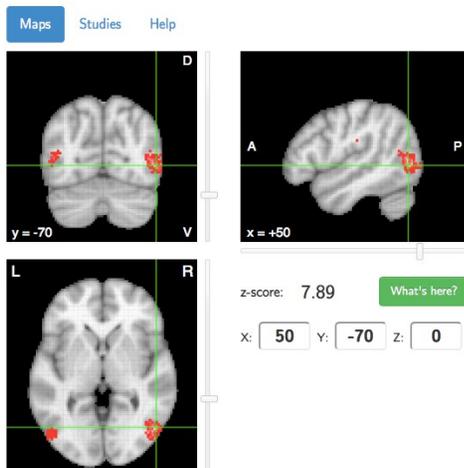
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body

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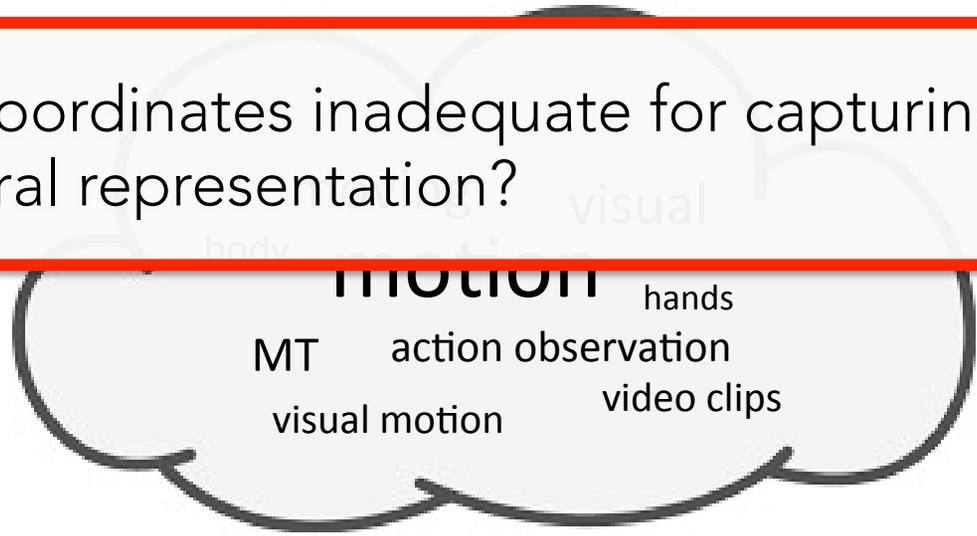
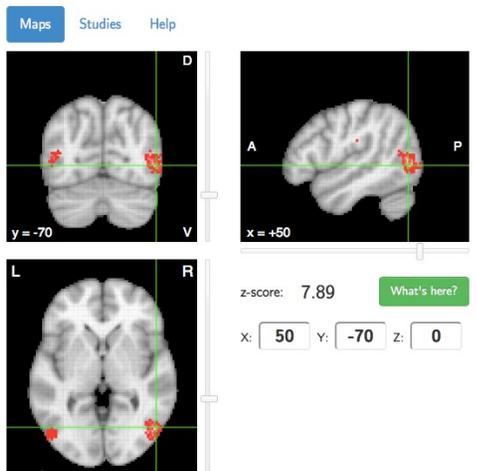
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Why are anatomical coordinates inadequate for capturing neural representation?

body

An automated meta-analysis of 376 studies

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# Real-life cognition challenge

(Hanke et al., Poster #3672, OHBM 2014)



nature.com

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SCIENTIFIC DATA | DATA DESCRIPTOR

**OPEN**

### A high-resolution 7-Tesla fMRI dataset from complex natural stimulation with an audio movie

Michael Hanke, Florian J. Baumgartner, Pierre Ibe, Falko R. Kaule, Stefan Pollmann  *et al.*

- **2 hours of 7-Tesla fMRI** (0.5Hz, 1.4mm), large sample of **natural language processing**
- Simultaneous respiratory and cardiac trace (200Hz)
- 0.7mm T1w, T2w
- SWI, angiography, DTI
- 20 human participants, plus phantom

<http://studyforrest.org>

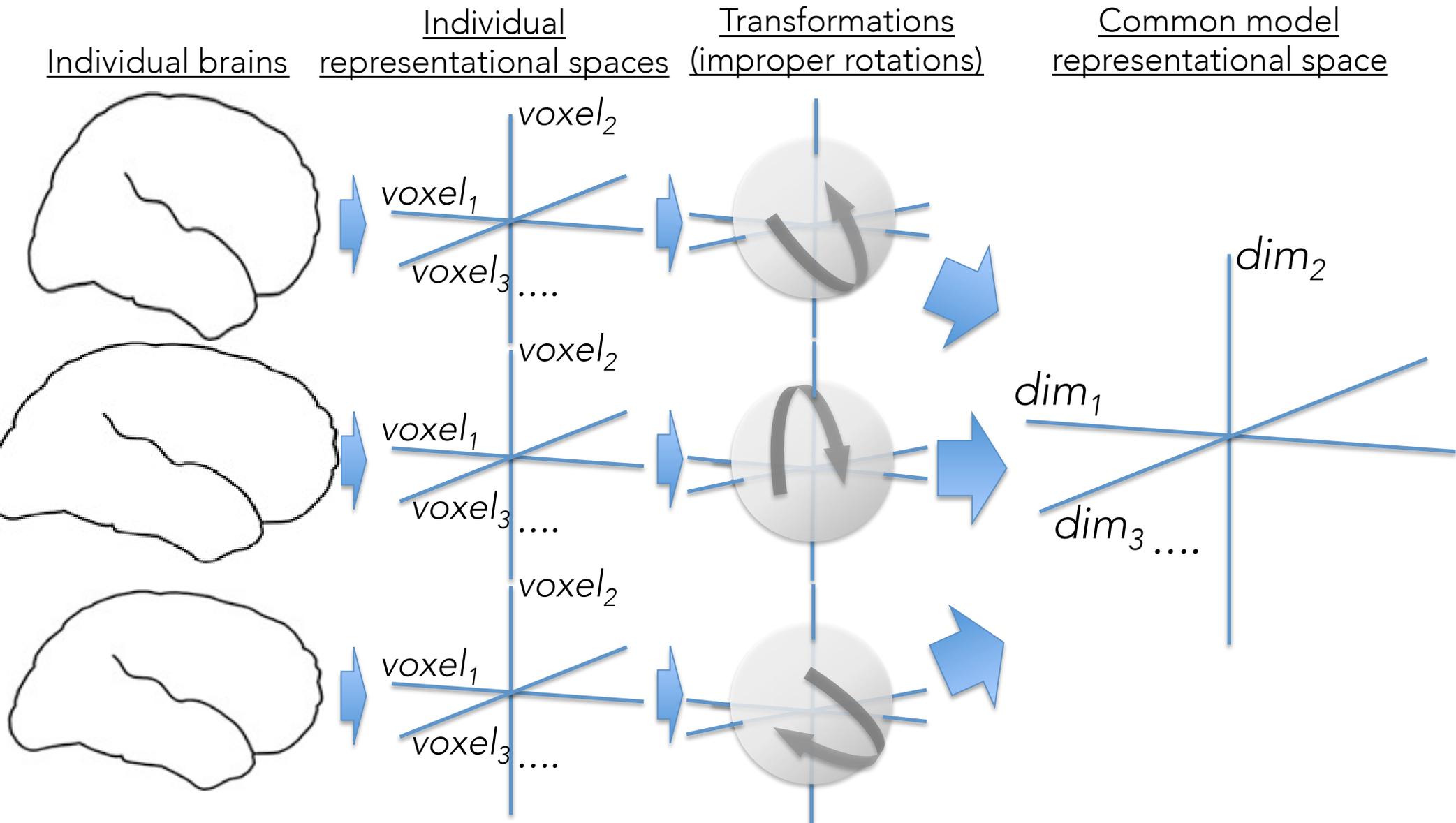
**Data in the public domain**

No registration needed

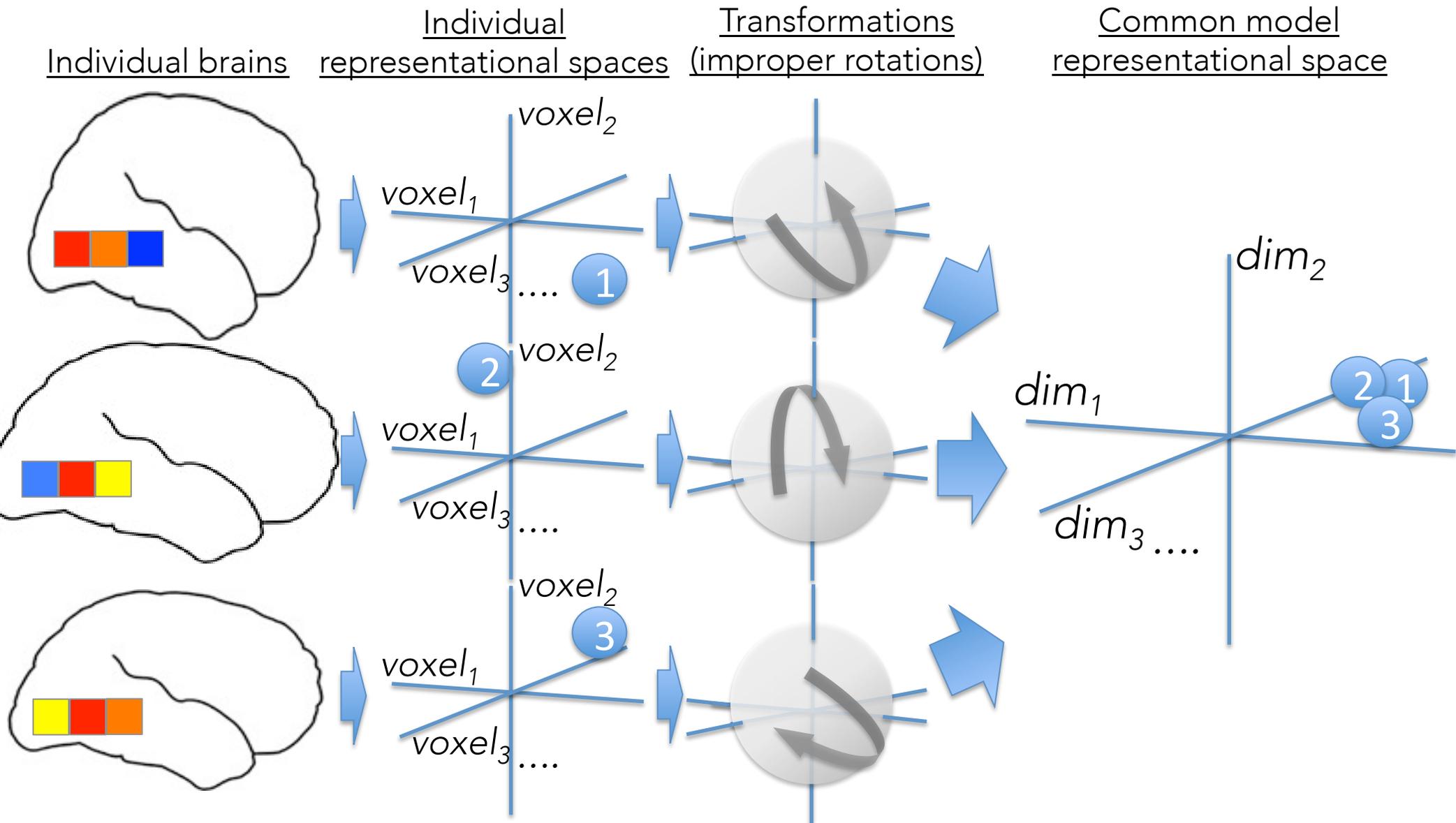
**Participate in the challenge  
and win 5000 Euro**



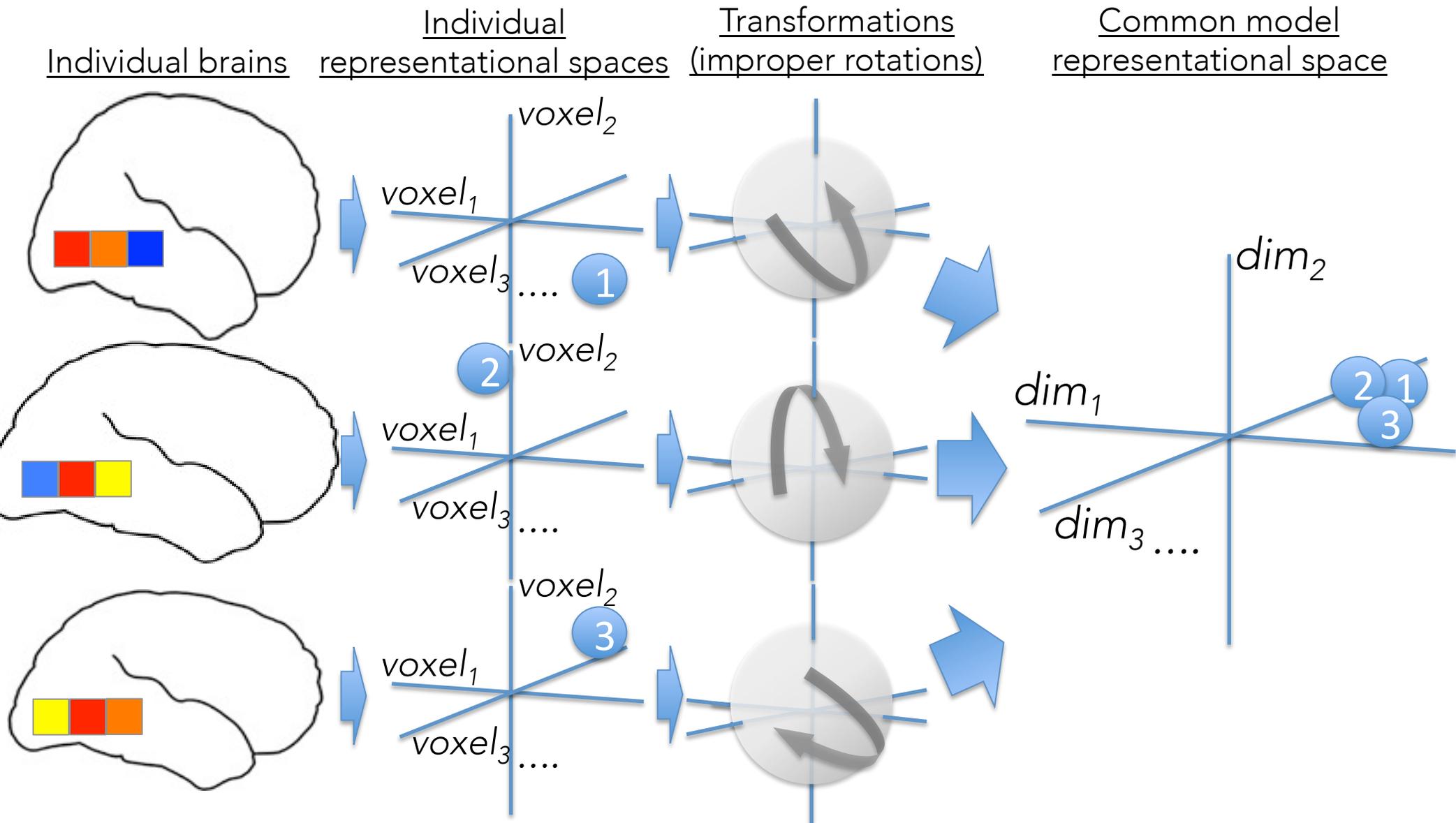
# Modeling functional architecture of the human cortex: Individual representational spaces $\Leftrightarrow$ common representational space

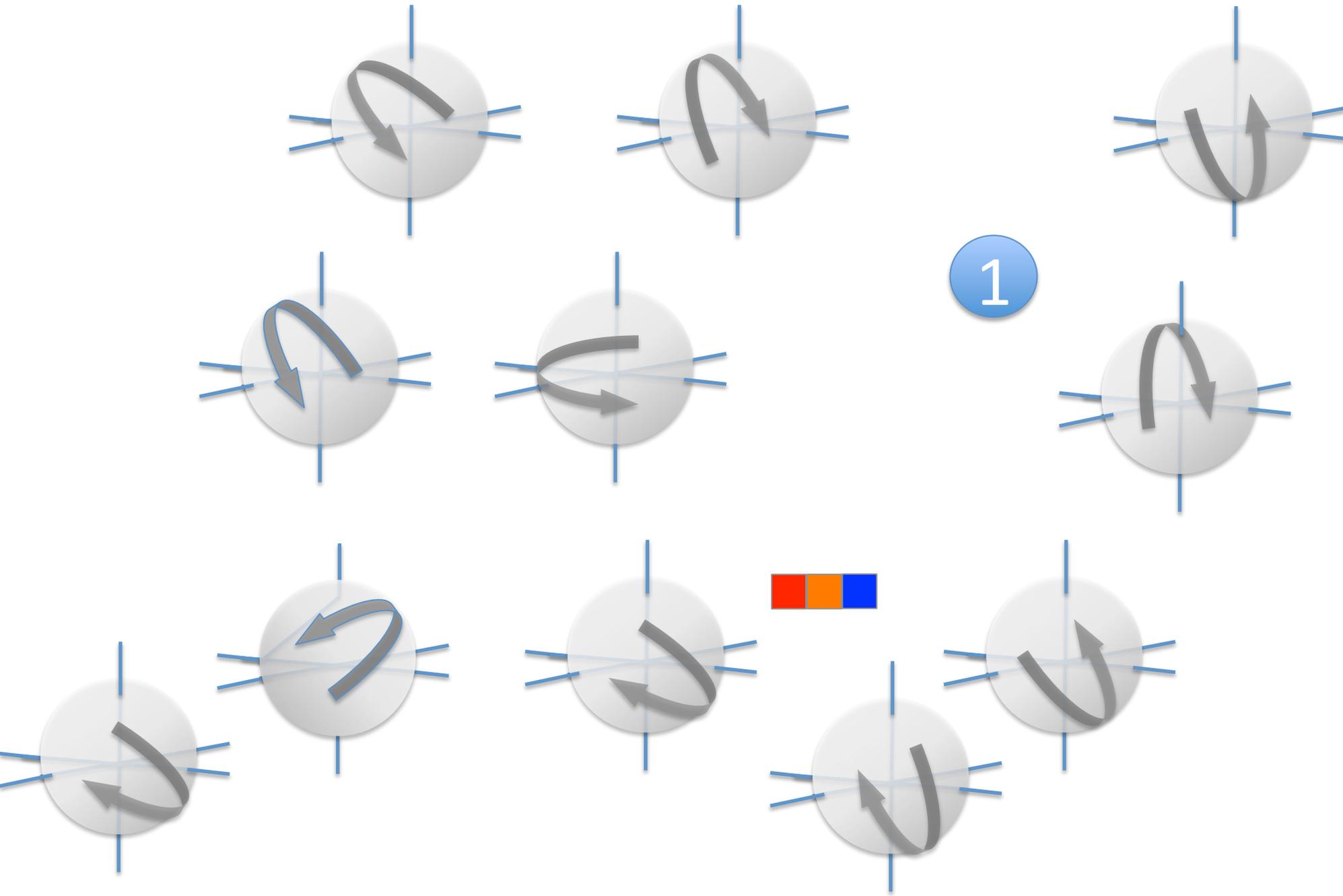


# Modeling functional architecture of the human cortex: Individual representational spaces $\Leftrightarrow$ common representational space



# Modeling functional architecture of the human cortex: Individual representational spaces $\Leftrightarrow$ common representational space





## Validation

Modeling fine distinctions in a model space based on response tuning functions that are common

Modeling topographies with basis functions that are grounded in common tuning functions

Single dimensions (or small numbers of dimensions) are inadequate to capture fine distinctions and the fine-structure of topographies that carry these distinctions

Functional brain atlas

Extensibility

Caveats

Other methods for hyperalignment

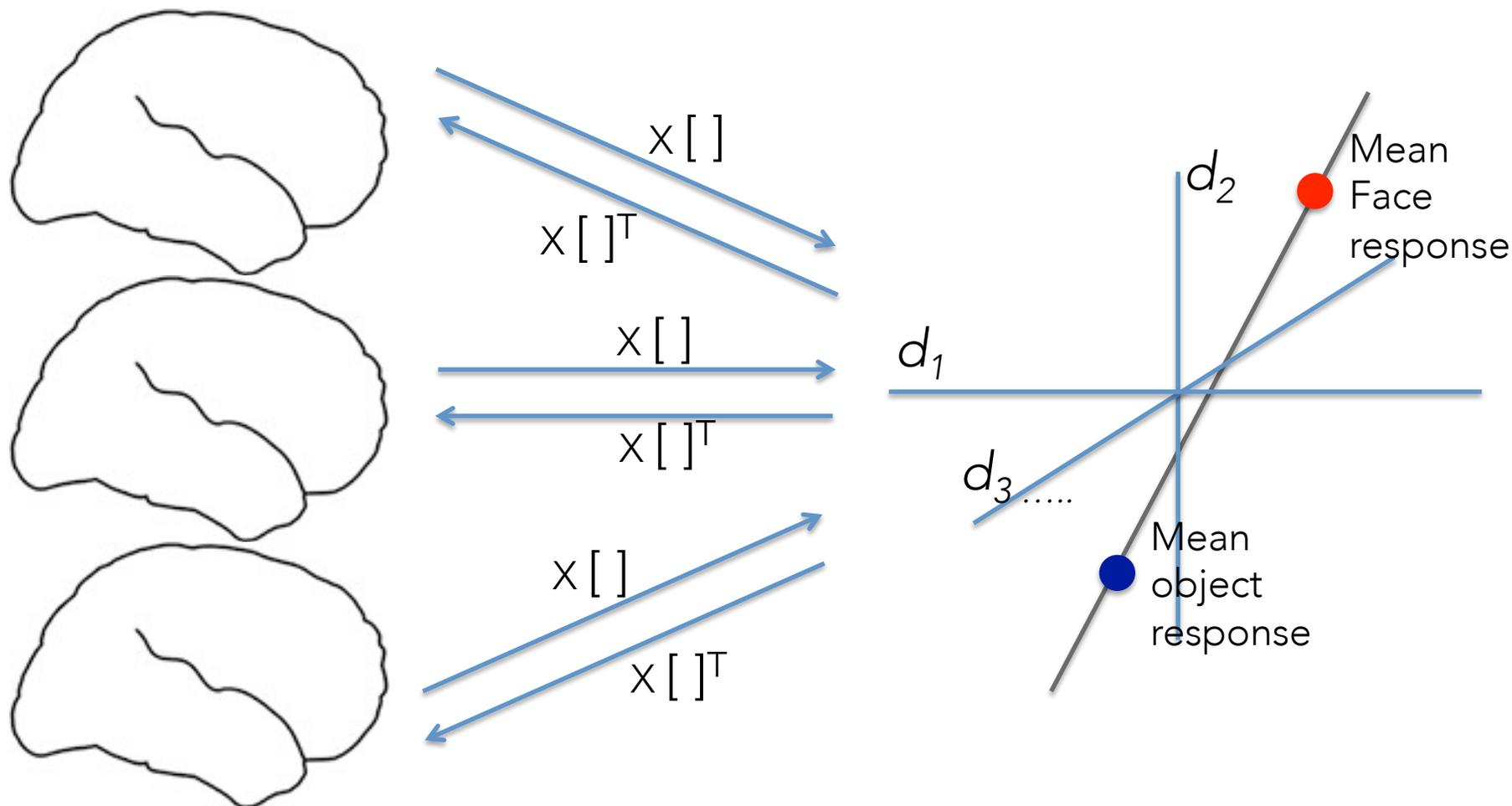
Other stimulus or task paradigms for sampling representational spaces

The face versus object topography can be found in common model space by projecting it into the cortical topography of individual brains

Individual brain spaces

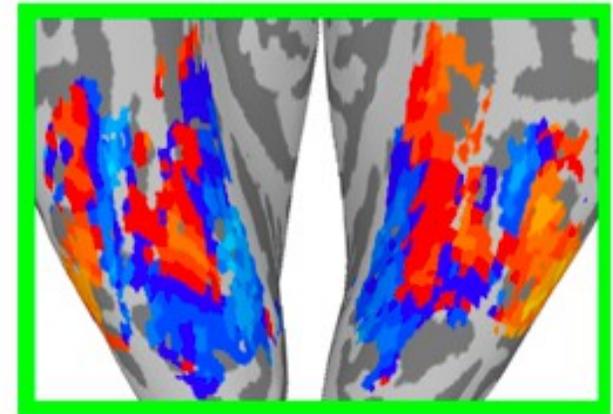
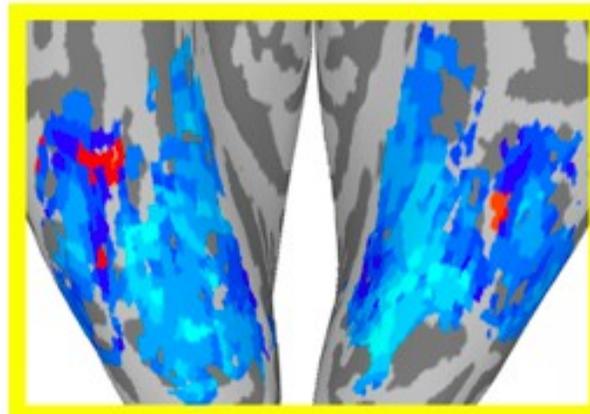
Transformation matrices

Common model space



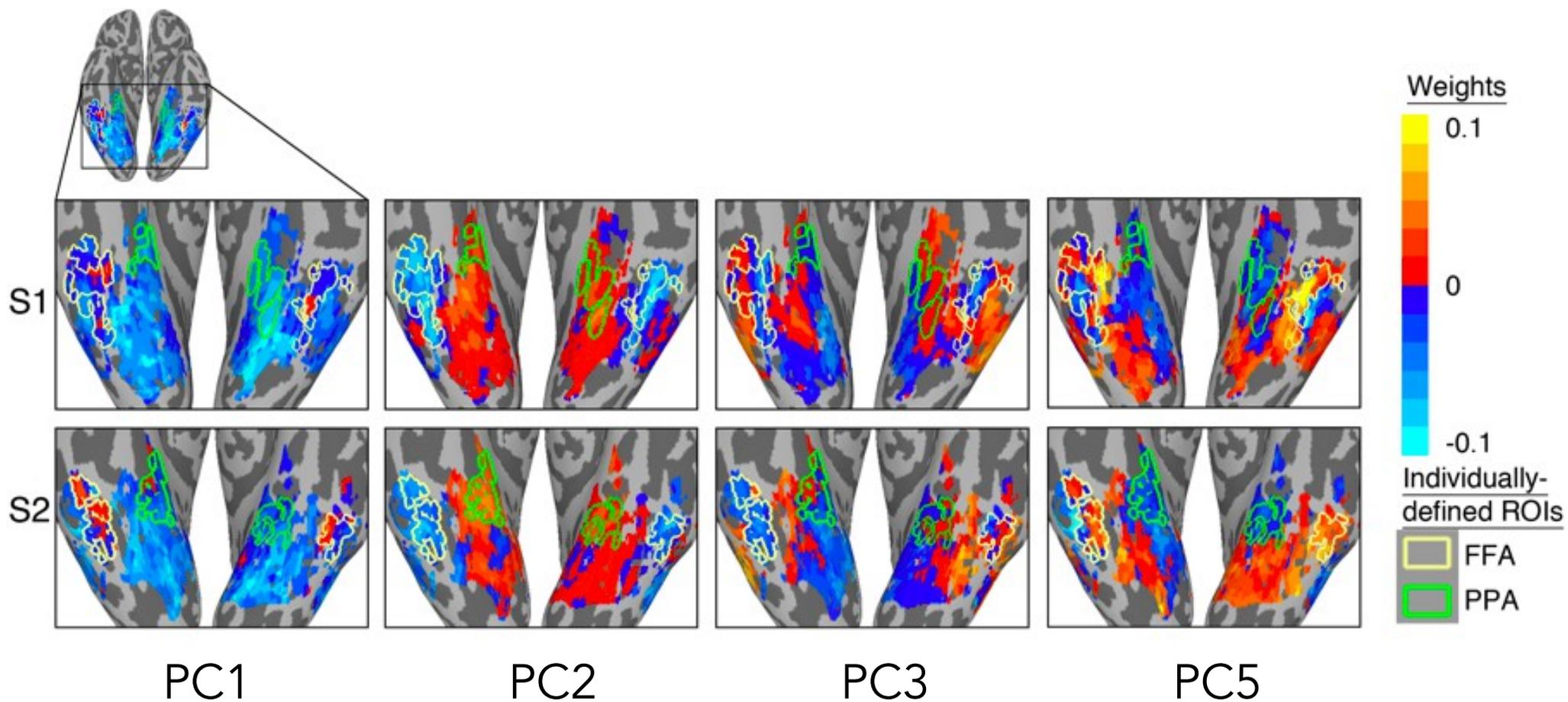
Each model dimension has an individual-specific cortical topography (weights in individual transformation matrix columns)

		Principal components				
$P$		$pc_1$	$pc_2$	$pc_3$	...	$pc_{35}$
Voxels	$v_1$	$w_{1,1}$	$w_{2,1}$	$w_{3,1}$	...	$w_{35,1}$
	$v_2$	$w_{1,2}$	$w_{2,2}$	$w_{3,2}$	...	$w_{35,2}$
	$v_3$	$w_{1,3}$	$w_{2,3}$	$w_{3,3}$	...	$w_{35,3}$
	...	...	...	...	...	...
	$v_{1000}$	$w_{1,1000}$	$w_{2,1000}$	$w_{3,1000}$	...	$w_{35,1000}$



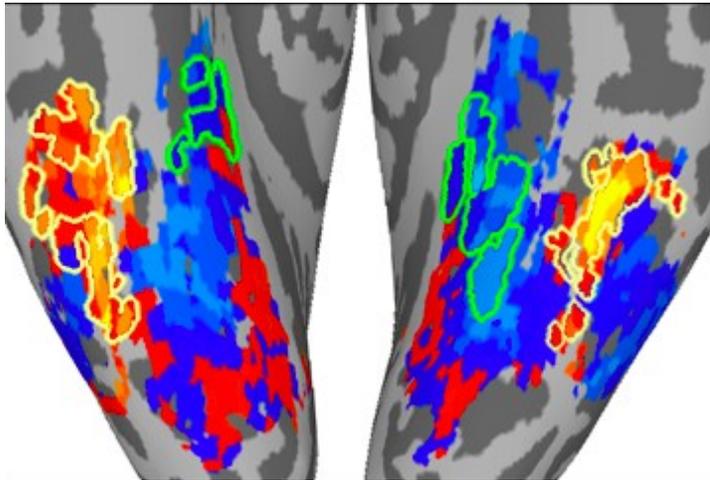
# VT topographies for 4 Top Principal Components

A face-specific topography is not evident



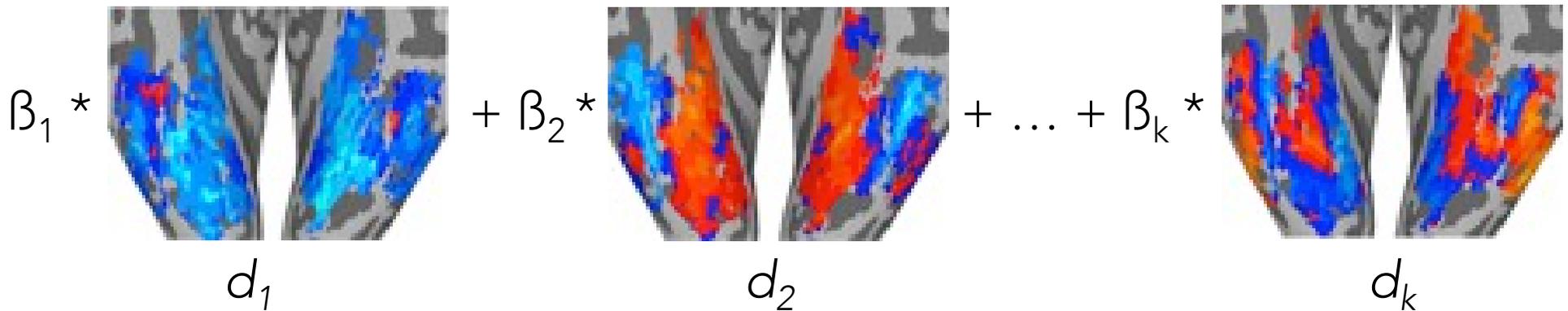
Faces vs objects is a simple contrast that can be modeled as a weighted sum of model dimension topographies

Face vs object contrast in Subject 1



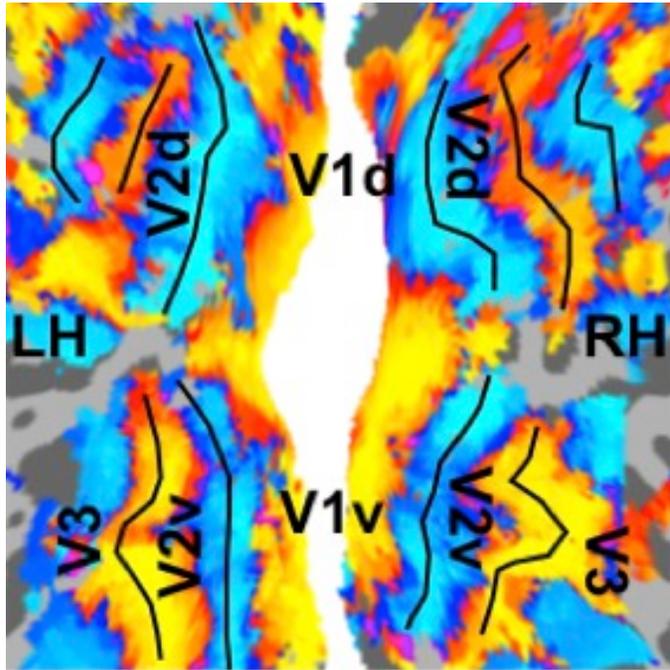
=

Pattern basis functions for each model dimension

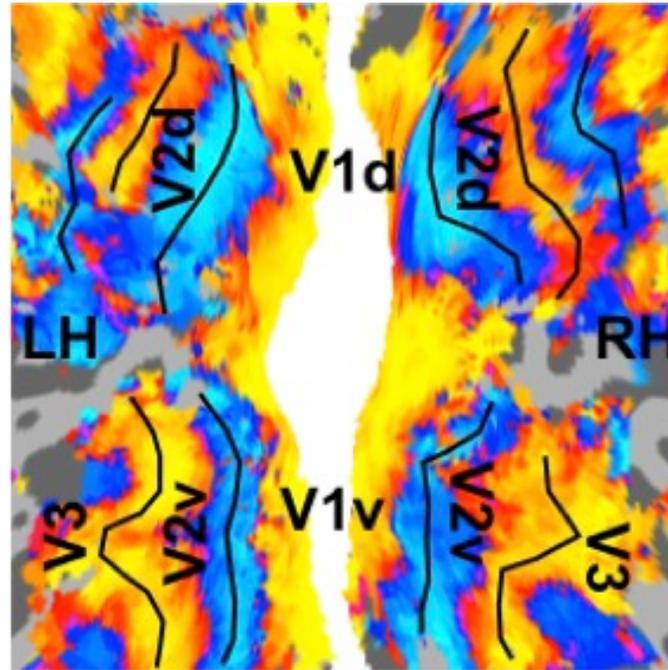


# Mapping retinotopy by projecting other subjects' polar angle maps into a different subject's occipital topography

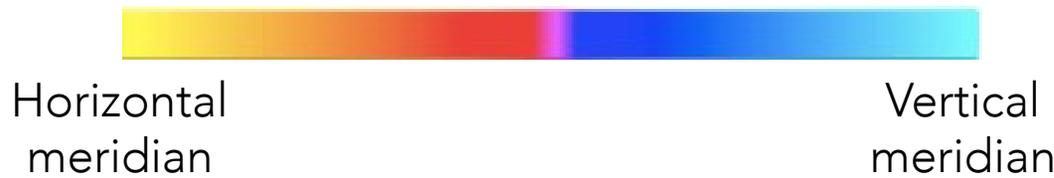
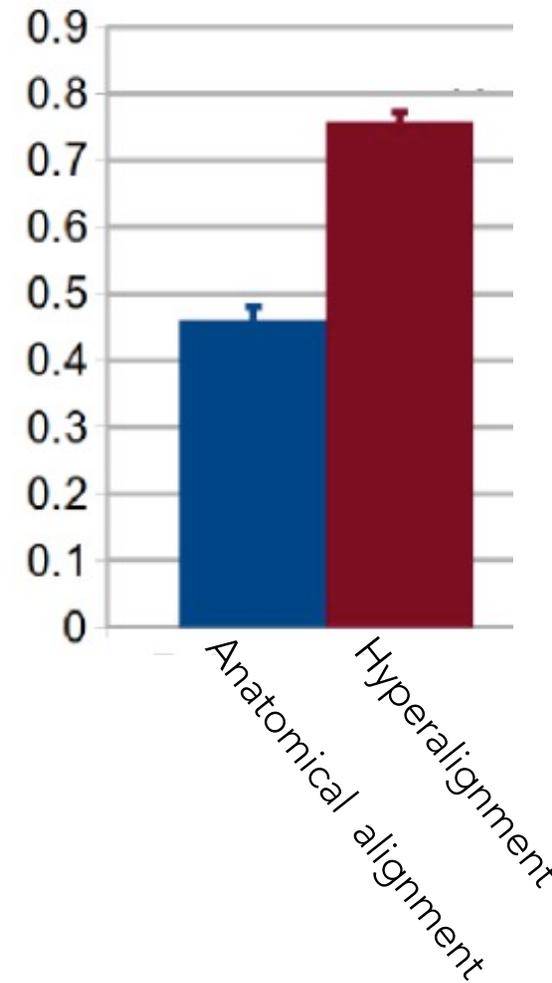
Polar angle from subject's own retinotopy data



Polar angle from other subjects' retinotopy data



Correlation between measured and projected



Why are anatomical coordinates inadequate for capturing neural representation?

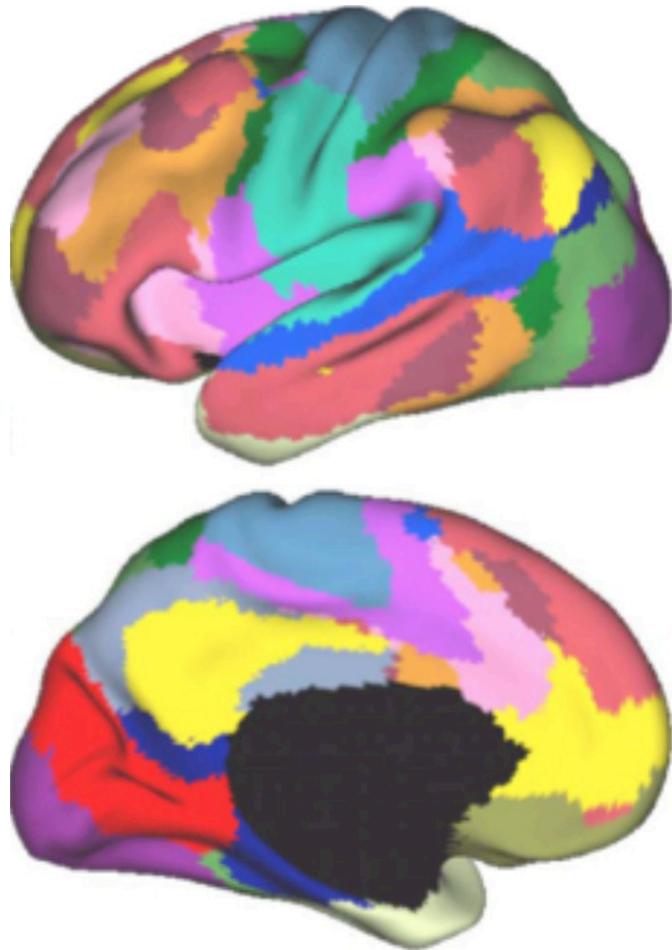
- Response tuning functions for voxels with the same anatomical coordinates are highly variable across brains.
- The basic unit for neural representation is the population response, not the responses of single voxels (or single neurons).



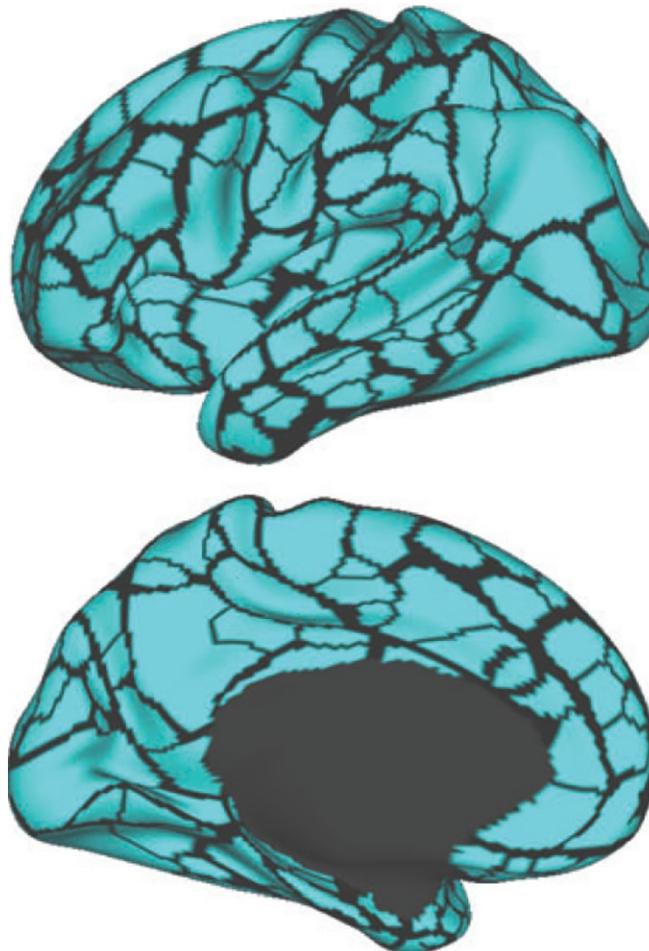
Hyperalignment  
Swaroop Guntupalli  
Post-doctoral fellow

# Parcellation using resting state fMRI connectivity

17 systems  
(Yeo et al. 2011)



422 areas (group)  
(Gordon et al. 2014)



616 areas (individual)  
(Laumann et al. 2015)

