SPM 12
Welcome to SPM12

Please refer to this version as "SPM12" in papers and communications.

The SPM12 Manual and Release Notes are available as PDF documents in the main directory of your SPM installation.

Updates will be made available from time to time and advertised on the SPM mailing list. You can also check for updates by clicking here.

We would love to hear your comments or bug reports - please contact us at <info@fil.ion.ucl.ac.uk>.

SPM is developed under the auspices of the Functional Imaging Laboratory (FIL), the Wellcome Trust Centre for Neuroimaging (WTCN), in the Institute of Neurology at University College London (UCL), UK.

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Pre-processing
Analysis
Pre-processing:
- Realignment
- Coregistration
- Slice timing
- Normalization
- Smooth
- Segmentation
Realignement: Goals

Why?
- Motion correction can (will) reduce noise.
- Movement possibly correlated with task.

Realignement:
- Match images of same modality
- Minimize cost-function: sum of squared difference
- Determine optimal rigid body transformation
Coregistration: Goals

Registration between modalities

Why?
1. Use high-resolution T1 for localization
2. Use high-resolution T1 for normalization
3. Many other operations

Coregistration:
1. Matches images of different modality
2. Again uses 6 parameter rigid body transformation (mostly)
3. Needs different cost function
Slice-timing correction

Why correct for slice timing?
• Correct for slice acquisition time differences

When not?
• Fast acquisition (e.g., multiband EPI, TR<1)
• 3D acquisition (e.g., 3D EPI, PRESTO)
• Slow block designs
Spatial normalization

Why?
• When studying more than one individual.
• Report coordinates in standard stereotactic space.

How?
• Transform / warp images to match functionally homologous regions from the different subjects
• Put all individuals in a standard space, e.g., Talairach or MNI (used in SPM)

Problems:
• No exact match between structure and function.
• Computational problems (e.g., local minima)
Smoothing

Why smooth?
- Potentially increase signal to noise (also in single subject)
- Inter-subject averaging (structure-function differences)

How?
- Smoothing is done using convolution with a Gaussian kernel (in SPM)
- Kernel defined in terms of FWHM (full width at half maximum)
Analysis
The design matrix defines the experimental design and the nature of hypothesis testing to be implemented. The design matrix has one row for each scan and one column for each effect or explanatory variable, e.g., regressor or stimulus function.

This allows you to build design matrices with separable session-specific partitions. Each partition may be the same-in which case it is only necessary to specify it once or different. Responses can be either event- or epoch-related, where the latter model involves prolonged and possibly time-varying responses to
SPM +
Segmentation
ROI analysis – Marsbar 2.0
xjView, MRIcron
Scripts using SPM batch