

Bayesian analysis of single-subject fMRI data:

User Guide

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Introduction

First of all, realign and spatially normalise your data. You may not want to upsample your data at this stage as the more slices your data have the longer the Bayesian analysis will take. Typically, the algorithm takes somewhere between 30s and 3 minutes per slice depending on how many information bearing voxels there are in that slice. You could upsample later (ie. after the Bayesian estimation) ie. upsample and smooth your contrast images prior to a second level analysis.

Do NOT spatially smooth your data.

The whole point of this algorithm is that it automatically finds the spatial scale that your signals lie in. Then set up a design matrix and assign your scans to it. Then press the **BAYESIAN** button in the first SPM window. Select your **SPM.mat** file. The following options will then appear.

Single subject fMRI – Yes/No

Press **YES**.

If you press **NO**, SPM will use a global shrinkage method described in earlier papers, see eg. (Friston and Penny, 2003). This is appropriate for 2nd level analysis.

AR model order

3 will do.

Select Prior

'Spatial-GMRF' – this uses a Gaussian Markov Random Field prior on the regression coefficients and the AR coefficients. The spatial precision of which is estimated automatically.

'Spatial-LORETA' – this uses a Laplacian prior on the regression coefficients and the AR coefficients. This prior is the same as that used by Pascual Marqui in his LORETA algorithm. It underestimates effect sizes at image edges (so does the GMRF, but not as much). The spatial precision is estimated automatically.

'Voxel – Shrinkage' – this uses the same prior as in the earlier method (Friston and Penny, 2003).

'Voxel – Uninformative' – this doesn't use any prior. This will approximate classical inference (interval estimation). This was the prior used in (Penny et al., 2003).

Unless you want to make particular comparisons *'Spatial-GMRF'* is the preferred option here.

Compute evidence YES/NO

Selecting YES allows you to do model comparison. But the algorithm takes longer, as the evidence needs to be computed. So, NO here is the usual option.

Select Space

'Volume' – applies the algorithm to the whole volume of data.

'Masked Volume' – applies algorithm to whole volume of data but allows user to then select a mask which restricts analysis to a subset of voxels.

'Slices' – applies algorithm to particular slices. If you select this option you will then be prompted to enter the numbers of the slices you want to analyse eg. 20 or 21 22 27.

Display

If you used the **'Slices'** option and selected a single slice (or a small number of slices) then when you display the results images (eg. images of regression or AR coefficients) you should select the 'nearest neighbour' interpolation option in the SPM display window (ie. switch from the default 'bilinear' interpolation method) – otherwise you won't see any results.

Results

The contrast manager can be used in the usual way. You need to specify the effect size threshold (which is '1' by default) and a display threshold that only includes voxels in a PPM if their posterior probability exceeds a certain value (this is 0.95 by default).

Reference List

1. Friston, K.J. and Penny, W. (2003). Posterior probability maps and SPMs. *Neuroimage*. 19, 1240-1249.
2. Penny, W., Kiebel, S., and Friston, K. (2003). Variational Bayesian inference for fMRI time series. *Neuroimage*. 19, 727-741.

