

Decoding and Classification of Category-Specific Visual Stimuli in the Fusiform Gyrus Using fMRI Data and Machine Learning

Kasapakis Nikolaos

Department of Physics
Aristotle University of Thessaloniki

nkasapak@auth.gr

September 23, 2024



Outline

1 Introduction

- Run-Through
- Decoding and Classification
- The Fusiform Gyrus
- Why fMRI?

2 Theoretical Background

- Visual Information Processing
- Mechanisms of fMRI

3 Data Acquisition and Manipulation

- The Human Connectome Project (*HCP*)
- Task-fMRI Battery of the HCP
- Analysis of fMRI Signal

4 Methods and Results

- Pipeline Overview
- Data Analysis - UPA
- Data Analysis - MVPA in the FFA
- Data Analysis - MVPA in the PPA

Outline

1 Introduction

- Run-Through
- Decoding and Classification
- The Fusiform Gyrus
- Why fMRI?

2 Theoretical Background

- Visual Information Processing
- Mechanisms of fMRI

3 Data Acquisition and Manipulation

- The Human Connectome Project (*HCP*)
- Task-fMRI Battery of the HCP
- Analysis of fMRI Signal

4 Methods and Results

- Pipeline Overview
- Data Analysis - UPA
- Data Analysis - MVPA in the FFA
- Data Analysis - MVPA in the PPA

Outline

- 1 **Introduction**
 - Run-Through
 - Decoding and Classification
 - The Fusiform Gyrus
 - Why fMRI?
- 2 **Theoretical Background**
 - Visual Information Processing
 - Mechanisms of fMRI
- 3 **Data Acquisition and Manipulation**

- The Human Connectome Project (*HCP*)
- Task-fMRI Battery of the HCP
- Analysis of fMRI Signal

- 4 **Methods and Results**

- Pipeline Overview
- Data Analysis - UPA
- Data Analysis - MVPA in the FFA
- Data Analysis - MVPA in the PPA

1 Introduction

- Run-Through
- Decoding and Classification
- The Fusiform Gyrus
- Why fMRI?

2 Theoretical Background

- Visual Information Processing
- Mechanisms of fMRI

3 Data Acquisition and Manipulation

- The Human Connectome Project (*HCP*)
- Task-fMRI Battery of the HCP
- Analysis of fMRI Signal

4 Methods and Results

- Pipeline Overview
- Data Analysis - UPA
- Data Analysis - MVPA in the FFA
- Data Analysis - MVPA in the PPA

Table of Contents

1 Introduction

- Run-Through
- Decoding and Classification
- The Fusiform Gyrus
- Why fMRI?

2 Theoretical Background

- Visual Information Processing
- Mechanisms of fMRI

3 Data Acquisition and Manipulation

- The Human Connectome Project (*HCP*)
- Task-fMRI Battery of the HCP
- Analysis of fMRI Signal

4 Methods and Results

- Pipeline Overview
- Data Analysis - UPA
- Data Analysis - MVPA in the FFA
- Data Analysis - MVPA in the PPA

Compact Run-Through

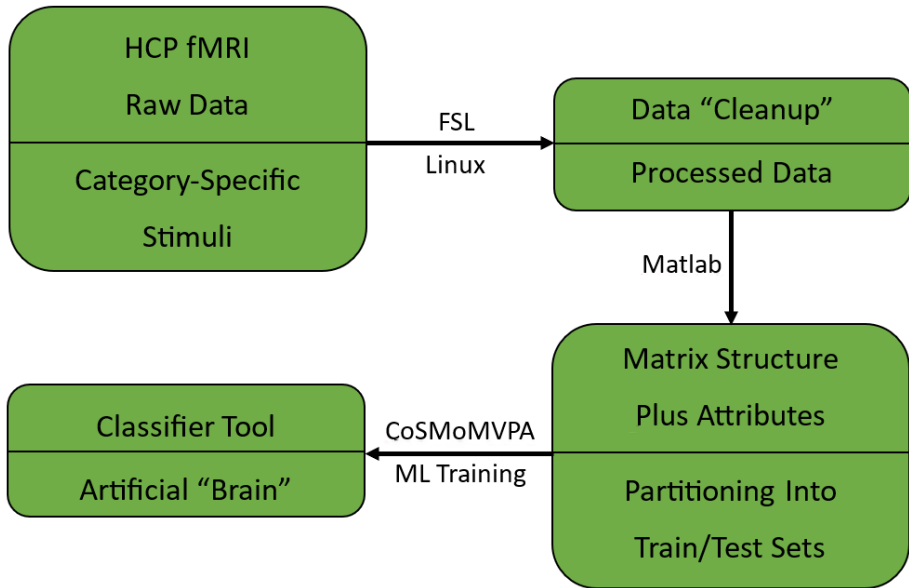


Table of Contents

1 Introduction

- Run-Through
- Decoding and Classification
- The Fusiform Gyrus
- Why fMRI?

2 Theoretical Background

- Visual Information Processing
- Mechanisms of fMRI

3 Data Acquisition and Manipulation

- The Human Connectome Project (*HCP*)
- Task-fMRI Battery of the HCP
- Analysis of fMRI Signal

4 Methods and Results

- Pipeline Overview
- Data Analysis - UPA
- Data Analysis - MVPA in the FFA
- Data Analysis - MVPA in the PPA

- To connect neural patterns with specific human functions
- From brain activation to identifying object of perception
- Certain areas are linked to category-specific stimuli processing
- Assessment of baseline BOLD signal magnitude (*UPA*)
- Comparison of pattern distributions (*MVPA*)

- To connect neural patterns with specific human functions
- From brain activation to identifying object of perception
- Certain areas are linked to category-specific stimuli processing
- Assessment of baseline BOLD signal magnitude (*UPA*)
- Comparison of pattern distributions (*MVPA*)

- To connect neural patterns with specific human functions
- From brain activation to identifying object of perception
- Certain areas are linked to category-specific stimuli processing
- Assessment of baseline BOLD signal magnitude (*UPA*)
- Comparison of pattern distributions (*MVPA*)

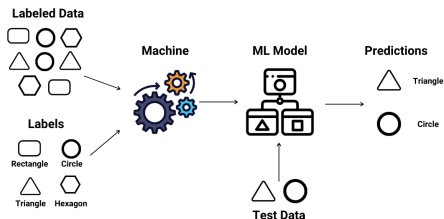
- To connect neural patterns with specific human functions
- From brain activation to identifying object of perception
- Certain areas are linked to category-specific stimuli processing
- Assessment of baseline BOLD signal magnitude (*UPA*)
- Comparison of pattern distributions (*MVPA*)

- To connect neural patterns with specific human functions
- From brain activation to identifying object of perception
- Certain areas are linked to category-specific stimuli processing
- Assessment of baseline BOLD signal magnitude (*UPA*)
- Comparison of pattern distributions (*MVPA*)

- Supervised Machine Learning
 - Train model on labeled data, predict labels of test data
 - Support Vector Machine algorithm to determine boundaries

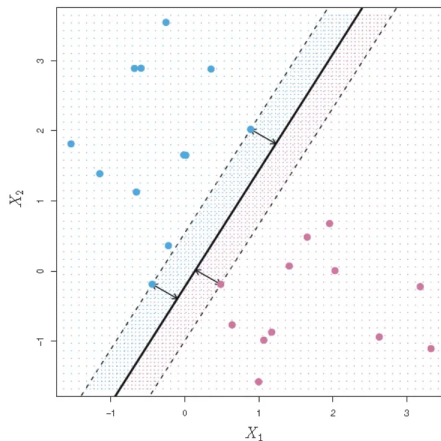
Classification

- Supervised Machine Learning
- Train model on labeled data, predict labels of test data
- Support Vector Machine algorithm to determine boundaries



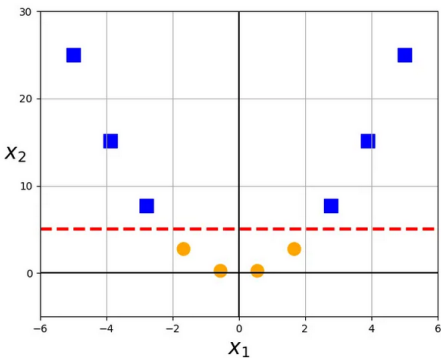
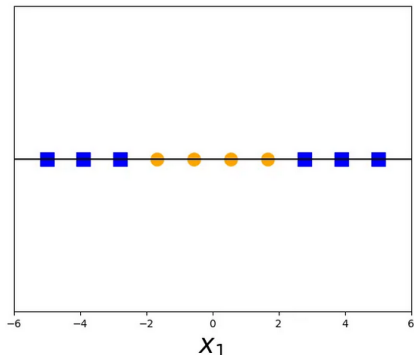
Classification

- Supervised Machine Learning
- Train model on labeled data, predict labels of test data
- Support Vector Machine algorithm to determine boundaries



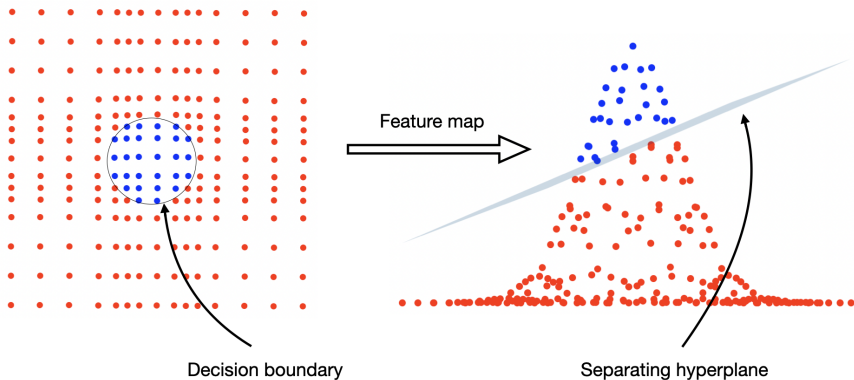
SVM - Linear Separation

SVM - Linear Separation - Kernel Trick



SVM - Linear Separation - Kernel Trick

SVM - Non-Linear Separation - Kernel Trick



SVM - Non-Linear Separation - Kernel Trick

Table of Contents

1

Introduction

- Run-Through
- Decoding and Classification
- The Fusiform Gyrus
- Why fMRI?

2

Theoretical Background

- Visual Information Processing
- Mechanisms of fMRI

3

Data Acquisition and Manipulation

- The Human Connectome Project (*HCP*)
- Task-fMRI Battery of the HCP
- Analysis of fMRI Signal

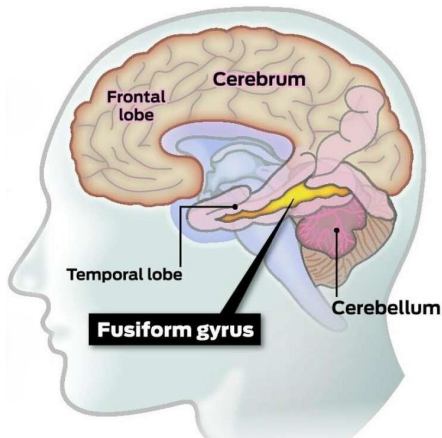
4

Methods and Results

- Pipeline Overview
- Data Analysis - UPA
- Data Analysis - MVPA in the FFA
- Data Analysis - MVPA in the PPA

The Fusiform Gyrus

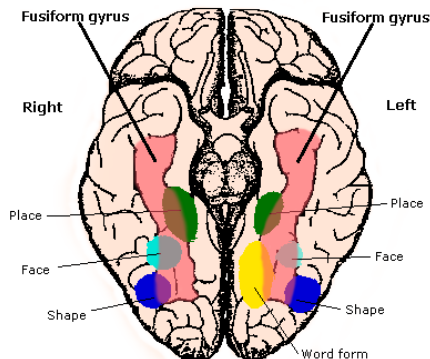
- Primarily located in the temporal lobe
- Home to the Fusiform Face Area (FFA) and the Parahippocampal Place Area (PPA), partly
- Category selectivity is more localized and stronger, based on literature



The Fusiform Gyrus Location in the Human Brain (*Saggital Plane*)

The Fusiform Gyrus

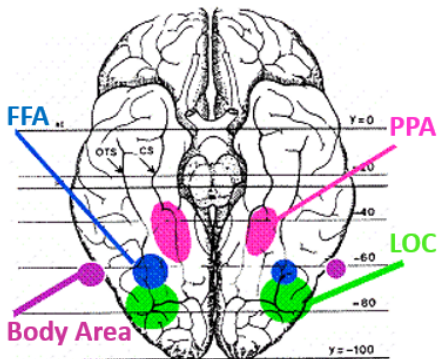
- Primarily located in the temporal lobe
- Home to the Fusiform Face Area (FFA) and the Parahippocampal Place Area (PPA), partly
- Category selectivity is more localized and stronger, based on literature



The Fusiform Gyrus Location in the Human Brain (*Horizontal Plane*)

The Fusiform Gyrus

- Primarily located in the temporal lobe
- Home to the Fusiform Face Area (*FFA*) and the Parahippocampal Place Area (*PPA*), partly
- Category selectivity is more localized and stronger, based on literature



Category-Specific Stimulus Information Processing Centers

Table of Contents

1

Introduction

- Run-Through
- Decoding and Classification
- The Fusiform Gyrus
- Why fMRI?

2

Theoretical Background

- Visual Information Processing
- Mechanisms of fMRI

3

Data Acquisition and Manipulation

- The Human Connectome Project (*HCP*)
- Task-fMRI Battery of the HCP
- Analysis of fMRI Signal

4

Methods and Results

- Pipeline Overview
- Data Analysis - UPA
- Data Analysis - MVPA in the FFA
- Data Analysis - MVPA in the PPA

Why fMRI?

- High spatial resolution (mm), ideal for studying localized functions
- Whole brain coverage, highlighting interaction among regions
- Measures BOLD signal, indirectly associated with neuronal activity
- Low temporal resolution, allowing the study of longer-term brain processes (s), but potential problem for quick responses

Why fMRI?

- High spatial resolution (mm), ideal for studying localized functions
- Whole brain coverage, highlighting interaction among regions
- Measures BOLD signal, indirectly associated with neuronal activity
- Low temporal resolution, allowing the study of longer-term brain processes (s), but potential problem for quick responses

Why fMRI?

- High spatial resolution (mm), ideal for studying localized functions
- Whole brain coverage, highlighting interaction among regions
- Measures BOLD signal, indirectly associated with neuronal activity
- Low temporal resolution, allowing the study of longer-term brain processes (s), but potential problem for quick responses

Why fMRI?

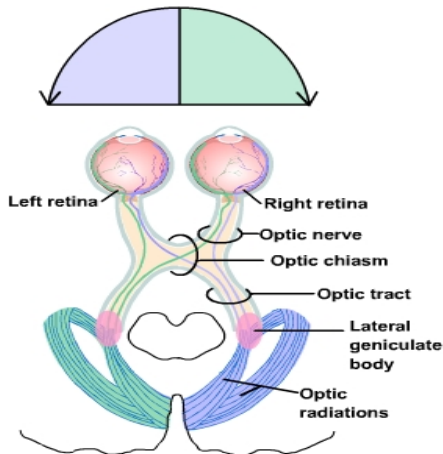
- High spatial resolution (mm), ideal for studying localized functions
- Whole brain coverage, highlighting interaction among regions
- Measures BOLD signal, indirectly associated with neuronal activity
- Low temporal resolution, allowing the study of longer-term brain processes (s), but potential problem for quick responses

Table of Contents

- 1 **Introduction**
 - Run-Through
 - Decoding and Classification
 - The Fusiform Gyrus
 - Why fMRI?
- 2 **Theoretical Background**
 - Visual Information Processing
 - Mechanisms of fMRI
- 3 **Data Acquisition and Manipulation**
 - The Human Connectome Project (*HCP*)
 - Task-fMRI Battery of the HCP
 - Analysis of fMRI Signal
- 4 **Methods and Results**
 - Pipeline Overview
 - Data Analysis - UPA
 - Data Analysis - MVPA in the FFA
 - Data Analysis - MVPA in the PPA

Visual Information Processing

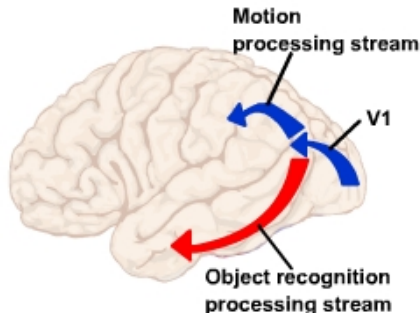
- Visual information route from the eyes to the visual cortex
- Distinction based on motion
- Assigned to category-specific information processing centers



Visual Information Flow to V1

Visual Information Processing

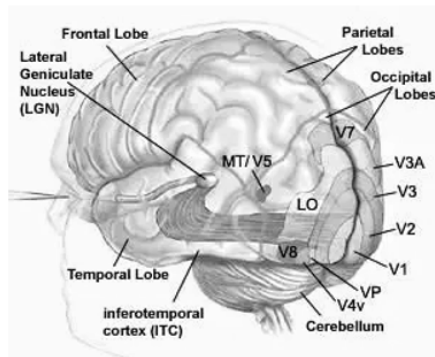
- Visual information route from the eyes to the visual cortex
- Distinction based on motion
- Assigned to category-specific information processing centers



Ventral and Dorsal Information Streams

Visual Information Processing

- Visual information route from the eyes to the visual cortex
- Distinction based on motion
- Assigned to category-specific information processing centers



Brain Region Specialization Regarding Visual Information Processing

Category-Specific Information Processing Centers

- Fusiform Face Area - Occipital Face Area
- Parahippocampal Place Area - Lateral Occipital Cortex
- Extrastriate Body Area - Fusiform Body Area

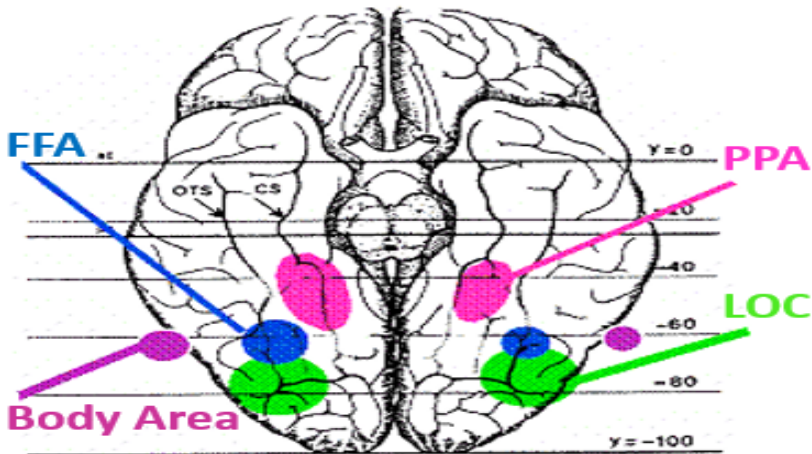


Table of Contents

1 Introduction

- Run-Through
- Decoding and Classification
- The Fusiform Gyrus
- Why fMRI?

2 Theoretical Background

- Visual Information Processing
- Mechanisms of fMRI

3 Data Acquisition and Manipulation

- The Human Connectome Project (*HCP*)
- Task-fMRI Battery of the HCP
- Analysis of fMRI Signal

4 Methods and Results

- Pipeline Overview
- Data Analysis - UPA
- Data Analysis - MVPA in the FFA
- Data Analysis - MVPA in the PPA

NMR Signal

- Scanner generates a powerful magnetic field \vec{B}_0
- Magnetic moments of nonzero spin nuclei (protons - water) weakly align with \vec{B}_0 , creating a net macroscopic magnetization \vec{M}_0
- Coil transmits RF transverse magnetic field pulse at resonant frequency tipping \vec{M}_0 from alignment
- \vec{M}_0 precesses around \vec{B}_0 to return to equilibrium
- Rotating M_{xy} component generates oscillating magnetic field inducing current, producing signal

NMR Signal

- Scanner generates a powerful magnetic field \vec{B}_0
- Magnetic moments of nonzero spin nuclei (protons - water) weakly align with \vec{B}_0 , creating a net macroscopic magnetization \vec{M}_0
- Coil transmits RF transverse magnetic field pulse at resonant frequency tipping \vec{M}_0 from alignment
- \vec{M}_0 precesses around \vec{B}_0 to return to equilibrium
- Rotating M_{xy} component generates oscillating magnetic field inducing current, producing signal

NMR Signal

- Scanner generates a powerful magnetic field \vec{B}_0
- Magnetic moments of nonzero spin nuclei (protons - water) weakly align with \vec{B}_0 , creating a net macroscopic magnetization \vec{M}_0
- Coil transmits RF transverse magnetic field pulse at resonant frequency tipping \vec{M}_0 from alignment
- \vec{M}_0 precesses around \vec{B}_0 to return to equilibrium
- Rotating M_{xy} component generates oscillating magnetic field inducing current, producing signal

NMR Signal

- Scanner generates a powerful magnetic field \vec{B}_0
- Magnetic moments of nonzero spin nuclei (protons - water) weakly align with \vec{B}_0 , creating a net macroscopic magnetization \vec{M}_0
- Coil transmits RF transverse magnetic field pulse at resonant frequency tipping \vec{M}_0 from alignment
- \vec{M}_0 precesses around \vec{B}_0 to return to equilibrium
- Rotating M_{xy} component generates oscillating magnetic field inducing current, producing signal

NMR Signal

- Scanner generates a powerful magnetic field \vec{B}_0
- Magnetic moments of nonzero spin nuclei (protons - water) weakly align with \vec{B}_0 , creating a net macroscopic magnetization \vec{M}_0
- Coil transmits RF transverse magnetic field pulse at resonant frequency tipping \vec{M}_0 from alignment
- \vec{M}_0 precesses around \vec{B}_0 to return to equilibrium
- Rotating M_{xy} component generates oscillating magnetic field inducing current, producing signal

T1 Relaxation

- The process by which the z component of the net magnetization M returns to its initial maximum value M_0 parallel to B_0
- Measured T1, modified by blood inflow relocating spins in-and-out of the imaging plane, is termed T1*

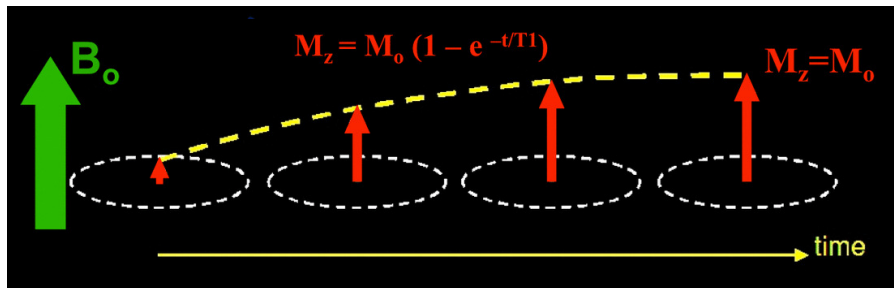


Illustration of T1 Relaxation

T1 Relaxation

- The process by which the z component of the net magnetization M returns to its initial maximum value M_0 parallel to B_0
- Measured T1, modified by blood inflow relocating spins in-and-out of the imaging plane, is termed T1*

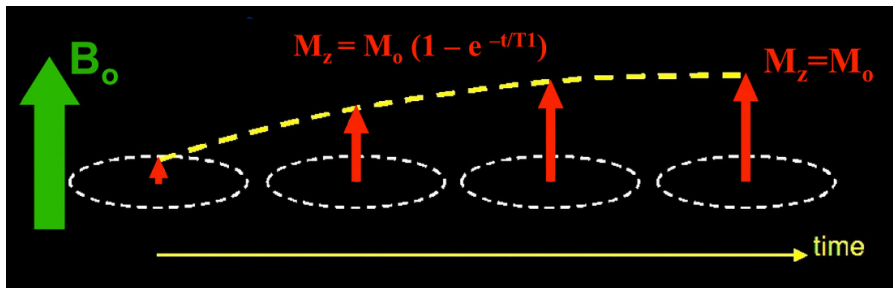


Illustration of T1 Relaxation

T2 Relaxation

- T2 is the time constant for dephasing of trasverse magnerization M_{xy}
- Following an RF pulse spin distribution is conserved, from the z axis to phase coherence in the xy plane, leading to precession of spins at the Larmor frequency

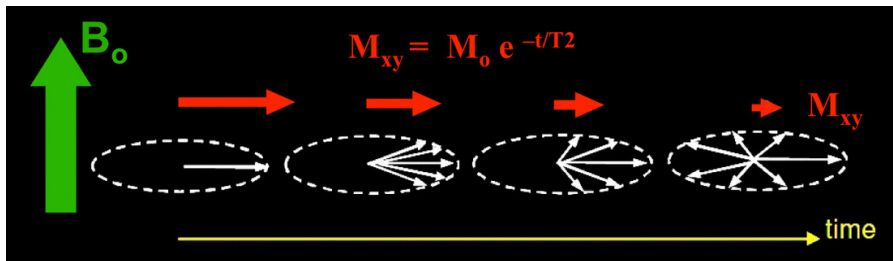


Illustration of T2 Relaxation

T2 Relaxation

- T2 is the time constant for dephasing of trasverse magnerization M_{xy}
- Following an RF pulse spin distribution is conserved, from the z axis to phase coherence in the xy plane, leading to precession of spins at the Larmor frequency

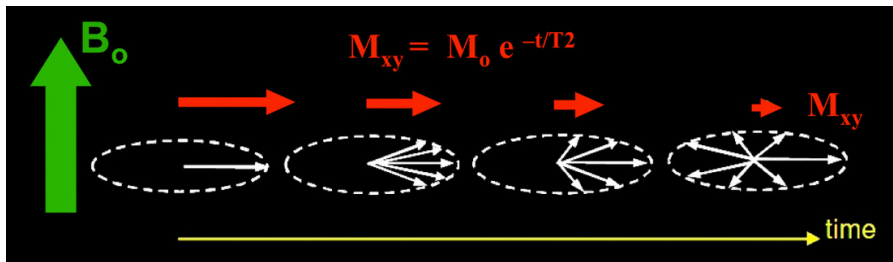
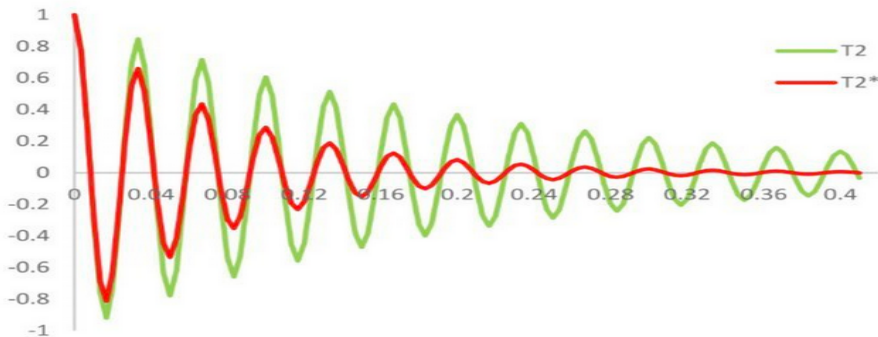


Illustration of T2 Relaxation

T2* Relaxation

Free Induction Decay (FID)



- "Effective" $T2^*$ is much shorter than "natural" $T2$ due to inhomogeneities in the main magnetic field

BOLD Signal

- Blood Oxygen-Level Dependent Signal
- Detects changes in HbR driven by localized changes in blood flow and blood oxygenation
- HbR is paramagnetic, making it a naturally occurring contrast agent
- Neural activity reduces the OEF which increases MR signal locally

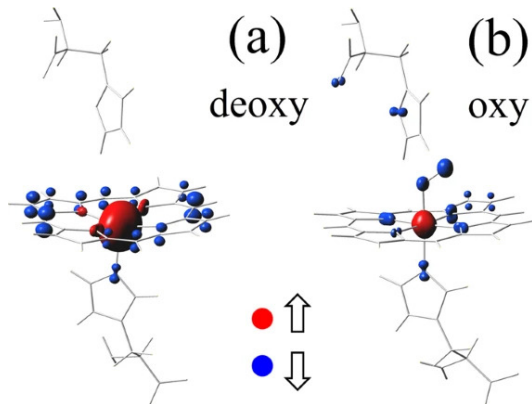


Illustration of Oxyhemoglobin and Deoxyhemoglobin Magnetic Moment Density

BOLD Signal

- Blood Oxygen-Level Dependent Signal
- Detects changes in HbR driven by localized changes in blood flow and blood oxygenation
- HbR is paramagnetic, making it a naturally occurring contrast agent
- Neural activity reduces the OEF which increases MR signal locally

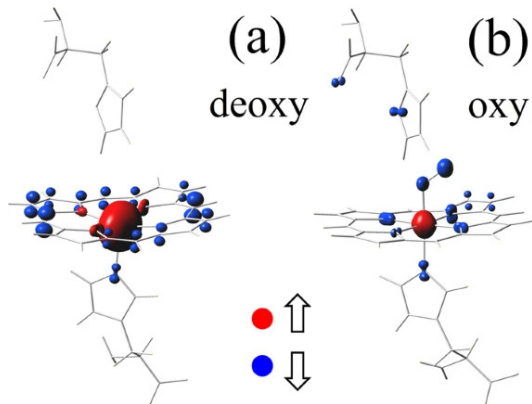


Illustration of Oxyhemoglobin and Deoxyhemoglobin Magnetic Moment Density

BOLD Signal

- Blood Oxygen-Level Dependent Signal
- Detects changes in HbR driven by localized changes in blood flow and blood oxygenation
- HbR is paramagnetic, making it a naturally occurring contrast agent
- Neural activity reduces the OEF which increases MR signal locally

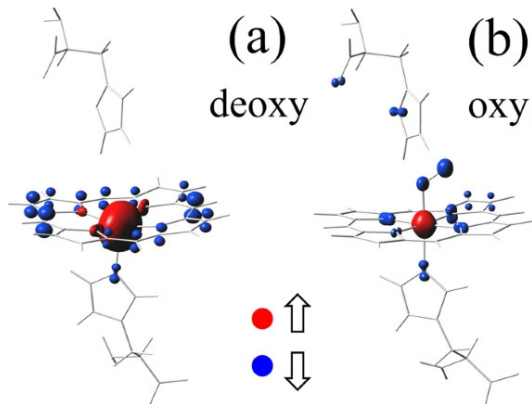


Illustration of Oxyhemoglobin and Deoxyhemoglobin Magnetic Moment Density

BOLD Signal

- Blood Oxygen-Level Dependent Signal
- Detects changes in HbR driven by localized changes in blood flow and blood oxygenation
- HbR is paramagnetic, making it a naturally occurring contrast agent
- Neural activity reduces the OEF which increases MR signal locally

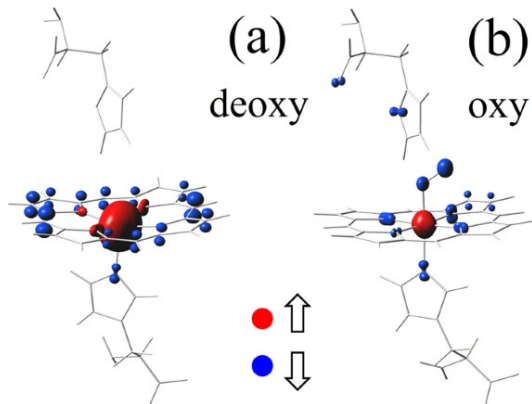
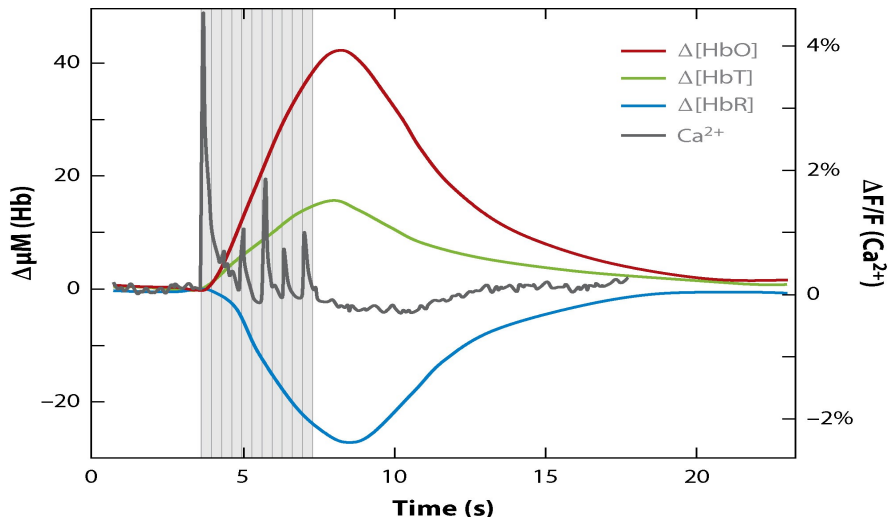


Illustration of Oxyhemoglobin and Deoxyhemoglobin Magnetic Moment Density

BOLD Response



Stimulus-Evoked Response in Somatosensory Cortex of Rats

Table of Contents

- 1 **Introduction**
 - Run-Through
 - Decoding and Classification
 - The Fusiform Gyrus
 - Why fMRI?
- 2 **Theoretical Background**
 - Visual Information Processing
 - Mechanisms of fMRI
- 3 **Data Acquisition and Manipulation**
 - The Human Connectome Project (*HCP*)
 - Task-fMRI Battery of the HCP
 - Analysis of fMRI Signal
- 4 **Methods and Results**
 - Pipeline Overview
 - Data Analysis - UPA
 - Data Analysis - MVPA in the FFA
 - Data Analysis - MVPA in the PPA

The Human Connectome Project (*HCP*)

- Five-year effort to characterize brain connectivity, function and their variability in healthy adults
- Multiple imaging modalities: dMRI, r-fMRI, t-fMRI, T1w and T2w MRI, MEG, and EEG
- 1200 subjects, 300 sibships mostly including a mono- or di-zygotic twin pair

The Human Connectome Project (*HCP*)

- Five-year effort to characterize brain connectivity, function and their variability in healthy adults
- Multiple imaging modalities: dMRI, r-fMRI, t-fMRI, T1w and T2w MRI, MEG, and EEG
- 1200 subjects, 300 sibships mostly including a mono- or di-zygotic twin pair

The Human Connectome Project (*HCP*)

- Five-year effort to characterize brain connectivity, function and their variability in healthy adults
- Multiple imaging modalities: dMRI, r-fMRI, t-fMRI, T1w and T2w MRI, MEG, and EEG
- 1200 subjects, 300 sibships mostly including a mono- or di-zygotic twin pair

Table of Contents

- 1 **Introduction**
 - Run-Through
 - Decoding and Classification
 - The Fusiform Gyrus
 - Why fMRI?
- 2 **Theoretical Background**
 - Visual Information Processing
 - Mechanisms of fMRI
- 3 **Data Acquisition and Manipulation**

- The Human Connectome Project (*HCP*)
- Task-fMRI Battery of the HCP
- Analysis of fMRI Signal

- 4 **Methods and Results**

- Pipeline Overview
- Data Analysis - UPA
- Data Analysis - MVPA in the FFA
- Data Analysis - MVPA in the PPA

Task-fMRI Battery of the HCP

Neural systems targeted by the tests:

- Visual and Somatosensory-Motor Systems
- **Category-Specific Representation**
- Language Function (semantic and phonological processing)
- Attention Systems
- **Working Memory/Cognitive Control System**
- Emotion Processing
- Decision-Making/Reward Processing
- Episodic Memory Systems

Working Memory Task

- Subjects presented with blocks of trials that consisted of pictures of places, tools, faces, and body parts
- N-Back paradigm was utilized
- Every 2 blocks separated by a fixation period
- 8 blocks per run, 2 runs per subject

Segment Type	Duration (s)	N-Back Paradigm	Target Category
Setup	10	-	-
Cue	2.5	-	-
Task	25	2-Back	Body
Cue	2.5	-	-
Task	25	0-Back	Face
Fixation	15	-	-
Cue	2.5	-	-
Task	25	2-Back	Tools
Cue	2.5	-	-
Task	25	0-Back	Body
Fixation	15	-	-
Cue	2.5	-	-
Task	25	0-Back	Place
Cue	2.5	-	-
Task	25	2-Back	Face
Fixation	15	-	-
Cue	2.5	-	-
Task	25	0-Back	Tools
Cue	2.5	-	-
Task	25	2-Back	Place
Fixation	15	-	-

Sequence of WM Events

Working Memory Task

- Subjects presented with blocks of trials that consisted of pictures of places, tools, faces, and body parts
- N-Back paradigm was utilized
- Every 2 blocks separated by a fixation period
- 8 blocks per run, 2 runs per subject

Segment Type	Duration (s)	N-Back Paradigm	Target Category
Setup	10	-	-
Cue	2.5	-	-
Task	25	2-Back	Body
Cue	2.5	-	-
Task	25	0-Back	Face
Fixation	15	-	-
Cue	2.5	-	-
Task	25	2-Back	Tools
Cue	2.5	-	-
Task	25	0-Back	Body
Fixation	15	-	-
Cue	2.5	-	-
Task	25	0-Back	Place
Cue	2.5	-	-
Task	25	2-Back	Face
Fixation	15	-	-
Cue	2.5	-	-
Task	25	0-Back	Tools
Cue	2.5	-	-
Task	25	2-Back	Place
Fixation	15	-	-

Sequence of WM Events

Working Memory Task

- Subjects presented with blocks of trials that consisted of pictures of places, tools, faces, and body parts
- N-Back paradigm was utilized
- Every 2 blocks separated by a fixation period
- 8 blocks per run,
2 runs per subject

Segment Type	Duration (s)	N-Back Paradigm	Target Category
Setup	10	-	-
Cue	2.5	-	-
Task	25	2-Back	Body
Cue	2.5	-	-
Task	25	0-Back	Face
Fixation	15	-	-
Cue	2.5	-	-
Task	25	2-Back	Tools
Cue	2.5	-	-
Task	25	0-Back	Body
Fixation	15	-	-
Cue	2.5	-	-
Task	25	0-Back	Place
Cue	2.5	-	-
Task	25	2-Back	Face
Fixation	15	-	-
Cue	2.5	-	-
Task	25	0-Back	Tools
Cue	2.5	-	-
Task	25	2-Back	Place
Fixation	15	-	-

Sequence of WM Events

Working Memory Task

- Subjects presented with blocks of trials that consisted of pictures of places, tools, faces, and body parts
- N-Back paradigm was utilized
- Every 2 blocks separated by a fixation period
- 8 blocks per run, 2 runs per subject

Segment Type	Duration (s)	N-Back Paradigm	Target Category
Setup	10	-	-
Cue	2.5	-	-
Task	25	2-Back	Body
Cue	2.5	-	-
Task	25	0-Back	Face
Fixation	15	-	-
Cue	2.5	-	-
Task	25	2-Back	Tools
Cue	2.5	-	-
Task	25	0-Back	Body
Fixation	15	-	-
Cue	2.5	-	-
Task	25	0-Back	Place
Cue	2.5	-	-
Task	25	2-Back	Face
Fixation	15	-	-
Cue	2.5	-	-
Task	25	0-Back	Tools
Cue	2.5	-	-
Task	25	2-Back	Place
Fixation	15	-	-

Sequence of WM Events

Table of Contents

1 Introduction

- Run-Through
- Decoding and Classification
- The Fusiform Gyrus
- Why fMRI?

2 Theoretical Background

- Visual Information Processing
- Mechanisms of fMRI

3 Data Acquisition and Manipulation

- The Human Connectome Project (*HCP*)
- Task-fMRI Battery of the HCP
- Analysis of fMRI Signal

4 Methods and Results

- Pipeline Overview
- Data Analysis - UPA
- Data Analysis - MVPA in the FFA
- Data Analysis - MVPA in the PPA

The Hemodynamic Response Function

- Impulse stimulus produces acute hemodynamic response function (*HRF*)
- Lasting stimulus produces boxcar HRF
- HRF shape can be modelled with a Gamma Distribution

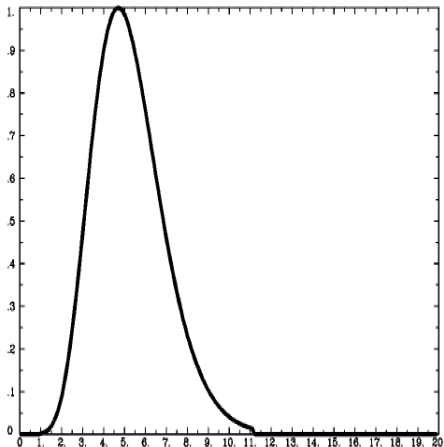


Illustration of Acute HRF.

The Hemodynamic Response Function

- Impulse stimulus produces acute hemodynamic response function (*HRF*)
- Lasting stimulus produces boxcar HRF
- HRF shape can be modelled with a Gamma Distribution

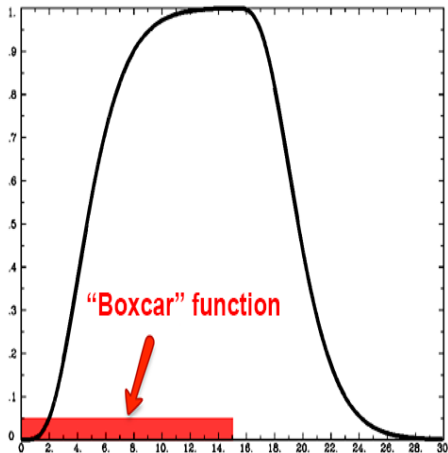
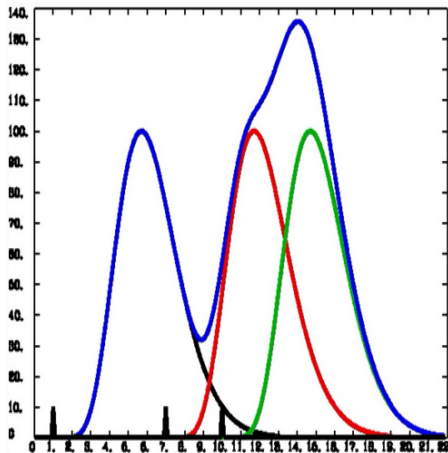


Illustration of Boxcar HRF.

The Hemodynamic Response Function

- Impulse stimulus produces acute hemodynamic response function (*HRF*)
- Lasting stimulus produces boxcar HRF
- HRF shape can be modelled with a Gamma Distribution



HRF Overlap and Fitting.

Analysis Process Overview

- General Linear Model fitting to the BOLD signal time-series
- Original explanatory variables (*EV*) defined by the experiment
- Beta-weights corresponding to each EV
- Contrast of parameter estimates (*COPE*) selected by researcher

$$Y = \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3 + \varepsilon$$

Analysis Process Overview

- General Linear Model fitting to the BOLD signal time-series
- Original explanatory variables (*EV*) defined by the experiment
- Beta-weights corresponding to each EV
- Contrast of parameter estimates (*COPE*) selected by researcher

$$Y = \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3 + \varepsilon$$

Analysis Process Overview

- General Linear Model fitting to the BOLD signal time-series
- Original explanatory variables (*EV*) defined by the experiment
- Beta-weights corresponding to each EV
- Contrast of parameter estimates (*COPE*) selected by researcher

$$Y = \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3 + \varepsilon$$

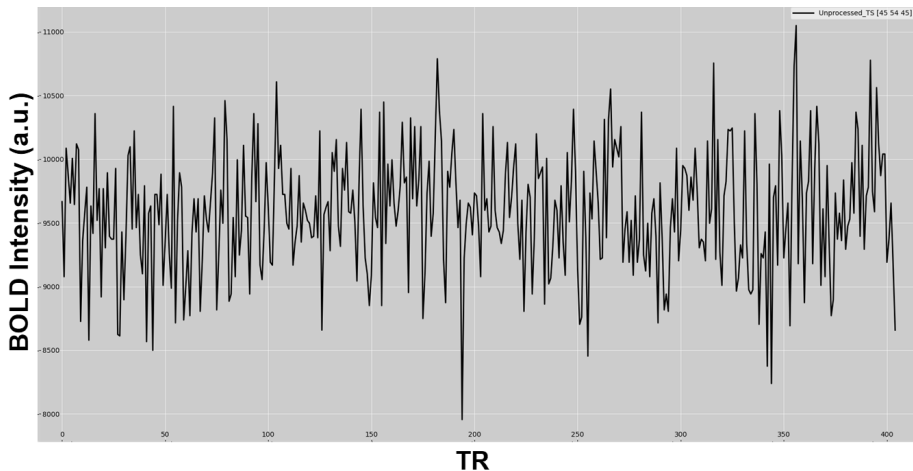
Analysis Process Overview

- General Linear Model fitting to the BOLD signal time-series
- Original explanatory variables (*EV*) defined by the experiment
- Beta-weights corresponding to each EV
- Contrast of parameter estimates (*COPE*) selected by researcher

$$Y = \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3 + \varepsilon$$

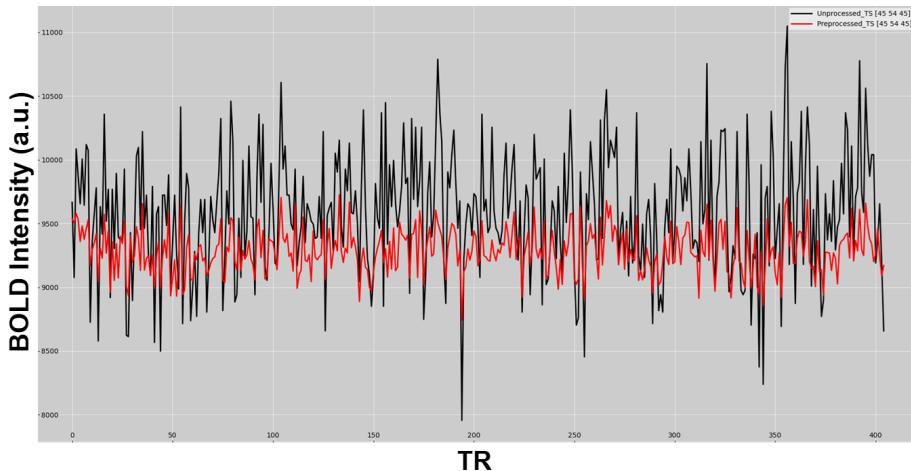
Unprocessed BOLD Time-Series.

■ Unprocessed BOLD Time-Series



Preprocessed BOLD Time-Series.

■ Unprocessed Versus Preprocessed BOLD Time-Series



Fitted BOLD Time-Series.

■ Preprocessed Versus Fitted BOLD Time-Series

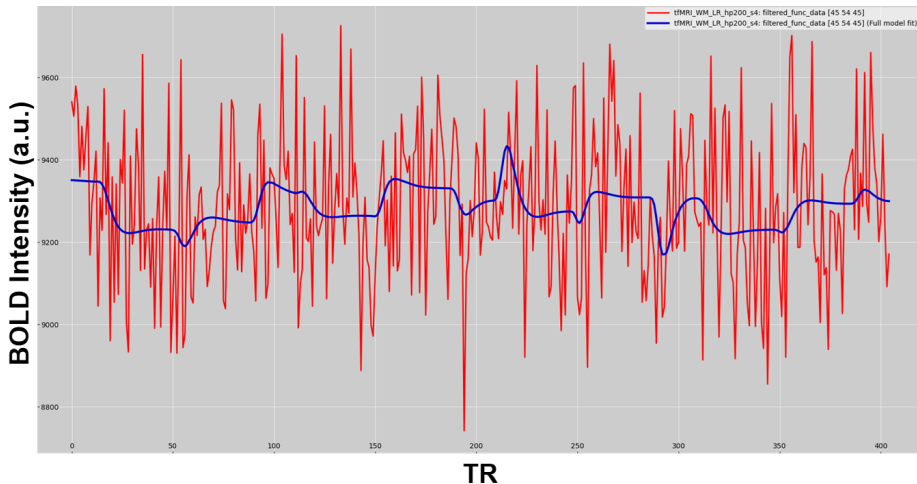


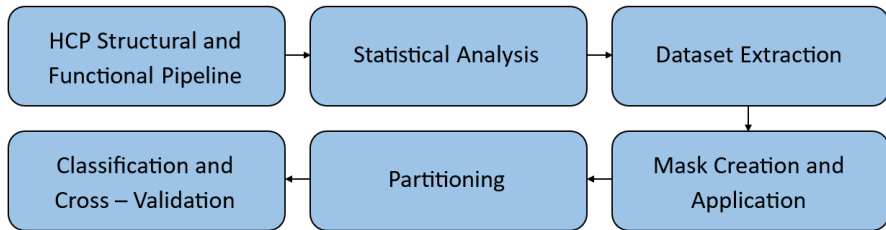
Table of Contents

- 1 **Introduction**
 - Run-Through
 - Decoding and Classification
 - The Fusiform Gyrus
 - Why fMRI?
- 2 **Theoretical Background**
 - Visual Information Processing
 - Mechanisms of fMRI
- 3 **Data Acquisition and Manipulation**
 - The Human Connectome Project (*HCP*)
 - Task-fMRI Battery of the HCP
 - Analysis of fMRI Signal
- 4 **Methods and Results**
 - Pipeline Overview
 - Data Analysis - UPA
 - Data Analysis - MVPA in the FFA
 - Data Analysis - MVPA in the PPA

Pipeline Overview

- Starting point is HCP preprocessed data
- Smoothing changed to 4mm
- Signal-to-noise ratio increase, registration to MNI-152, enables statistical comparisons

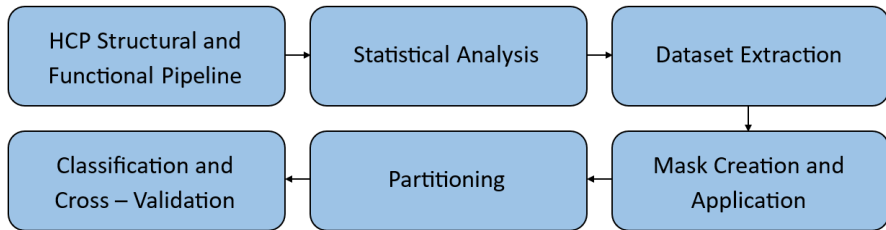
- Two analyses conducted (20s)
- N-Back combination, 4 copies/run, 2 chunks/subject (2C), 160 patterns total
- N-Back distinction, 8 copies/run, 4 chunks/subject (4C), 320 patterns total



Pipeline Overview

- Starting point is HCP preprocessed data
- Smoothing changed to 4mm
- Singal-to-noise ratio increase, registrastion to MNI-152, enables statistical comparisons

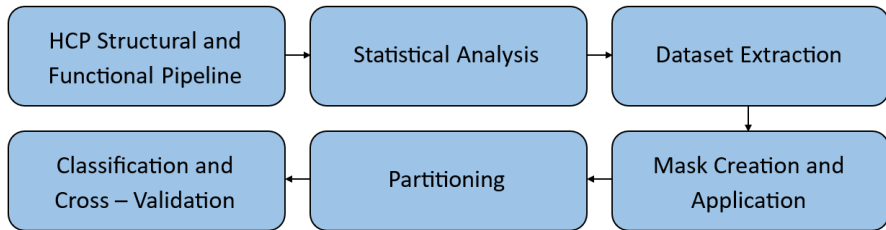
- Two analyses conducted (20s)
- N-Back combination, 4 copes/run, 2 chunks/subject (2C), 160 patterns total
- N-Back distinction, 8 copes/run, 4 chunks/subject (4C), 320 patterns total



Pipeline Overview

- Starting point is HCP preprocessed data
- Smoothing changed to 4mm
- Signal-to-noise ratio increase, registration to MNI-152, enables statistical comparisons

- Two analyses conducted (20s)
- N-Back combination, 4 copies/run, 2 chunks/subject (2C), 160 patterns total
- N-Back distinction, 8 copies/run, 4 chunks/subject (4C), 320 patterns total

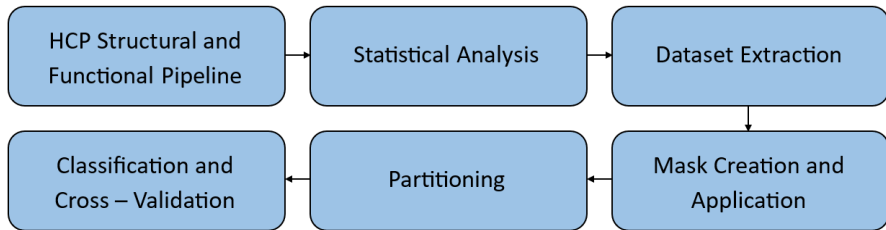


Pipeline Overview

- Starting point is HCP preprocessed data
- Smoothing changed to 4mm
- Signal-to-noise ratio increase, registration to MNI-152, enables statistical comparisons

- Two analyses conducted (20s)

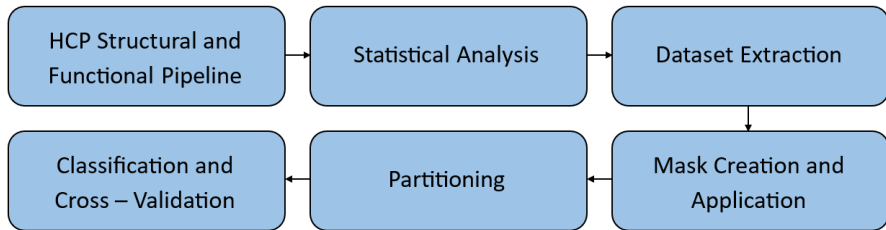
- N-Back combination, 4 copes/run, 2 chunks/subject (2C), 160 patterns total
- N-Back distinction, 8 copes/run, 4 chunks/subject (4C), 320 patterns total



Pipeline Overview

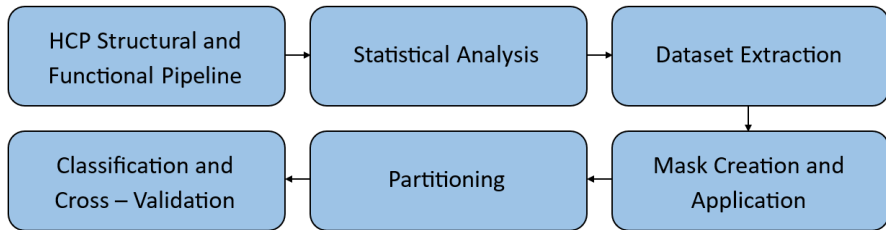
- Starting point is HCP preprocessed data
- Smoothing changed to 4mm
- Signal-to-noise ratio increase, registration to MNI-152, enables statistical comparisons

- Two analyses conducted (20s)
- N-Back combination, 4 copies/run, 2 chunks/subject (2C), 160 patterns total
- N-Back distinction, 8 copies/run, 4 chunks/subject (4C), 320 patterns total



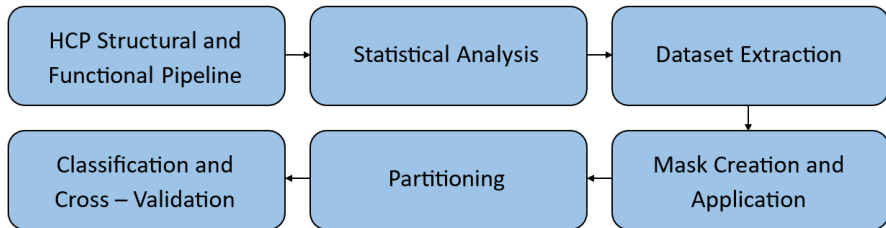
Pipeline Overview

- Starting point is HCP preprocessed data
- Smoothing changed to 4mm
- Signal-to-noise ratio increase, registration to MNI-152, enables statistical comparisons
- Two analyses conducted (20s)
- N-Back combination, 4 copies/run, 2 chunks/subject (2C), 160 patterns total
- N-Back distinction, 8 copies/run, 4 chunks/subject (4C), 320 patterns total



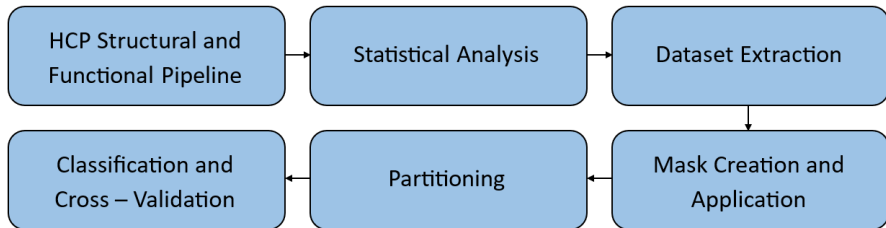
Extraction and Masks

- From separate copes across different runs of various subjects into one dataset structure
- Samples by Features matrix with attributes, targets, labels, chunks (320 X 900k)
- Two masks created for FFA and PPA with 12 voxel radius
- Application of masks, focus on specific region, data is manageable (320 X 1k)



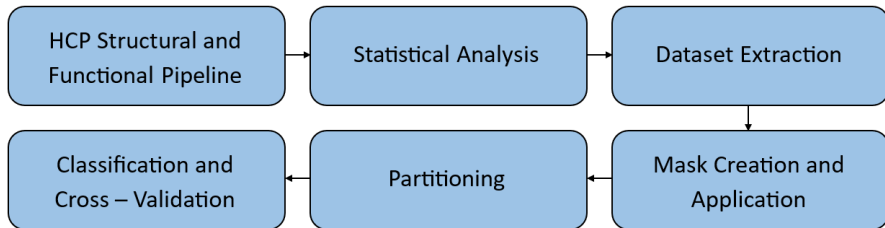
Extraction and Masks

- From separate copies across different runs of various subjects into one dataset structure
- Samples by Features matrix with attributes, targets, labels, chunks (**320 X 900k**)
- Two masks created for FFA and PPA with 12 voxel radius
- Application of masks, focus on specific region, data is manageable (**320 X 1k**)



Extraction and Masks

- From separate copies across different runs of various subjects into one dataset structure
- Samples by Features matrix with attributes, targets, labels, chunks (**320 X 900k**)
- Two masks created for FFA and PPA with 12 voxel radius
- Application of masks, focus on specific region, data is manageable (**320 X 1k**)



Extraction and Masks

- From separate copies across different runs of various subjects into one dataset structure
- Samples by Features matrix with attributes, targets, labels, chunks (**320 X 900k**)
- Two masks created for FFA and PPA with 12 voxel radius
- Application of masks, focus on specific region, data is manageable (**320 X 1k**)

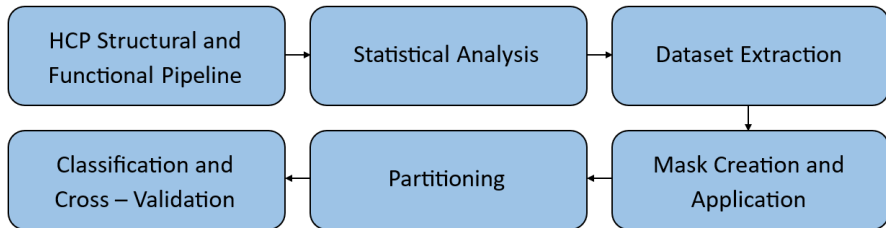
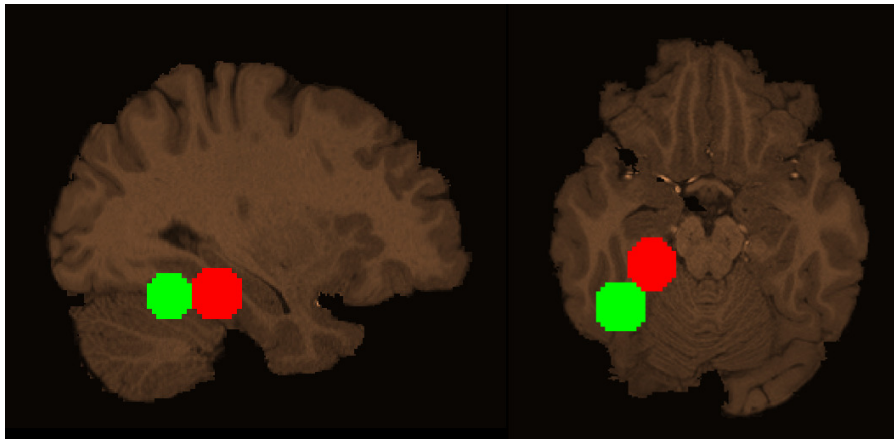


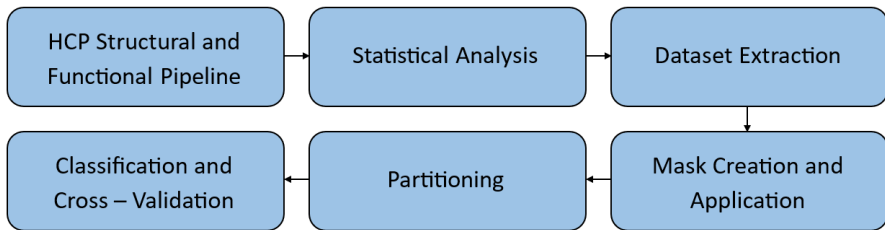
Illustration of Masks



FSL Snapshots of FFA (green) and PPA (red) Masks at Maximum Overlap in the Sagittal and Horizontal Planes

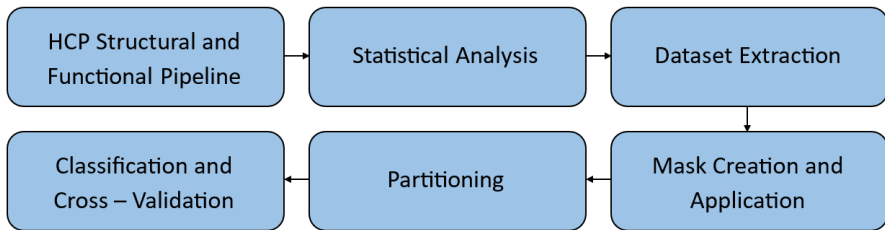
Partitioning, Classification and Cross-Validation

- Partition data into folds, based on chunks
- Each fold contains independent train and test sets (80/20)
- SVM classification
- Predict test set targets/labels
- Repeat across multiple folds (cross-validate)



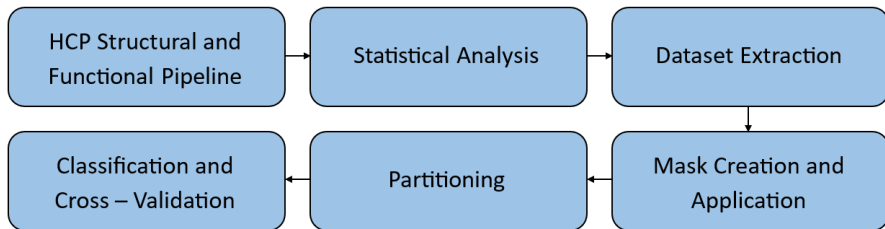
Partitioning, Classification and Cross-Validation

- Partition data into folds, based on chunks
- Each fold contains independent train and test sets (80/20)
- SVM classification
- Predict test set targets/labels
- Repeat across multiple folds (cross-validate)



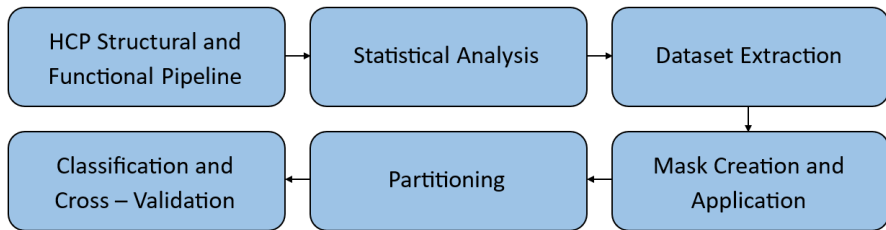
Partitioning, Classification and Cross-Validation

- Partition data into folds, based on chunks
- Each fold contains independent train and test sets (80/20)
- SVM classification
- Predict test set targets/labels
- Repeat across multiple folds (cross-validate)



Partitioning, Classification and Cross-Validation

- Partition data into folds, based on chunks
- Each fold contains independent train and test sets (80/20)
- SVM classification
- Predict test set targets/labels
- Repeat across multiple folds (cross-validate)



Partitioning, Classification and Cross-Validation

- Partition data into folds, based on chunks
- Each fold contains independent train and test sets (80/20)
- SVM classification
- Predict test set targets/labels
- Repeat across multiple folds (cross-validate)

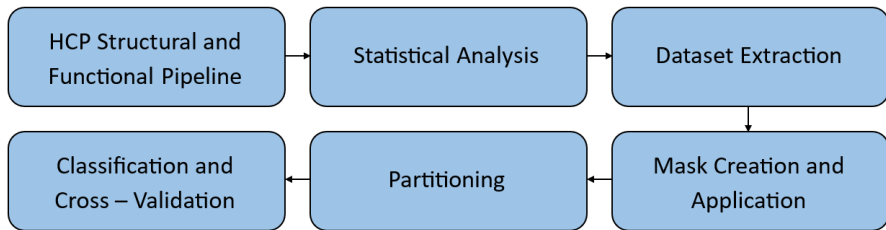
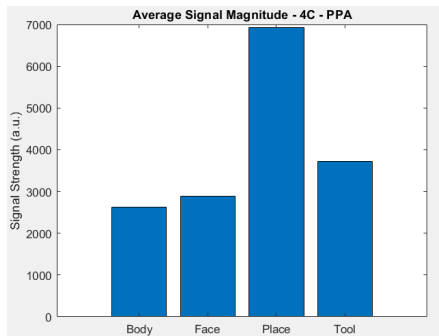
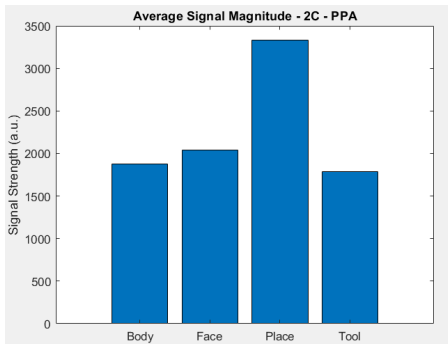


Table of Contents

- 1 **Introduction**
 - Run-Through
 - Decoding and Classification
 - The Fusiform Gyrus
 - Why fMRI?
- 2 **Theoretical Background**
 - Visual Information Processing
 - Mechanisms of fMRI
- 3 **Data Acquisition and Manipulation**
 - The Human Connectome Project (*HCP*)
 - Task-fMRI Battery of the HCP
 - Analysis of fMRI Signal
- 4 **Methods and Results**
 - Pipeline Overview
 - Data Analysis - UPA
 - Data Analysis - MVPA in the FFA
 - Data Analysis - MVPA in the PPA

Category-Specific BOLD Signal (*UPA*) - PPA



- Average magnitude of brain activation in the PPA across different stimulus categories in the 2C and 4C analyses
- UPA based on COPE values -
Statistical value of BOLD over time and voxels
- Baseline signal for the region's specificity stands out, with higher magnitude

Classifier Performance Variables

- Classification accuracy was treated as a function of three variables:
 - Chunks Per Subject
 - Fold Count
 - Subject Count
- Outlier subjects were identified and excluded
- Only subject with 0% accuracy in both regions
- Inability attributed to left FFA/PPA predominant activation or artifacts

Classifier Performance Variables

- Classification accuracy was treated as a function of three variables:
- Chunks Per Subject
 - Fold Count
 - Subject Count
- Outlier subjects were identified and excluded
- Only subject with 0% accuracy in both regions
- Inability attributed to left FFA/PPA predominant activation or artifacts

Classifier Performance Variables

- Classification accuracy was treated as a function of three variables:
- Chunks Per Subject
- Fold Count
- Subject Count
- Outlier subjects were identified and excluded
- Only subject with 0% accuracy in both regions
- Inability attributed to left FFA/PPA predominant activation or artifacts

Classifier Performance Variables

- Classification accuracy was treated as a function of three variables:
- Chunks Per Subject
- Fold Count
- Subject Count
- Outlier subjects were identified and excluded
- Only subject with 0% accuracy in both regions
- Inability attributed to left FFA/PPA predominant activation or artifacts

Classifier Performance Variables

- Classification accuracy was treated as a function of three variables:
 - Chunks Per Subject
 - Fold Count
 - Subject Count
- Outlier subjects were identified and excluded
 - Only subject with 0% accuracy in both regions
 - Inability attributed to left FFA/PPA predominant activation or artifacts

Classifier Performance Variables

- Classification accuracy was treated as a function of three variables:
 - Chunks Per Subject
 - Fold Count
 - Subject Count
- Outlier subjects were identified and excluded
- Only subject with 0% accuracy in both regions
- Inability attributed to left FFA/PPA predominant activation or artifacts

Classifier Performance Variables

- Classification accuracy was treated as a function of three variables:
 - Chunks Per Subject
 - Fold Count
 - Subject Count
- Outlier subjects were identified and excluded
- Only subject with 0% accuracy in both regions
- Inability attributed to left FFA/PPA predominant activation or artifacts

Table of Contents

- 1 **Introduction**
 - Run-Through
 - Decoding and Classification
 - The Fusiform Gyrus
 - Why fMRI?
- 2 **Theoretical Background**
 - Visual Information Processing
 - Mechanisms of fMRI
- 3 **Data Acquisition and Manipulation**
 - The Human Connectome Project (*HCP*)
 - Task-fMRI Battery of the HCP
 - Analysis of fMRI Signal
- 4 **Methods and Results**
 - Pipeline Overview
 - Data Analysis - UPA
 - Data Analysis - MVPA in the FFA
 - Data Analysis - MVPA in the PPA

MVPA - FFA - Chunks per Subject

2C

- Optimal mean accuracy of 70% across 3000 folds

- Distribution **not normal**
Lilliefors: $p = 10^{-4}$

- Two-Sample F-Test showed different variances with $p < 10^{-16}$
- Wilcoxon Rank-Sum Test showed:
statistically significant difference in distribution means with $p < 1^{-16}$

4C

- Optimal mean accuracy of 61.9% across 3000 folds

- Distribution **not normal**
Lilliefors: $p = 10^{-4}$

MVPA - FFA - Chunks per Subject

2C

- Optimal mean accuracy of 70% across 3000 folds
- Distribution **not normal**
Lilliefors: $p = 10^{-4}$

4C

- Optimal mean accuracy of 61.9% across 3000 folds
- Distribution **not normal**
Lilliefors: $p = 10^{-4}$

- Two-Sample F-Test showed different variances with $p < 10^{-16}$
- Wilcoxon Rank-Sum Test showed:
statistically significant difference in distribution means with $p < 1^{-16}$

MVPA - FFA - Chunks per Subject

2C

- Optimal mean accuracy of 70% across 3000 folds
- Distribution **not normal**
Lilliefors: $p = 10^{-4}$

4C

- Optimal mean accuracy of 61.9% across 3000 folds
- Distribution **not normal**
Lilliefors: $p = 10^{-4}$
- Two-Sample F-Test showed different variances with $p < 10^{-16}$
- Wilcoxon Rank-Sum Test showed:
statistically significant difference in distribution means with $p < 1^{-16}$

MVPA - FFA - Chunks per Subject

2C

- Optimal mean accuracy of 70% across 3000 folds
- Distribution **not normal**
Lilliefors: $p = 10^{-4}$

- Two-Sample F-Test showed different variances with $p < 10^{-16}$
- Wilcoxon Rank-Sum Test showed:
statistically significant difference in distribution means with $p < 1^{-16}$

4C

- Optimal mean accuracy of 61.9% across 3000 folds
- Distribution **not normal**
Lilliefors: $p = 10^{-4}$

MVPA - FFA - Chunks per Subject - Conclusions

- The different methods of integrating separate N-Back data provide significantly different results
- The tool should preferentially be trained and utilized on data belonging to only one N-Back paradigm
- Supervised learning data should come from a study separating N-Back paradigms, in different sessions, not just blocks or trials
- If a generic approach is unavoidable, efficiency prevails

MVPA - FFA - Chunks per Subject - Conclusions

- The different methods of integrating separate N-Back data provide significantly different results
- The tool should preferentially be trained and utilized on data belonging to only one N-Back paradigm
- Supervised learning data should come from a study separating N-Back paradigms, in different sessions, not just blocks or trials
- If a generic approach is unavoidable, efficiency prevails

MVPA - FFA - Chunks per Subject - Conclusions

- The different methods of integrating separate N-Back data provide significantly different results
- The tool should preferentially be trained and utilized on data belonging to only one N-Back paradigm
- Supervised learning data should come from a study separating N-Back paradigms, in different sessions, not just blocks or trials
- If a generic approach is unavoidable, efficiency prevails

MVPA - FFA - Chunks per Subject - Conclusions

- The different methods of integrating separate N-Back data provide significantly different results
- The tool should preferentially be trained and utilized on data belonging to only one N-Back paradigm
- Supervised learning data should come from a study separating N-Back paradigms, in different sessions, not just blocks or trials
- If a generic approach is unavoidable, efficiency prevails

- Data from 19 subjects classified across 250:250:3000 folds
- Accuracy stabilized to 2nd decimal by 250 folds
with $\sigma = 0.15\%$ and $\sigma = 0.17\%$
for analysis 2C and 4C, respectively
- Slight overperformance until 1000 folds
- Practical fold count was determined for each analysis

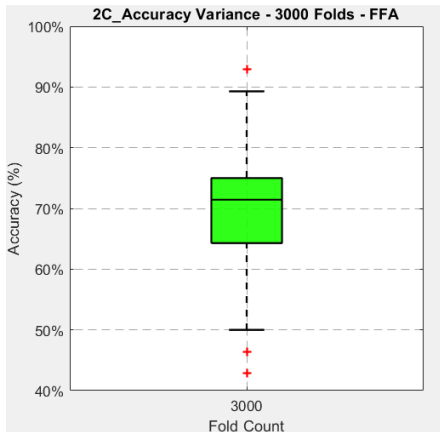
- Data from 19 subjects classified across 250:250:3000 folds
- Accuracy stabilized to 2nd decimal by 250 folds
with $\sigma = 0.15\%$ and $\sigma = 0.17\%$
for analysis 2C and 4C, respectively
- Slight overperformance until 1000 folds
- Practical fold count was determined for each analysis

- Data from 19 subjects classified across 250:250:3000 folds
- Accuracy stabilized to 2nd decimal by 250 folds
with $\sigma = 0.15\%$ and $\sigma = 0.17\%$
for analysis 2C and 4C, respectively
- Slight overperformance until 1000 folds
- Practical fold count was determined for each analysis

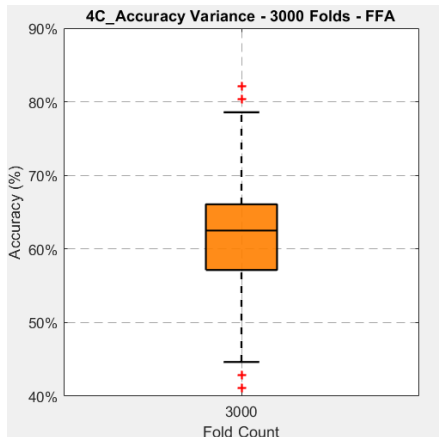
- Data from 19 subjects classified across 250:250:3000 folds
- Accuracy stabilized to 2nd decimal by 250 folds
with $\sigma = 0.15\%$ and $\sigma = 0.17\%$
for analysis 2C and 4C, respectively
- Slight overperformance until 1000 folds
- Practical fold count was determined for each analysis

MVPA - FFA - 3000 Folds Analysis

■ Mean: 70% σ : 8.4%
Median: 71.4%

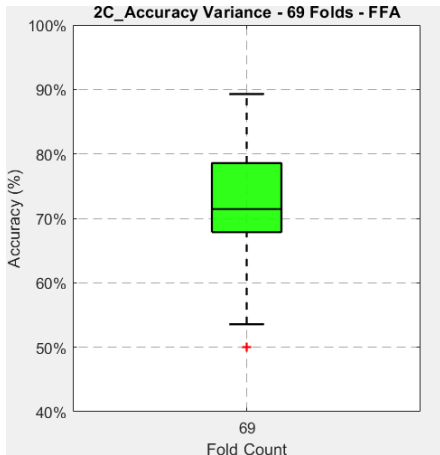


■ Mean: 61.9% σ : 6.3%
Median: 62.5%

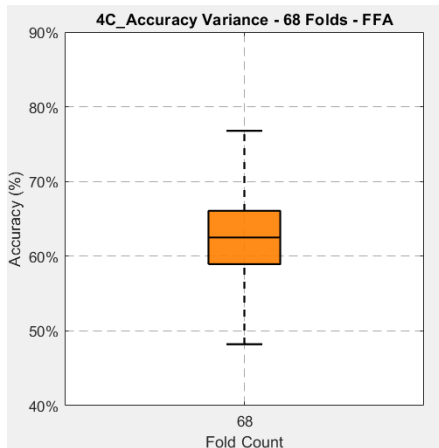


MVPA - FFA - Practical Fold Count

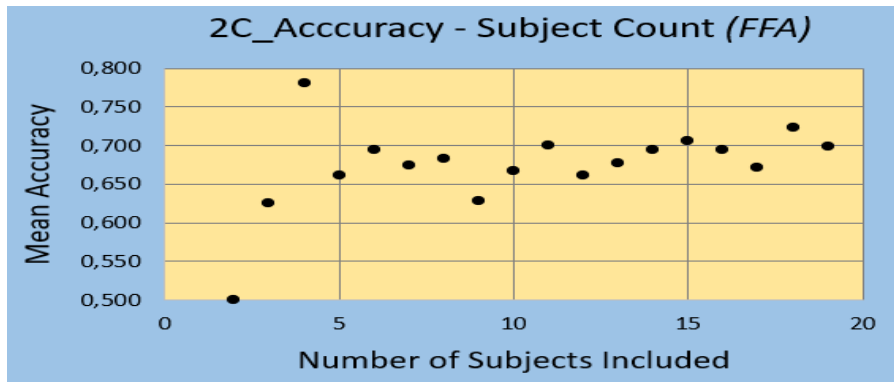
■ Mean: 72.3% σ : 8.0%
Median: 71.4%



■ Mean: 62.2% σ : 6.0%
Median: 62.5%

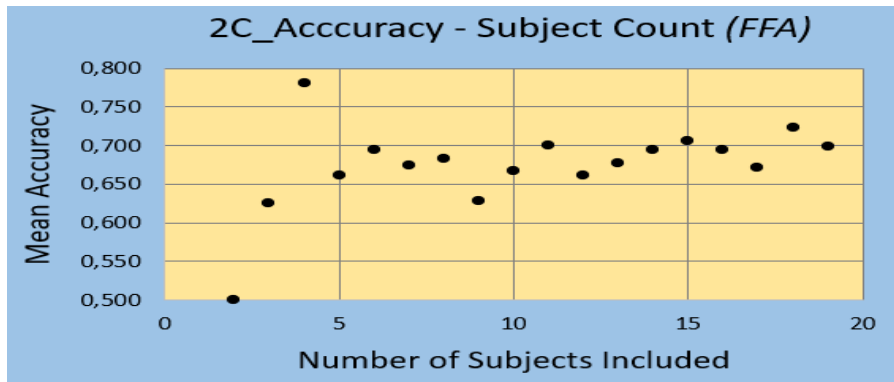


MVPA - FFA - 2C Subject Count



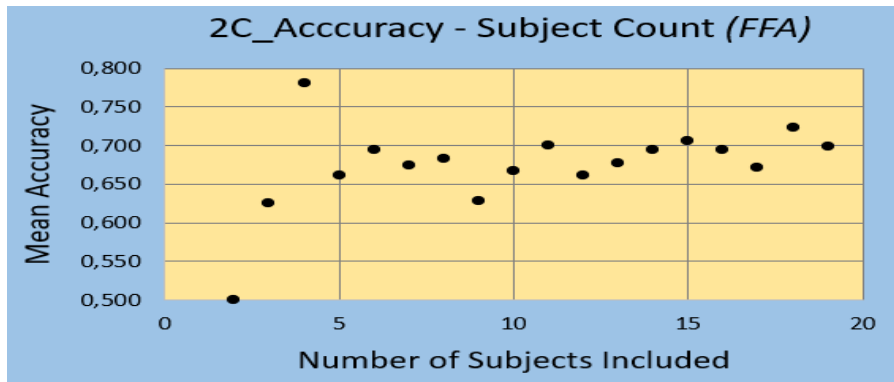
- Surprisingly accurate at 2 subjects only (50%)
- Irregularity at 4 subjects (78.1%), affected by low fold counts
- Realistic values over 6 subjects
- Oscillates in the 65-70% range thereafter

MVPA - FFA - 2C Subject Count



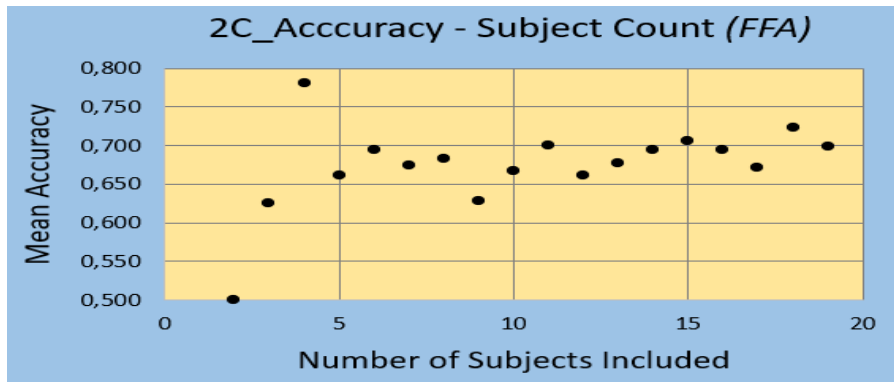
- Surprisingly accurate at 2 subjects only (50%)
- Irregularity at 4 subjects (78.1%), affected by low fold counts
- Realistic values over 6 subjects
- Oscillates in the 65-70% range thereafter

MVPA - FFA - 2C Subject Count



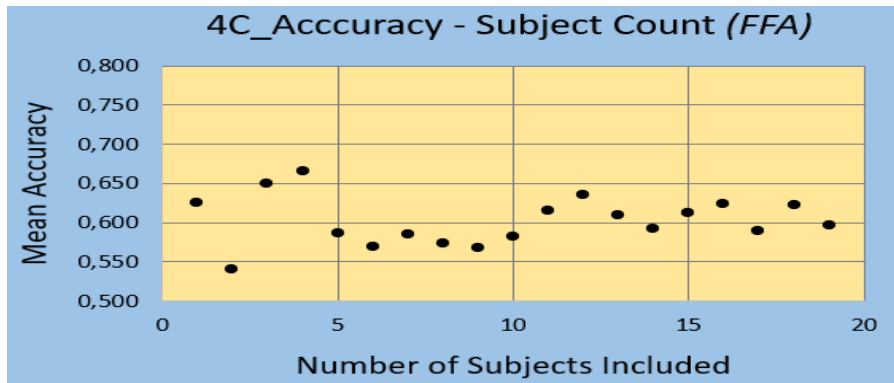
- Surprisingly accurate at 2 subjects only (50%)
- Irregularity at 4 subjects (78.1%), affected by low fold counts
- Realistic values over 6 subjects
- Oscillates in the 65-70% range thereafter

MVPA - FFA - 2C Subject Count



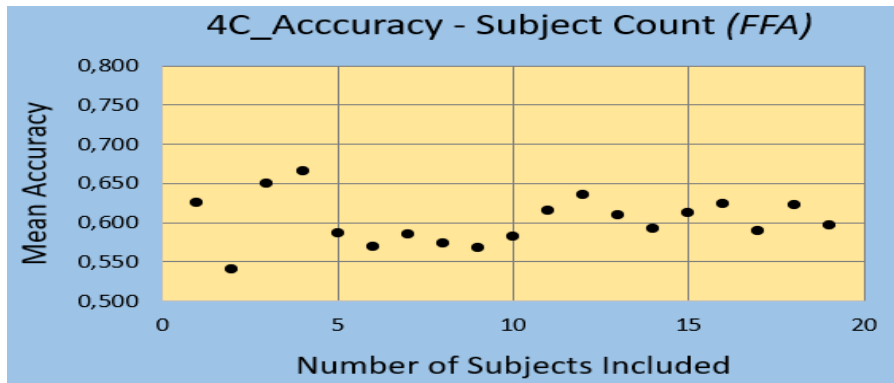
- Surprisingly accurate at 2 subjects only (50%)
- Irregularity at 4 subjects (78.1%), affected by low fold counts
- Realistic values over 6 subjects
- Oscillates in the 65-70% range thereafter

MVPA - FFA - 4C Subject Count



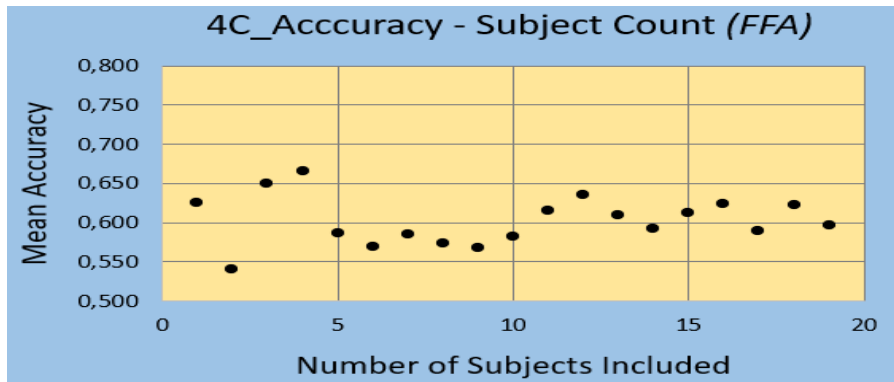
- Similar overperformance before 5 subjects
- Stabilizes around 57% initially at 5 subjects
- Realistic values over 11 subjects

MVPA - FFA - 4C Subject Count



- Similar overperformance before 5 subjects
- Stabilizes around 57% initially at 5 subjects
- Realistic values over 11 subjects

MVPA - FFA - 4C Subject Count



- Similar overperformance before 5 subjects
- Stabilizes around 57% initially at 5 subjects
- Realistic values over 11 subjects

Table of Contents

- 1 **Introduction**
 - Run-Through
 - Decoding and Classification
 - The Fusiform Gyrus
 - Why fMRI?
- 2 **Theoretical Background**
 - Visual Information Processing
 - Mechanisms of fMRI
- 3 **Data Acquisition and Manipulation**
 - The Human Connectome Project (*HCP*)
 - Task-fMRI Battery of the HCP
 - Analysis of fMRI Signal
- 4 **Methods and Results**
 - Pipeline Overview
 - Data Analysis - UPA
 - Data Analysis - MVPA in the FFA
 - Data Analysis - MVPA in the PPA

MVPA - PPA - Chunks per Subject

2C

- Optimal mean accuracy of 66.4% across 3000 folds
- Distribution **not normal**
Lilliefors: $p = 10^{-4}$

4C

- Optimal mean accuracy of 50.6% across 3000 folds
- Distribution **not normal**
Lilliefors: $p = 10^{-4}$
- Two-Sample F-Test showed different variances with $p < 10^{-16}$
- Wilcoxon Rank-Sum Test showed:
statistically significant difference in distribution means with $p < 10^{-16}$
- Choice of data integration shows identical pattern in both brain regions

MVPA - PPA - Chunks per Subject

2C

- Optimal mean accuracy of 66.4% across 3000 folds
- Distribution **not normal**
Lilliefors: $p = 10^{-4}$

4C

- Optimal mean accuracy of 50.6% across 3000 folds
- Distribution **not normal**
Lilliefors: $p = 10^{-4}$

- Two-Sample F-Test showed different variances with $p < 10^{-16}$
- Wilcoxon Rank-Sum Test showed:
statistically significant difference in distribution means with $p < 10^{-16}$
- Choice of data integration shows identical pattern in both brain regions

MVPA - PPA - Chunks per Subject

2C

- Optimal mean accuracy of 66.4% across 3000 folds
- Distribution **not normal**
Lilliefors: $p = 10^{-4}$

4C

- Optimal mean accuracy of 50.6% across 3000 folds
- Distribution **not normal**
Lilliefors: $p = 10^{-4}$
- Two-Sample F-Test showed different variances with $p < 10^{-16}$
- Wilcoxon Rank-Sum Test showed:
statistically significant difference in distribution means with $p < 10^{-16}$
- Choice of data integration shows identical pattern in both brain regions

MVPA - PPA - Chunks per Subject

2C

- Optimal mean accuracy of 66.4% across 3000 folds
- Distribution **not normal**
Lilliefors: $p = 10^{-4}$

4C

- Optimal mean accuracy of 50.6% across 3000 folds
- Distribution **not normal**
Lilliefors: $p = 10^{-4}$
- Two-Sample F-Test showed different variances with $p < 10^{-16}$
- Wilcoxon Rank-Sum Test showed:
statistically significant difference in distribution means with $p < 1^{-16}$
- Choice of data integration shows identical pattern in both brain regions

MVPA - PPA - Chunks per Subject

2C

- Optimal mean accuracy of 66.4% across 3000 folds
- Distribution **not normal**
Lilliefors: $p = 10^{-4}$

4C

- Optimal mean accuracy of 50.6% across 3000 folds
- Distribution **not normal**
Lilliefors: $p = 10^{-4}$
- Two-Sample F-Test showed different variances with $p < 10^{-16}$
- Wilcoxon Rank-Sum Test showed:
statistically significant difference in distribution means with $p < 10^{-16}$
- Choice of data integration shows identical pattern in both brain regions

MVPA - PPA - Fold Count

- Data from 19 subjects classified across 250:250:3000 folds
- Accuracy stabilized to 2nd decimal by 250 folds
with $\sigma = 0.12\%$ and $\sigma = 0.07\%$
- Slight underperformance until 750 folds
- Absolute stability by 750 folds (third decimal)
Improvement might be due to signal baseline
- Practical fold count was determined for each analysis

MVPA - PPA - Fold Count

- Data from 19 subjects classified across 250:250:3000 folds
- Accuracy stabilized to 2nd decimal by 250 folds
with $\sigma = 0.12\%$ and $\sigma = 0.07\%$
- Slight underperformance until 750 folds
- Absolute stability by 750 folds (third decimal)
Improvement might be due to signal baseline
- Practical fold count was determined for each analysis

MVPA - PPA - Fold Count

- Data from 19 subjects classified across 250:250:3000 folds
- Accuracy stabilized to 2nd decimal by 250 folds
with $\sigma = 0.12\%$ and $\sigma = 0.07\%$
- Slight underperformance until 750 folds
- Absolute stability by 750 folds (third decimal)
Improvement might be due to signal baseline
- Practical fold count was determined for each analysis

MVPA - PPA - Fold Count

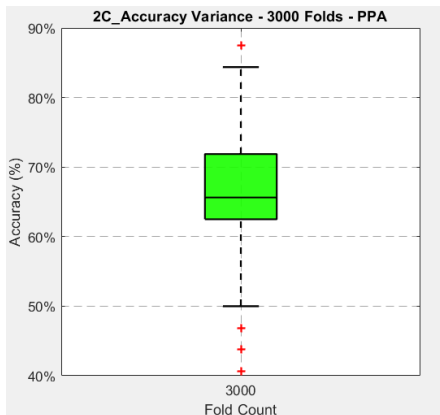
- Data from 19 subjects classified across 250:250:3000 folds
- Accuracy stabilized to 2nd decimal by 250 folds
with $\sigma = 0.12\%$ and $\sigma = 0.07\%$
- Slight underperformance until 750 folds
- Absolute stability by 750 folds (third decimal)
Improvement might be due to signal baseline
- Practical fold count was determined for each analysis

MVPA - PPA - Fold Count

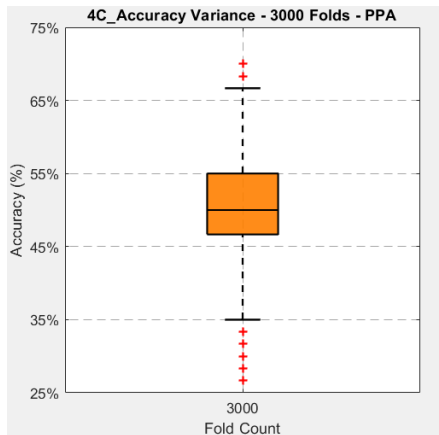
- Data from 19 subjects classified across 250:250:3000 folds
- Accuracy stabilized to 2nd decimal by 250 folds
with $\sigma = 0.12\%$ and $\sigma = 0.07\%$
- Slight underperformance until 750 folds
- Absolute stability by 750 folds (third decimal)
Improvement might be due to signal baseline
- Practical fold count was determined for each analysis

MVPA - PPA - 3000 Folds

■ Mean: 66.4% σ : 7.9%
Median: 65.6%

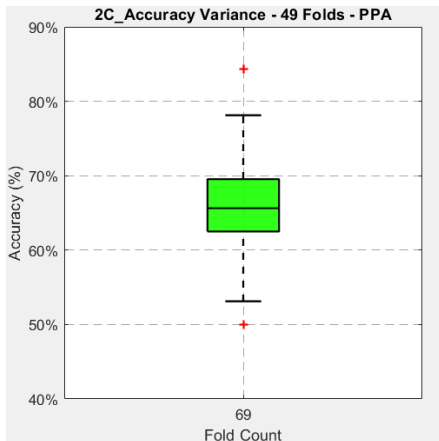


■ Mean: 50.6% σ : 6.1%
Median: 50.0%

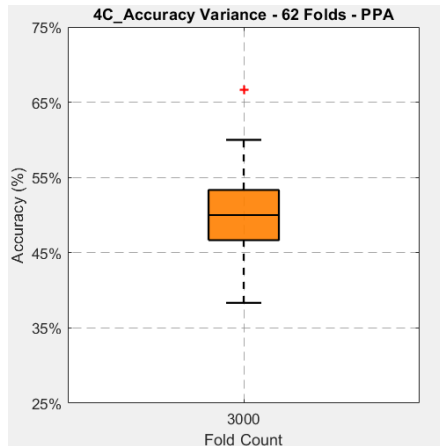


MVPA - PPA - Practical Fold Count

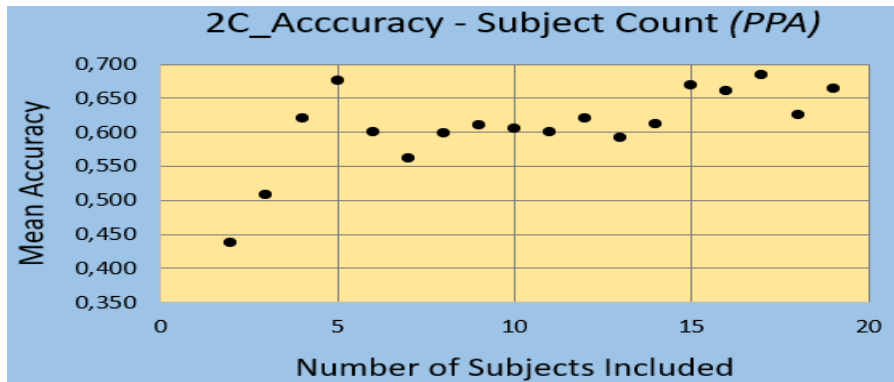
■ Mean: 66.4% σ : 7.0%
Median: 65.6%



■ Mean: 50.1% σ : 5.7%
Median: 50.0%

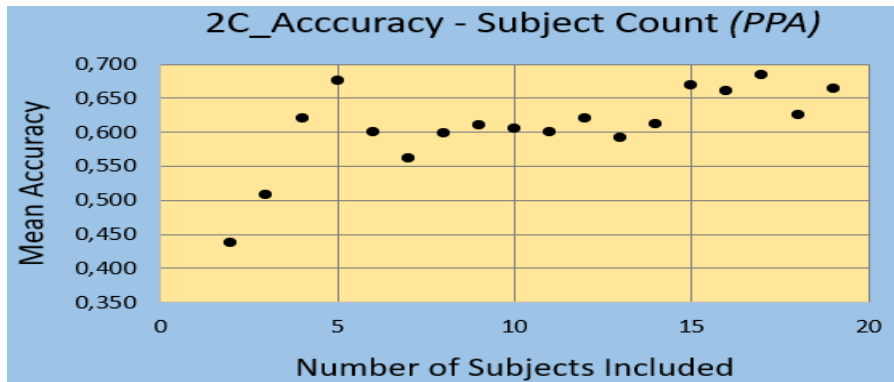


MVPA - PPA - 2C Subject Count



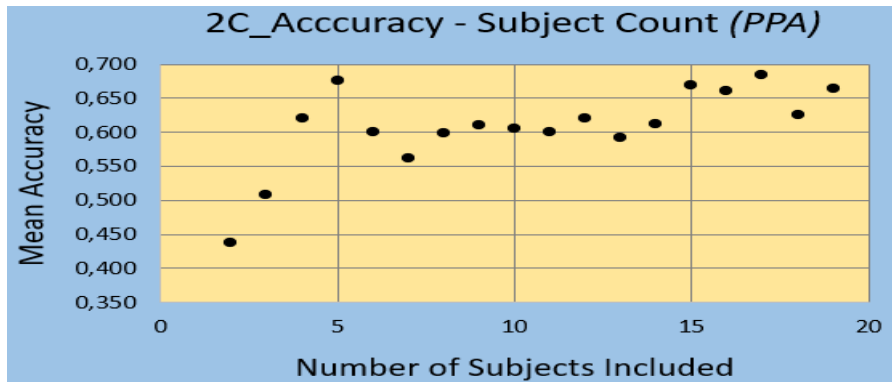
- Rapid linear increase until 5 subjects
- Overperformance at 5 (67.5%), cannot be generalized
- Consistency over 5 subjects around 60%
- Approaches optimal accuracy at 15 subjects (66.8% - 66.4%)

MVPA - PPA - 2C Subject Count



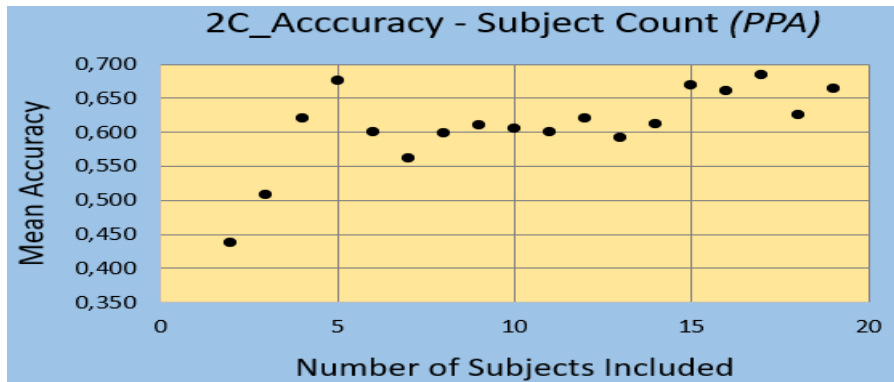
- Rapid linear increase until 5 subjects
- Overperformance at 5 (67.5%), cannot be generalized
- Consistency over 5 subjects around 60%
- Approaches optimal accuracy at 15 subjects (66.8% - 66.4%)

MVPA - PPA - 2C Subject Count



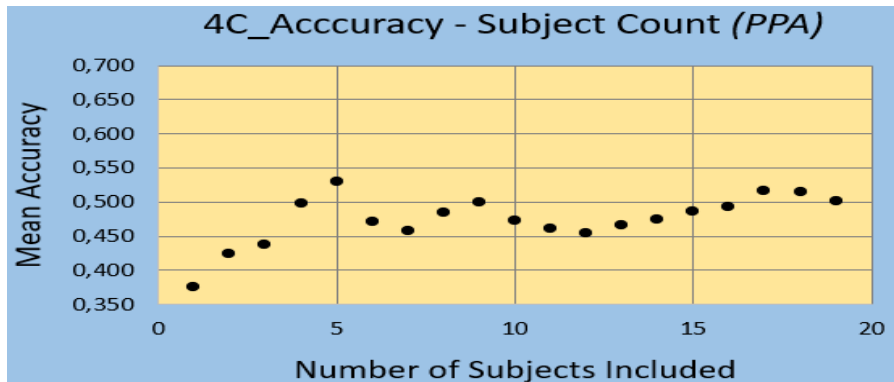
- Rapid linear increase until 5 subjects
- Overperformance at 5 (67.5%), cannot be generalized
- Consistency over 5 subjects around 60%
- Approaches optimal accuracy at 15 subjects (66.8% - 66.4%)

MVPA - PPA - 2C Subject Count



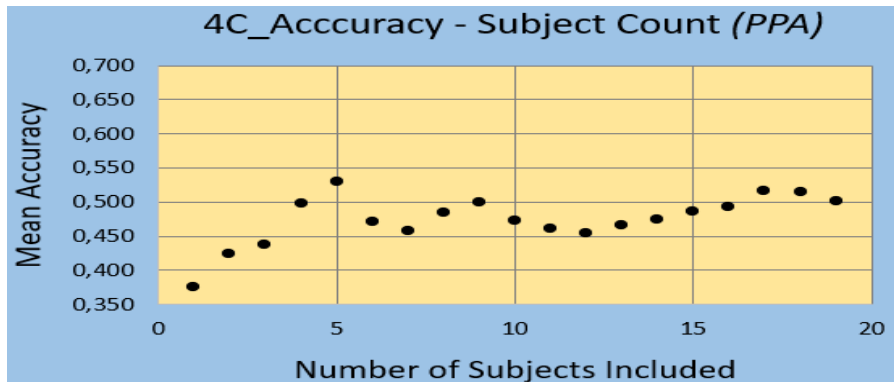
- Rapid linear increase until 5 subjects
- Overperformance at 5 (67.5%), cannot be generalized
- Consistency over 5 subjects around 60%
- Approaches optimal accuracy at 15 subjects (66.8% - 66.4%)

MVPA - PPA - 4C Subject Count



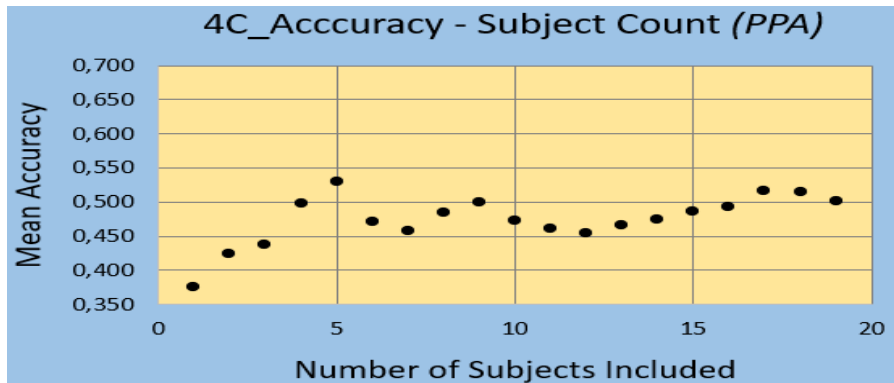
- Similar pattern showing even more stability
- Linear increase into irregularity at 5
- Oscillation around optimal accuracy (50.1%)

MVPA - PPA - 4C Subject Count



- Similar pattern showing even more stability
- Linear increase into irregularity at 5
- Oscillation around optimal accuracy (50.1%)

MVPA - PPA - 4C Subject Count



- Similar pattern showing even more stability
- Linear increase into irregularity at 5
- Oscillation around optimal accuracy (50.1%)

Summary

- Automated and provided protocol for data cleanup and selection
- Automated data extraction and consolidation
- Linked base signal to performance
- Significance of reasearcher's choice of data interpretation proven
- Provided framework for tool's optimal performance, efficiency, practicality

Summary

- Automated and provided protocol for data cleanup and selection
- Automated data extraction and consolidation
- Linked base signal to performance
- Significance of reasearcher's choice of data interpretation proven
- Provided framework for tool's optimal performance, efficiency, practicality

Summary

- Automated and provided protocol for data cleanup and selection
- Automated data extraction and consolidation
- Linked base signal to performance
- Significance of reasearcher's choice of data interpretation proven
- Provided framework for tool's optimal performance, efficiency, practicality

Summary

- Automated and provided protocol for data cleanup and selection
- Automated data extraction and consolidation
- Linked base signal to performance
- Significance of reasearcher's choice of data interpretation proven
- Provided framework for tool's optimal performance, efficiency, practicality

Summary

- Automated and provided protocol for data cleanup and selection
- Automated data extraction and consolidation
- Linked base signal to performance
- Significance of reasearcher's choice of data interpretation proven
- Provided framework for tool's optimal performance, efficiency, practicality

Future Work

- Script optimization, grouping and potentially GUI
- Cross-model decoding
- Utilization of more specialized data
- Expansion to other brain regions, not only visual
- Big Picture, Clinical Applications, Diagnosis, Cure
- Bigger Picture, Brain-Computer Interface

Future Work

- Script optimization, grouping and potentially GUI
- Cross-model decoding
- Utilization of more specialized data
- Expansion to other brain regions, not only visual
- Big Picture, Clinical Applications, Diagnosis, Cure
- Bigger Picture, Brain-Computer Interface

Future Work

- Script optimization, grouping and potentially GUI
- Cross-model decoding
- Utilization of more specialized data
- Expansion to other brain regions, not only visual
- Big Picture, Clinical Applications, Diagnosis, Cure
- Bigger Picture, Brain-Computer Interface

Future Work

- Script optimization, grouping and potentially GUI
- Cross-model decoding
- Utilization of more specialized data
- Expansion to other brain regions, not only visual
- Big Picture, Clinical Applications, Diagnosis, Cure
- Bigger Picture, Brain-Computer Interface

Future Work

- Script optimization, grouping and potentially GUI
- Cross-model decoding
- Utilization of more specialized data
- Expansion to other brain regions, not only visual
- Big Picture, Clinical Applications, Diagnosis, Cure
- Bigger Picture, Brain-Computer Interface

Future Work

- Script optimization, grouping and potentially GUI
- Cross-model decoding
- Utilization of more specialized data
- Expansion to other brain regions, not only visual
- Big Picture, Clinical Applications, Diagnosis, Cure
- Bigger Picture, Brain-Computer Interface

License

All author's original content of this work is licensed under the **Creative Commons Attribution-Sharealike 4.0** license, except otherwise noted.



<https://creativecommons.org/licenses/by-sa/4.0/>

Everything can be found on the **GitHub** repository:

[https://github.com/
kasapakis-nk/BSc_Thesis_MVPA_Decoding_Classification](https://github.com/kasapakis-nk/BSc_Thesis_MVPA_Decoding_Classification)

Thank You!

Kasapakis Nikolaos
nkasapak@auth.gr

<https://github.com/kasapakis-nk>