



fMRI analysis using machine learning approaches

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Outline

Preliminaries

- > Task-based Neuroimaging
- > Representational Space
- > Multi-Subject fMRI analysis
- > Classification Analysis

Functional Alignment

- > Def: Functional Alignment
- > Multi-View Learning
- > Deep Hyperalignment

Reconstructing Images from fMRI

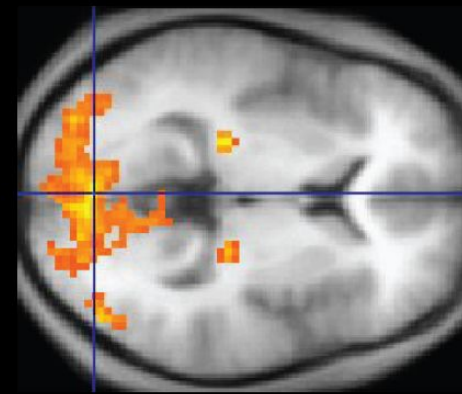
- > Classification Analysis
- > Our Proposed TIGAN

Diagnosing pediatric anxiety

- > Predicting Negative Emotional
- > Diagnosing Anxiety
- > Creating Neural Signatures

Preliminaries

> functional Magnetic Resonance Imaging (fMRI) machine



> Task-based fMRI dataset

Subject

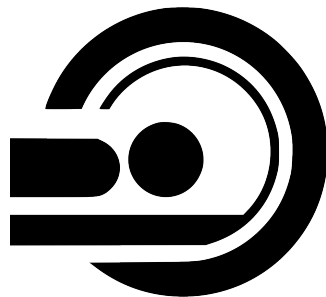


Subject

> Task-based fMRI dataset

Subject

fMRI scan



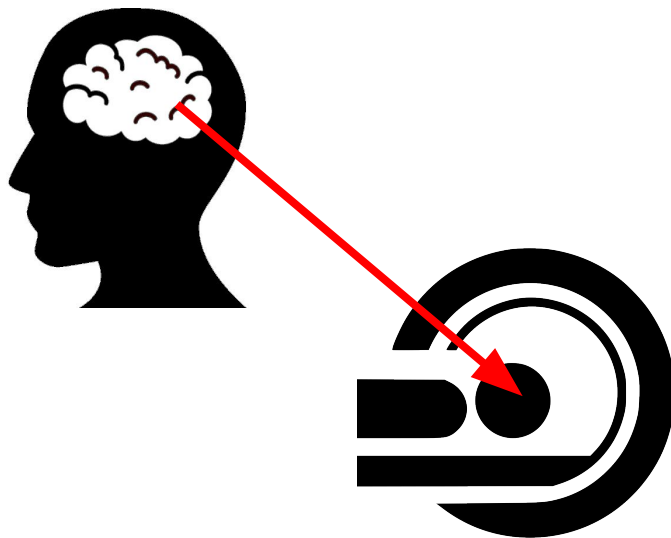
Subject

> Task-based fMRI dataset

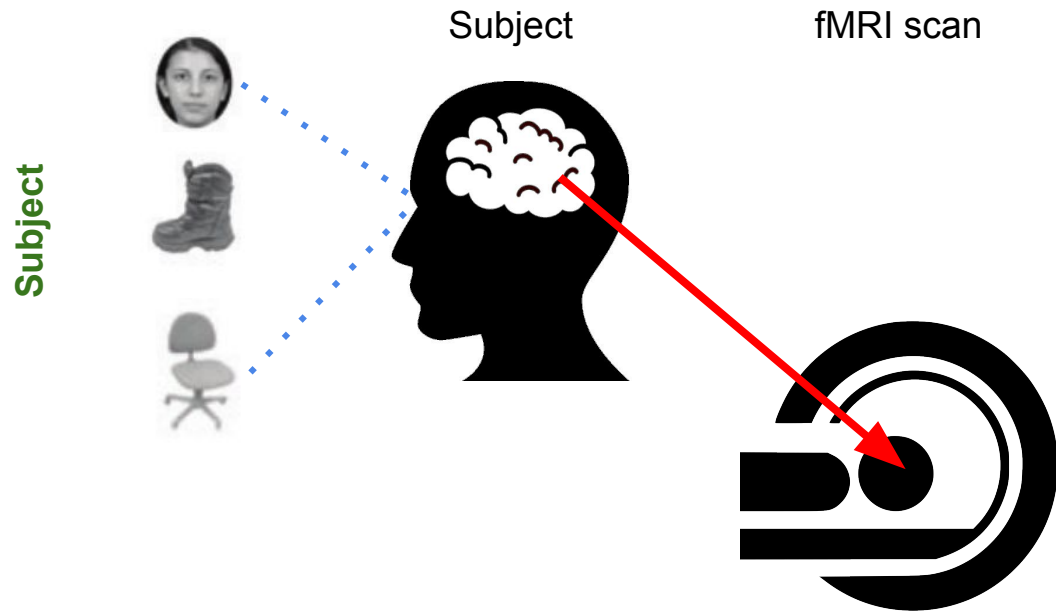
Subject

Subject

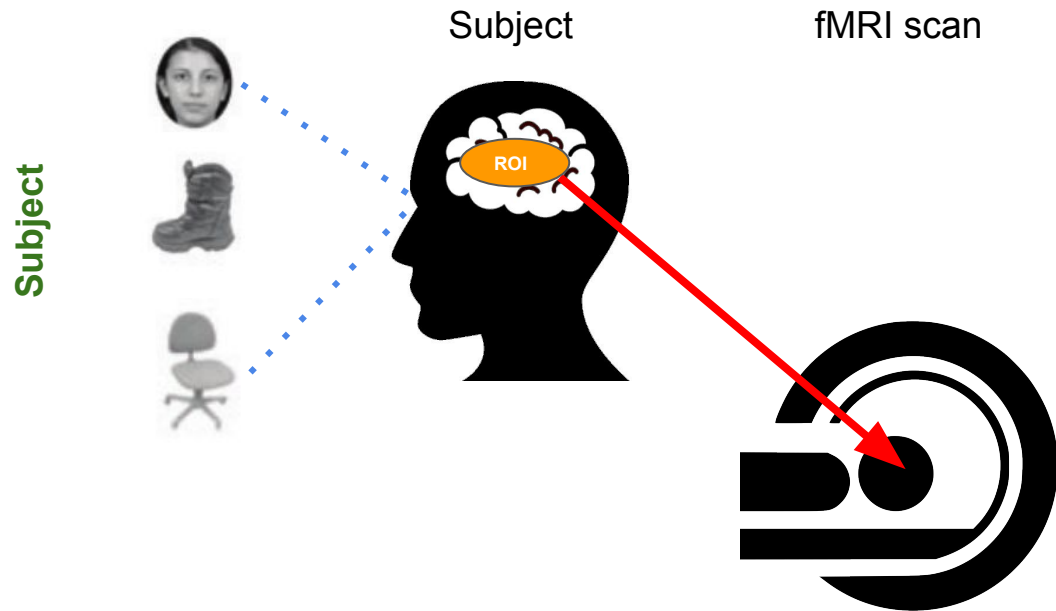
fMRI scan



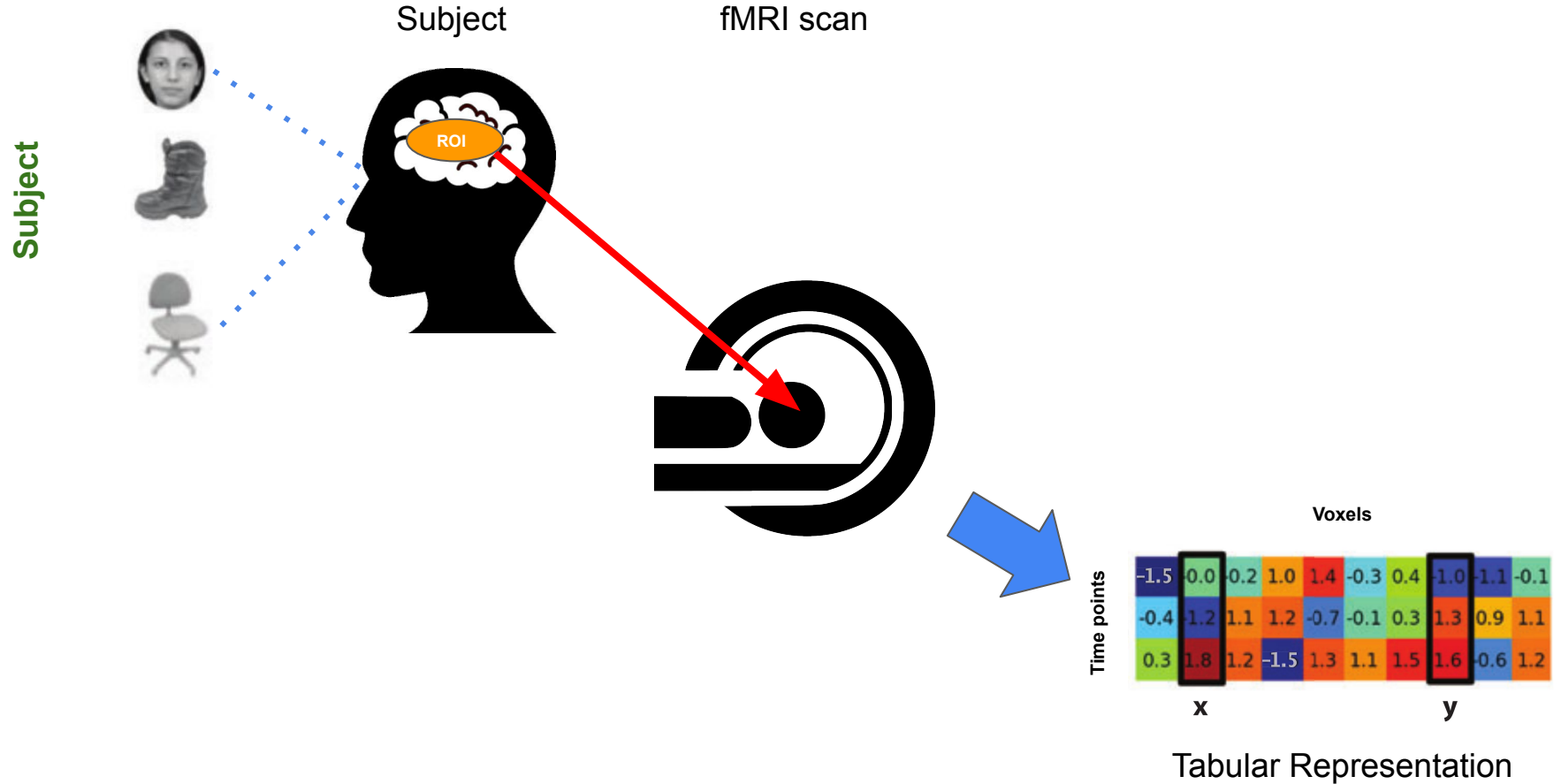
> Task-based fMRI dataset



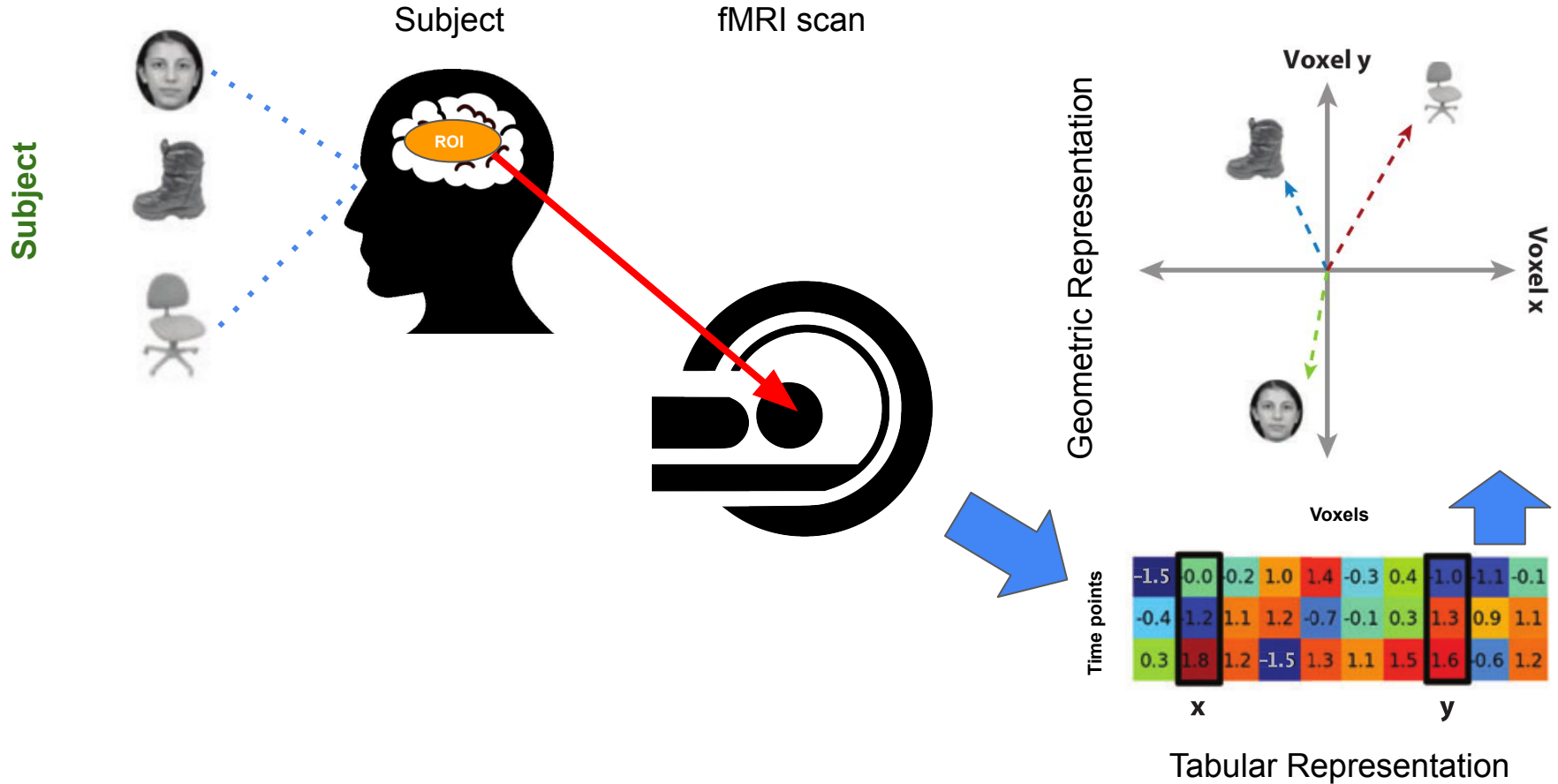
> Task-based fMRI dataset



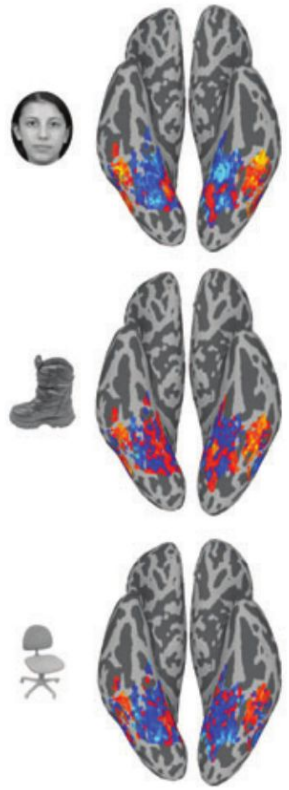
> Task-based fMRI dataset



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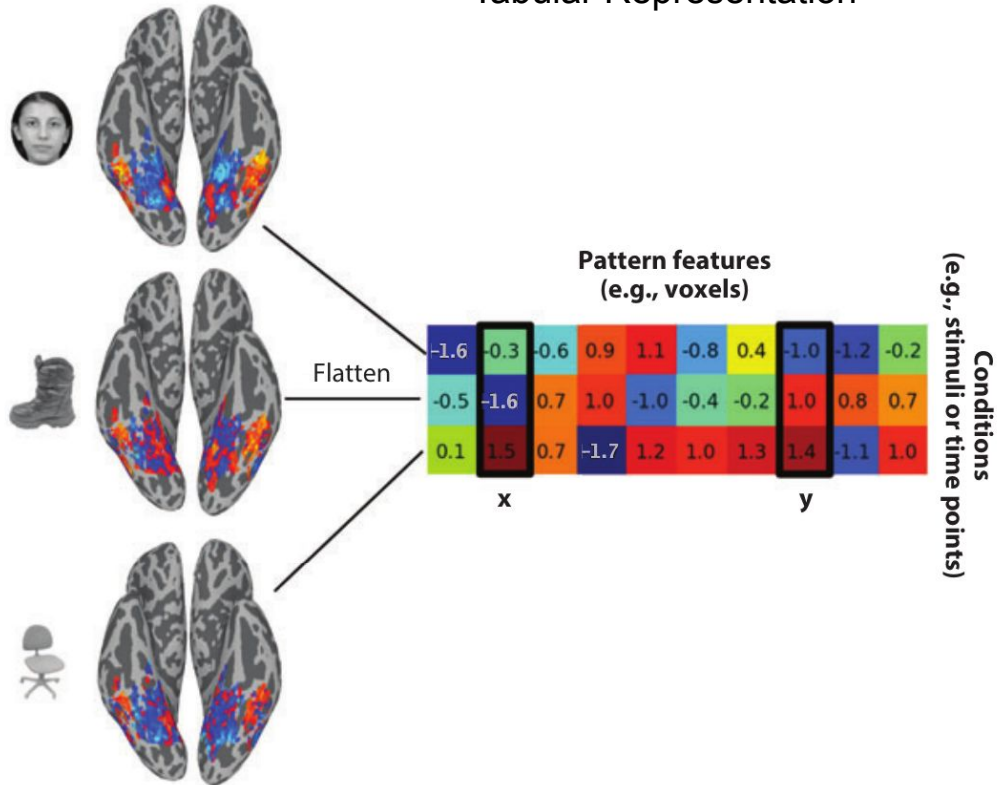


> Representational Space



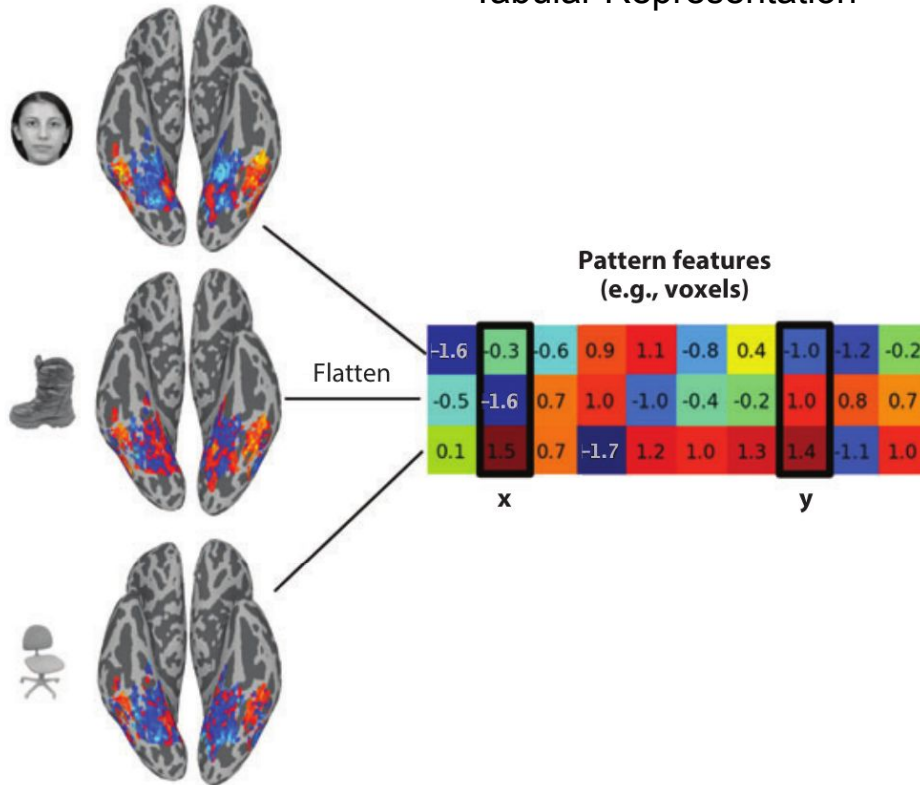
> Representational Space

Tabular Representation

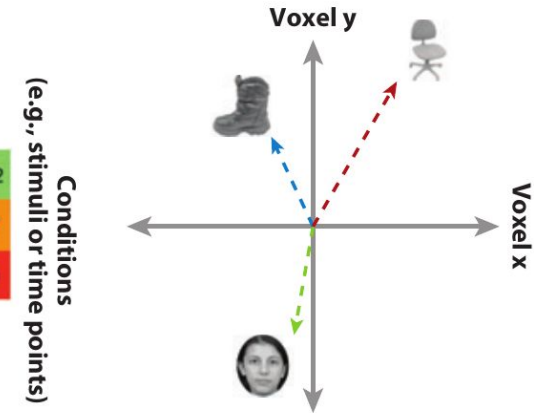


> Representational Space

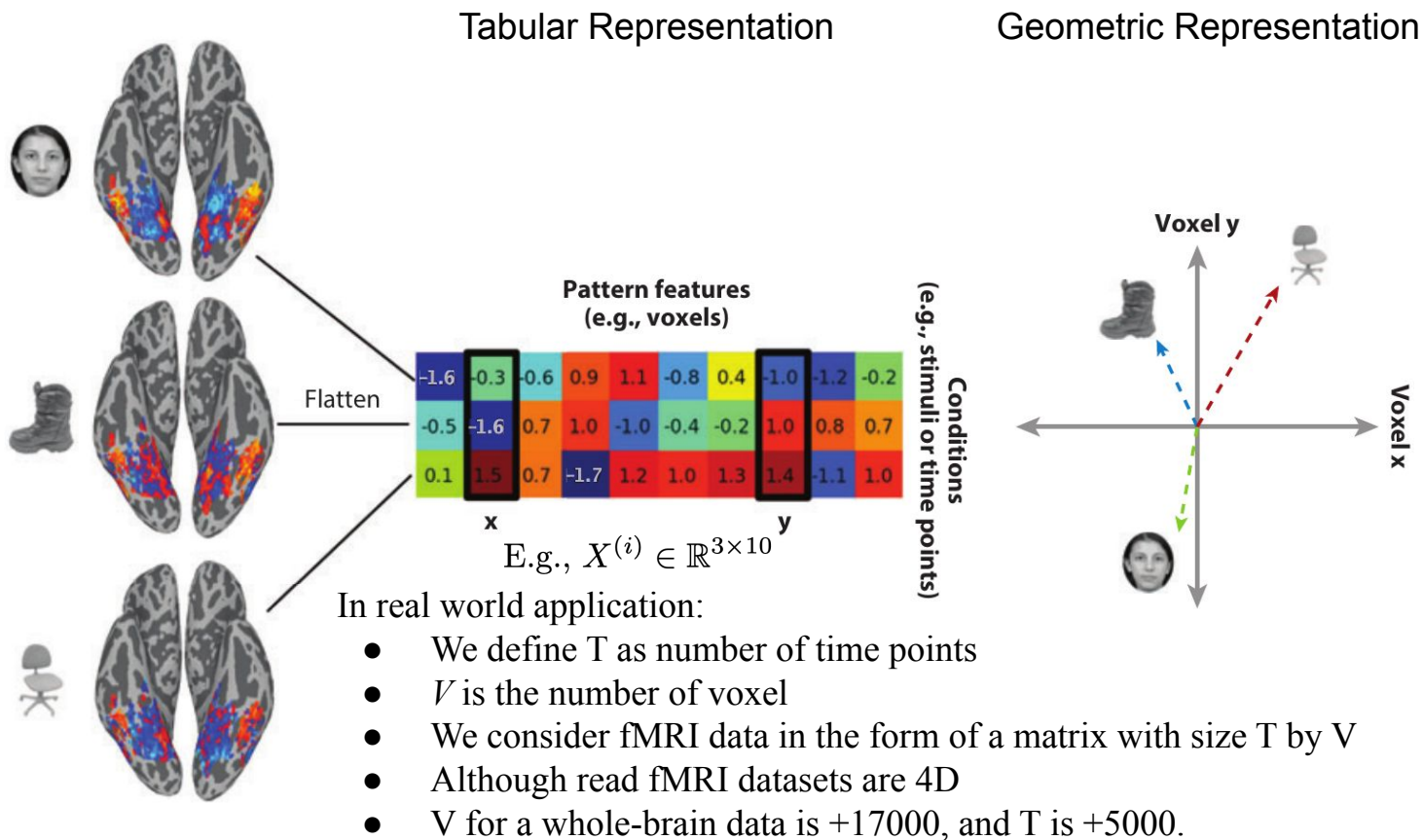
Tabular Representation



Geometric Representation



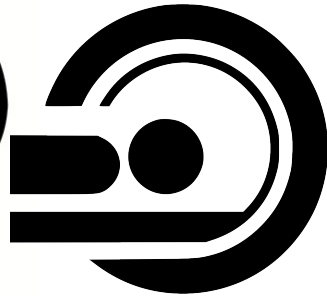
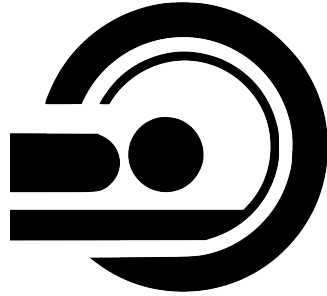
> Representational Space



> Multi-subject fMRI dataset

Subjects

An fMRI Scanner



Subject 1



Subject N

> Multi-subject fMRI dataset

Stimuli

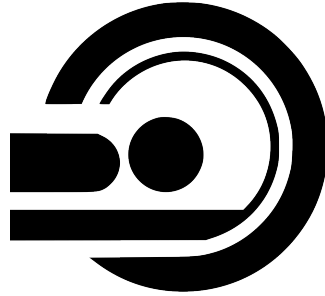
Subjects

An fMRI Scanner

Subject 1



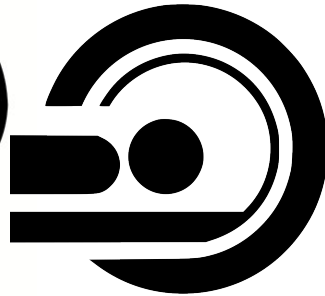
Watching



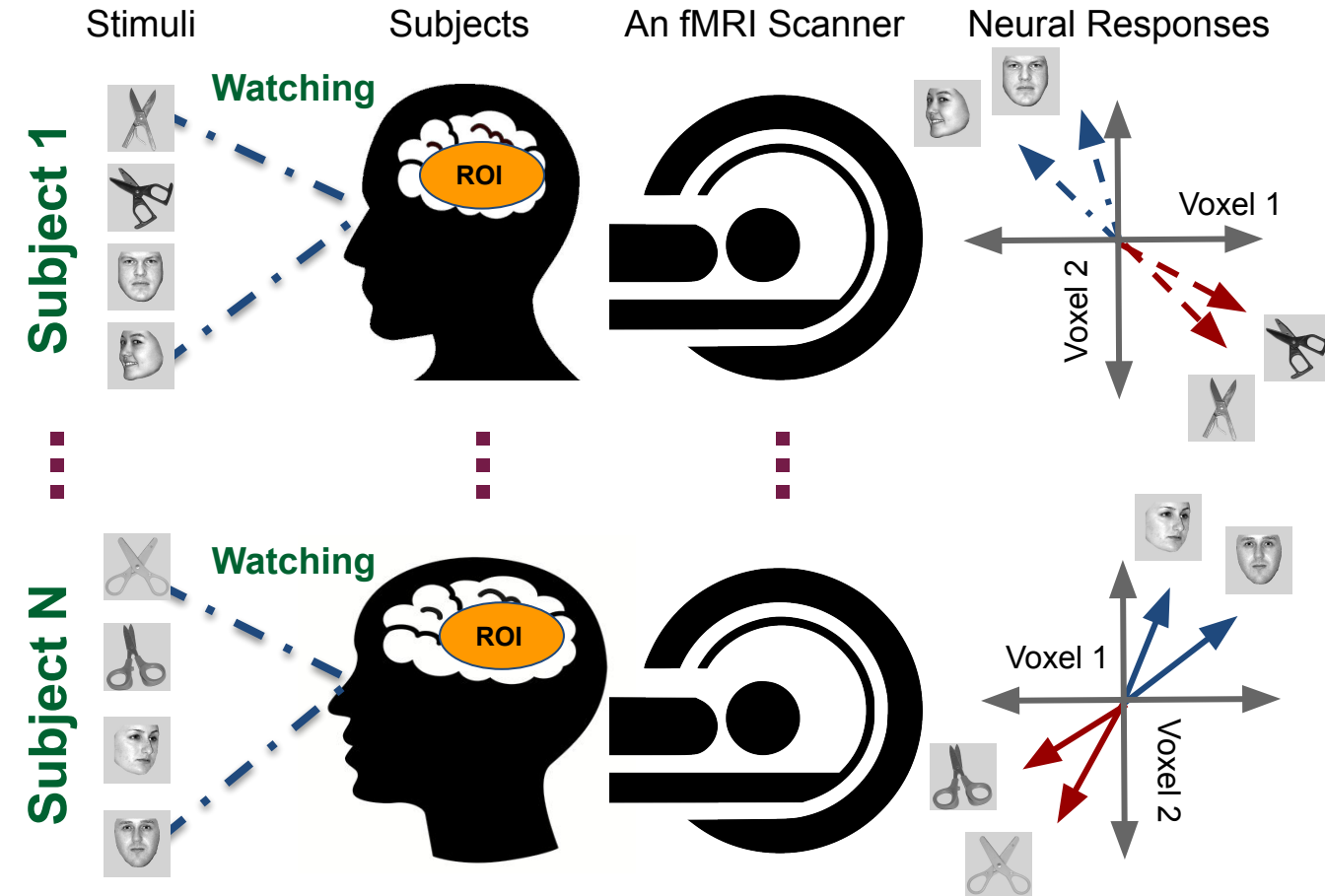
Subject N



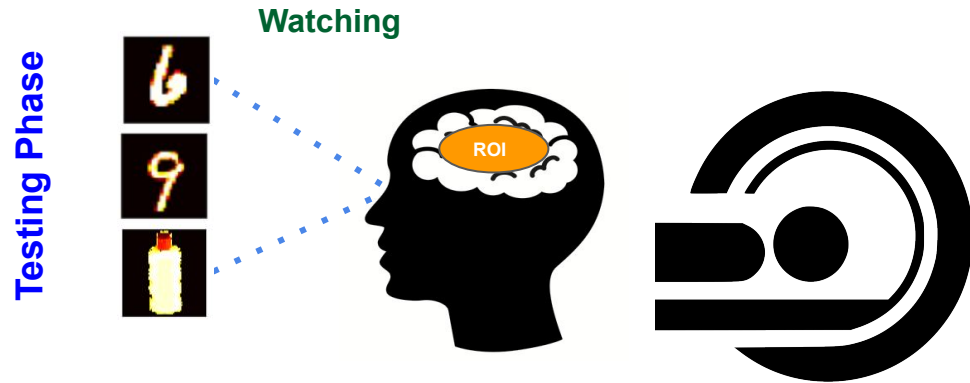
Watching



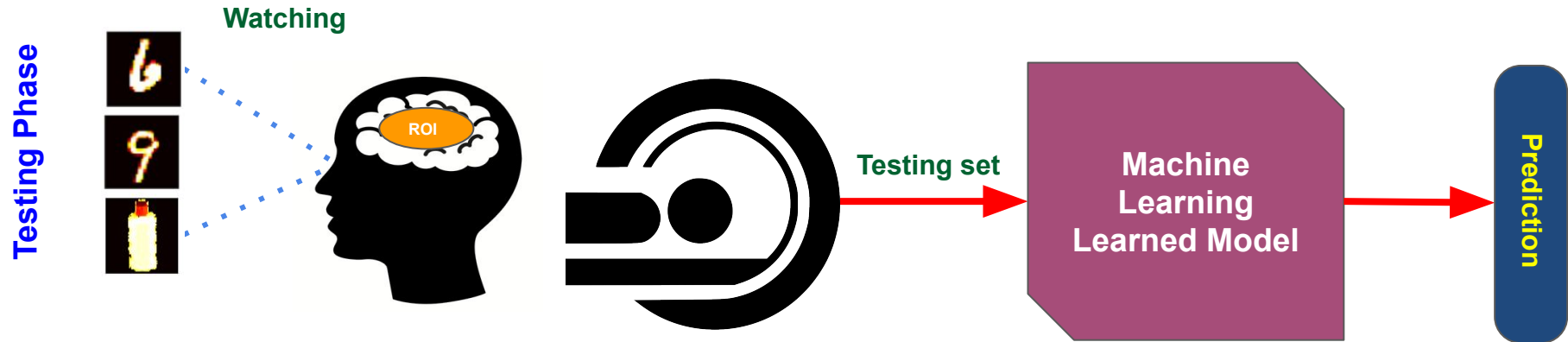
> Multi-subject fMRI dataset



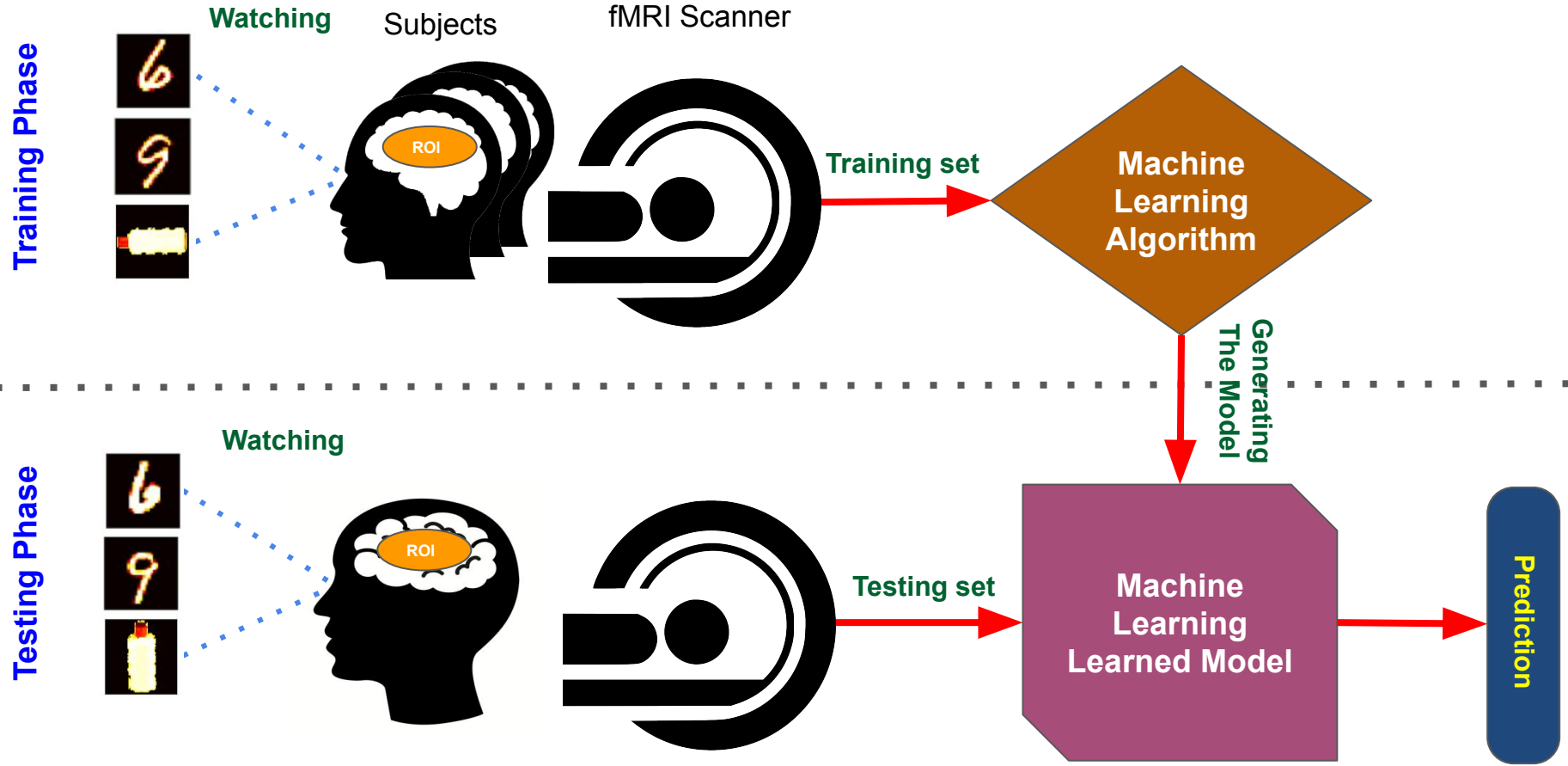
> Classification Analysis for fMRI data



> Classification Analysis for fMRI data



> Classification Analysis for fMRI data



> Classification Analysis for fMRI data

- Prediction can be categories of stimuli
 - *E.g.*, six, nine, or bottle
- It also can be the actual stimuli
 - *E.g.*,



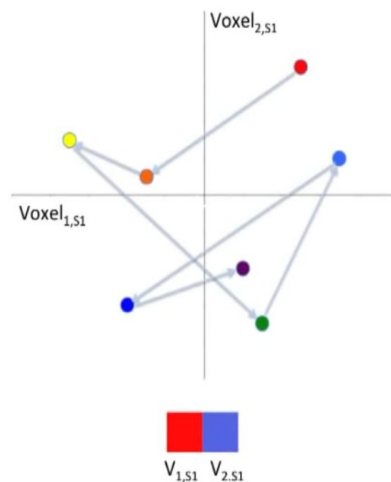
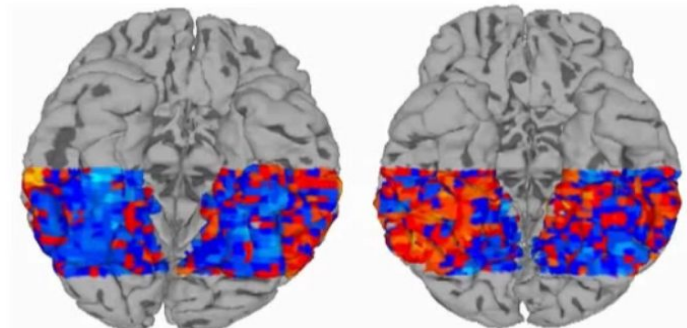
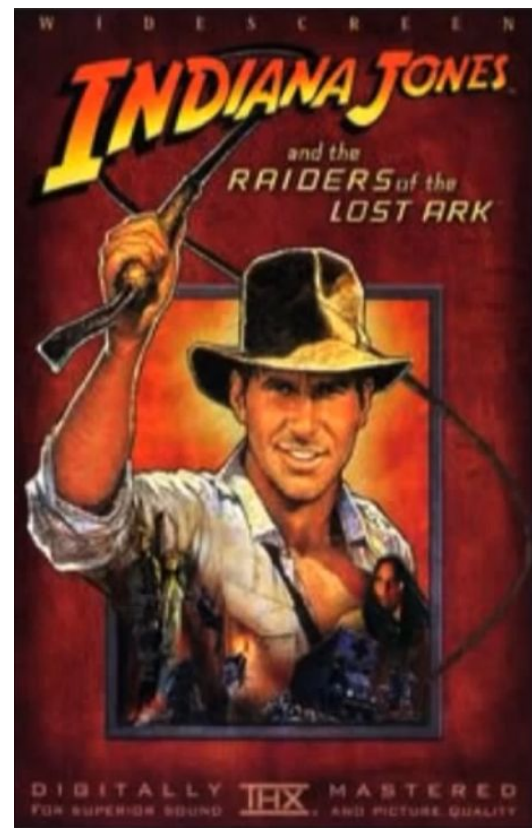
- Alternatively, it can be something related to the cognitive task:
 - *E.g.*, Anxiety versus Control, defined **in the term of subject**

Prediction

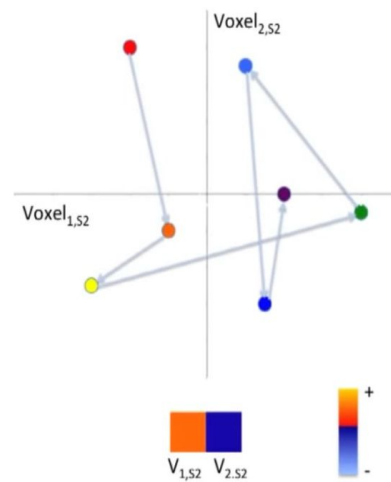
Functional Neuroimaging

Task-based fMRI analysis

> Pattern vector trajectories for 2 subjects in a 2-voxel representation space



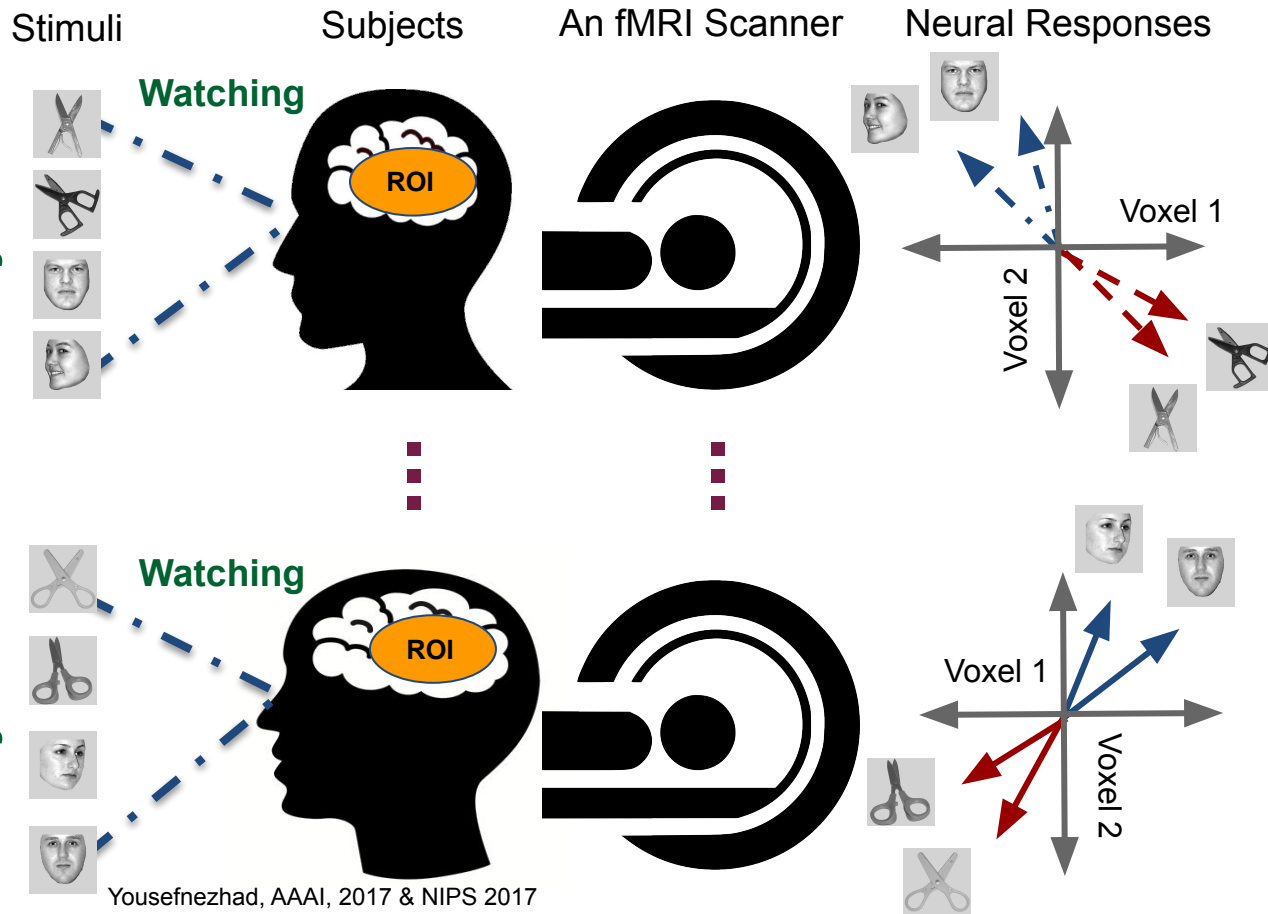
Subject 1



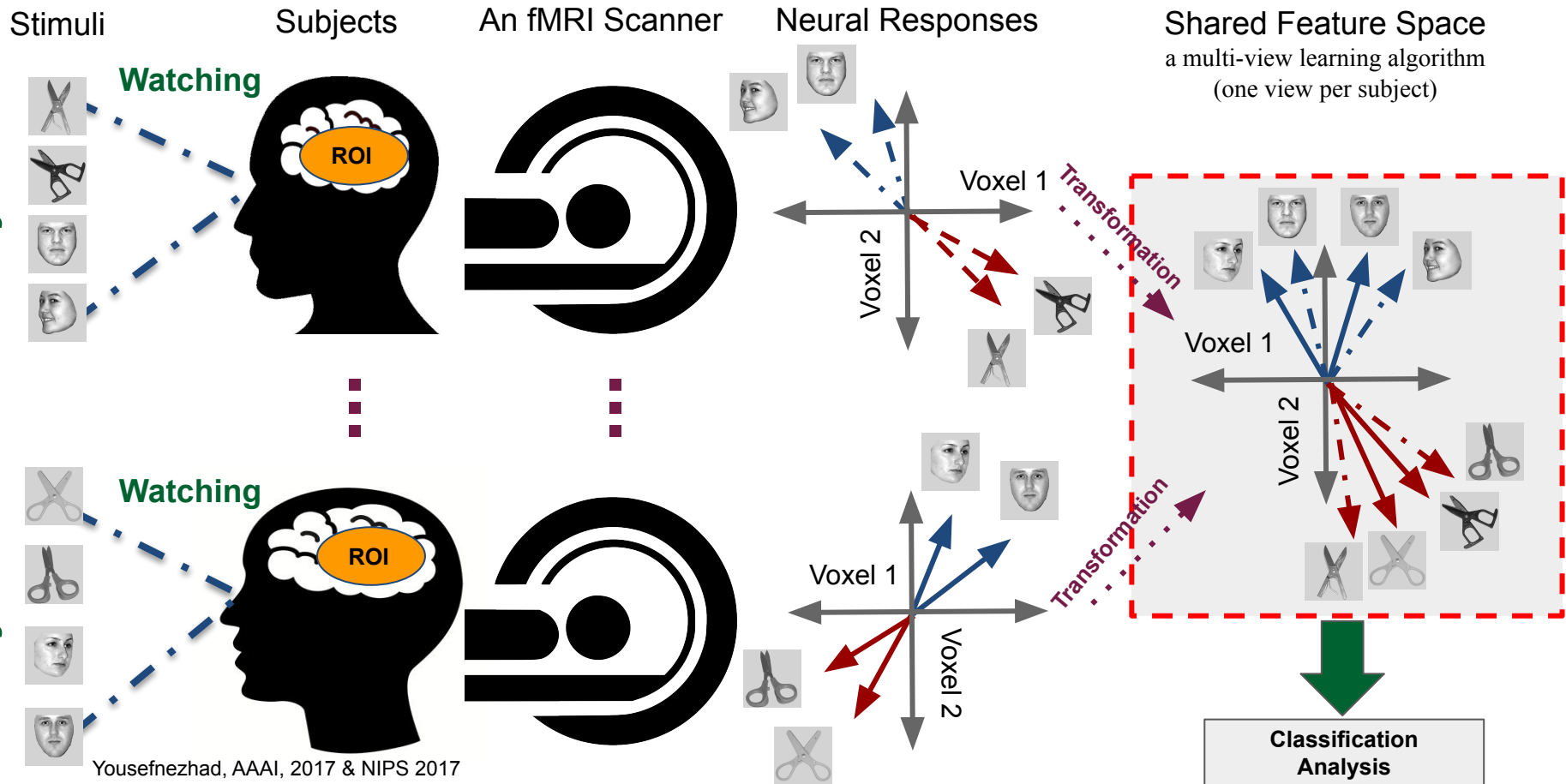
Subject 2

This slide is part of [Haxby, 2011] talk in Dartmouth College
Link <https://youtu.be/jaR9PmlalPs>

> Functional Alignment for Multi-subject fMRI Analysis



> Functional Alignment for Multi-subject fMRI Analysis



> Classic Functional Alignment: Main Idea

- We let $\mathbf{x}^{(i)} \in \mathbb{R}^{T \times V}$ be the neural responses of i-th subject
- V is the number of voxels (after vectorization)
- T is the number of time points
- Inter-Subject Correlation (ISC)

$$\text{ISC}(\mathbf{X}^{(i)}, \mathbf{X}^{(j)}) = \left(\frac{1}{V}\right) \text{tr}\left(\left(\mathbf{X}^{(i)}\right)^\top \mathbf{X}^{(j)}\right)$$

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- Multi-subject Hyperalignment

$$\begin{aligned} & \max_{\mathbf{R}^{(i)}, \mathbf{R}^{(j)}} \sum_{i=1}^S \sum_{j=i+1}^S \text{ISC}(\mathbf{X}^{(i)} \mathbf{R}^{(i)}, \mathbf{X}^{(j)} \mathbf{R}^{(j)}) \\ & \text{s.t.} \quad \left(\mathbf{R}^{(\ell)}\right)^\top \tilde{\Phi}^{(\ell)} \mathbf{R}^{(\ell)} = \mathbf{I}, \ell = 1:S \end{aligned}$$

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- Covariance Matrix:

$\tilde{\Phi}^{(\ell)} = \mathbf{I} \rightarrow$ Multi-set orthogonal Procrustes problem

$\tilde{\Phi}^{(\ell)} = \left(\mathbf{X}^{(\ell)}\right)^\top \mathbf{X}^{(\ell)} \rightarrow$ Multi-set Canonical Correlation Analysis (CCA)
Generalized Canonical Correlation Analysis (CCA)

> Classic Functional Alignment: HA & Pearson Correlation

- By Considering $\widetilde{\Phi}^{(\ell)} = (\mathbf{X}^{(\ell)})^\top \mathbf{X}^{(\ell)}$, we have:

$$\max_{\mathbf{R}^{(i)}, \mathbf{R}^{(j)}} \sum_{i=1}^S \sum_{j=i+1}^S \text{tr} \left(\frac{(\mathbf{X}^{(i)} \mathbf{R}^{(i)})^\top \mathbf{X}^{(i)} \mathbf{R}^{(j)}}{\sqrt{((\mathbf{R}^{(i)})^\top \widetilde{\Phi}^{(i)} \mathbf{R}^{(i)})} \sqrt{((\mathbf{R}^{(j)})^\top \widetilde{\Phi}^{(j)} \mathbf{R}^{(j)})}} \right)$$

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- Since $(\mathbf{X}^{(\ell)} \mathbf{R}^{(\ell)})^\top \mathbf{X}^{(\ell)} \mathbf{R}^{(\ell)} = \mathbf{I}$, we have:

$$\max_{\mathbf{R}^{(i)}, \mathbf{R}^{(j)}} \sum_{i=1}^S \sum_{j=i+1}^S \text{tr} \left((\mathbf{X}^{(i)} \mathbf{R}^{(i)})^\top \mathbf{X}^{(i)} \mathbf{R}^{(j)} \right)$$

> Classic Functional Alignment: Objective Function

- The classic functional alignment:

$$\begin{aligned} & \min_{\mathbf{R}^{(i)}, \mathbf{R}^{(j)}} \sum_{i=1}^S \sum_{j=i+1}^S \left\| \mathbf{X}^{(i)} \mathbf{R}^{(i)} - \mathbf{X}^{(j)} \mathbf{R}^{(j)} \right\|_F^2 \\ \text{s.t.} \quad & \left(\mathbf{X}^{(\ell)} \mathbf{R}^{(\ell)} \right)^\top \mathbf{X}^{(\ell)} \mathbf{R}^{(\ell)} = \mathbf{I}, \ell = 1:S \end{aligned}$$

> Classic Functional Alignment: Objective Function

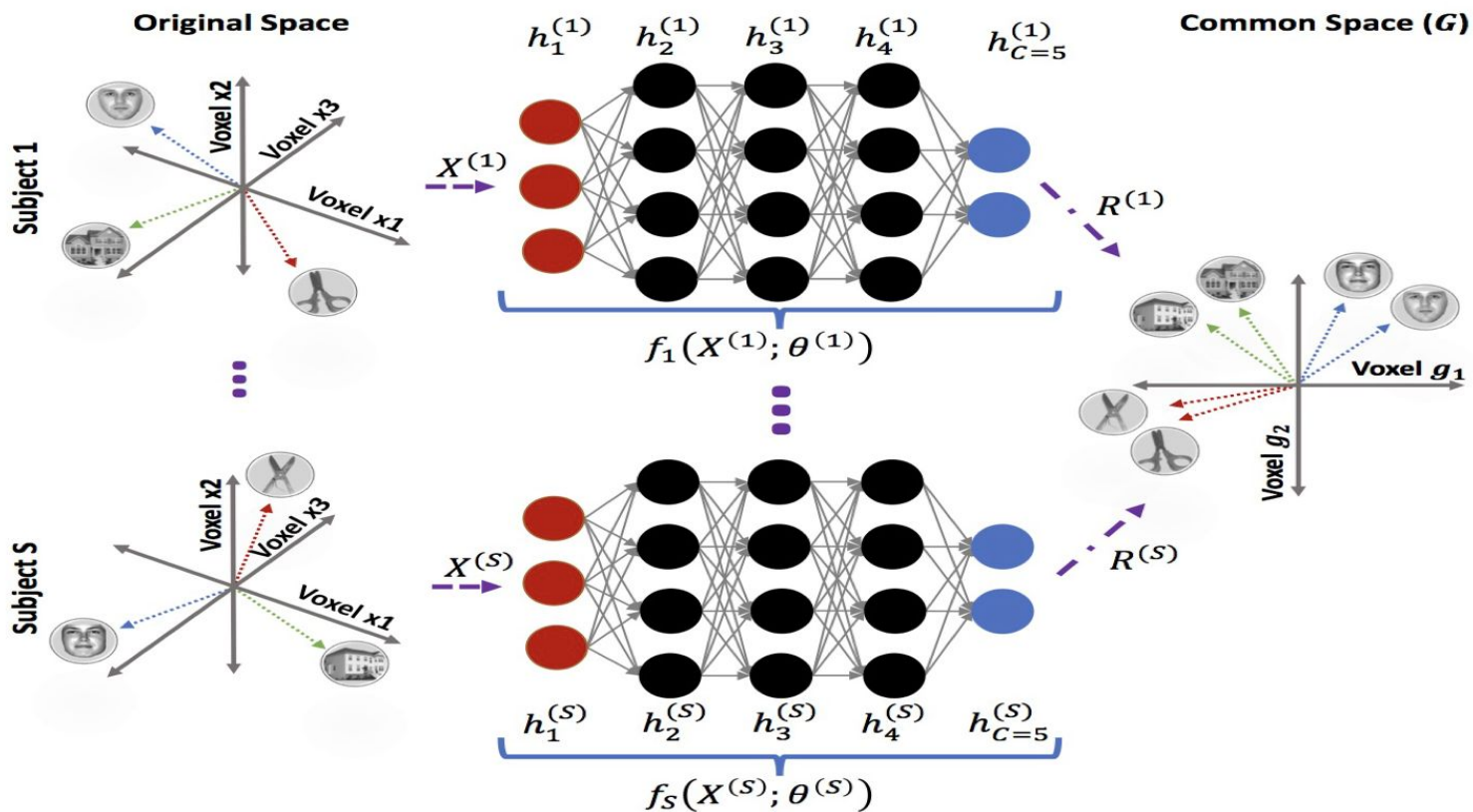
- The classic functional alignment:

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- Also, can be written as follows, which is computationally efficient for the testing stage:

$$\begin{aligned} & \min_{\mathbf{R}^{(i)}, \mathbf{G}} \sum_{i=1}^S \left\| \mathbf{X}^{(i)} \mathbf{R}^{(i)} - \mathbf{G} \right\|_F^2 \\ & \text{Shared Space:} \quad \mathbf{G} = \frac{1}{S} \sum_{j=1}^S \mathbf{X}^{(j)} \mathbf{R}^{(j)} \\ & \text{s.t.} \quad \left(\mathbf{X}^{(\ell)} \mathbf{R}^{(\ell)} \right)^\top \mathbf{X}^{(\ell)} \mathbf{R}^{(\ell)} = \mathbf{I}, \quad \ell = 1:S \end{aligned}$$

> Deep Hyperalignment (DHA)



> DHA: Objective Function

- The deep functional alignment:

$$\begin{aligned} \min_{\mathbf{G}, \mathbf{R}^{(i)}, \theta^{(i)}} \sum_{i=1}^S \left\| \mathbf{G} - f_i(\mathbf{X}^{(i)}; \theta^{(i)}) \mathbf{R}^{(i)} \right\|_F^2 \\ \text{s.t. } \mathbf{G}^\top \mathbf{G} = \mathbf{I} \end{aligned}$$

where the deep network is defined as follows:

$$f_\ell(\mathbf{X}^{(\ell)}; \theta^{(\ell)}) = \text{mat}\left(\mathbf{h}_C^{(\ell)}, T, V_{new}\right)$$

$$\mathbf{h}_m^{(\ell)} = \mathbf{g}\left(\mathbf{W}_m^{(\ell)} \mathbf{h}_{m-1}^{(\ell)} + \mathbf{b}_m^{(\ell)}\right), \quad \text{where } \mathbf{h}_1^{(\ell)} = \text{vec}(\mathbf{X}^{(\ell)}) \quad \text{and } m = 2:C$$

> DHA: Definitions for Optimization

- Rank-m SVD:

$$f_\ell(\mathbf{X}^{(\ell)}; \theta^{(\ell)}) \stackrel{SVD}{=} \mathbf{\Omega}^{(\ell)} \mathbf{\Sigma}^{(\ell)} (\mathbf{\Psi}^{(\ell)})^\top, \quad \ell = 1:S$$

- Projection Matrix:

$$\begin{aligned} \mathbf{P}^{(\ell)} &= f_\ell(\mathbf{X}^{(\ell)}; \theta^{(\ell)}) \left(\left(f_\ell(\mathbf{X}^{(\ell)}; \theta^{(\ell)}) \right)^\top f_\ell(\mathbf{X}^{(\ell)}; \theta^{(\ell)}) + \epsilon \mathbf{I} \right)^{-1} \left(f_\ell(\mathbf{X}^{(\ell)}; \theta^{(\ell)}) \right)^\top \\ &= \mathbf{\Omega}^{(\ell)} (\mathbf{\Sigma}^{(\ell)})^\top \left(\mathbf{\Sigma}^{(\ell)} (\mathbf{\Sigma}^{(\ell)})^\top + \epsilon \mathbf{I} \right)^{-1} \mathbf{\Sigma}^{(\ell)} (\mathbf{\Omega}^{(\ell)})^\top = \mathbf{\Omega}^{(\ell)} \mathbf{D}^{(\ell)} \left(\mathbf{\Omega}^{(\ell)} \mathbf{D}^{(\ell)} \right)^\top \end{aligned}$$

where $\mathbf{D}^{(\ell)} (\mathbf{D}^{(\ell)})^\top = (\mathbf{\Sigma}^{(\ell)})^\top \left(\mathbf{\Sigma}^{(\ell)} (\mathbf{\Sigma}^{(\ell)})^\top + \epsilon \mathbf{I} \right)^{-1} \mathbf{\Sigma}^{(\ell)}$.

- Sum of Projection Matrices

$$\mathbf{A} = \sum_{i=1}^S \mathbf{P}^{(i)} = \widetilde{\mathbf{A}} \widetilde{\mathbf{A}}^\top, \quad \text{where } \widetilde{\mathbf{A}} \in \mathbb{R}^{T \times mS} = [\mathbf{\Omega}^{(1)} \mathbf{D}^{(1)} \dots \mathbf{\Omega}^{(S)} \mathbf{D}^{(S)}].$$

 Cholesky Decomposition

> DHA: Optimization

- Objective Function can be reformulated as follows:

$$\min_{\mathbf{G}, \mathbf{R}^{(i)}, \theta^{(i)}} \sum_{i=1}^S \left\| \mathbf{G} - f_i(\mathbf{X}^{(i)}; \theta^{(i)}) \mathbf{R}^{(i)} \right\| \propto \max_{\mathbf{G}} \left(\text{tr}(\mathbf{G}^\top \mathbf{A} \mathbf{G}) \right).$$

- So, we have:

$$\mathbf{A} \mathbf{G} = \mathbf{G} \mathbf{\Lambda}, \text{ where } \mathbf{\Lambda} = \{ \lambda_1 \dots \lambda_T \} \quad \text{and} \quad \widetilde{\mathbf{A}} = \mathbf{G} \widetilde{\mathbf{\Sigma}} \widetilde{\mathbf{\Psi}}^\top$$

- DHA mappings can be calculated as follows:

$$\mathbf{R}^{(\ell)} = \left(\left(f_\ell(\mathbf{X}^{(\ell)}; \theta^{(\ell)}) \right)^\top f_\ell(\mathbf{X}^{(\ell)}; \theta^{(\ell)}) + \epsilon \mathbf{I} \right)^{-1} \left(f_\ell(\mathbf{X}^{(\ell)}; \theta^{(\ell)}) \right)^\top \mathbf{G}.$$

- In order to use back-propagation algorithm for seeking an optimized parameters for the deep network, we also have:

$$\frac{\partial \mathbf{Z}}{\partial f_\ell(\mathbf{X}^{(\ell)}; \theta^{(\ell)})} = 2\mathbf{R}^{(\ell)} \mathbf{G}^\top - 2\mathbf{R}^{(\ell)} (\mathbf{R}^{(\ell)})^\top \left(f_\ell(\mathbf{X}^{(\ell)}; \theta^{(\ell)}) \right)^\top \text{ where } \mathbf{Z} = \sum_{\ell=1}^T \lambda_\ell$$

 Incremental SVD

> Datasets

Title	ID	S	K	T	V	X	Y	Z	Scanner	TR	TE
Mixed-gambles task	DS005	48	2	240	450	53	63	52	S 3T	2	30
Visual Object Recognition	DS105	71	8	121	1963	79	95	79	G 3T	2.5	30
Word and Object Processing	DS107	98	4	164	932	53	63	52	S 3T	2	28
Auditory and Visual Oddball	DS116	102	2	170	2532	53	63	40	P 3T	2	25
Multi-subject, multi-modal	DS117	171	2	210	524	64	61	33	S 3T	2	30
Forrest Gump	DS113	20	10	451	2400	160	160	36	S 7T	2.3	22
Raiders of the Lost Ark	<i>N/A</i>	10	7	924	980	78	78	54	S 3T	3	30

S is the number of subject; K denotes the number of stimulus categories; T is the number of scans in unites of TRs (Time of Repetition); V denotes the number of voxels in ROI; X, Y, Z are the size of 3D images; Scanners include S=Siemens, G = General Electric, and P = Philips in 3 Tesla or 7 Tesla; TR is Time of Repetition in millisecond; TE denotes Echo Time in second; Please see openfmri.org for more information.

> Simple Cognitive Tasks Analysis

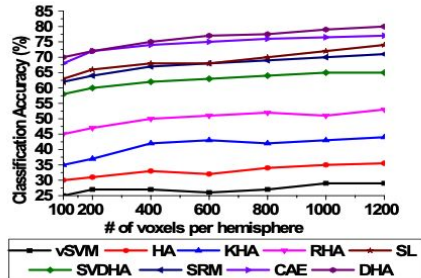
Table 1: Simple Task Analysis: Accuracy of HA methods

↓Algorithms, Datasets→	DS005	DS105	DS107	DS116	DS117
ν -SVM	71.65±0.97	22.89±1.02	38.84±0.82	67.26±1.99	73.32±1.67
Hyperalignment (HA)	81.27±0.59	30.03±0.87	43.01±0.56	74.23±1.40	77.93±0.29
Regularized HA	83.06±0.36	32.62±0.52	46.82±0.37	78.71±0.76	84.22±0.44
Kernel HA	85.29±0.49	37.14±0.91	52.69±0.69	78.03±0.89	83.32±0.41
SVD-HA	90.82±1.23	40.21±0.83	59.54±0.99	81.56±0.54	95.62±0.83
Shared Response Model	91.26±0.34	48.77±0.94	64.11±0.37	83.31±0.73	95.01±0.64
SearchLight	90.21±0.61	49.86±0.4	64.07±0.98	82.32±0.28	94.96±0.24
Convolutional Autoencoder	94.25±0.76	54.52±0.80	72.16±0.43	91.49±0.67	95.92±0.67
Deep HA	97.92±0.82	60.39±0.68	73.05±0.63	90.28±0.71	97.99±0.94

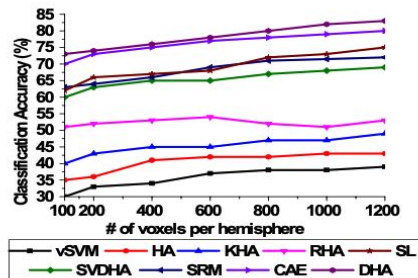
Table 2: Simple Task Analysis: AUC of different HA methods

↓Algorithms, Datasets→	DS005	DS105	DS107	DS116	DS117
ν -SVM [17]	68.37±1.01	21.76±0.91	36.84±1.45	62.49±1.34	70.17±0.59
Hyperalignment (HA)	70.32±0.92	28.91±1.03	40.21±0.33	70.67±0.97	76.14±0.49
Regularized HA	82.22±0.42	30.35±0.39	43.63±0.61	76.34±0.45	81.54±0.92
Kernel HA	80.91±0.21	36.23±0.57	50.41±0.92	75.28±0.94	80.92±0.28
SVD-HA	88.54±0.71	37.61±0.62	57.54±0.31	78.66±0.82	92.14±0.42
Shared Response Model	90.23±0.74	44.48±0.75	62.41±0.72	79.20±0.98	93.65±0.93
SearchLight	89.79±0.25	47.32±0.92	61.84±0.32	80.63±0.81	93.26±0.72
Convolutional Autoencoder	91.24±0.61	52.16±0.63	72.33±0.79	87.53±0.72	91.49±0.33
Deep HA	96.91±0.82	59.57±0.32	70.23±0.92	89.93±0.24	96.13±0.32

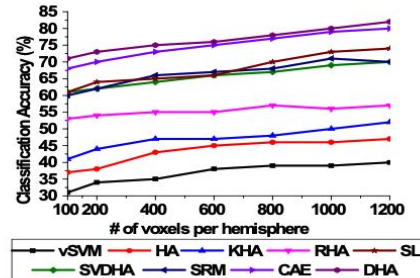
> Movie Stimulus Analysis



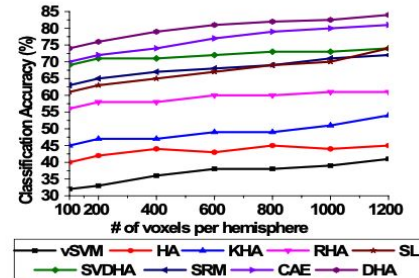
(a) Forrest Gump
(TRs = 100)



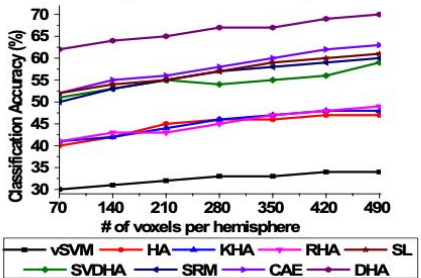
(b) Forrest Gump
(TRs = 400)



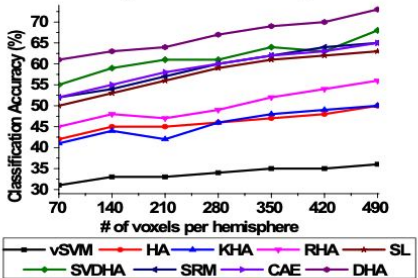
(c) Forrest Gump
(TRs = 800)



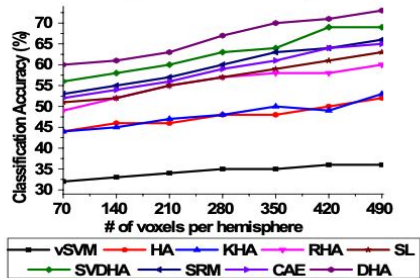
(d) Forrest Gump
(TRs = 2000)



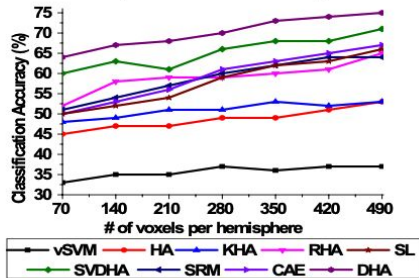
(e) Raiders
(TRs = 100)



(f) Raiders
(TRs = 400)



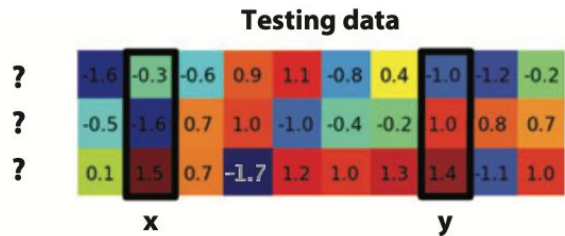
(g) Raiders
(TRs = 800)



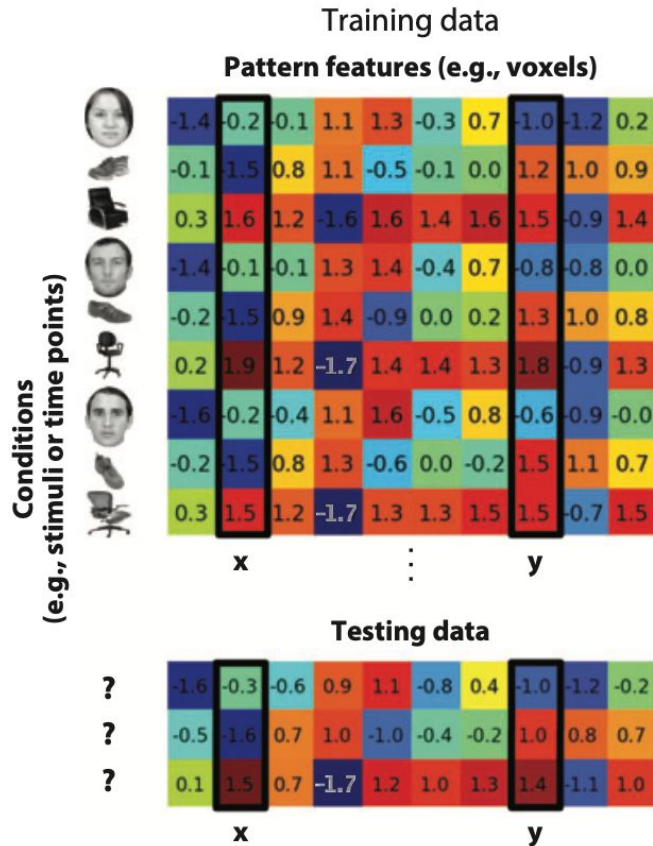
(h) Raiders
(TRs = 2000)

Reconstructing Images from fMRI

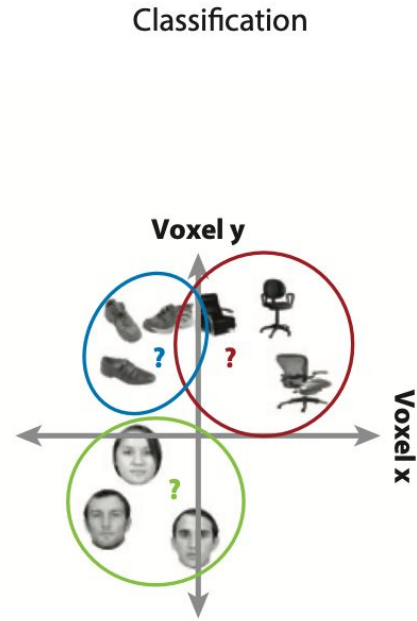
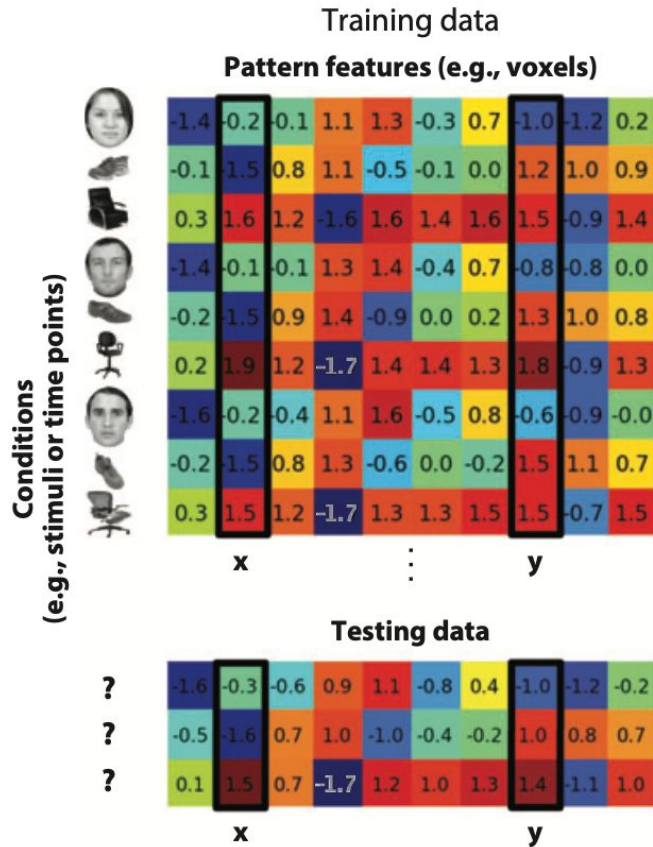
> Classification Analysis



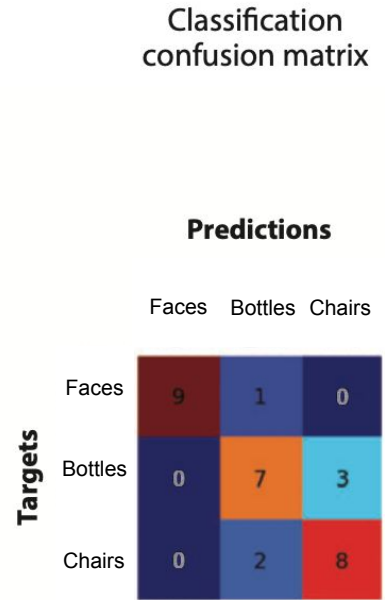
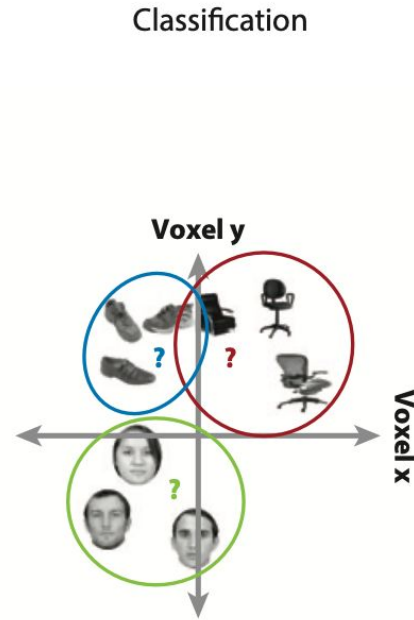
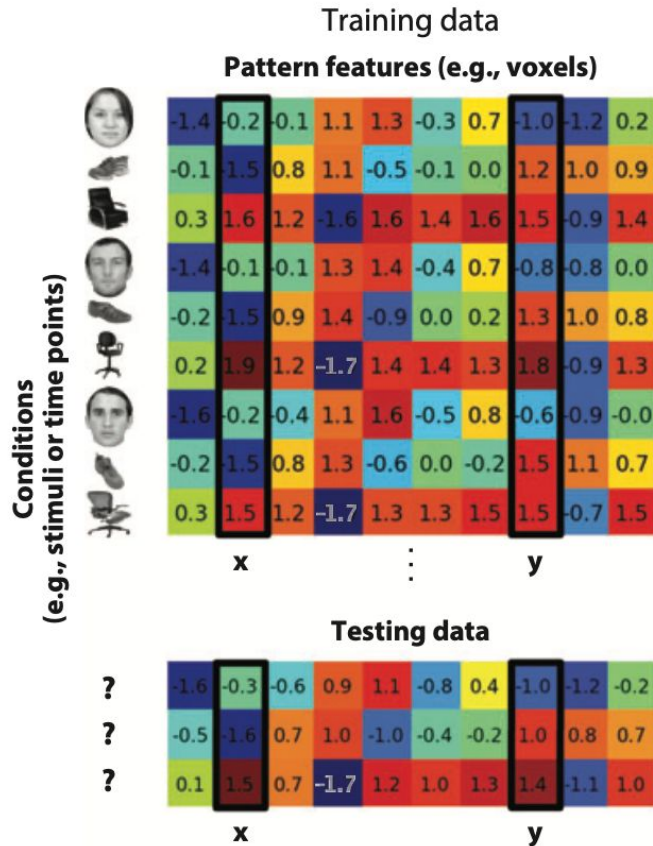
> Classification Analysis



> Classification Analysis

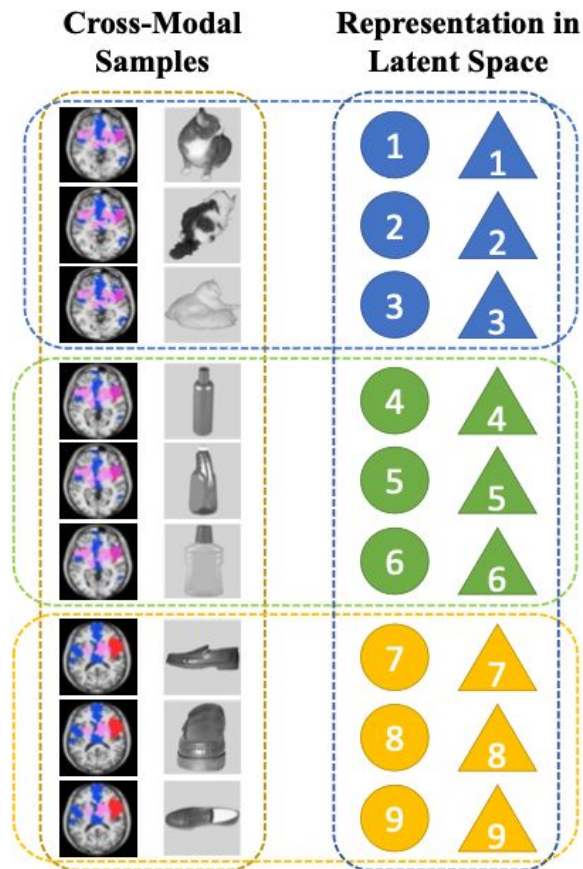


> Classification Analysis



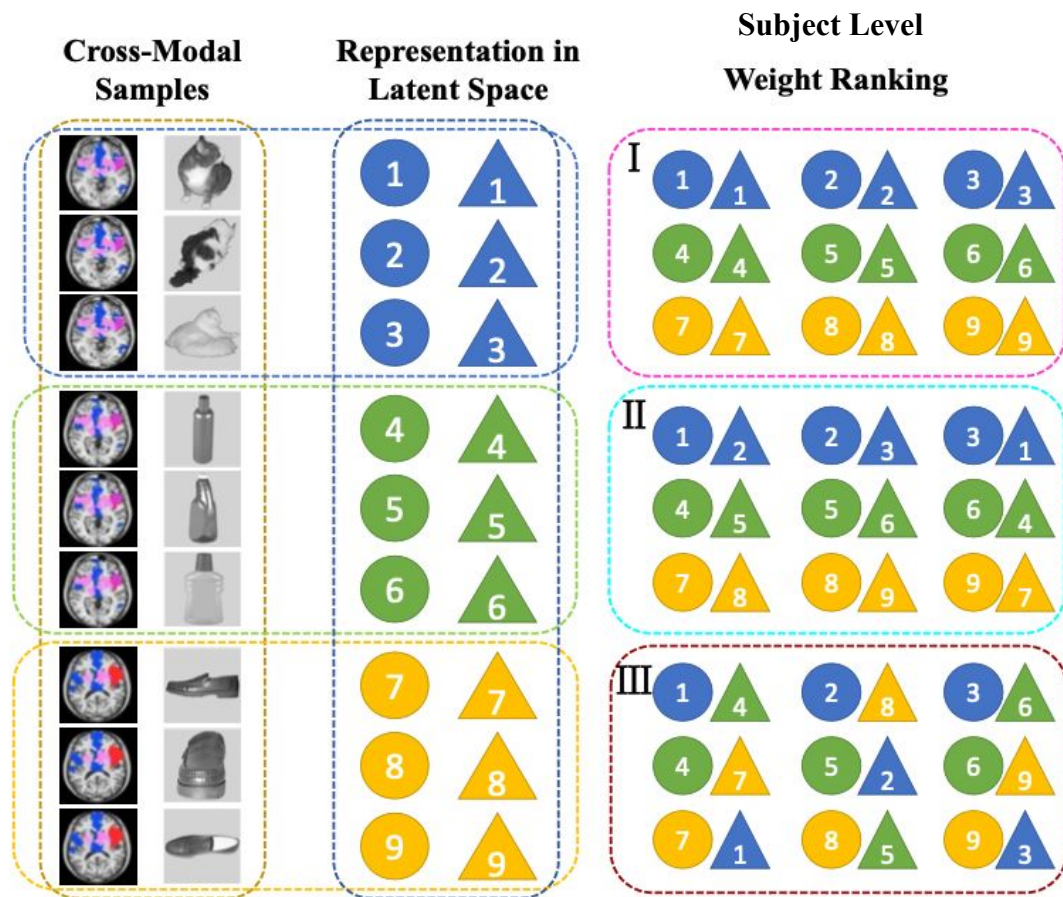
> Pairwise ranking loss

- The schematic diagram of pairwise ranking loss in visual stimuli reconstruction.
- Circles represent the fMRI data
- Triangles represent the stimuli images.
- Different colors means different categories:
 - blue=cats
 - green=bottles
 - yellow=shoes

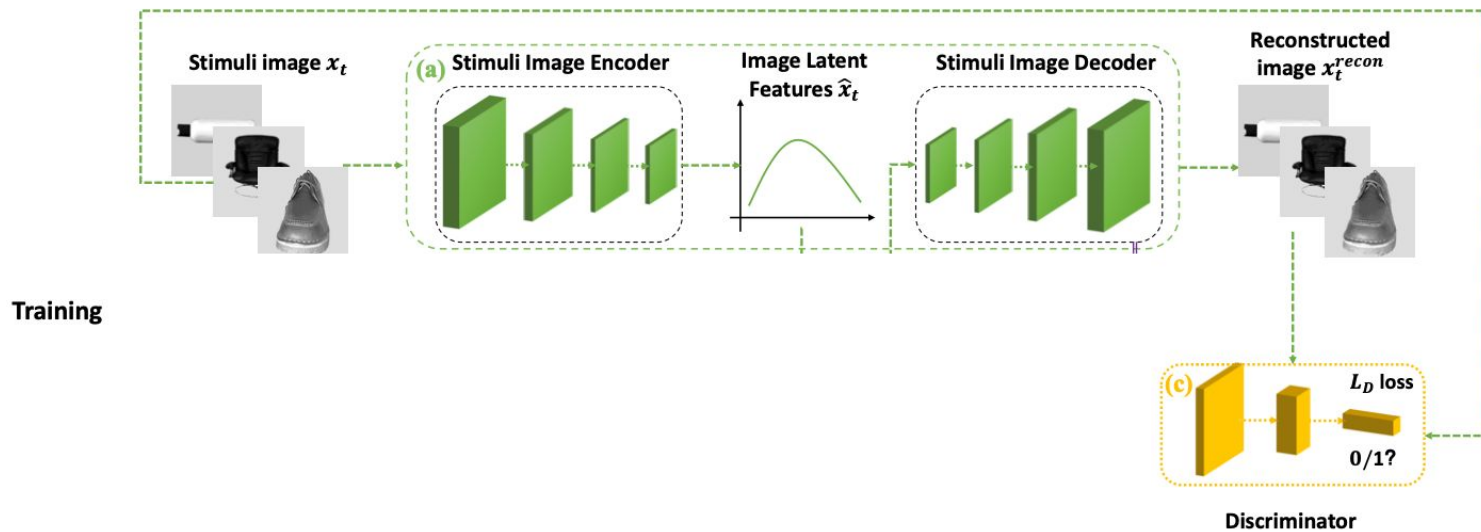


> Pairwise ranking loss

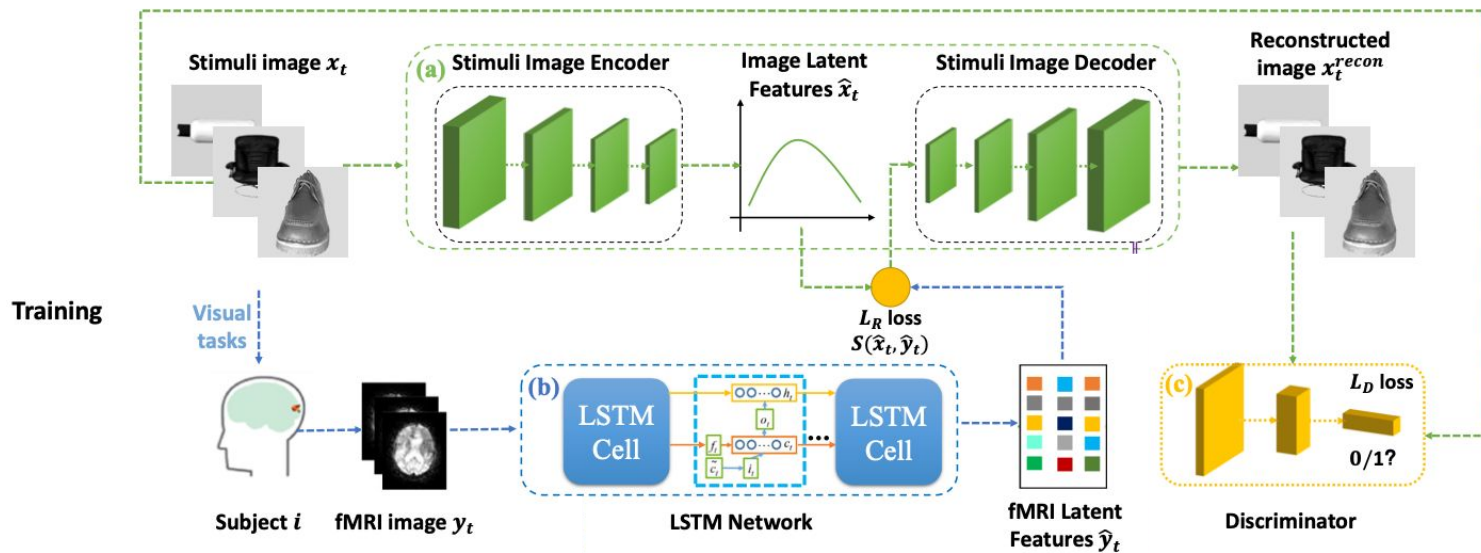
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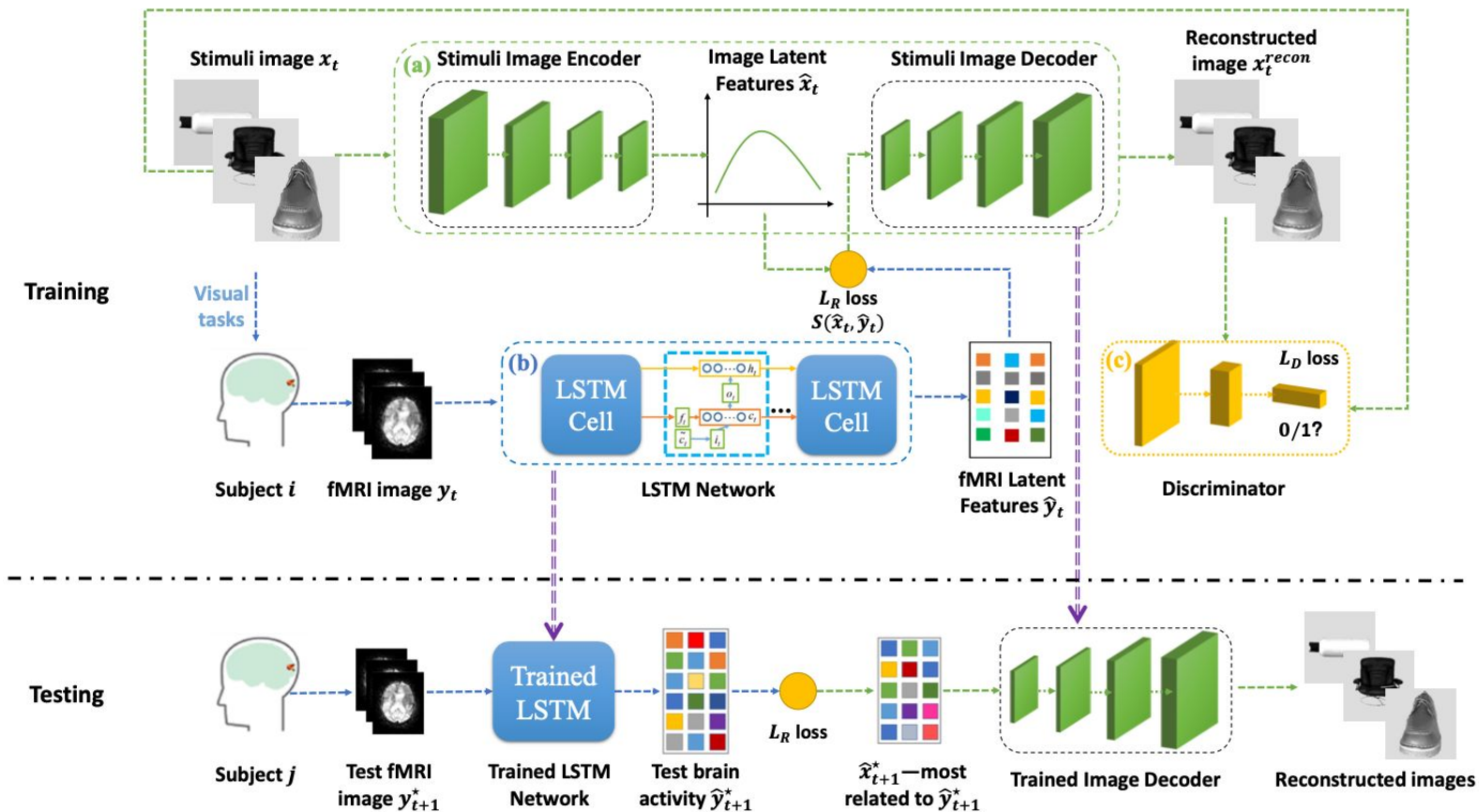
> Our proposed Temporal Information Generative Adversarial Networks (TIGAN)



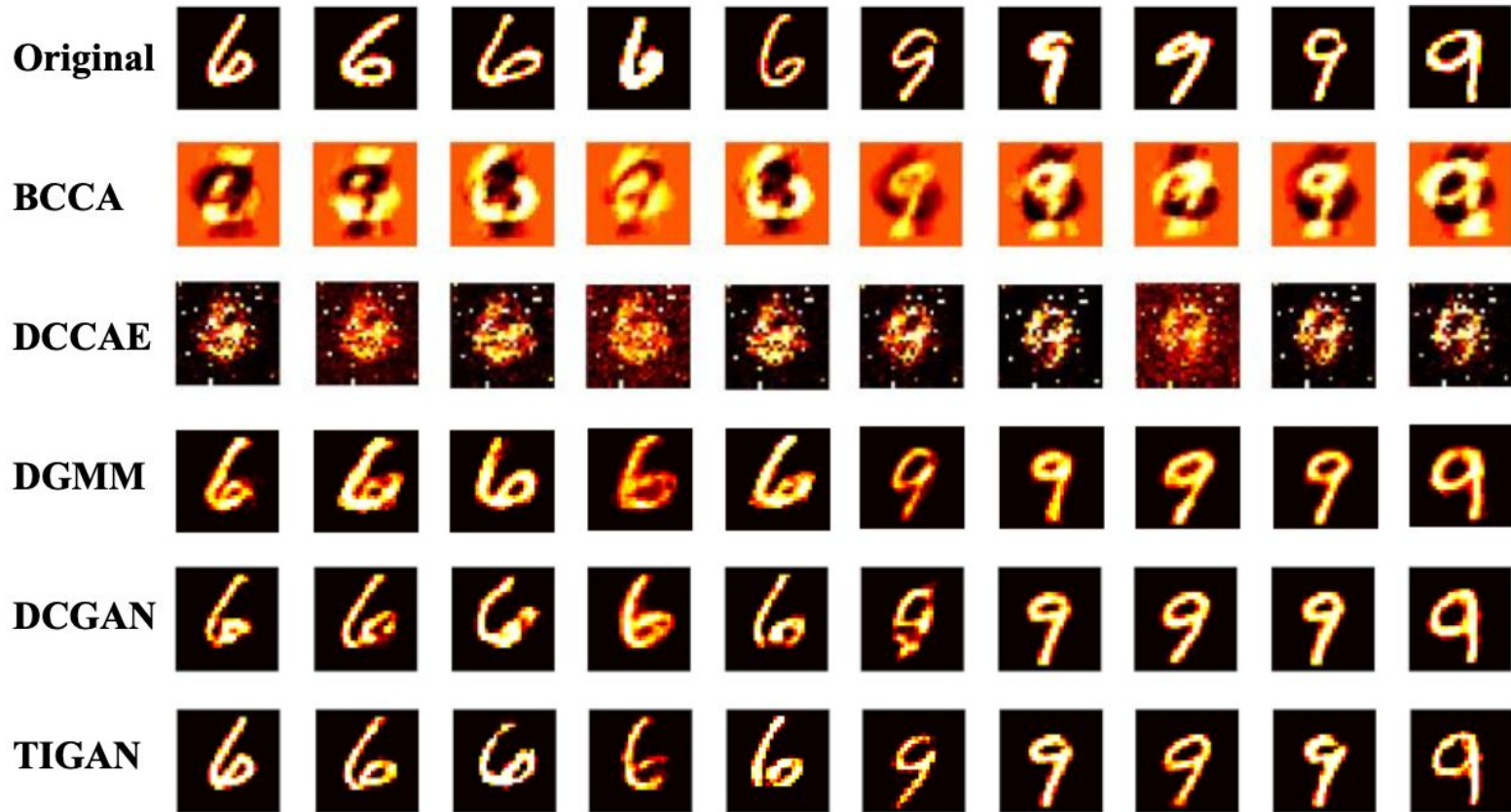
> Our proposed Temporal Information Generative Adversarial Networks (TIGAN)



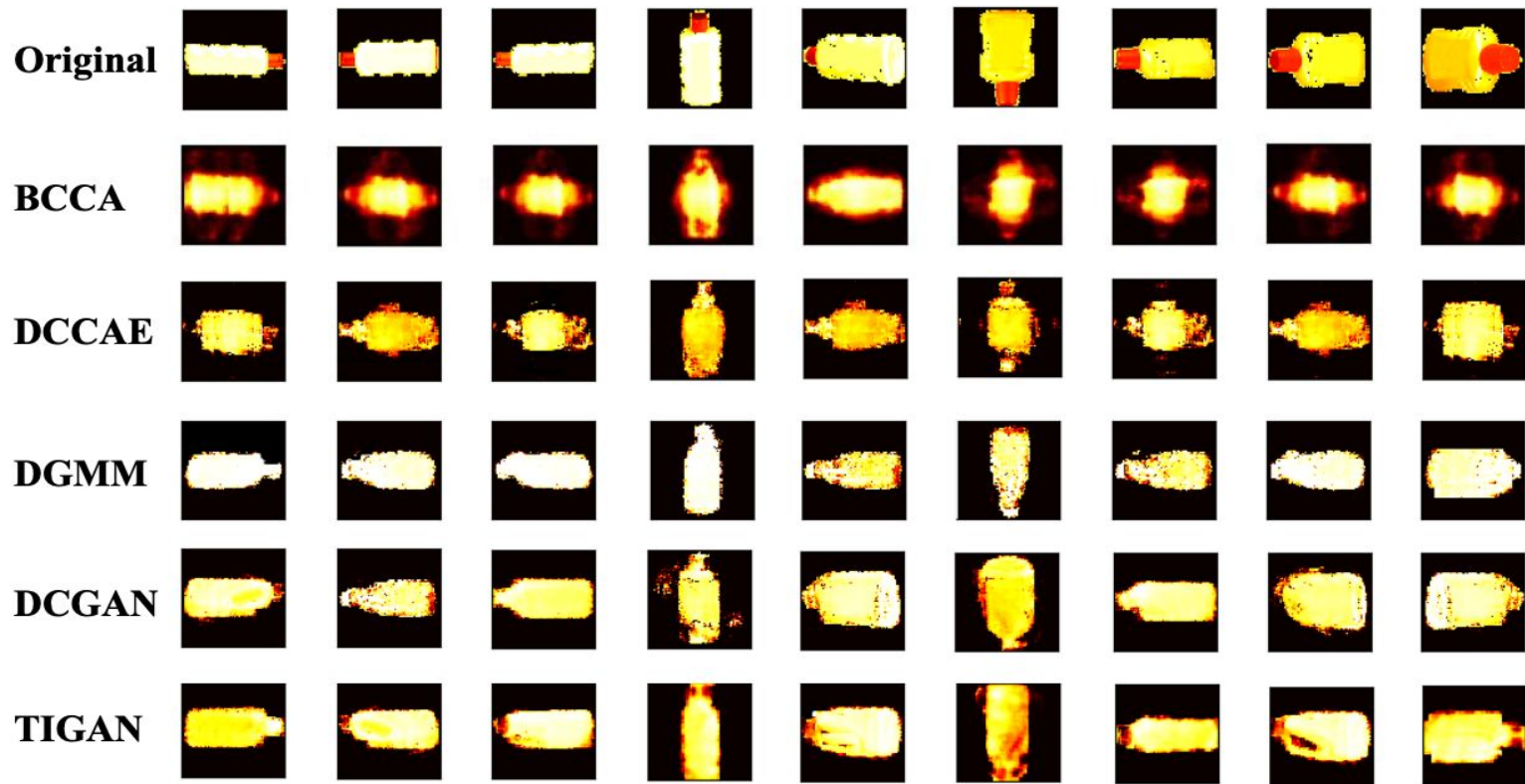
> Our proposed Temporal Information Generative Adversarial Networks (TIGAN)



> Comparing image reconstruction – on number stimuli

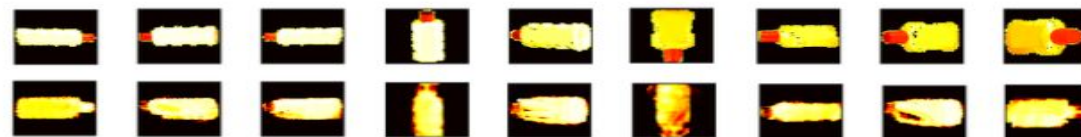


> Comparing image reconstruction – on bottle stimuli

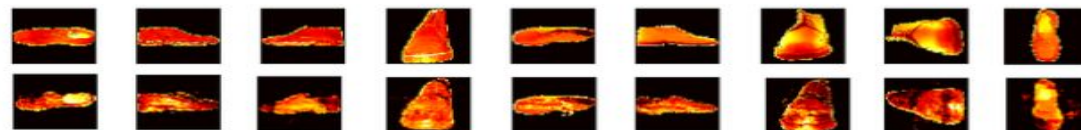


> More examples

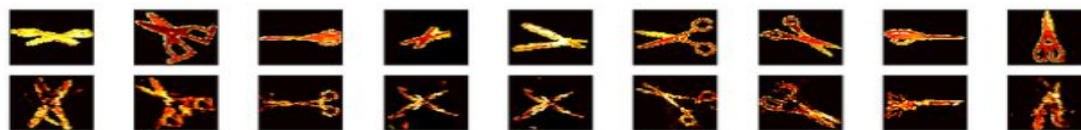
bottles



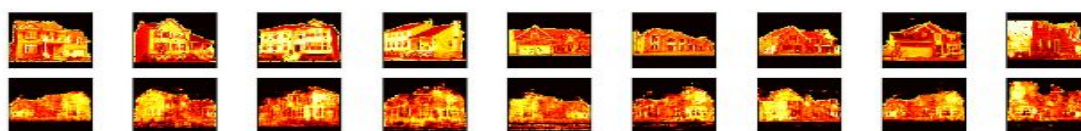
shoes



scissors



houses



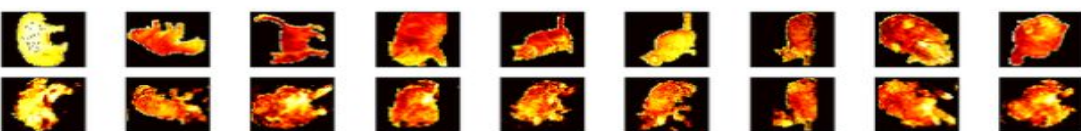
faces



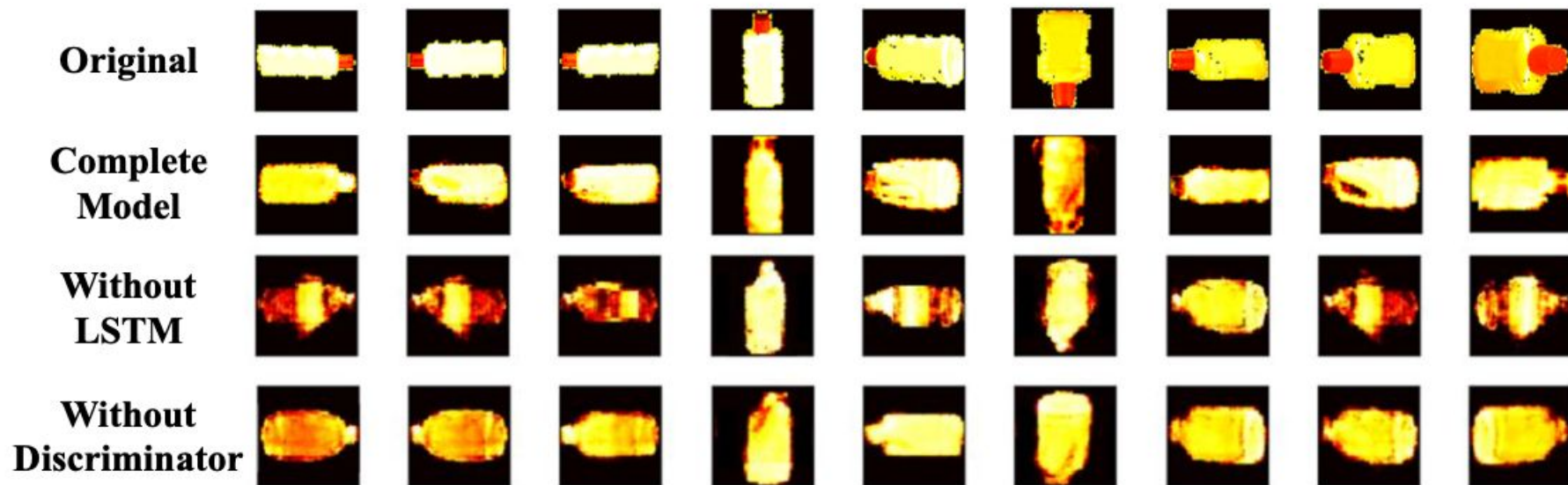
chairs



cats



> Comparing different components of TIGAN



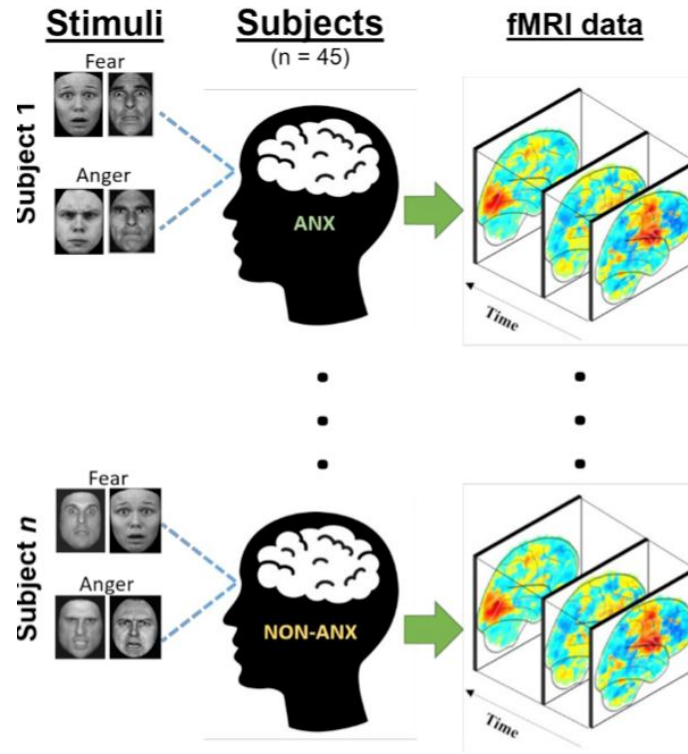
Diagnosing pediatric anxiety by using fMRI

> Pediatric anxiety dataset

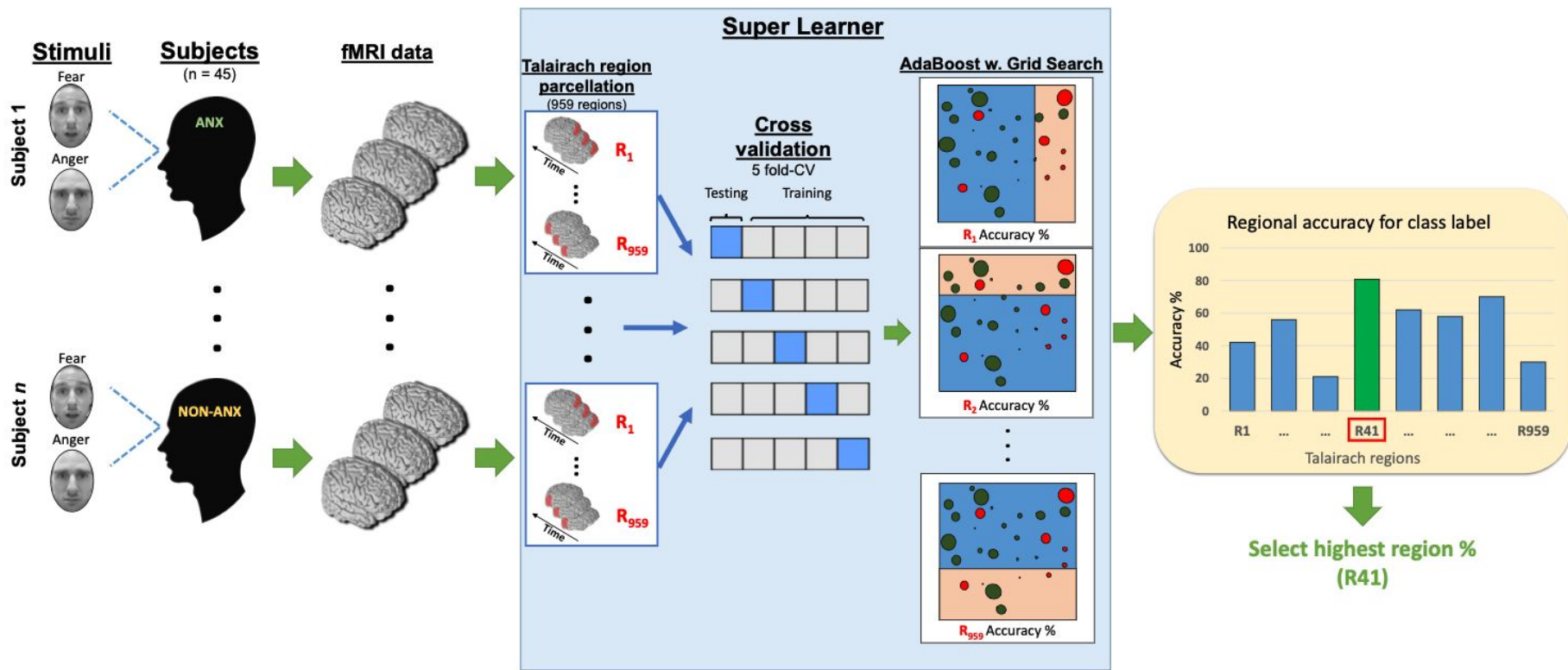
	Non-anxious (N=23)	Anxious (N=22)	Generalized Anxiety (N=15)	Separation Anxiety (N=10)	Social Phobia (N=11)
Demographics					
Age at scan	7.48 (1.04)	6.86 (0.99)*	6.86 (1.06)	7.00 (1.33)	6.63 (0.81)*
Female	13	16	12	7	8
Ethnicity	12	10	8	6	3
Below poverty	4	6	5	5	2
Handedness (right)	16	18	14	7	8
IQ	104.48 (14.02)	103.86 (10.81)	103.52 (11.51)	103.20 (10.63)	106.18 (9.54)
Symptoms					
Impairment (0-10)	0.74 (1.09)	3.5 (2.35)**	3.93 (2.66)**	3.80 (2.62)**	3.28 (1.68)**
Emotional symptoms (0-14)	2.17 (1.99)	6.54 (2.91)**	7.26 (3.13)**	8.40 (2.91)**	5.81 (2.40)**

Kimberly L. H. Carpenter and Adrian Angold and Nan-Kuei Chen and William E. Copeland and Pooja Gaur and Kevin Pelphrey and Allen W. Song and Helen L. Egger (2018). Preschool Anxiety Disorders. OpenNeuro: <https://openneuro.org/datasets/ds000144/versions/00002>

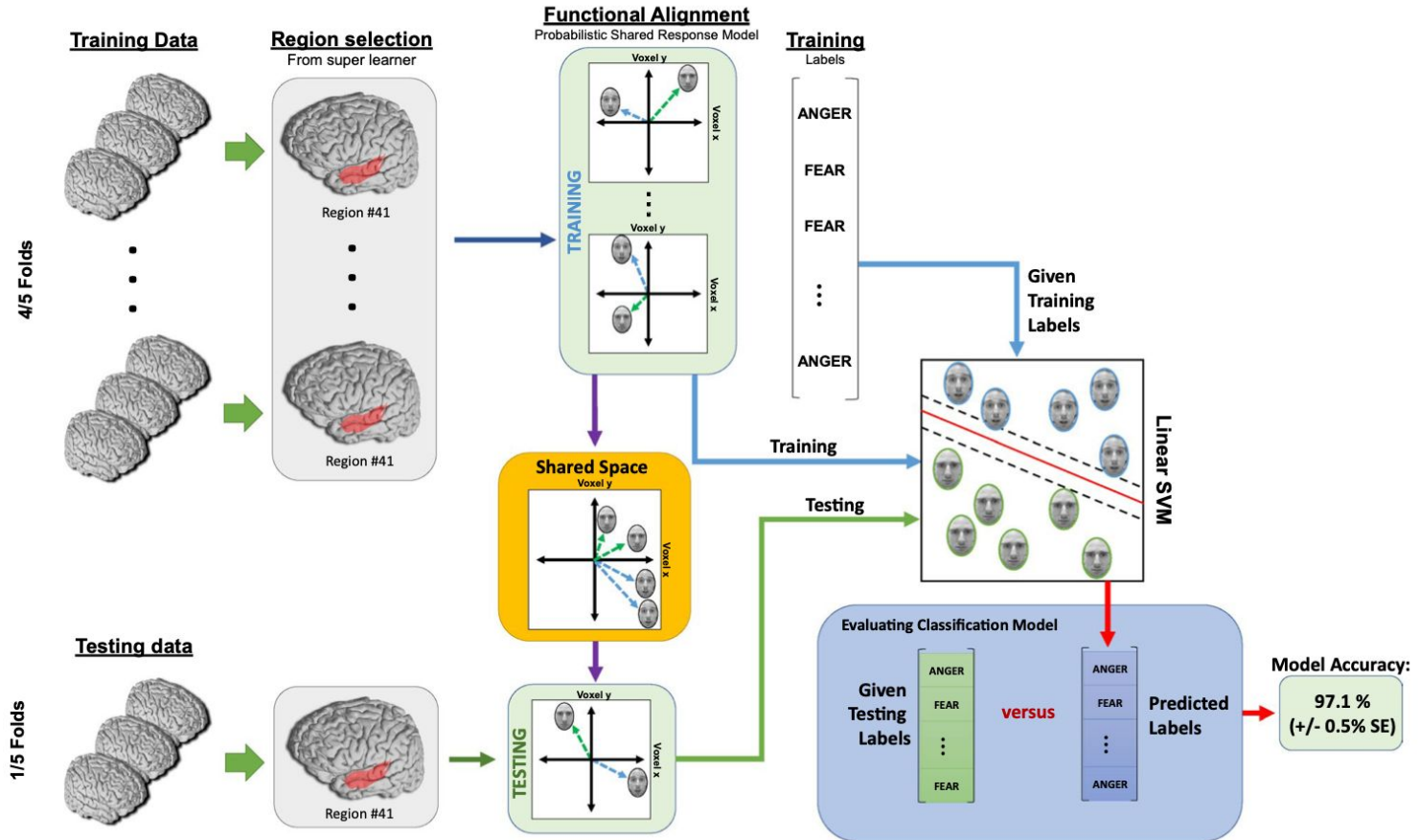
> Pediatric anxiety: cognitive tasks



> Finding the best region of interest to predict pediatric anxiety

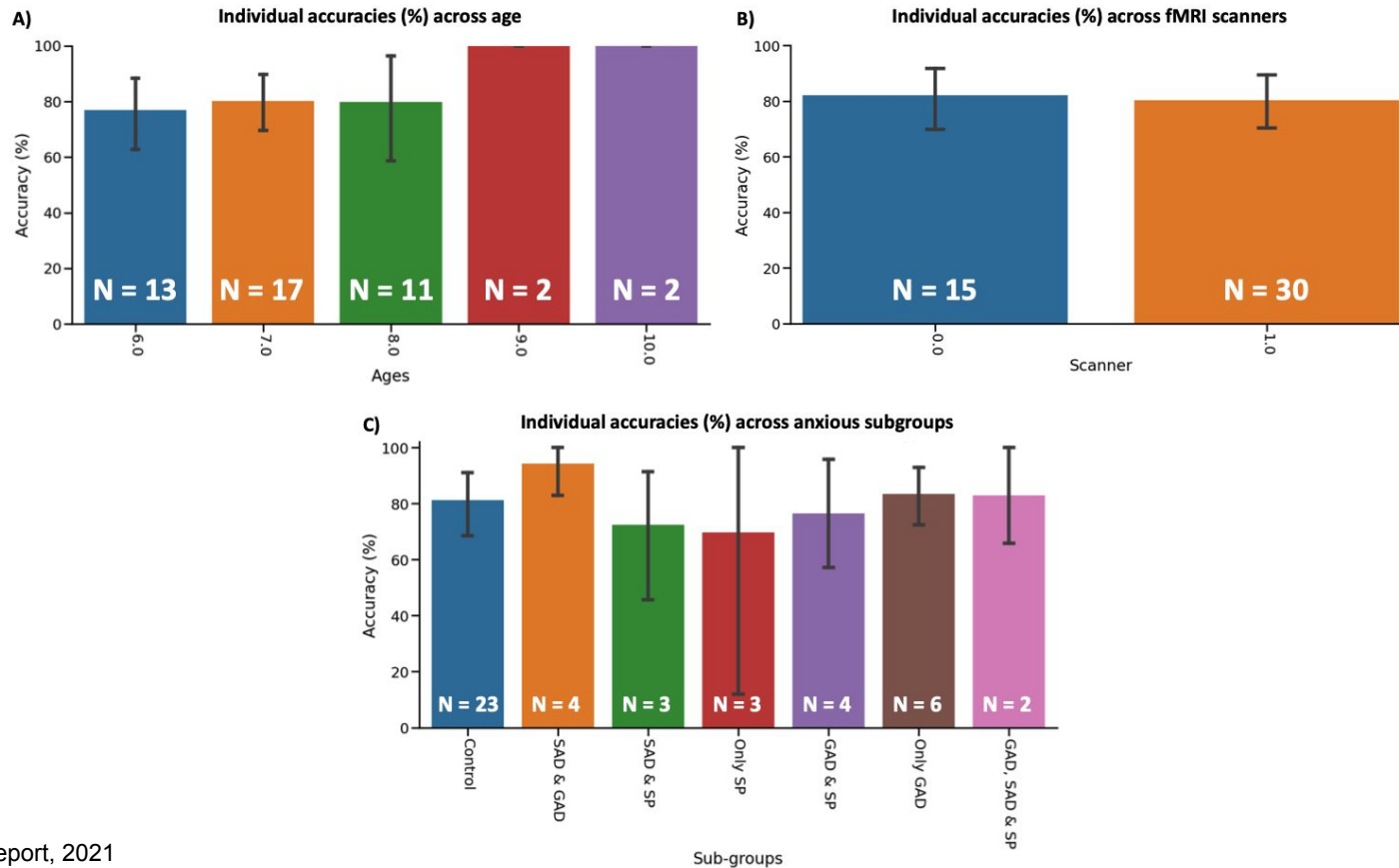


> Predicting Negative Emotion Faces

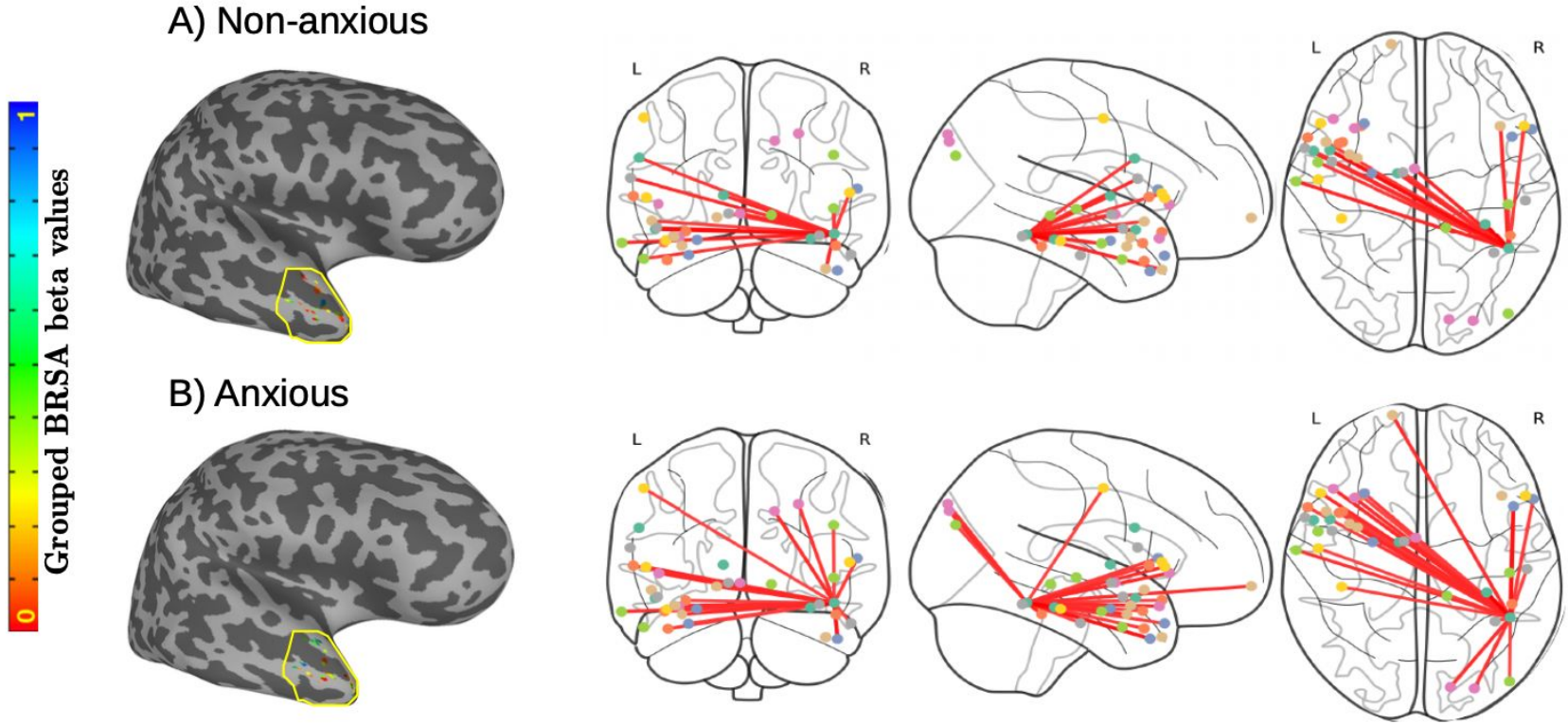


> Predicting Pediatric Anxiety: Prediction Rate

- Our model average accuracy is **81%**.



> Predicting Pediatric Anxiety: Group-Level Connection



Conclusion

> Our Related Studies

- Image/Video decoding from human brain:
 - Temporal Information Guided Generative Adversarial Networks [TCDS 2021]
 - Perceived Image Reconstruction [ICONIP 2020]
- Functional Alignment
 - Shared Space Transfer Learning [NurIPS 2020]
 - Supervised Hyperalignment [TCDS 2020]
 - Deep Hyperalignment [NIPS 2017]
 - Local Discriminant Hyperalignment [AAAI 2017]
- Mental Health
 - Predicting Pediatric Anxiety [Nature Scientific Reports 2021]
 - Deep Representational Similarity Learning [Neuroinformatics 2020]
 - Detecting Presence of PTSD Using Sentiment Analysis From Text Data [Frontiers in Psychiatry 2022]

> The easyX project

- easyX is a simple Python library for saving big complex data structure

The screenshot shows the GitLab repository page for the 'easyX' project. At the top, the repository name 'easyX' is displayed with a globe icon and the Project ID '20549491'. To the right are icons for notifications, stars (0), and forks (0). Below this, the repository statistics are shown: 10 Commits, 1 Branch, 0 Tags, 143 KB Files, and 143 KB Storage. A description reads: 'A simple library for saving big data with complex structure'. The main content area shows the 'master' branch selected, with a 'Clone' button. A recent commit is highlighted: 'fixing \\n issue for converting binary var by using base64' by Muhammad Yousefnezhad, authored 4 months ago, with commit hash 7876e94b. Below the commit list are buttons for 'Upload File', 'README', 'MIT License', 'Add CHANGELOG', 'Add CONTRIBUTING', 'Add Kubernetes cluster', 'Set up CI/CD', and 'Add Security Testing'. A table lists the repository files with their last commit and update dates. The 'README.md' file is expanded, showing the project's description: 'easyX: a simple Python library for saving complex data structure'. The text explains that the library saves Python dictionaries with complex structures to a single file, tested up to 150 GB. It details the internal procedure of encoding data into a base64 format and storing it as a vector in a 'binary' group.

Project ID: 20549491

10 Commits 1 Branch 0 Tags 143 KB Files 143 KB Storage

A simple library for saving big data with complex structure

master easyX / +

History Find file Web IDE Clone

fixing \\n issue for converting binary var by using base64
Muhammad Yousefnezhad authored 4 months ago 7876e94b

Upload File README MIT License Add CHANGELOG Add CONTRIBUTING Add Kubernetes cluster

Set up CI/CD Add Security Testing

Name	Last commit	Last update
LICENSE	Add LICENSE	11 months ago
README.md	README is updated	11 months ago
easyX.py	fixing \\n issue for converting binary var by ...	4 months ago
requirements.txt	adding requirements.txt	11 months ago

README.md

easyX: a simple Python library for saving complex data structure

This library enables you to save a Python dictionary with a complex structure to a single file. We have tested this library to save files in size 150 GB — i.e., you need a computer with 155 GB memory.

The procedure is simple. The library tries to save homogeneous tensors by using the regular algorithm that is used for [Hierarchical Data Format 5 \(HDF5\)](#). We will store them in a group called "raw." If the dictionary has other complex structures — such as another dictionary or nonhomogeneous tensors — the library will first dump the bytes of data from memory and encode it in a [base64](#) format. The encoded data will be stored as a vector in a group called "binary." This library is originally developed for the [easy fMRI project](#) — a toolbox for analyzing task-based fMRI datasets.

Available at

<https://gitlab.com/myousefnezhad/easyx>

Multi-Site Neuroimage Analysis: Domain Adaptation and Batch Effects

About this Research Topic

Neuroimaging is a vital tool for brain science in both basic and applied studies — including, for example, studies of cognitive processes and neurodevelopmental trends, and prediction or diagnosis of brain pathology. Despite the advantages of modern imaging technologies, this is still challenging as the data is noisy, high-dimensional, and typically only small sample sizes (as it is expensive to acquire).

Increased access to public neuroimaging datasets has motivated the field to investigate multi-site datasets, which promise an improvement of accuracy rates in the application of advanced computational learning procedures (i.e., machine learning). However, forming a dataset by merely concatenating data from various sites/sources often fails due to batch effects, where the accuracy on a dataset of a model trained on a multi-site dataset is often worse than the accuracy of a model trained on that single site. A promising area for tackling these issues is that of domain adaptation techniques — e.g., transfer learning, which leverages source data to improve related target data performance.

This Research Topic calls for papers focusing on advanced machine learning approaches that can address current challenges in multi-site neuroimaging analysis. Contributions may address homogeneous domain adaptation problems, where the source and target sites have the same modularity of neuroimage data — e.g., multi-site fMRI analysis. Another class of submissions may tackle nonhomogeneous problems, where the source and target sites have different modalities of images. One prevalent use of nonhomogeneous approaches is to improve the quality of low-resolution medical images (such as CT scans) through leveraging high-resolution features (e.g., MRIs). This Research Topic will also cover theoretical studies, which may focus on the development of novel machine learning techniques for multi-site neuroimage analysis — such as probabilistic graphical models, deep learning, multi-view methods, reinforcement learning, etc. Basic and applied studies should indicate successful analyses that relied on advanced domain adaptation techniques to improve the performance of analysis in real-world applications.

Keywords: Multi-Site Neuroimage Analysis, Domain Adaptation, Batch Effects, Transfer Learning

Important Note: All contributions to this Research Topic must be within the scope of the section and journal to which they are submitted, as defined in their mission statements. Frontiers reserves the right to guide an out-of-scope manuscript to a more suitable section or journal at any stage of peer review.

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