**Supplemental Material**

# **fMRI Methods**

## Data acquisition

Acquisition sequences alternated between phase encoding in an anterior-posterior (AP) direction in one run, and phase encoding in a posterior-anterior (PA) direction in another run for every participant. This was performed to reduce the signal loss and distortions from the high-resolution multiband acquisition. Split slice-GRAPPA (leak block) reconstruction algorithm was applied to correct for potential signal leakage during slice separation (unaliasing) to recover the whole brain volume (Risk et al., 2018). The order of run presentation was counterbalanced across participants.

## Preprocessing

Images were first converted from DICOM to BIDS format. The first 17 scans (~ 12 secs) of every encoding and retrieval run were discarded to ensure that images have reached steady-state magnetization. Scan images were preprocessed using fMRIPrep 20.2.7 (Esteban et al., 2019), which is based on Nipype 1.7.0 (Gorgolewski et al., 2018) and implements tools from various software packages including Advanced Normalization Tools version 2.3.3 (ANTs), FMRIB Software Library version 5.0.9 (FSL), and FreeSurfer 6.0.1. The creators of the fMRIPrep 20.2.7 software recommend reporting the preprocessing steps using their generated boilerplate. Below is an edited version of these steps that were simplified for clarity purposes.

### ***Anatomical data preprocessing***

The T1-weighted (T1w) images were corrected for intensity non-uniformity and skull-stripped using ANTs via Nipype(Avants et al., 2008; Tustison et al., 2010). Brain tissue segmentation of cerebrospinal fluid (CSF), white-matter (WM) and gray-matter (GM) was performed on the brain-extracted T1w using FSL (Zhang et al., 2001). Brain surfaces were reconstructed via FreeSurfer (Dale et al., 1999), and the brain masks estimated previously were refined with a custom variation of the method to reconcile ANTs-derived and FreeSurfer-derived segmentations of the cortical gray-matter (Klein et al., 2017). Finally, the T1w were spatially normalized to the MNI 152 template (Nonlinear Asymmetrical template version 2009c, MNI152NLin2009cAsym; Fonov et al., 2009) using ANTs.

### ***Functional data preprocessing***

Reference image estimation: For each of the 8 BOLD runs found per subject (4 encoding runs and 4 retrieval runs), a reference volume and its skull-stripped version were generated by aligning and averaging 1 single-band references (SBRefs). Susceptibility distortion correction: A B0-nonuniformity map (or fieldmap) was estimated and co-registered to a corrected target EPI (echo-planar imaging) reference run and converted to a displacements field map with FSL. Co-registration: The BOLD reference was co-registered to the T1w reference with six degrees of freedom using FreeSurfer’s bbregister function (Greve & Fischl, 2009). Motion correction: Head-motion parameters with respect to the BOLD reference (transformation matrices, and six corresponding rotation and translation parameters) were estimated using FSL’s mcflirt function (Jenkinson et al., 2002). Normalization: The co-registered BOLD time-series were then resampled into standard space, generating a preprocessed BOLD run in MNI152NLin2009cAsym space. Confound estimations: Based on the preprocessed BOLD, the confounding time-series of framewise displacement (FD) and three region-wise global signals were calculated (Jenkinson et al., 2002; Power et al., 2014).

### ***Additional preprocessing steps***

Additional preprocessing steps were carried out using custom code in Python 3.0 and Nilearn libraries (Abraham et al., 2014). The normalized scans from fMRIprep were scrubbed for motion artefacts (if there were one or two consecutive volumes that exceeded 1mm movement, the volume was replaced by the average of the previous and the subsequent volume in time). The scans were then smoothed using a Gaussian filter (FWHM=6mm). Finally, confounds such as white matter, CSF and 6 motion parameters were regressed out from all the runs.

Our high-resolution, fast TR multiband sampling sequence reduces the need for slice timing correction since slices within each volume were acquired much closer together than in a typical fMRI acquisition sequence (TR ~ 2.5 secs). As such, no slice timing correction was employed in the current study. Due to unforeseen circumstances, four participants from the final sample size did not complete all four runs of the AET. Due to time constraints, one participant only completed three runs. Due to an error in the order of run presentation, two runs out of four were excluded for two participants. Finally, due to a technical issue with the scanner halfway through the experiment, the last participant only completed two runs.

## fMRI GLM analysis with parametric modulation

### ***Matrix design***

For each subject, we constructed a design matrix for classical contrast analysis and parametric modulation analysis, in which trial onsets for each of the following conditions were modeled with a separate regressor:

1. Encoding with RT: encoding trials for which a RT was provided before (pre-stimulus RT) *and* after (post-stimulus RT) the trial presentation.
2. Encoding without RT: encoding trials that are not included in the encoding-with-RT condition.
3. Retrieval old: retrieval trials where objects previously shown at encoding were presented.
4. Retrieval new: retrieval trials where new objects were presented.
5. Retrieval no response: retrieval trials where the participant didn’t provide a response.

Post-stimulus RTs were entered as a separate parametric modulator for the *Encoding with RT* trial onsets regressor. In order to make the parametric modulator orthogonal to the regressor it is modulating, post-stimulus RT values were mean-centered, as recommended by Mumford and colleagues (2015). Since the orthogonalization was already satisfied, the default option of orthogonalize modulations was set to “No” when specifying the first-level analysis in SPM (option available from SPM 9 and earlier versions).

## fMRI GLM analysis for subsequent memory effects

### ***Matrix design***

For each subject, we computed a second GLM regression analysis where 8 regressors were modeled and convolved with the SPM canonical hemodynamic response function and its temporal derivative. The regressors were coded as follows:

1. Encoding source hit: encoding trials associated with subsequent source hits.
2. Encoding source failure: encoding trials associated with subsequent source failure (i.e., collapsing item memory, context misattribution, and misses responses).
3. Encoding no response: encoding trials for which the participants didn’t provide a RT to the expanding cross.
4. Retrieval source hit: retrieval trials associated with source hits.
5. Retrieval source failure: retrieval trials associated with source failure (i.e., collapsing item memory, context misattribution, and misses response).
6. Retrieval false alarms: retrieval trials associated with false alarms responses.
7. Retrieval correct rejection: retrieval trials associated with correct rejections.
8. Retrieval no response: retrieval trials with no associated response.

# **Results**

## fMRI Results

**Table S1**

*Brain encoding-related activations and deactivations*

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Cluster Level | | Peak Level | | | MNI coordinates | | |
| Region | *k* | p(FDR-corr) | p(FDR-corr) | *T* value | Peak BA | *x* | *y* | *z* |
|  | | | | |  |  |  |  |
| Encoding activations | | | | |  |  |  |  |
| R middle occipital gyrus (extending to L lingual gyrus) | 5931 | <.001 | <.001 | 15.82 | 18, 19 | 32 | -88 | 18 |
| L precentral gyrus (extending to L middle frontal gyrus) | 191 | <.001 | .007 | 5.55 | 6, 46 | -42 | 6 | 32 |
|  |  |  |  |  |  |  |  |  |
| Encoding deactivations |  |  |  |  |  |  |  |  |
| L medial frontal gyrus (extending to L superior temporal gyrus and R insula) | 9150 | <.001 | <.001 | 11.75 | 6, 13 | -4 | -6 | 56 |
| R precuneus (extending to bilateral cuneus) | 570 | <.001 | <.001 | 11.20 | 7, 31 | 12 | -52 | 36 |
| L superior/middle frontal gyrus | 322 | <.001 | .001 | 6.30 | 8, 9 | -40 | 44 | 24 |
|  |  |  |  |  |  |  |  |  |

*Note*. R = right hemisphere, L = left hemisphere, *k* = number of voxels, MNI = Montreal Neurological Institute, BA = Brodmann area.

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