**SPM12 Guide to fMRI Data Analysis**

*Preprocessing & First-Level Univariate Modeling*  
*Applicable to standard fMRI experiments using SPM12*

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**1. Data Structure & Preparation**

Before preprocessing, organize your raw data as follows:

/sub-01/

/anat/ → anatomical T1-weighted scan

/func/ → EPI runs (e.g., run1–run4)

/fmap/ → optional fieldmap images

Typical data types include:

* **DICOM files** (raw scanner output)
* **Fieldmaps** (phase + magnitude images)
* **BOLD runs** (multiple sessions)
* **Anatomy** (T1 image)

**2. DICOM Conversion**

1. Open MATLAB → enter: spm fmri
2. Open the **Batch Editor**  
   → Use the **"DICOM Import"** module  
   → Output: NIfTI files (e.g., f\*.nii, s\*.nii)
3. Group and rename files by scan type:
   * Functional runs (f\*.nii)
   * Structural image (s\*.nii)
   * Fieldmaps (magnitude & phase images)
4. Discard dummy scans:
   * Remove first N volumes (e.g., 5 volumes) per run
   * These are unstable scanner signals not used in analysis

**3. Fieldmap Correction *(optional)***

1. Open the **Fieldmap Toolbox** in SPM
2. Load:
   * **Phase image** (TE2 – TE1)
   * **Magnitude image** (use shorter TE for better SNR)
3. Enter required metadata:
   * **TE1 / TE2** (e.g., 4.89ms, 7.35ms)
   * **Total EPI readout time**: e.g., 64 × 0.42ms = 26.88ms
4. Load the first EPI volume from the run the fieldmap applies to
5. Click “Calculate” → “Write”

Output: vdm5\_\*.nii = voxel displacement map used for unwarping

Repeat this process for each fieldmap-to-run pair if needed.

**4. Preprocessing (via SPM Batch)**

**a. Realign & Unwarp**

* **Input:** All EPI images (each run as one session)
* **Fieldmap (VDM):** Add corresponding vdm5\_\* file per session
* **Output:** u\*.nii, mean\*.nii

**b. Slice Timing Correction**

* Number of slices (e.g., 32)
* TR (e.g., 2s)
* TA = TR – (TR / #slices)
* Slice order: e.g., descending [32 31 30 … 1]
* Reference slice = middle slice
* **Output:** au\*.nii

**c. Coregistration**

* **Reference:** mean EPI (mean\*.nii)
* **Source:** structural (T1) image
* Aligns structural and functional spaces

**d. Segmentation**

* Segments T1 image into GM, WM, CSF
* Generates normalization parameters
* **Output:** y\_\*.nii, native-space tissue maps

**e. Normalization**

* Applies warps from segmentation to functional data
* **Voxel size:** [3 3 3]
* **Output:** wau\*.nii

**f. Smoothing**

* Input: normalized functional images
* Kernel: FWHM = [8 8 8] mm
* **Output:** swau\*.nii

**5. First-Level Analysis (GLM)**

**a. Specify the Design Matrix**

* Define condition names, onsets, durations
* Optional: parametric modulators (pmod)
* Include 6 motion regressors as nuisance covariates

**Example design specification:**

names = {'delay', 'encoding', 'retrieval', 'feedback'};

onsets = {...}; % vectors of onset times

durations = {[4], [0], [6.5], [0]};

pmod(1).name{1} = 'load';

pmod(1).param{1} = load\_vec;

pmod(1).poly{1} = 1; % linear modulation

**b. Model Estimation**

* Use SPM’s **Model Estimation** module
* Input: SPM.mat, preprocessed time series, and onset file

**6. Define Contrasts**

Specify contrast vectors to test hypotheses:

| **Contrast** | **Description** | **Weights (example)** |
| --- | --- | --- |
| Del-Zero | Delay activation | 1 0 0 0 |
| Del-Load+ | Positive load modulation | 0 1 0 0 |
| Enc-Zero | Encoding | 0 0 1 0 |
| Ret-Zero | Retrieval | 0 0 0 1 |

Set contrasts via the **Contrast Manager** in SPM.

**7. Second-Level Analysis**

If you have multiple subjects:

* Collect first-level contrast images (e.g., con\_0001.nii)
* Set up a **one-sample t-test** for each contrast of interest
* Model inter-subject variance → interpret at the group level

**Best Practices & Tips**

| **Topic** | **Recommendation** |
| --- | --- |
| Folder structure | Organize by raw/, preproc/, firstlevel/, etc. |
| Documentation | Record TR, slice order, onset definitions, etc. clearly |
| Debugging | Visually inspect: alignment, normalization, design matrix |
| Reproducibility | Use batch jobs or MATLAB scripts rather than only GUI |
| Fieldmap use | Ensure TE and readout time are correct; apply per session |