

## SPM8 Release Notes

These Release Notes summarize changes made in the latest release of the SPM software, SPM8. This is a major update, containing theoretical, algorithmic, structural and interface enhancements over previous versions. Some of the changes described below were already available in the most recent updates of SPM5, while most of them have been introduced in this new release.

Although we have tried hard to produce high quality software, in a project of this size and complexity there are certainly some remaining bugs. Please assist us by reporting them to the SPM manager <spm@fil.ion.ucl.ac.uk>.

We would like to thank everyone who has provided feedback on the beta version.

### ***Batch interface***

SPM8 incorporates a new batch machinery, `matlabbatch`, that has been derived from the SPM5 batch system. The main new feature is the handling of dependencies: if you have several jobs that you want to execute, where the input to one job depends on the output of another, you can specify that dependency explicitly in the interface. It becomes then straightforward to apply the same operations on several datasets (for example, re-using the same batch for multiple subject analyses).

This batch system is compatible with the previous, SPM5, job structure.

**Matlabbatch:** <http://sourceforge.net/projects/matlabbatch>

### ***File formats***

SPM8 attempts to follow the recommendations of the Data Format Working Group (DFWG: <http://nifti.nih.gov/dfwg/>) that aims at proposing solutions to the problem of multiple data formats used in fMRI research.

- NIfTI-1 is the image file format used in SPM8. See <http://nifti.nih.gov/>
- GIFTI-1 is the geometry file format used to store a variety of surface-based data. See <http://www.nitrc.org/projects/gifti/>

Functions to read/write files with these formats are implemented in the Matlab classes `@nifti` and `@gifti`.

### ***New Segmentation***

This toolbox is an extension of the default unified segmentation. The algorithm is essentially the same as that described in the Unified Segmentation paper (Ashburner and Friston, 2005), except for:

- A different treatment of the mixing proportions,
- The use of an improved registration model,
- The ability to use multi-spectral data,
- An extended set of tissue probability maps, which allows a different treatment of voxels outside the brain,
- A more robust initial affine registration.

Some of the options in the toolbox may not yet work, and it has not yet been seamlessly integrated into the rest of the SPM software. Also, the extended tissue probability maps may need further refinement. The current versions were crudely generated (by JA) using data that was kindly provided by Cynthia Jongen of the Imaging Sciences Institute at Utrecht, NL.

This toolbox can be accessed from the Batch Editor in menu `SPM > Tools > New Segment`.

J. Ashburner and K.J. Friston. **Unified segmentation**. *NeuroImage*, 26:839-851, 2005.

## **DARTEL**

This toolbox is based around the “A Fast Diffeomorphic Registration Algorithm” paper (Ashburner, 2007). The idea is to register images by computing a “flow field” which can then be “exponentiated” to generate both forward and backward deformations.

Processing begins with the “import” step. This involves taking the parameter files produced by the segmentation, and writing out rigidly transformed versions of the tissue class images, such that they are in as close alignment as possible with the tissue probability maps.

The next step is the registration itself. This involves the simultaneous registration of e.g. GM with GM, WM with WM and 1-(GM+WM) with 1-(GM+WM) (when needed, the 1-(GM+WM) class is generated implicitly, so there is no need to include this class yourself). This procedure begins by creating a mean of all the images, which is used as an initial template. Deformations from this template to each of the individual images are computed, and the template is then re-generated by applying the inverses of the deformations to the images and averaging. This procedure is repeated a number of times. Finally, warped versions of the images (or other images that are in alignment with them) can be generated.

This toolbox is not yet seamlessly integrated into the SPM package. Eventually, the plan is to use many of the ideas here as the default strategy for spatial normalisation. The toolbox may change with future updates.

There will also be a number of other (as yet unspecified) extensions, which may include a variable velocity version. Note that the Fast Diffeomorphism paper only describes a sum of squares objective function. The multinomial objective function is an extension, based on a more appropriate model for aligning binary data to a template (Ashburner & Friston, 2009).

J. Ashburner. A **Fast Diffeomorphic Image Registration Algorithm**. *NeuroImage*, 38(1):95-113, 2007.

J. Ashburner and K.J. Friston. **Computing average shaped tissue probability templates**. *NeuroImage*, 45(2):333-341, 2009.

## **Extended hemodynamic model in DCM for fMRI**

The classical model of blood oxygen level dependent (BOLD) responses by Buxton et al. (1998) has been very important in providing a biophysically plausible framework for explaining different aspects of hemodynamic responses. We have derived a generalized model that has been included in SPM8 as part of DCM for fMRI. Bayesian model selection using empirical fMRI data from a group of twelve subjects showed that this model outperforms other variants of hemodynamic models. This extended hemodynamic

model has a non-linear BOLD function and includes a new parameter per region. This parameter,  $\varepsilon$ , represents the region-specific ratio of intra- and extravascular signals and makes DCM more robust for applications to data acquired at higher field strengths.

K.E. Stephan, N. Weiskopf, P.M. Drysdale, P.A. Robinson, K.J. Friston. **Comparing hemodynamic models with DCM.** *NeuroImage* 38: 387-401, 2008.

### ***Nonlinear DCM for fMRI***

In its original formulation, DCM was based on bilinear equations, where the bilinear term models the effect of experimental manipulations on neuronal interactions. The bilinear framework, however, precludes an important aspect of neuronal interactions that has been established with invasive electrophysiological recording studies; *i.e.*, how the connection between two neuronal units is enabled or gated by activity in other units. These gating processes are critical for controlling the gain of neuronal populations and are mediated through interactions between synaptic inputs (e.g. by means of voltage-sensitive ion channels). They represent a key mechanism for various neurobiological processes, including top-down (e.g. attentional) modulation, learning and neuromodulation. We have developed a nonlinear extension of DCM that models such processes (to second order) at the neuronal population level. In this way, the modulation of network interactions can be assigned to an explicit neuronal population.

K.E. Stephan, L. Kasper, L.M. Harrison, J. Daunizeau, H.E.M. den Ouden, M. Breakspear, K.J. Friston. **Nonlinear Dynamic Causal Models for fMRI.** *NeuroImage* 42: 649-662, 2008.

### ***DCM for fMRI: Slice timing***

DCM, in its original inception, was not informed about slice timings of each acquired slice in echo-planar images (EPI) and assumed that all slices were acquired simultaneously. In the first DCM paper (Friston et al., 2003), it has been shown that DCM can cope with slice timing differences of up to 1 s. However, many fMRI studies employ a repetition time (TR) of 3 to 5 s, which precludes a straightforward DCM of these data.

We removed this limitation by including slice timing information into the DCM specification. When entering parameters for a DCM, the user is now asked for the slice timings of each area. In principle, this simple model extension makes it possible to use DCM even on fMRI data acquired with long repetition times and slice-wise acquisition.

K.J. Friston, L. Harrison, and W.D. Penny. **Dynamic Causal Modelling.** *NeuroImage*, 19(4):1273-1302, 2003.

S.J. Kiebel, S. Klöppel, N. Weiskopf, and K.J. Friston. **Dynamic causal modeling: A generative model of slice timing in fMRI.** *NeuroImage*, 34:1487-1496, 2007.

### ***Bayesian Model Selection for Group Studies***

SPM8 includes a new method for performing a random effects analysis of models at the between-subject or group level. This 2nd-level facility is added to all DCM modalities (DCM for fMRI, DCM for ERPs etc.). Bayesian model selection (BMS) is a term given to a procedure which identifies the best model among a set of competing models (*i.e.* the most likely in a set of competing hypotheses). This can be done at the single subject level

by examining each model's log evidence, where the greatest evidence gives the 'winning' model. At the second level however, making inferences across the population requires a random-effects treatment that is not sensitive to outliers and accounts for heterogeneity across the population of subjects studied. To this end, a group BMS procedure has been implemented using a Bayesian approach which provides a probability density on the models themselves. This function uses a novel, hierarchical model which specifies a Dirichlet distribution that, in turn, defines the parameters of a multinomial distribution. By sampling from this distribution for each subject we obtain a posterior Dirichlet distribution that specifies the conditional density of the model probabilities. SPM returns the expected multinomial parameters for the models under test which allows users to rank the models from most to least likely at the population level.

K.E. Stephan, W.D. Penny, J. Daunizeau, R. Moran and K.J. Friston. **Bayesian Model Selection for Group Studies**. In press.

### ***PPMs for Bayesian Model Selection at the group level***

SPM8 includes new routines that allow the construction of Posterior Probability Maps for Bayesian Model Selection (BMS) at the group level. This technique allows neuroimagers to make inferences about regionally specific effects using imaging data from a group of subjects. These effects are characterised using Bayesian model comparisons. These comparisons are analogous to classical inference using F-tests, with the advantage that the models to be compared do not need to be nested, and therefore can be very useful, for example, in comparing computational models of learning and decision-making, for which there may be no natural nesting. Additionally, an arbitrary number of models can be compared together.

The 'BMS Maps' functions receive as input previously estimated log-model evidence maps for each subject and model to be compared. These maps can be obtained, for example, using the first-level Bayesian estimation routines available in the software. These functions then return between-subject Posterior Probability Maps, which are created by applying the new Random Effects approach for inference on model space at the group level in a voxel-wise manner to the log-model evidence data.

Bayesian Model Selection can be implemented and visualised via the user interface (`Stats > Bayesian Model Selection > BMS: Maps` or `BMS: Maps (Results)`).

M. J. Rosa, S. Bestmann, L. Harrison and W. Penny. **Bayesian Model Selection Maps for Group Studies**. Under review.

K.E. Stephan, W. Penny, J. Daunizeau, R. Moran and K. Friston. **Bayesian Model Selection for Group Studies**. In press.

W.D. Penny, G. Flandin, and N. Trujillo-Barreto. **Bayesian Comparison of Spatially Regularised General Linear Models**. *Human Brain Mapping*, 28(4):275–293, 2007.

### ***Graph Laplacian priors for fMRI***

Users of spatial priors for fMRI now have additional flexibility as to which voxels they analyze. Previously, either the full volume or specified slices could be selected, whereas now sub-volumes, e.g. using a mask generated from an effect of interest computed from smoothed data and a standard mass-univariate SPM analysis, can be analyzed. The

options available in “Bayesian 1st-Level”, under “Analysis space” are now; “Volume”, “Slices” or “Clusters”. In addition, after this, the user can choose how these volumes are divided into smaller blocks, which is necessary for computational reasons, c.f. in `spm_spm` a slice is also divided into blocks. These blocks can be either slices (by selecting “Slices”) or 3D segments (“Subvolumes”), whose extent is computed using a graph partitioning algorithm. The latter option means that the spatial prior is truly 3D, instead of 2D spatial priors stacked one on another.

Two additional spatial precision matrices have been included; unweighted graph-Laplacian, ‘UGL’, and weighted graph-Laplacian, ‘WGL’. The priors ‘GMRf’ and ‘LORETA’ are functions of the ‘UGL’, i.e. normalized and squared respectively. The ‘WGL’ empirical prior uses the ordinary least squares estimate of regression coefficients to inform the precision matrix, which has the advantage of preserving edges of activations.

Explicit spatial basis priors (Flandin & Penny 2007) will be included and generalized in the near future, which will include eigenvectors of the graph-Laplacian (see Harrison et al 2007-2008). In general these can be global, i.e. the spatial extent of each basis covers the whole graph, local, or multiscale. The benefit here is in the flexibility to explore ‘natural’ bases that provide a sparse representation of neuronal responses.

G. Flandin & W.D. Penny. **Bayesian fMRI data analysis with sparse spatial basis function priors.** *NeuroImage*, 34:1108-1125, 2007.

L. Harrison, W.D. Penny, J. Daunizeau, and K.J. Friston. **Diffusion-based spatial priors for functional magnetic resonance images.** *NeuroImage*, 41(2):408-423, 2008.

### ***Multivariate Bayes (MVB)***

The MVB facility allows one to compare different hypotheses about the mapping from functional or structural anatomy to perceptual and behavioural consequences. Typical use would be to infer whether a local cortical representation is sparse or distributed. The aim of MVB is not to predict brain states or classify outcomes (because these will be known) but to enable inference on different models of structure–function mappings. This allows one to optimise the model itself and produce predictions that outperform standard pattern classification approaches, like support vector machines.

K.J. Friston, C. Chu, J. Mourão-Miranda, O. Hulme, G. Rees, W.D. Penny, and J. Ashburner. **Bayesian decoding of brain images.** *NeuroImage*, 39(1):181-205, 2008.

### ***Canonical Variates Analysis (Results section)***

This routine allows one to make inferences about effects that are distributed in a multivariate fashion or pattern over voxels. It uses conventional canonical variates (CVA) analysis (also known as canonical correlation analysis, ManCova and linear discriminant analysis). CVA is a complement to MVB, in that the predictor variables remain the design matrix and the response variable is the imaging data in the usual way. However, the multivariate aspect of this model allows one to test for designed effects that are distributed over voxels and thereby increase the sensitivity of the analysis.

Because there is only one test, there is no multiple comparison problem. The results are shown in terms of the maximum intensity projection of the (positive) canonical image or

vector and the canonical variates based on (maximally) correlated mixtures of the explanatory variables and data.

CVA uses the generalised eigenvalue solution to the treatment and residual sum of squares and products of a general linear model. The eigenvalues (i.e., canonical values), after transformation, have a chi-squared distribution and allow one to test the null hypothesis that the mapping is D or more dimensional. This inference is shown as a bar plot of p-values. The first p-value is formally identical to that obtained using Wilks' Lambda and tests for the significance of any mapping.

This routine uses the current contrast to define the subspace of interest and treats the remaining design as uninteresting. Conventional results for the canonical values are used after the data (and design matrix) have been whitened; using the appropriate ReML estimate of non-sphericity.

CVA can be used to for decoding because the model employed by CVA design not care about the direction of the mapping (hence canonical correlation analysis). However, one cannot test for mappings between nonlinear mixtures of regional activity and some experimental variable (this is what MVB was introduced for).

K.J. Friston, C.D. Frith, R.S. Frackowiak and R. Turner. **Characterizing dynamic brain responses with fMRI: a multivariate approach.** *NeuroImage*, 2(2):166-172, 1995.

K.J. Friston, K.M. Stephan, J.D. Heather, C.D. Frith, A.A Ioannides, L.C. Liu, M.D. Rugg, J. Vieth, H. Keber, K. Hunter, R.S. Frackowiak. **A multivariate analysis of evoked responses in EEG and MEG data.** *NeuroImage*, 3(3 Pt 1):167-174, 1996.

### ***Topological False Discovery Rate (FDR)***

FDR control is an alternative to the more conservative “family-wise error” control for multiple comparisons. Historically, SPM has aimed to control FDR on voxels (the expected fraction of false-positive/total-positive decisions made about individual voxels in an image). This is now superseded by FDR control of topological properties of the signal (i.e. control of properties that pertain to the spatial organization of activations - e.g. height and extent - and are not reducible to individual voxels). SPM is now able to identify significantly voluminous blobs according to a decision procedure that controls spatial-extent FDR. Thus, on average, the fraction of blobs falsely deemed to have significant spatial extent is controlled beneath say  $5/100 = .05$  or  $1/100 = .01$ . More recent work is examining FDR control over local maxima.

J. Chumbley and K.J. Friston. **False discovery rate revisited: FDR and topological inference using Gaussian random fields.** *Neuroimage*, 44:62-70, 2009.

J. Chumbley, K.J. Worsley, G. Flandin and K.J. Friston. **Topological FDR for NeuroImaging.** Under review.

### ***Changes to Smoothness Estimation***

The spatial smoothness estimation in SPM5 (`spm_est_smoothness.m`) normalised the residual data (residual gradients were divided by standard deviation, instead of gradients being computed on standardized residuals). Image data that has fairly homogeneous variance will show little difference in the estimated smoothness, but data with highly structured variance images (e.g. VBM data) may give noticeably different estimated smoothness and, as a result, corrected p-values. This change will generally

increase the estimated smoothness (i.e. smoothness was previously underestimated) and RESEL count will decrease. All other things equal, larger FWHM smoothness results in increased voxel-level corrected significance; larger FWHM decreases *uncorrected* cluster-level significance, but smaller RESEL count may counter this effect in terms of corrected significance.

K.J. Worsley. **An unbiased estimator for the roughness of a multivariate Gaussian random field.** *Technical Report, Department of Mathematics and Statistics, McGill University, 1996.*

S.J. Kiebel, J.B. Poline, K.J. Friston, A.P. Holmes and K.J. Worsley. **Robust smoothness estimation in Statistical Parametric Maps using standardized residuals from the General Linear Model.** *NeuroImage*, 10:756-766, 1999.

S. Hayasaka, K. Phan, I. Liberzon, K.J. Worsley, T.E. Nichols. **Nonstationary cluster-size inference with random field and permutation methods.** *NeuroImage*, 22:676-687, 2004.

## **SPM for M/EEG**

In SPM for M/EEG, there are several major changes from SPM5 to SPM8.

First, we changed the internal M/EEG format of SPM in many ways to make reading/writing and manipulating M/EEG data more robust and straightforward for the user. Effectively, we invested a lot of effort into rebuilding almost from scratch the ‘SPM for EEG’ machinery.

Second, there are now three ways of implementing M/EEG analyses in SPM. These are the graphical user interface, SPM8 batch and MATLAB scripting. The batch and scripting facilities come in handy for multi-subject studies. As in fMRI analysis, many processing steps are repetitive and it is now quite straightforward to automatize the software to a high degree.

Third, we now have a collaboration with the Fieldtrip software developers from the Donders Institute for Brain, Cognition and Behaviour, Centre for Cognitive Neuroimaging. Fieldtrip and SPM are pooling resources for converting data from the native format to our software. We also share code for M/EEG forward modelling, and other functions. A full version of Fieldtrip is included with SPM8 and Fieldtrip code is updated with every SPM update. It is now possible to convert M/EEG data, within SPM8, from SPM to Fieldtrip representation, and back. This powerful feature makes it possible to use, within SPM, many Fieldtrip functions. For example, it is quite straightforward, using a script, to work within SPM, and use Fieldtrip functions to do different aspects of the preprocessing, time-frequency analysis and source analysis. This extends SPM8 functionality to a high degree.

SPM8 now uses ‘*forwinv*’ toolbox originally developed for Fieldtrip to create M/EEG head models. Unlike in SPM5, the same head models are used for imaging source reconstruction and DCM. There are presently two kinds of EEG head models and three kinds of MEG head models and the range will possibly be extended in the future. SPM8 makes it straightforward to create head models integrating all the available measurements such as individual structural scans and Polhemus head shape measurements. Coregistration of head models with EEG or MEG sensors is done with a graphical user interface. The resulting head models and sensor representations can then be also used for analyses implemented in Fieldtrip (i.e. beamforming).

**Fieldtrip:** <http://www.ru.nl/neuroimaging/fieldtrip/>

## **Canonical Source Reconstruction for MEG**

SPM8 uses a simple and efficient solution to the problem of reconstructing electromagnetic sources into a canonical or standard anatomical space. Its simplicity rests upon incorporating subject-specific anatomy into the forward model in a way that eschews the need for cortical surface extraction. The forward model starts with a set of canonical mesh, defined in a standard stereotactic space. These meshes are warped, in a nonlinear fashion, to match the subject's anatomy. This warping is the inverse of the transformation derived from spatial normalization of the subject's structural MRI image. Electromagnetic lead fields for the warped cortical mesh are computed using a head model based on the warped scalp and skull meshes. The ensuing forward model is inverted using an empirical Bayesian scheme (see Multiple Sparse Priors). Critically, because anatomical information enters the forward model, there is no need to spatially normalize the reconstructed source activity. In other words, each source, comprising the mesh, has a predetermined and unique anatomical attribution within standard stereotactic space. This enables the pooling of data from multiple subjects and the reporting of results in stereotactic coordinates. Furthermore, it allows the graceful fusion of fMRI and MEG data within the same anatomical framework.

The canonical cortical mesh surfaces are stored in the `canonical` directory of SPM, in GIFTI format. Importantly, they are different from those available in SPM5 and were created by D. Wakeman and R.N.A. Henson using FreeSurfer from a canonical brain in MNI space. See `canonical/spm_mesh.man` for more details.

J. Mattout, R.N.A. Henson, and K.J. Friston. **Canonical Source Reconstruction for MEG**. *Comput Intell Neurosci.*, 2007(67613), 2007.

R.N.A. Henson, J. Mattout, C. Phillips and K.J. Friston. **Selecting forward models for MEG source-reconstruction using model-evidence**. *NeuroImage*, In press.

## **Multiple sparse priors for the M/EEG inverse problem**

SPM8 exploits hierarchical or empirical Bayes to solve the distributed source reconstruction problem in electro- and magnetoencephalography (EEG and MEG). This rests on the automatic selection of multiple cortical sources with compact spatial support that are specified in terms of empirical priors. This obviates the need to use priors with a specific form (e.g., smoothness or minimum norm) or with spatial structure (e.g., priors based on depth constraints or functional magnetic resonance imaging results). Furthermore, the inversion scheme allows for a sparse solution for distributed sources, of the sort enforced by equivalent current dipole (ECD) models. This means the approach automatically selects either a sparse or a distributed model, depending on the data. Conventional applications of Bayesian solutions are also implemented to quantify the improvement in performance.

K.J. Friston, L. Harrison, J. Daunizeau, S.J. Kiebel, C. Phillips, N. Trujillo-Bareto, R.N.A. Henson, G. Flandin, and J. Mattout. **Multiple sparse priors for the M/EEG inverse problem**. *NeuroImage*, 39(3):1104-1120, 2008.

## **Variational Bayes for equivalent current dipoles (VB-ECD)**

Much methodological research has been devoted to developing sophisticated Bayesian source imaging inversion schemes, while dipoles have received less attention. Dipole



models have their advantages; they are often appropriate summaries of evoked responses or helpful first approximations. In SPM8, we have implemented a variational Bayesian algorithm that enables the fast Bayesian inversion of dipole models. The approach allows for specification of priors on all the model parameters. The posterior distributions can be used to form Bayesian confidence intervals for interesting parameters, like dipole locations. Furthermore, competing models (e.g., models with different numbers of dipoles) can be compared using their evidence or marginal likelihood. At the time of release, only EEG data are supported in VB-ECD.

S.J. Kiebel, J. Daunizeau, C. Phillips, and K.J. Friston. **Variational Bayesian inversion of the equivalent current dipole model in EEG/MEG.** *NeuroImage*, 39(2):728-741, 2008.

### ***Electromagnetic source reconstruction for group studies***

SPM8 incorporates a simple procedure for electromagnetic (EEG or MEG) source reconstruction, in the context of group studies. This entails a simple extension of existing source reconstruction techniques based upon the inversion of hierarchical models. The extension ensures that evoked or induced responses are reconstructed in the same subset of sources, over subjects. Effectively, the procedure aligns the deployment of reconstructed activity over subjects and increases, substantially, the detection of differences between evoked or induced responses at the group or between-subject level.

V. Litvak and K.J. Friston. **Electromagnetic source reconstruction for group studies.** *NeuroImage*, 42:1490-1498, 2008.

### ***DCM for M/EEG: intrinsic connectivity***

The original DCM for M/EEG publications looked at the modulation of connectivity between sources only. However, one could also formulate hypotheses that posit a modulation of within-source (intrinsic) connectivity. This feature has been implemented in SPM8 and is useful for testing hypotheses about adaptation of neuronal responses to local influences, in relation to influences that are mediated by long-range extrinsic connections (forward, backward, and lateral) from other sources.

S.J. Kiebel, M.I. Garrido, and K.J. Friston. **Dynamic causal modelling of evoked responses: The role of intrinsic connections.** *NeuroImage*, 36:332-345, 2007.

### ***DCM for Steady State Responses***

Dynamic causal models (DCM) of steady-state responses is a new methodology available for the analysis of M/EEG or intracranial data in the frequency domain. This new DCM follows previous DCM frameworks by offering a mechanistic description of how a distributed neuronal network produces observed data. The key difference lies in the type of data this model can explain, namely, stationary oscillatory dynamics. Frequency responses that occur without time-dependency during some experimental event are summarised in terms of their cross-spectral density.

These M/EEG or intracranial responses in the frequency domain form the data feature which is explained in terms of neuronal parameters by employing a Bayesian inversion of a coupled neural mass model. The parameterisation takes into account the types

(inhibitory/excitatory) and direction of extrinsic (between source) cortical connections and also includes meaningful physiological parameters of within-source activity e.g., post-synaptic receptor density and time constants.

Under linearity and stationarity assumptions, the biophysical parameters of this model prescribe the cross-spectral density of responses measured directly (e.g., local field potentials) or indirectly through some lead-field (e.g., M/EEG data). Inversion of the ensuing DCM provides conditional probabilities on the synaptic parameters of intrinsic and extrinsic connections in the underlying neuronal network. Thus inferences about synaptic physiology, as well as changes induced by pharmacological or behavioural manipulations can be made.

R. Moran, K.E. Stephan, T. Seidenbecher, H.-C. Pape, R. Dolan and K.J. Friston. **Dynamic Causal Models of steady-state responses.** *NeuroImage*. 44:796-811, 2009.

### ***Induced responses***

DCM for induced responses aims to model coupling within and between frequencies that are associated with linear and non-linear mechanisms respectively. This is a further extension of DCM for ERP/ERF to cover the spectrum dynamics as measured with the electroencephalogram (EEG) or the magnetoencephalogram (MEG). The model parameters encode the frequency response to exogenous input and coupling among sources and different frequencies. One key aspect of the model is that it differentiates between linear and nonlinear coupling; which correspond to within and between-frequency coupling respectively. Furthermore, a bilinear form for the state equations can be used to model the modulation of connectivity by experimental manipulations.

C.C. Chen, S.J. Kiebel, K.J. Friston. **Dynamic causal modelling of induced responses.** *NeuroImage*, 41(4):1293-1312, 2008.

### ***DCM for Phase-Coupling***

DCM for phase coupling uses a weakly coupled oscillator model to describe dynamic phase changes in a network of oscillators. Combined with the use of Bayesian model comparison, one can use these models to infer the mechanisms underlying synchronization processes in the brain. For example, whether activity leading to synchronization is driven by master-slave or mutual entrainment mechanisms. Earlier methods for studying phase coupling, such as the Evolution Map Approach, were restricted to pairs of brain regions. DCM for phase coupling allows connectivity to be analysed in networks with arbitrary numbers of regions.

W.D. Penny et al. **Dynamical Causal Models for Phase Coupling.** Under review.

### ***Mean-field and neural-mass models***

These demonstrations illustrate the behaviour of mean-field and neural mass models of cortical sources through simulations and stability analyses. These models are exactly the same models used in DCM for evoked, induced and steady-state responses. It is anticipated that people will deconstruct the code after viewing the demos, to understand

the nature of the models in more depth and how they are specified, integrated and used. Many of the figures produced are in the peer reviewed articles associated with each demonstration.

Although MEG/EEG signals are highly variable, systematic changes in distinct frequency bands are commonly encountered. These frequency-specific changes represent robust neural correlates of cognitive or perceptual processes (for example, alpha rhythms emerge on closing the eyes). However, their functional significance remains a matter of debate. Some of the mechanisms that generate these signals are known at the cellular level and rest on a balance of excitatory and inhibitory interactions within and between populations of neurons. The kinetics of the ensuing population dynamics determine the frequency of oscillations. In these demonstrations we extend the classical nonlinear lumped-parameter model of alpha rhythms, initially developed by Lopes da Silva and colleagues, to generate more complex dynamics and consider conduction based models.

R. Moran, S.J. Kiebel, N. Rombach, W.T. O'Connor, K.J. Murphy, R.B. Reilly, and K.J. Friston. **Bayesian estimation of synaptic physiology from the spectral responses of neural masses.** *NeuroImage*, 42(1):272-284, 2008.

### **DEM toolbox**

Dynamic expectation maximisation (DEM) is a variational treatment of hierarchical, nonlinear dynamic or static models. It uses a fixed-form Laplace assumption to approximate the conditional, variational or ensemble density of unknown states and parameters. This is an approximation to the density that would obtain from Variational Filtering (VF) in generalized coordinates of motion. The first demonstration with VF uses a simple convolution model and allows one to compare DEM and VF. We also demonstrate the inversion of increasingly complicated models; ranging from a simple General Linear Model to a Lorenz attractor. It is anticipated that the reader will examine the routines called to fully understand the nature of the scheme.

DEM presents a variational treatment of dynamic models that furnishes time-dependent conditional densities on the trajectory of a system's states and the time-independent densities of its parameters. These are obtained by maximising a variational action with respect to conditional densities, under a fixed-form assumption about their form. The action or path-integral of free-energy represents a lower bound on the model's log-evidence required for model selection and averaging. This approach rests on formulating the optimisation dynamically, in generalised coordinates of motion. The resulting scheme can be used for online Bayesian inversion of nonlinear dynamic causal models and is shown to outperform existing approaches, such as Kalman and particle filtering. Furthermore, it provides for dual and triple inferences on a system's states, parameters and hyperparameters using exactly the same principles. DEM can be regarded as the fixed-form homologue of variational filtering (which is covered in the demonstrations):

Variational filtering represents a simple Bayesian filtering scheme, using variational calculus, for inference on the hidden states of dynamic systems. Variational filtering is a stochastic scheme that propagates particles over a changing variational energy landscape, such that their sample density approximates the conditional density of hidden states and inputs. Again, the key innovation, on which variational filtering rests, is a formulation in generalised coordinates of motion. This renders the scheme much simpler and more

versatile than existing approaches, such as those based on particle filtering. We demonstrate variational filtering using simulated and real data from hemodynamic systems studied in neuroimaging and provide comparative evaluations using particle filtering and the fixed-form homologue of variational filtering, namely dynamic expectation maximisation.

K.J. Friston. **Variational filtering**. *NeuroImage*, 41(3):747-766, 2008.

K.J. Friston, N. Trujillo-Barreto, and J. Daunizeau. **DEM: A variational treatment of dynamic systems**. *NeuroImage*, 41(3):849-885, 2008.

### ***Mixture toolbox***

This toolbox implements Bayesian Clustering based on Bayesian Gaussian Mixture models. The algorithm (`spm_mix`) will cluster multidimensional data and report on the optimal number of clusters. The toolbox also contains code for a Robust General Linear Model (`spm_rglm`), where the error processes comprise a two-component univariate mixture model. There is no user interface but there are many demo files.

U. Noppeney, W. D. Penny, C. J. Price, G. Flandin, and K. J. Friston. **Identification of degenerate neuronal systems based on intersubject variability**. *Neuroimage*, 30:885-890, 2006.

W. Penny, J. Kilner and F. Blankenburg. **Robust Bayesian General Linear Models**. *Neuroimage*, 36(3):661-671, 2007.

### ***Spectral toolbox***

This toolbox implements routines based on univariate (`spm_ar`) and multivariate autoregressive modelling (`spm_mar`), including time and frequency domain Granger-causality analysis, coherence and power spectral analysis. The routines allow you to estimate the optimal number of time lags in the AR/MAR models. There is also a routine for robust autoregressive modelling (`spm_rar`) in which the error process is a two-component mixture model (to run this routine you will need the mixture toolbox on your search path). There is no user interface but there are many demo files.

W.D. Penny and S.J. Roberts. **Bayesian Multivariate Autoregressive Models with structured priors**. *IEE Proceedings on Vision, Image and Signal Processing*, 149(1):33-41, 2002.