SPM5 – New Features

EEG/MEG analysis

A major new feature of SPM5 is the functionality to analyze epoched EEG and MEG data. This functionality can be divided into two components: (i) preprocessing and (ii) statistical analysis. Preprocessing contains the usual steps; *e.g.* epoching, filtering, artifact detection, time-frequency decomposition and averaging. After preprocessing, the data is projected into voxel space. This space can be either the 2D-scalp (interpolation) or 3D-brain space (source density reconstruction – see below). Conversion to voxel-space allows one to use SPM's existing functionality for model specification, parameter estimation and adjusting p-values. In particular, we make use of Random Field Theory to adjust p-values to account for the multiple comparisons over brain space.

Time-frequency EEG/MEG analysis

This combines the time-frequency components of preprocessing for basic EEG/MEG pre-processing with extant Random Field Theory adjusted p-values. In this application the adjustment is for searches over 2D time-frequency domains. There have been suitable extensions for graceful and more general handling of 2D SPMs.

Source localisation

Features will include:

- Co-registration of structural MRI (sMRI) and EEG/MEG
- A forward solution based on the 3 sphere shell model
- Individual forward solutions based on a deformed template mesh of the cortical surface. This is based on a simple spherical forward solution provided by BrainStorm
- Equivalent Current Dipole (ECD) source localisation
- Distributed source localisation using Empirical Bayes with smoothness and/or functional priors.
- Interpolation of the reconstructed source activity into sMRI voxel-space

Spatial normalisation and segmentation

Because of the confusion about "optimized VBM" and "customized templates", there will be a new integrated spatial normalisation and segmentation routine. This enables spatial normalisation of images acquired using a wider range of sequences (so fewer "customized templates" are likely to be needed). More

accurate results can potentially be achieved by combining tissue classification, bias correction and nonlinear warping into the same generative of forward model.

Bayesian fMRI analysis with spatial priors

This analysis method potentially improves the sensitivity of fMRI analysis by spatially regularising signal and noise parameters in the context of a Gaussian Markov Random Field. Smoothing fMRI data an arbitrary amount in a pre-processing stage is no longer required, as the optimal amount of spatial regularisation can be determined automatically and separately for each putative experimental effect.

User interface

There will be a new User-Interface (UI) for the pre-processing steps. Some stats utilities may also have the new UI. The idea is to allow easier batching, and flexibility of the order in which operations are defined. The batch files should serve as documentation about how the data were processed. The user-interface will include explanations of what the various options mean. Most of the code behind SPM2 is just for the user interface. Code for the SPM5 user-interface should be much simpler.

Data formats

Data will be written as NIFTI-1 format instead of Analyze, although the old Analyze format will still be read directly by the various SPM functions. MINC and ECAT7 will no longer be read directly, but will instead need to be converted. Tools will be provided for doing this. For more information on NIFTI-1, see http://nifti.nimh.nih.gov/dfwg/ . The motivation for this is to reduce confusion about whether the images are flipped or not, and increase inter-operability among packages.

DCM for ERPs

DCM for ERPs is a toolbox with a standalone GUI that enables inferences about large scale neural networks, based on epoched ERP data. The user interface allows you to specify the data, experimental design and lead fields (that implicitly specify the sources or nodes of the network). Having specified this information, and the network connectivity, a model is constructed and identified in terms of the conditional distribution of the its parameters using **EM**. In addition, the log-evidence, for that particular model, is returned to facilitate Bayesian model comparison.