



Università
di Genova



Re-Parcellation of The Human Brain Using the Harvard Oxford Atlas

Performed on the The Midnight Scan Club (MSC)
dataset from OpenNeuro (ds000224)

Prepared by: Nagham Mohamed - 7200337
Supervised by: Prof. Storace and Prof. Lodi

TABLE OF CONTENTS

- 01 Dataset Description
- 02 Slice-Time & Motion Correction
- 03 Skull-Stripping of T1 Images
- 04 Coregistration of T1 to EPI
- 05 Skull-Stripping of Functional EPI
- 06 Projecting the HO Atlas on the warped EPI Image
- 07 Time-Series Extraction and ROI Functional Connectivity
- 08 Visualization of the overlaid Atlas on the brain

01 - Dataset Description



1.1 Dataset Overview

- Dataset name: Midnight Scanning Club (MSC)
- OpenNeuro ID: [ds000224, version 00002](#)
- Purpose: To provide high-quality, multi-session resting-state and task fMRI data for studying individual differences in brain organization.

1.2 Participants

- Number of subjects: 10 healthy adults (5 males, 5 females)
- Age range: 24–34 years
- Right-handed, with normal or corrected-to-normal vision.
- Each subject participated in 10 separate scanning sessions, allowing within-subject reproducibility studies.

1.3 Image Acquisition

- Each subject's dataset includes:
 - Structural MRI (T1-weighted): High-resolution anatomical images for alignment and normalization.
 - Functional MRI (fMRI):
 - Resting-state scans: Eyes open, fixating on a cross.
 - Task scans: Motor, memoryfaces, memorywords, memoryscenes, glasslexical.

02 - Slice-Time and Motion Correction



Goal of this Stage

A- Objective:

Remove timing offsets between slices and head-motion artifacts before modeling.

B- Steps implemented (SPM):

1. Slice-Timing Correction (STC) → temporal interpolation to a common reference time.
2. Realignment (6-DOF rigid-body) → estimate motion; reslice images.

C- What is SPM?

SPM (**S**tatistical **P**arametric **M**apping) is a MATLAB toolbox for preprocessing and statistical analysis of brain imaging (fMRI, PET, MRI). It provides standardized pipelines (batch/scripting) for slice-timing correction, realignment, coregistration, normalization, smoothing, and model estimation.

D- Why it matters?

Slice offsets distort the BOLD (**B**lood-**O**xigen-**L**evel-**D**ependent) phase; motion induces spurious correlations and false activations.

02 - Slice-Time and Motion Correction



STC - Concept Behind the Scene

A- Problem:

EPI acquires slices sequentially, so each volume's slices are sampled at different times within the same TR.

TR (Repetition Time): the time between successive excitations of the same slice (or volume). In fMRI, it's the sampling interval of the BOLD time series.

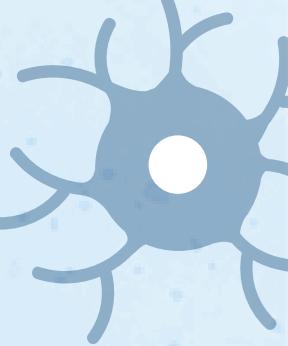
B- Significance:

Temporal misalignment of voxel time series and task regressors. This can reduce detection power, especially in event-related designs and for longer TRs.

C- What STC does:

STC interpolates each voxel's time series to a common reference time (a “reference slice”; often the middle slice to minimize average shift). Only the reference slice is not interpolated; all others are shifted in time toward it.

02 - Slice-Time and Motion Correction



STC - SPM Implementation

A- Inputs:

- Repetition Time (TR) and SliceTiming (one time per slice).
- Compute $TA = TR - TR/nslices$ (time from first to last slice within a volume).

B- Derive SPM Batch Parameters:

- $nslices = \text{length}(\text{SliceTiming})$
- $\text{slice_order} = \text{sort}(\text{SliceTiming}) \rightarrow$ converts true acquisition times to an ascending order list for SPM.
- $\text{refslice} = \text{round}(nslices/2) \rightarrow$ use the middle slice as reference to minimize average temporal shift.

C- What STC does:

First step is to pull TR and exact per-slice times from BIDS, compute TA, recover the true acquisition order, and align all slices to the middle-slice time using SPM's sinc-based interpolation. Outputs are assigned a prefix (a*.nii) for the next step.

02 - Slice-Time and Motion Correction



Motion Correction - Concept Behind the Scene

A- What is modeled?

- Treat the head as a rigid body: every fMRI volume is related to a reference by 6 parameters → 3 translations (x,y,z) and 3 rotations (pitch, roll, yaw).
- Realignment estimates these per-volume transforms so all frames describe the brain in a common coordinate system

B- How it is done:

SPM minimizes sum of squared differences between each volume and the reference, using iterative optimization. Mild smoothing (FWHM) and a sampling step (sep) make the cost function well-behaved; after parameter estimation, volumes are resliced (interpolated) onto the reference grid.

C- Choice of the reference:

- First image: preserves original intensity framing; avoids circularity from averaging across motion.
- Mean image: sharper target and better SNR, but built from already-misaligned frames.
- **In this pipeline, the choice is the first image.**

02 - Slice-Time and Motion Correction



Motion Correction - SPM Implementation

A- Overview:

- we feed all $a^*.nii$ volumes to SPM Realign (Estimate & Reslice), registering each volume with a 6-DOF rigid transform to the first image ($rtm=0$).
- SPM then writes the resliced series $ra^*.nii$ and a mean EPI $meana^*.nii$, and saves $rp_*.txt$ (6 motion parameters/TR) for nuisance regression and QC.

B- SPM Batch Parameters:

- **sep = 3 mm (sampling separation)**

Grid step for sampling the cost function during estimation. Smaller = finer search (better convergence on subtle motion) but slower. Typical: 2–4 mm; we use 3 mm as an accuracy–speed compromise.

- **fwhm = 6 mm (estimation smoothing)**

Temporary Gaussian smoothing during parameter estimation only to stabilize the SSD cost function under noise/edges. Larger values ease optimization but can blur features; 6 mm is a well-used default.

02 - Slice-Time and Motion Correction



Motion Correction - SPM Implementation

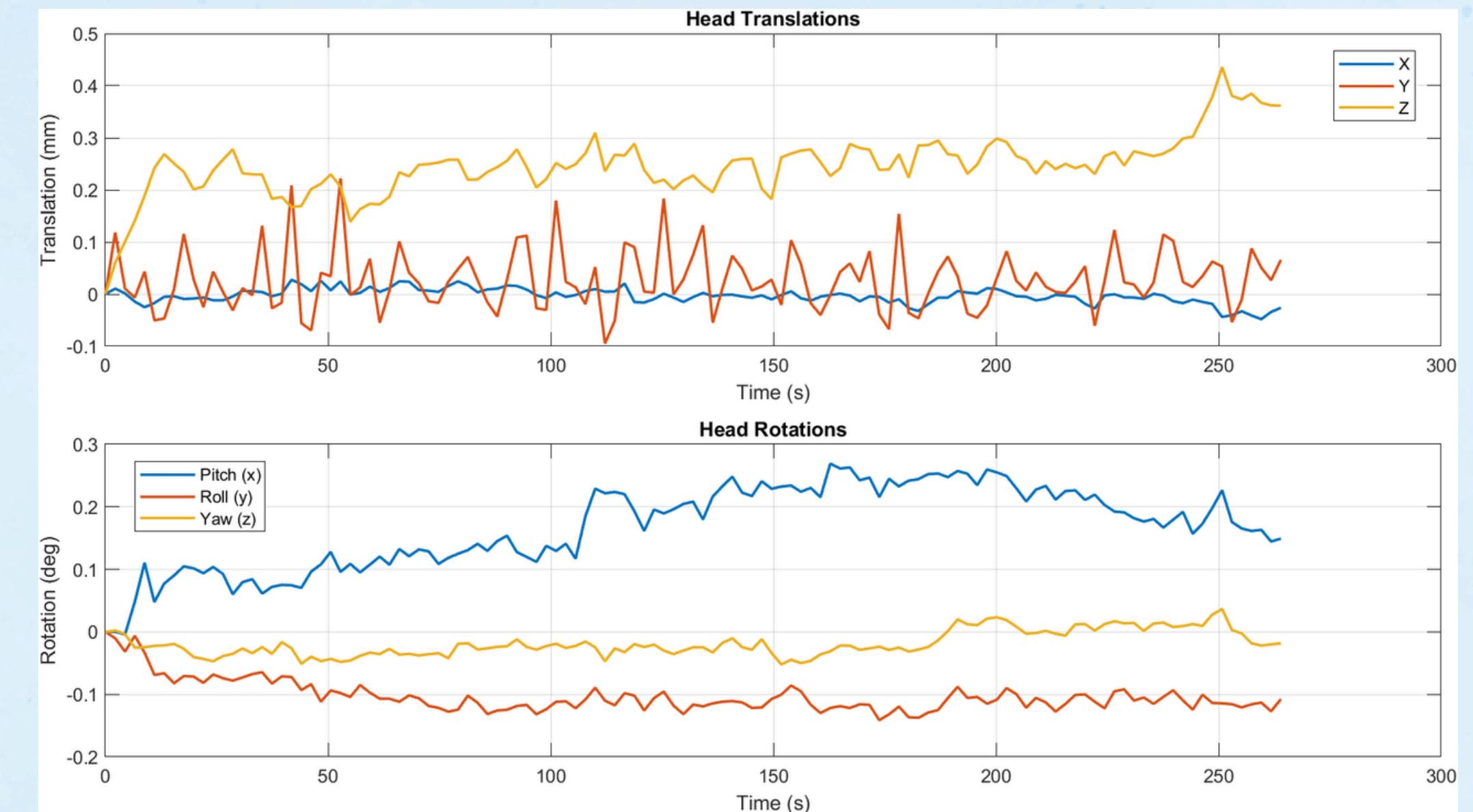
- **interp** (interpolation order)

Estimation: eoptions.interp = 2 (B-spline, smooth derivatives for the optimizer).

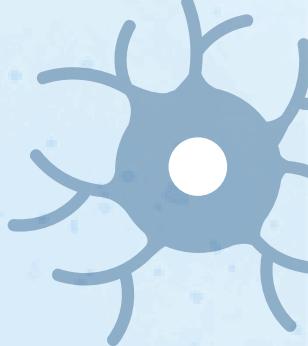
Final reslice: roptions.interp = 4 (higher-order B-spline → better spatial fidelity than trilinear).

C- Visualization of Motion Parameters:

- There's a gradual drift in Z translation and Pitch rotation over time, which may indicate slow head movement
- The most stable parameter is X translation, while Z translation and Pitch rotation show the greatest drift.



03 - Skull-Stripping of T1 Images



Goal of this Stage

A- Rationale:

Remove non-brain tissues (scalp, skull, dura) from the anatomical T1 so downstream coregistration and normalization and atlas projection are more accurate and faster.

B- Approach:

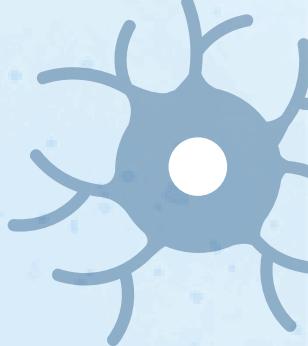
1. Use SPM Unified Segmentation on the T1 to estimate GM/WM/CSF probability maps.,
2. Derive an intracranial mask (ICV), and apply it to a bias-corrected mean T1 (averaged across two runs).

Simple averaging improves SNR approximately with \sqrt{N}

C- What is Unified Segmentation?

- Unified Segmentation jointly models bias-field, tissue classes (mixture of Gaussians), and priors (TPMs) within one generative framework.
- **mask = GM+WM+CSF.** These three classes (**Grey Matter, White Matter, Cerebrospinal Fluid**) define intracranial contents; summing their posteriors approximates ICV and excludes skull/skin tissues. (SPM also defines 6 tissue priors including non-brain.)

03 - Skull-Stripping of T1 Images



SPM Implementation

A- Steps:

1. Run SPM Unified Segmentation on T1#1 and on the mean of T1#1+T1#2.
2. Build a brain mask as **(GM+WM+CSF)>0.3**
3. Apply it to the bias-corrected mean T1 to produce **mean_T1_stripped.nii**.
4. On reruns, the cached outputs are used to regenerate the Quality Check (**QC**) figures without rerunning the pipeline.

B- Outputs:

- **mean_T1.nii** → anatomical target for coregistration.
- **mmean_T1.nii** → bias-corrected mean T1.
- **brain_mask_meanT1.nii** → intracranial mask (GM+WM+CSF).
- **mean_T1_stripped.nii** → brain-only T1 for coregistration to EPI and for atlas work.

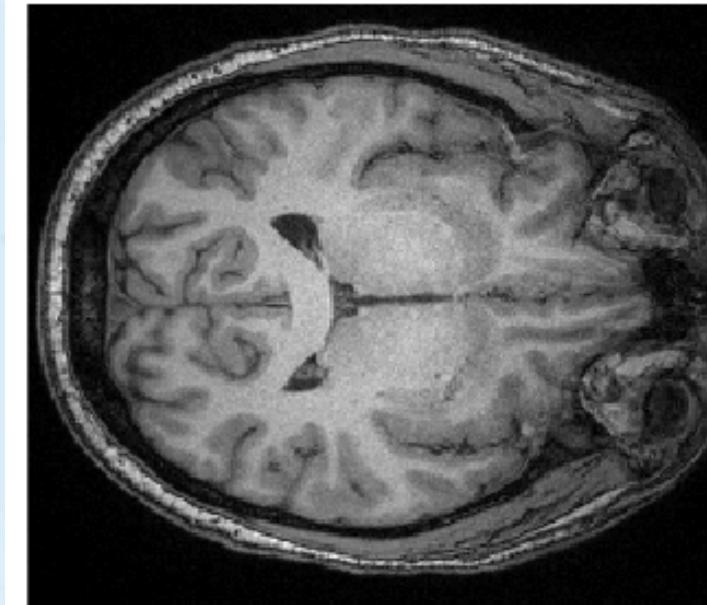
03 - Skull-Stripping of T1 Images

Visualization of the 2x2 QC Figure

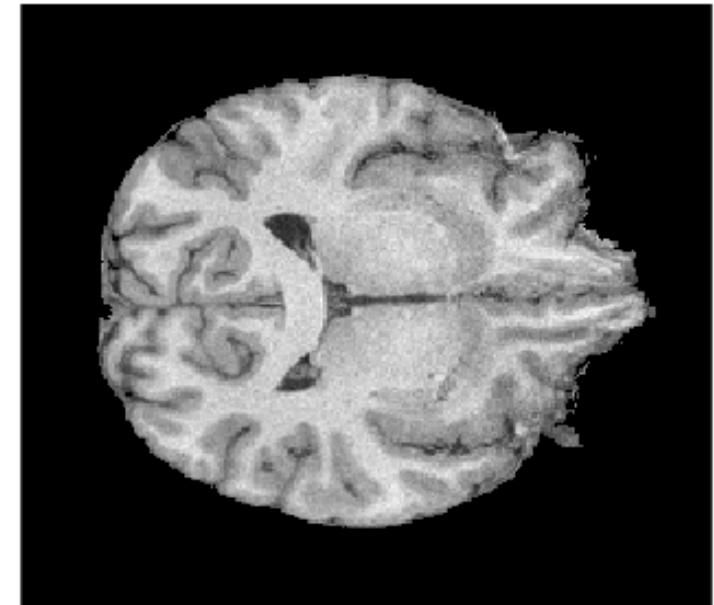
- The bias-corrected stripped image (bottom right) has sharper tissue boundaries and more uniform intensity, ideal for processing pipelines
- The mean images suggest good alignment and averaging — no obvious blurring from motion.

Comparison of Original vs Skull-Stripped T1

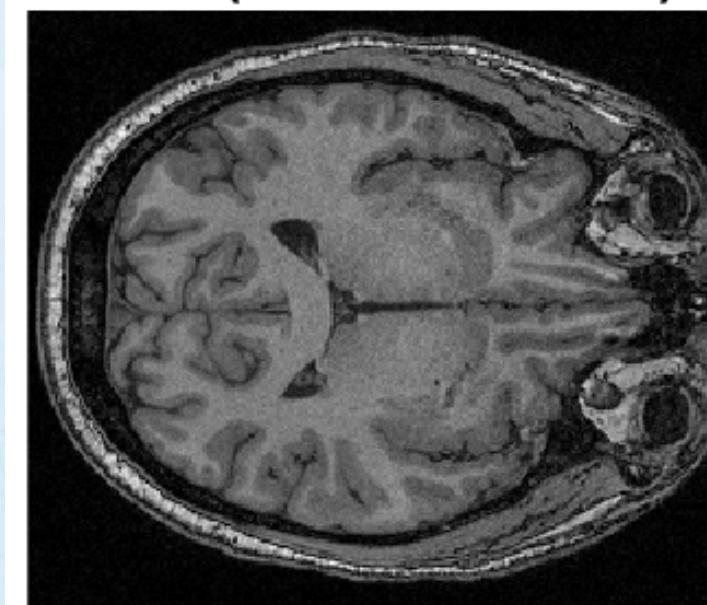
Mean T1



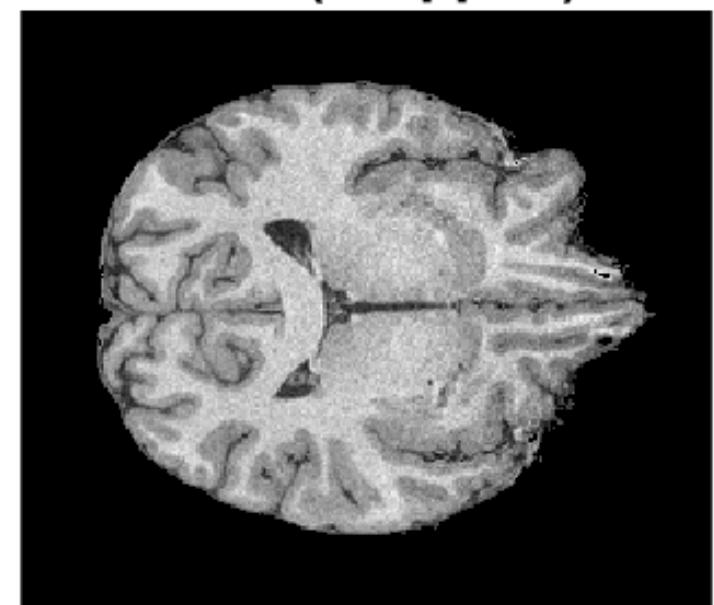
Mean T1 (stripped)



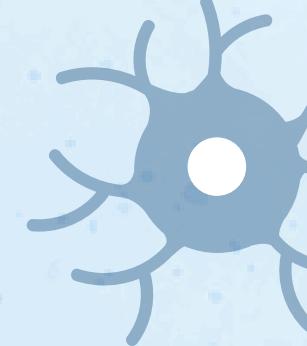
T1#1 (bias-corrected)



T1#1 (stripped)



04 - Coregistration of T1 to EPI



Goal of this Stage

A- Approach:

1. Put the mean EPI (**BOLD, distorted & low-contrast**) into the T1 (**high-contrast, undistorted**) anatomical frame using a rigid **6-DOF transform—without resampling yet**.
2. Then apply the same header transform to the entire 4D EPI, so later steps reslice just once (**one-interpolation principle**).

B- Why NMI (Normalized Mutual Information)?

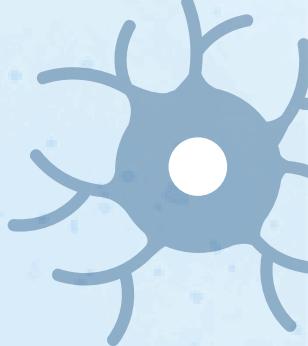
1. Problem:

EPI (BOLD) and T1 images come from different MRI contrasts:

- T1 → bright white matter, dark CSF
- EPI (BOLD) → the opposite: dark white matter, bright CSF

That means their intensity patterns don't match — so similarity measures like Sum of Squared Differences (SSD) or Correlation fail, because they assume a linear intensity relationship.

04 - Coregistration of T1 to EPI



Goal of this Stage

2. Solution:

- Mutual Information (MI) measures how much knowing the intensity in one image reduces uncertainty about the other — it captures statistical dependence, not direct intensity matching.
- Normalized MI (NMI) is a version that's scale-invariant, so it works even if the images have different dynamic ranges or partial overlaps (like when fields of view differ).
- NMI computes the joint histogram of intensities between the two images and finds the rigid transform that maximizes shared information.

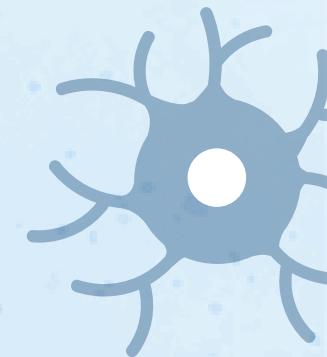
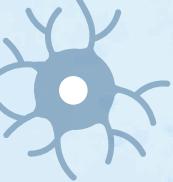
Formally,

$$\text{NMI} = \frac{H(A) + H(B)}{H(A, B)}$$

where $H(A)$, $H(B)$ are marginal entropies, and $H(A, B)$ is joint entropy.

Maximizing NMI \Rightarrow best spatial alignment between modalities.

04 - Coregistration of T1 to EPI



SPM Implementation

A- Design

- **Reference (fixed)**: skull-stripped T1 → removes scalp/skull edges that can mislead the optimizer.
- **Source (moving)**: mean EPI → higher SNR & less noise than a single EPI frame.
- **Apply to “other”**: the full 4D EPI → headers updated in-place; voxel data untouched (no blur yet).

B- SPM Batch Parameters:

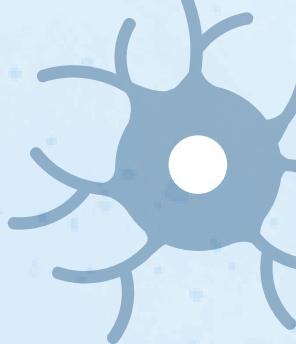
1. **sep = [4 2]** : Multi-resolution sampling step, mm

2. **tol = [0.02 0.02 0.02 0.001 0.001 0.001 0.01 0.01 0.01 0.001 0.001 0.001]** : Small step-size thresholds for translations (mm) and rotations (rad) (first six entries)

Estimate-only; header update

No voxel interpolation now. SPM writes the 6-DOF transform into the headers of the source and “other” images to limit blur

05 - Skull-Stripping of Functional EPI



Goal of this Stage

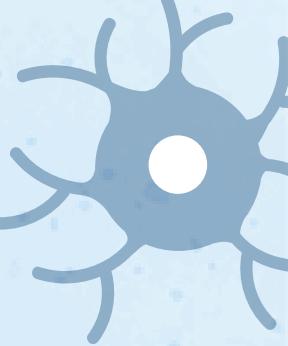
A- Rationale:

Remove non-brain voxels from the mean EPI and the full 4D EPI (in EPI space) using a single static mask, so later modeling isn't confounded by scalp/skull/air signals.

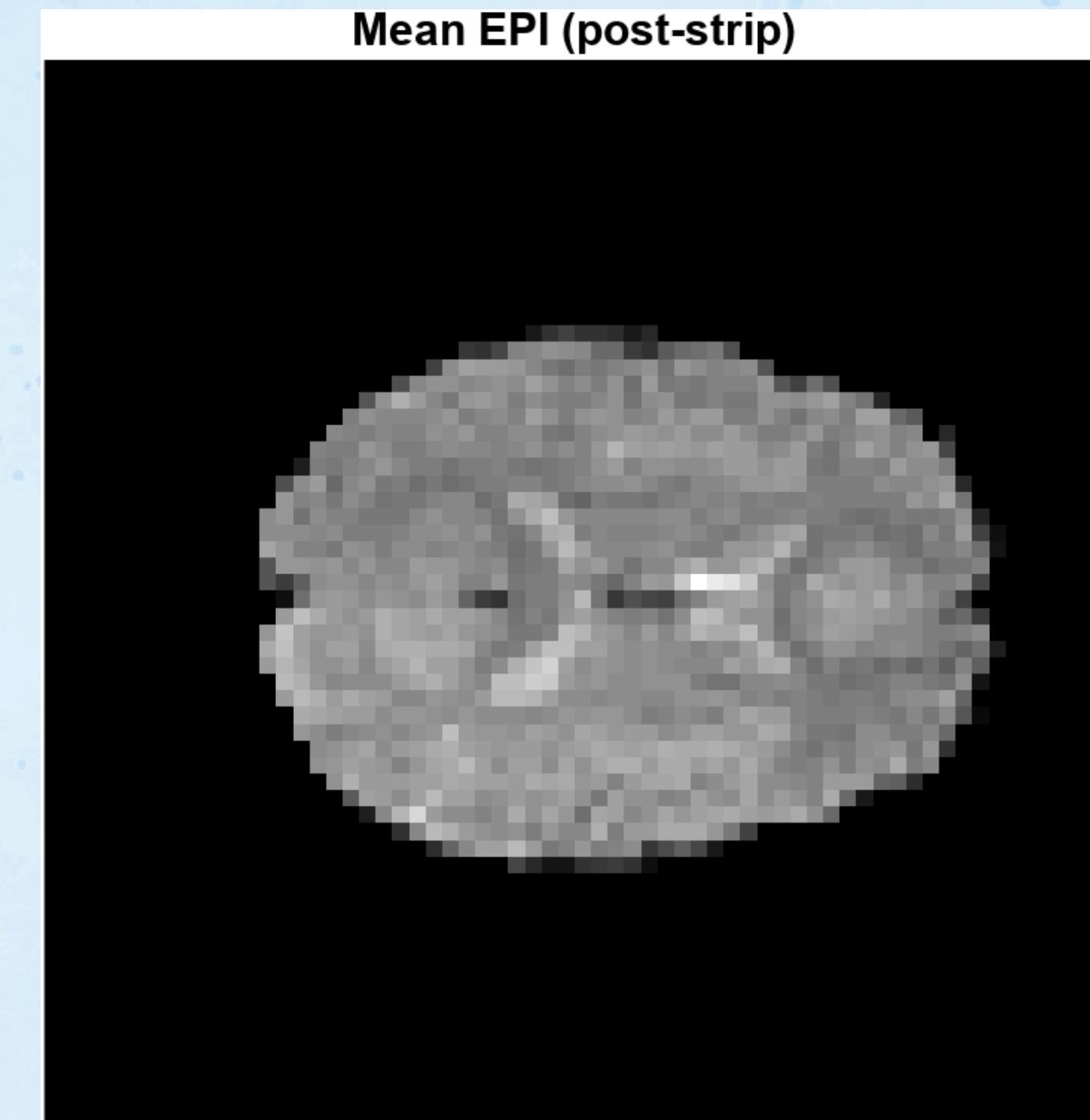
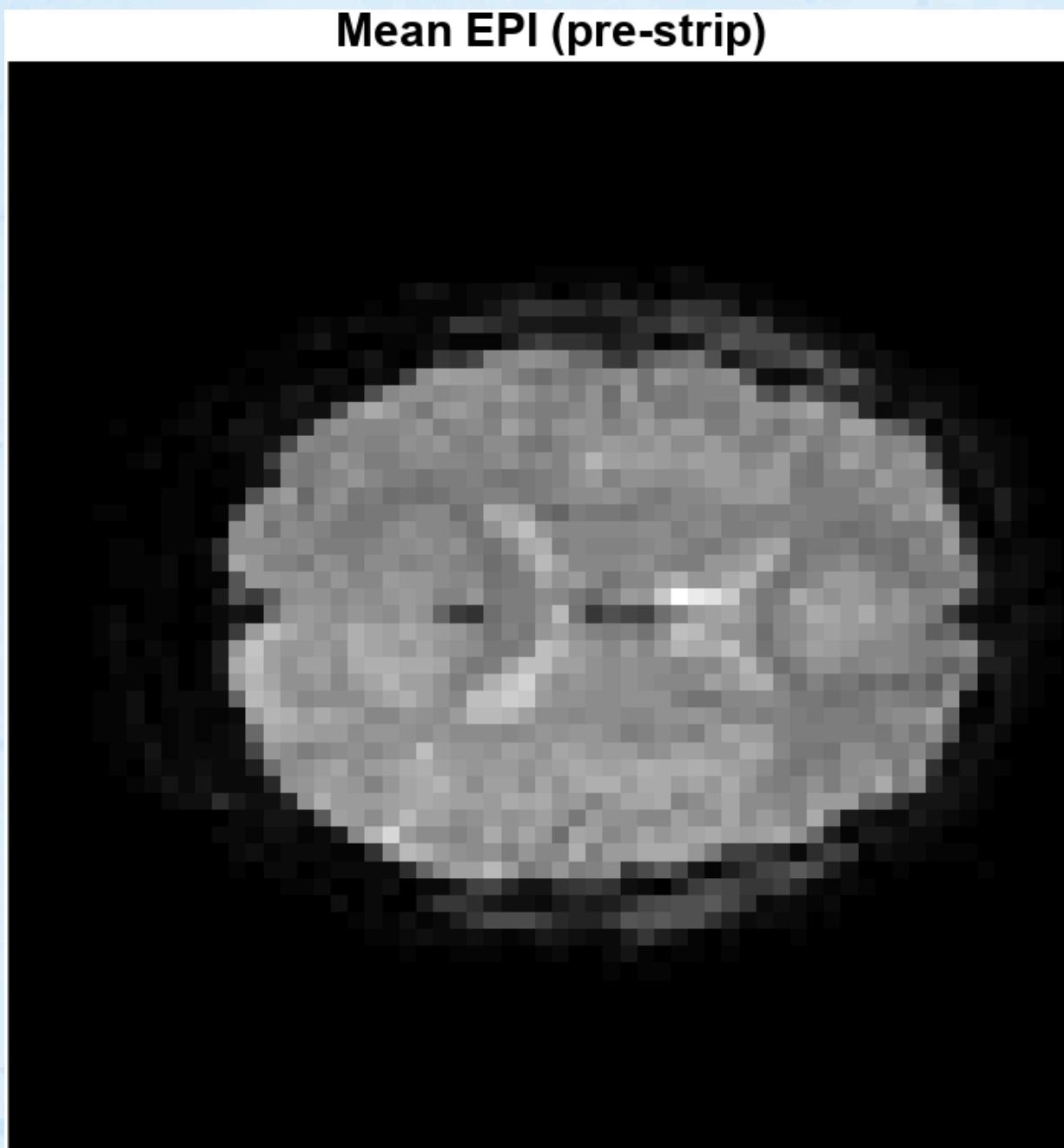
B- Approach and Implementation:

1. One mask for all timepoints: apply the same 3D mask to every TR which avoids time-varying censoring that can introduce artifactual dynamics and connectivity biases.
2. Binary labels stay binary: resample masks with **nearest-neighbor** only (no partial voluming). This prevents fuzzy edges and unintended erosion/dilation of brain borders.

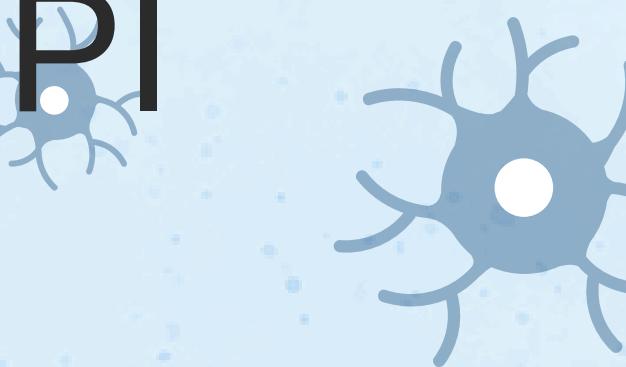
05 - Skull-Stripping of Functional EPI



Visualization of the QC Figures:

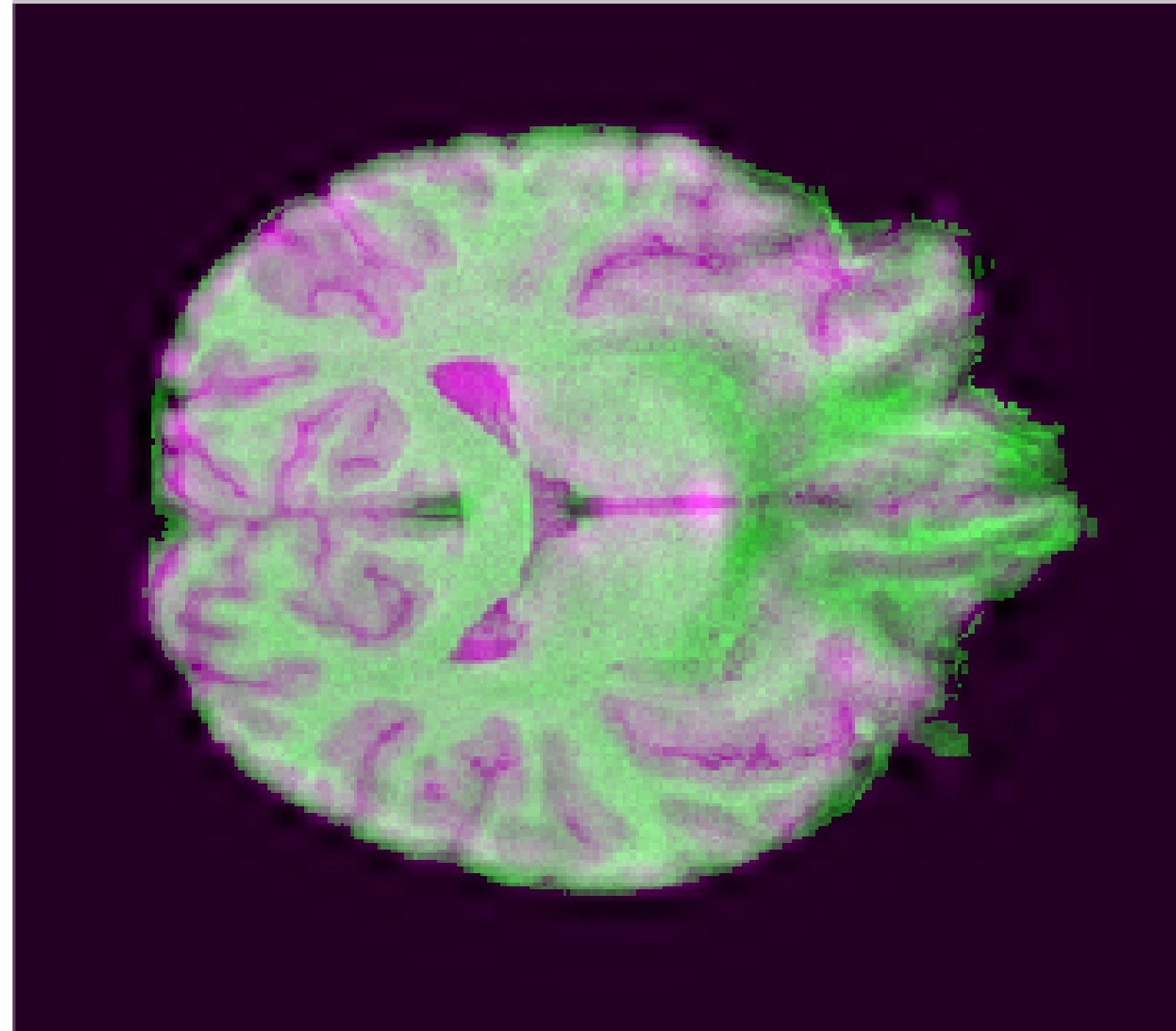


05 - Skull-Stripping of Functional EPI



Visualization of the QC Figures:

T1 and Functional Image Overlay (Axial Slice)



06 - Projecting the HO Atlas on the warped EPI Image

Goal of this Stage

A- Rationale:

To bring the subject's functional (EPI) data and the Harvard–Oxford atlas into the same anatomical space and grid, enabling extraction of region-level (parcel-based) time series.

B- 3-sub-step pipeline (They ensure all three datasets (EPI, T1, and HO atlas) are perfectly aligned voxel-to-voxel in MNI space, allowing direct extraction of BOLD time series per ROI).

Sub-step	Operation	Direction	Purpose
(A) Normalize T1 to MNI	Estimate nonlinear deformation fields (y_- , jy_-)	Native \leftrightarrow MNI	Define mapping between subject anatomy and standard MNI space
(B) Warp EPI to MNI	Apply y_- to EPI (and T1)	Native \rightarrow MNI	Bring functional data into MNI space for analysis and group alignment
(C) Project HO Atlas onto EPI grid	<u>Reslice</u> atlas using NN interpolation	MNI \rightarrow MNI (grid match)	Match atlas labels to the exact EPI voxel grid for parcel-based analysis

06 - Projecting the HO Atlas on the warped EPI Image

Step A: Normalizing T1 to MNI

A- What it does:

- Estimates a nonlinear deformation field between subject's native T1 and the MNI152 template.
- Outputs two warp fields:
 - `y_<T1>.nii` — Forward (native to MNI)
 - `iy_<T1>.nii` — Inverse (MNI to native)

B- Purpose:

- Defines how to move any image to or from MNI space — **the standard coordinate system used by Harvard–Oxford and other atlases.**
- This field becomes the "**bridge**" between the subject's brain and the MNI template.

06 - Projecting the HO Atlas on the warped EPI Image

Step B: Warping EPI and Projecting the Atlas

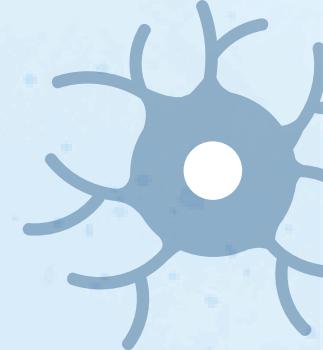
A- Step B1 — Warp the EPI to MNI space

- Applies forward deformation (y_*) to the 4D EPI using high-order B-spline interpolation
- Output:
 - wEPI.nii — the functional image in MNI space.
- Simultaneously, T1 is also warped to MNI and resliced onto the same wEPI grid for perfect overlay and QC.
- Ensures only one interpolation step for EPI to minimize blur

B- Step B2 — Project the Harvard–Oxford Atlas

- Uses SPM's Coreg: Write to reslice the Harvard–Oxford atlas onto the exact voxel grid of the warped EPI.
- Interpolation: Nearest Neighbor (NN) to preserve integer parcel labels.
- Output:
 - rHarvardOxford.nii — the atlas perfectly aligned to EPI space.
- Now every EPI voxel corresponds to a specific anatomical parcel label.

07 - Time-Series Extraction and ROI FC



Goal of this Stage

A- Rationale:

To summarize the BOLD signal within each anatomical region (ROI) defined by the Harvard–Oxford atlas, then compute functional connectivity between regions.

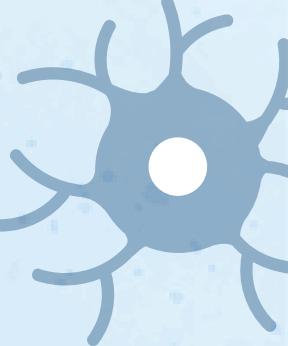
B- Pipeline Concept:

- Extract ROI-wise mean time series from the MNI-aligned EPI (using the resliced HO atlas).
- Standardize (z-score) each ROI's time series across time.
- Compute correlation matrix between all ROI pairs → functional connectivity (FC).
- Identify strongly correlated ROI pairs using statistical thresholds.

C- Purpose:

Convert high-dimensional voxel-wise data into region-wise interactions, revealing how brain regions fluctuate together during rest or task.

07 - Time-Series Extraction and ROI FC



Time-Series Extraction

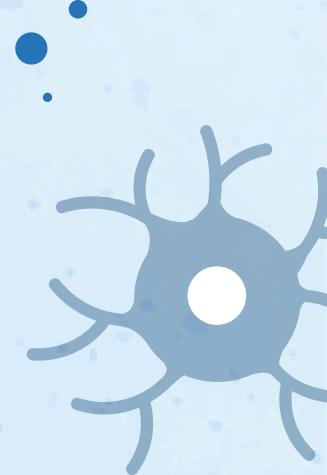
A- How:

1. Loads the 4D warped EPI ([X Y Z T]) and the Harvard–Oxford atlas (resliced to EPI grid).
2. For each ROI label:
3. Extracts all voxels belonging to that region.
4. Computes the mean BOLD intensity across those voxels for each timepoint.
5. Produces a $[T \times R]$ matrix, where each column is one region's time series.

B- Key Outputs:

1. **roi_timeseries**: Raw mean time series per ROI
2. **roi_ts_z**: Z-scored version (mean=0, std=1)
3. **roi_labels**: Atlas label IDs
4. **fc_matrix**: ROI \times ROI correlation matrix

07 - Time-Series Extraction and ROI FC

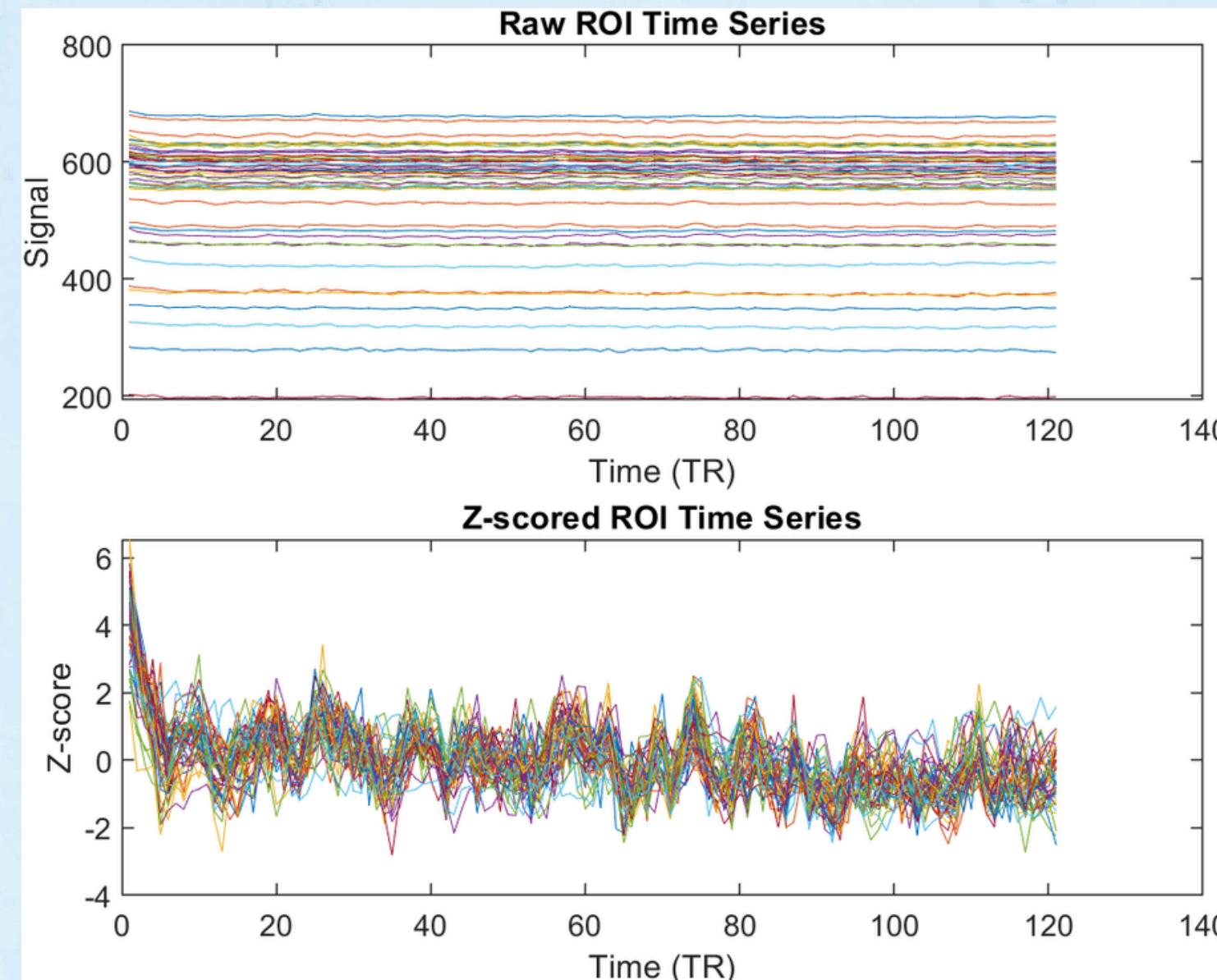


Visualization and Standardization

A- Z-Scoring per ROI:

- Removes baseline amplitude differences.
- Ensures comparability across ROIs and subjects.

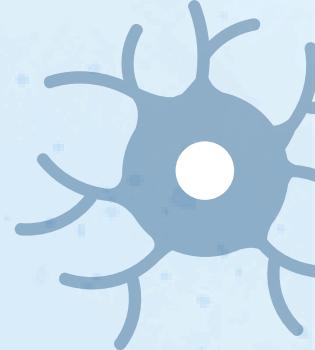
$$z_{t,r} = \frac{x_{t,r} - \mu_r}{\sigma_r}$$



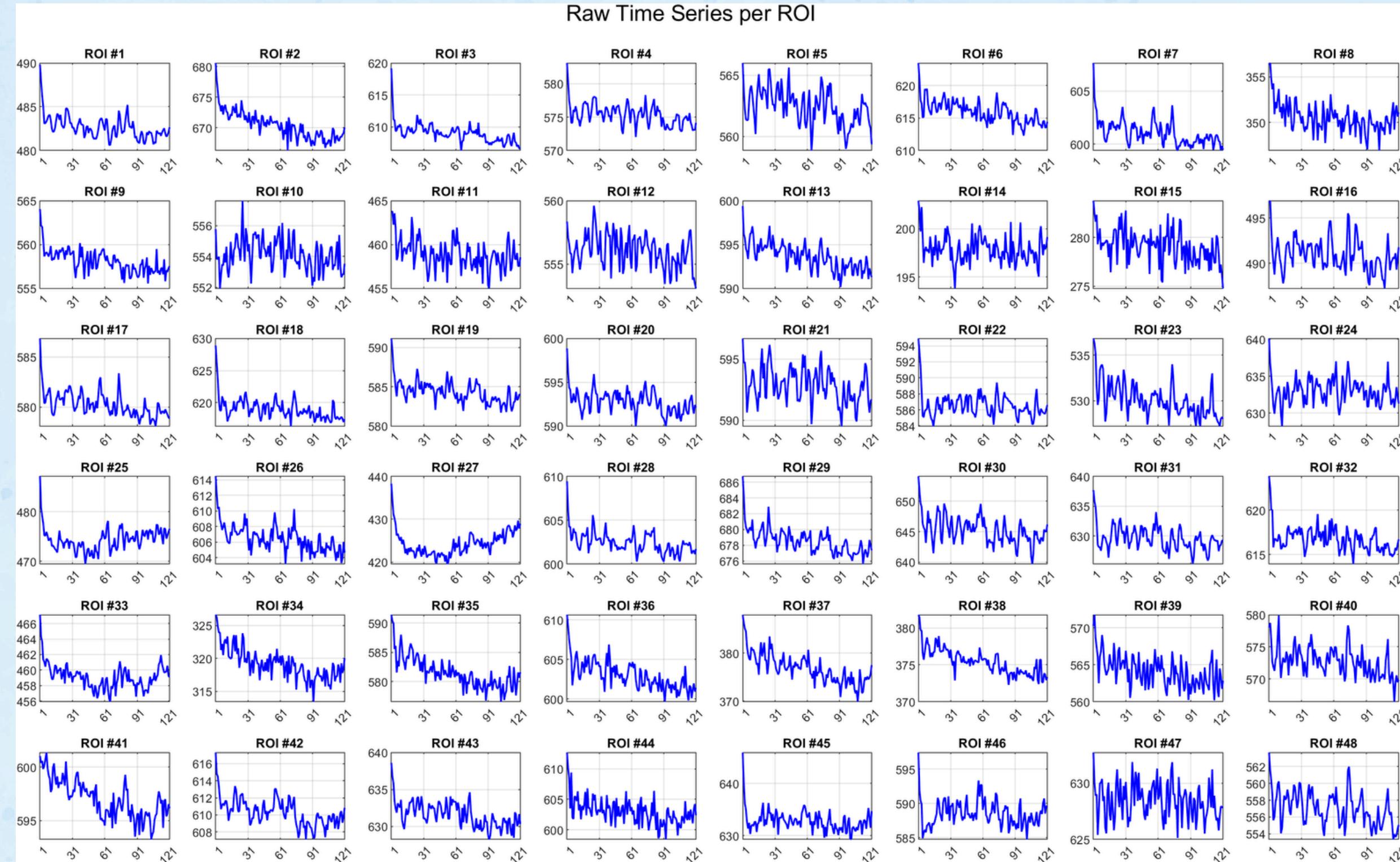
B- QC Outputs:

- Raw timeseries:
 - Each line represents the mean BOLD signal (in raw scanner intensity units) within one Harvard–Oxford ROI across the 121 timepoints (TRs).
- Z-scored timeseries:
 - After z-scoring, amplitude scaling differences are removed, leaving only relative temporal fluctuations. This makes the signals suitable for FC computation because correlation is sensitive to shared temporal structure.

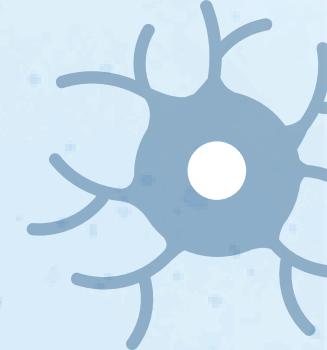
07 - Time-Series Extraction and ROI FC



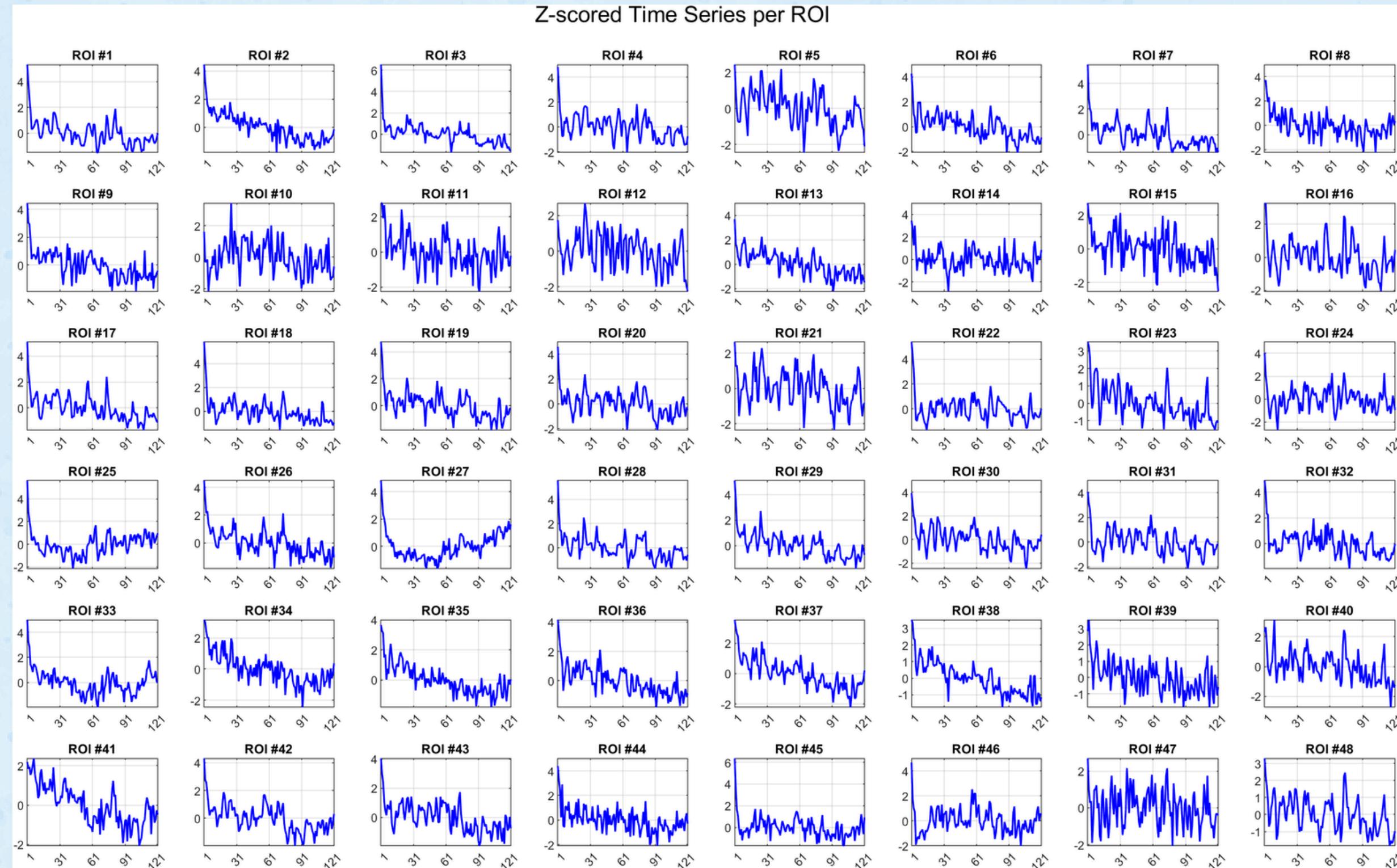
Visualization of Raw Timeseries per ROI



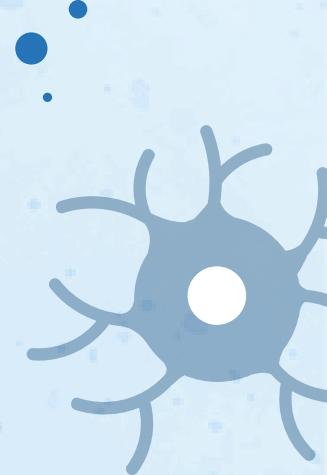
07 - Time-Series Extraction and ROI FC



Visualization of Z-scored Timeseries per ROI

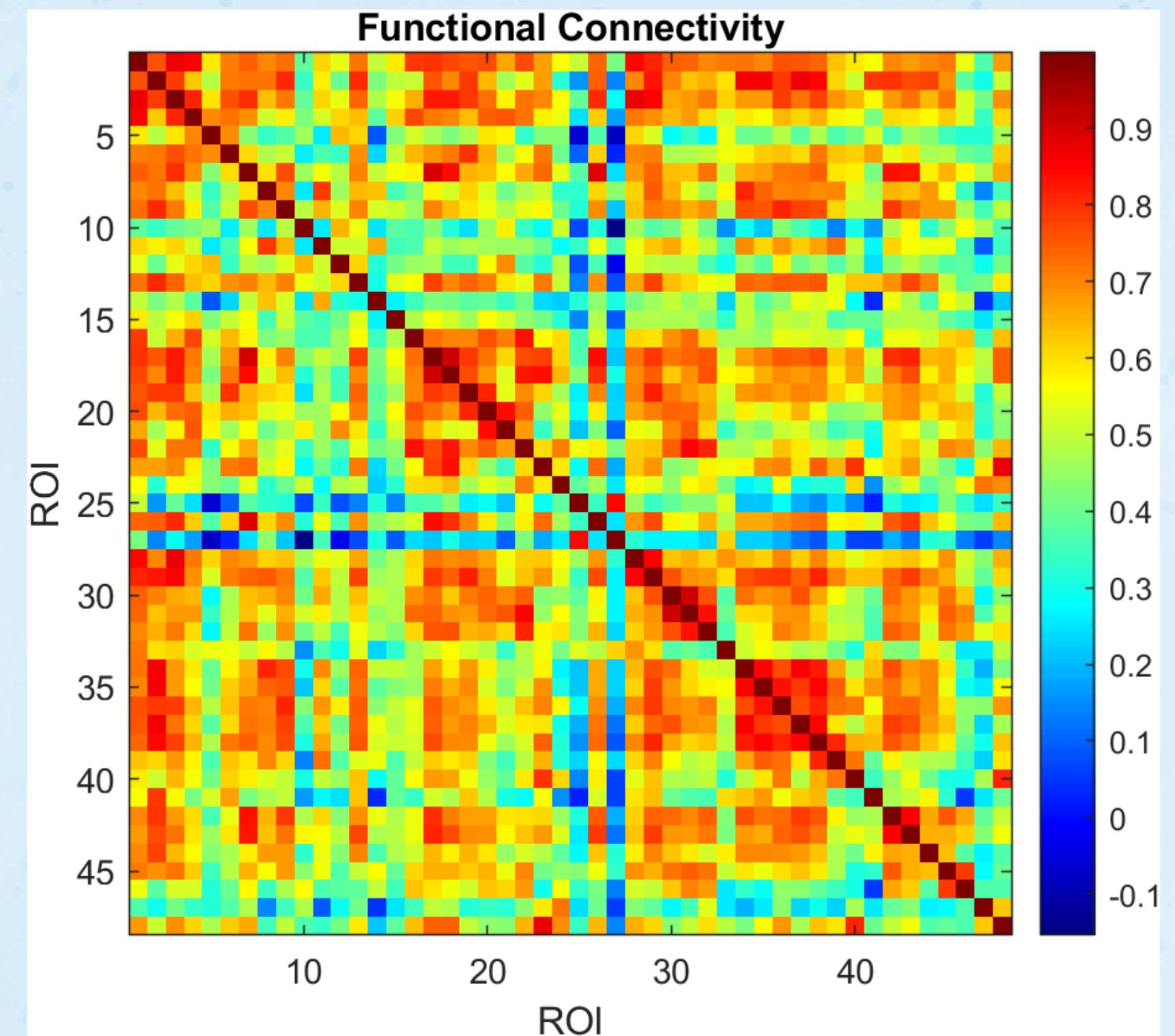


07 - Time-Series Extraction and ROI FC

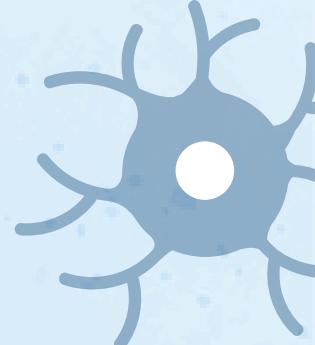


Visualization of FC Matrix

- Each cell shows the temporal correlation between the z-scored mean BOLD signals of two regions (Harvard–Oxford atlas).
- The symmetric structure and clustered red blocks indicate coherent functional subnetworks, reflecting intrinsic coordination between cortical and subcortical regions during rest.



07 - Time-Series Extraction and ROI FC



Identifying Strong ROI-ROI Connection

A- What it does:

1. Reads the **FC matrix** and **HO XML** (ROI names).
2. Finds ROI pairs whose correlation exceeds a statistical threshold
3. Builds a table of high-FC pairs with labels and correlation values.
4. Optionally saves results as a CSV report.

$$r \geq \text{mean}(r_{\text{offdiag}}) + k_{\text{std}} \cdot \text{std}(r_{\text{offdiag}})$$

B- Output Table Example:

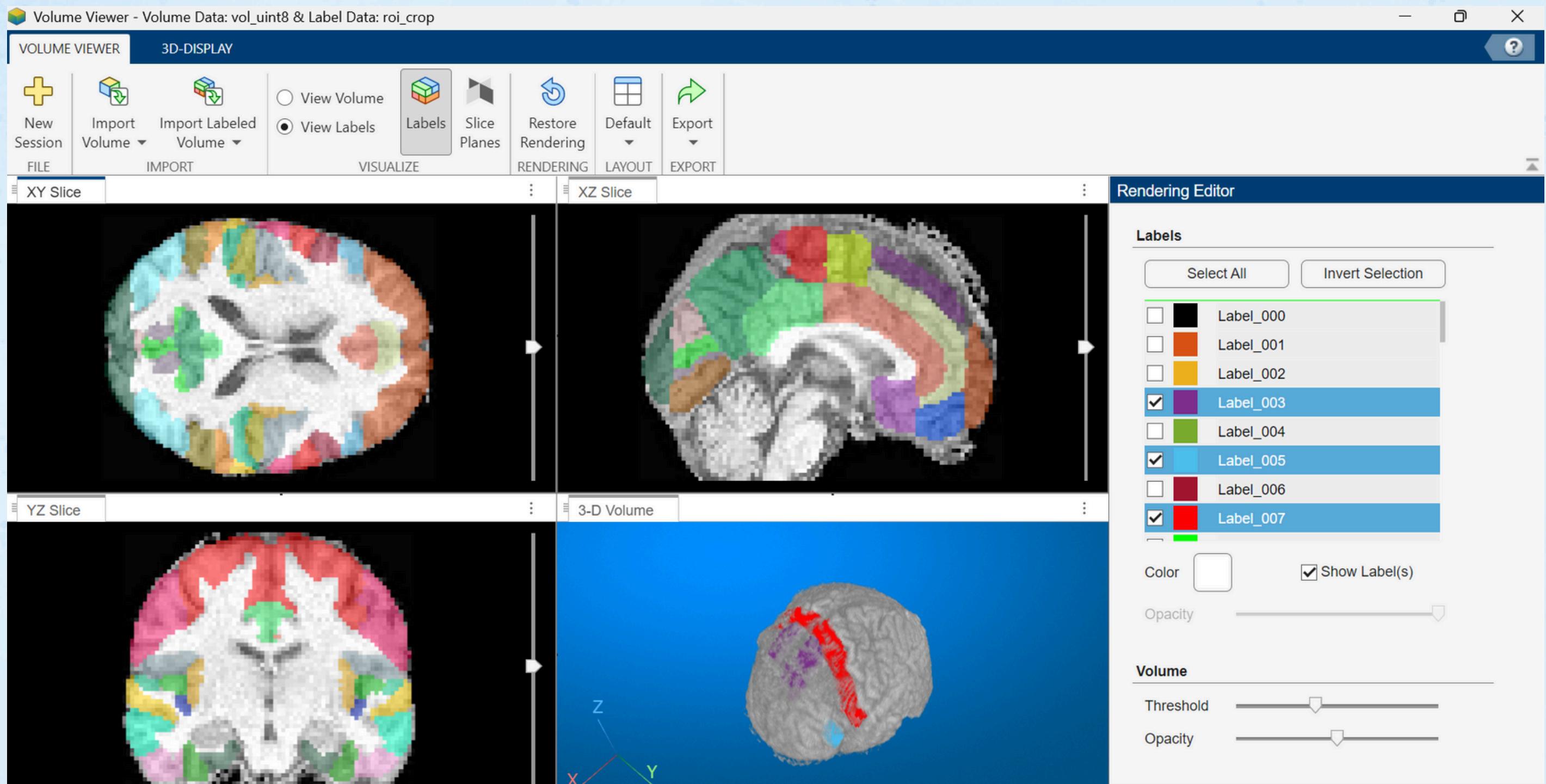
ROI_1	Label_1	ROI_2	Label_2	Correlation
17	Superior Frontal Gyrus	42	Precuneus	0.82

C- Purpose:

- Highlight pairs of brain regions that show strong functional coupling, suggesting network-level communication or co-activation.

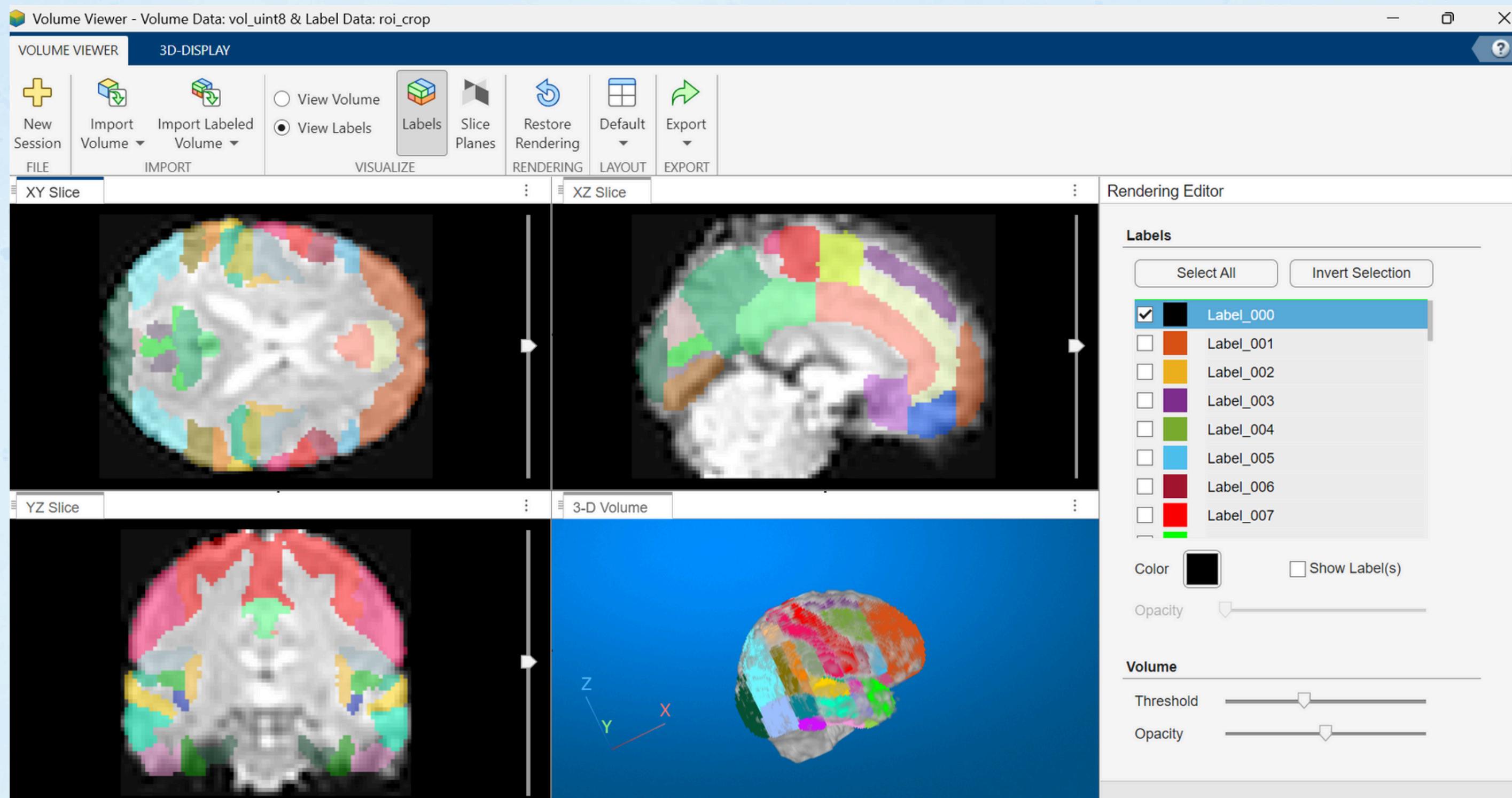
08 - Visualization of the overlaid Atlas on the brain

HO-T1-Underlay



08 - Visualization of the overlaid Atlas on the brain

HO-EPI-Underlay



References

1.Dataset

OpenNeuro. (n.d.). Dataset ds000224: Multi-modal fMRI data. OpenNeuro. Retrieved from [OpenNeuro Dataset Description: https://openneuro.org/datasets/ds000224](https://openneuro.org/datasets/ds000224)

2.Slice Timing Correction (STC)

Sladky, R., Friston, K. J., Tröstl, J., Cunnington, R., Moser, E., & Windischberger, C. (2011). Slice-timing effects and their correction in functional MRI. *NeuroImage*, 58(2), 588–594. <https://doi.org/10.1016/j.neuroimage.2011.06.078>

SPM12 Documentation. (n.d.). Slice timing. Wellcome Centre for Human Neuroimaging. https://www.fil.ion.ucl.ac.uk/spm/docs/wikibooks/Slice_Timing/

SPM12 Tutorial. (n.d.). fMRI preprocessing: Slice timing. Wellcome Centre for Human Neuroimaging. https://www.fil.ion.ucl.ac.uk/spm/docs/tutorials/fmri/preprocessing/slice_timing/

3.Realignment

Roche A. (2011). A four-dimensional registration algorithm with application to joint correction of motion and slice timing in fMRI. *IEEE transactions on medical imaging*, 30(8), 1546–1554. <https://doi.org/10.1109/TMI.2011.2131152>

References

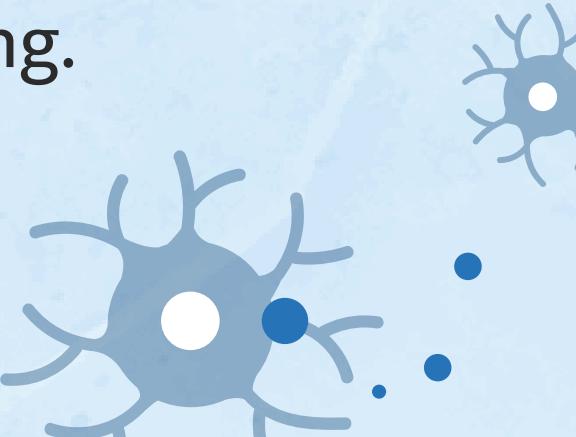
Andy's Brain Book. (n.d.). SPM: Realign & Unwarp. Retrieved from https://andysbrainbook.readthedocs.io/en/latest/SPM/SPM_Short_Course/SPM_04_Preprocessing/01_SPM_Realign_Unwarp.html

SPM12 Manual. (2014). Statistical Parametric Mapping: The Analysis of Functional Brain Images. Wellcome Centre for Human Neuroimaging. https://www.fil.ion.ucl.ac.uk/spm/doc/spm12_manual.pdf

Mikl, M., Marecek, R., Hlustík, P., Pavlicová, M., Drastich, A., Chlebus, P., Brázdil, M., & Krupa, P. (2008). Effects of spatial smoothing on fMRI group inferences. Magnetic resonance imaging, 26(4), 490–503.
<https://doi.org/10.1016/j.mri.2007.08.006>

4. Skull Stripping

SPM12 Tutorial. (n.d.). Segmentation and normalization. Wellcome Centre for Human Neuroimaging. https://www.fil.ion.ucl.ac.uk/spm/docs/tutorials/fmri_preprocessing/segmentation/



References

5.Coregistration of T1 to EPI

Pluim, J. P. W., Maintz, J. B. A., & Viergever, M. A. (2003). Mutual-information-based registration of medical images: A survey. *IEEE Transactions on Medical Imaging*, 22(8), 986-1004. <https://doi.org/10.1109/TMI.2003.815867>

Ashburner, J., & Friston, K. J. (1997). Multimodal image coregistration and partitioning—a unified framework. *NeuroImage*, 6(3), 209–217. <https://sci-hub.st/https://doi.org/10.1006/nimg.1997.0290>

6.Timeseries and FC

Biswal, B., Yetkin, F. Z., Haughton, V. M., & Hyde, J. S. (1995). Functional connectivity in the motor cortex of resting human brain using echo-planar MRI. *Magnetic Resonance in Medicine*, 34(4), 537-541. <https://sci-hub.st/https://doi.org/10.1002/mrm.1910340409>

Brkić, D., Sommariva, S., Schuler, A.-L., Pascarella, A., Belardinelli, P., Isabella, S. L., Di Pino, G., Zago, S., Ferrazzi, G., Rasero, J., Arcara, G., Marinazzo, D., & Pellegrino, G. (2023). The impact of ROI extraction method for MEG connectivity estimation: Practical recommendations for the study of resting state data. *NeuroImage*, 284, Article 120424. <https://www.sciencedirect.com/science/article/pii/S105381192300575X?via%3Dihub>

References

7. General References (Applicable to the Entire Pipeline)

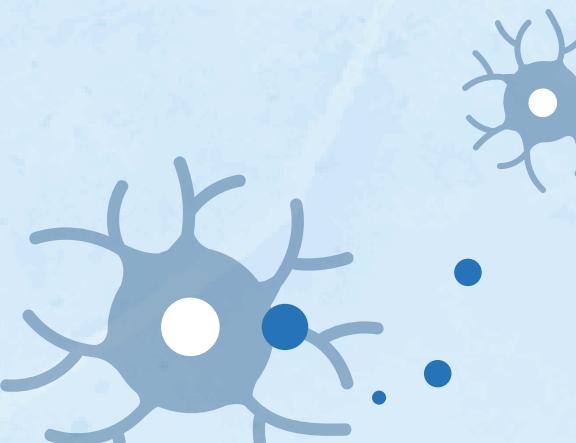
(2022). The role of the arousal system in age-related differences in cortical functional network architecture. [Manuscript on ResearchGate]. Retrieved from
https://www.researchgate.net/publication/355762769_The_role_of_the_arousal_system_in_age-related_differences_in_cortical_functional_network_architecture

Orlichenko, A., Su, K.-J., Shen, H., Deng, H.-W., & Wang, Y.-P. (2024). Somatomotor-Visual resting state functional connectivity increases after two years in the UK Biobank longitudinal cohort. Journal of Medical Imaging (Bellingham), 11(2), 024010. <https://doi.org/10.1117/1.JMI.11.2.024010> [SPIE Digital Library+1](#)

(2017). *NeuroImage: Clinical*, 14, [Article-ID]. <https://doi.org/10.1016/j.nicl.2017.05.001>

Ashburner, J., & Friston, K. J. (2004). Unified segmentation. *NeuroImage*, 22(3), 839-851.
<https://doi.org/10.1016/j.neuroimage.2004.07.051>

Sporns, O. (2010). Networks of the brain. *Nature Reviews Neuroscience*, 10(6), 463-474.
<https://doi.org/10.1038/nrn756>



References

Penny, W., Friston, K., Ashburner, J., Kiebel, S., & Nichols, T. (n.d.). SPM: Statistical Parametric Mapping – Installation guide [Software documentation]. University College London.
<https://www.fil.ion.ucl.ac.uk/spm/docs/installation/>

Radiopaedia. (n.d.). Multiplanar reformation (MPR). In Radiopaedia.org. Retrieved [date you accessed] from <https://radiopaedia.org/articles/multiplanar-reformation-mpr?lang=us>

Zhang, X., Ying, X., & Toga, A. W. (2022). Human Brain Mapping. Advance online publication.
<https://doi.org/10.1002/hbm.25841>

Ashburner, J., & Friston, K. J. (2010). Voxel-based morphometry — The methods. *NeuroImage*, 53(2), 936-940.
<https://doi.org/10.1016/j.neuroimage.2010.08.063>

Gordon, E. M., Laumann, T. O., Adeyemo, B., Huckins, J. F., Kelley, W. M., & Petersen, S. E. (2017). Precision functional mapping of individual human brains. *Neuron*, 95(4), 791-807.e7.
<https://doi.org/10.1016/j.neuron.2017.07.011>

References

Finn, E. S., Shen, X., Scheinost, D., Rosenberg, M. D., Huang, J., Chun, M. M., Papademetris, X., & Constable, R. T. (2015). Functional connectome fingerprinting: identifying individuals using patterns of brain connectivity. *Nature neuroscience*, 18(11), 1664–1671. <https://doi.org/10.1038/nn.4135>

Local-global parcellation of the human cerebral cortex from intrinsic functional connectivity MRI | Cerebral Cortex | Oxford academic. (n.d.-a). <https://academic.oup.com/cercor/article/28/9/3095/3978804>

THANKS!

Do you have any questions?
7200337@studenti.unige.it

