README BFAST3D

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This document describes the Bayesian Fast Accurate Spatial Tricks in 3D (BFAST3D) code that can be used to run the Spatial variational Bayes (SVB) and Markov chain Monte Carlo (MCMC) methods for fMRI analysis in Sidén et al. (2016). The code is an add-on to the SPM12 software (Ashburner et al., 2013) and to its Bayesian single subject method (Penny et al., 2003, 2005b,a, 2007; Penny and Flandin, 2005). To use the code, follow these steps

- (1) Download/duplicate your spm12-directory (downloadable at http://www.fil.ion.ucl.ac.uk/spm/software/spm12/).
- (2) Delete the spm_spm_vb.m-file in the new spm12-directory.
- (3) Copy the svb-folder from this package into the new spm12-directory.

runExample.m gives an example on how to run the code and calls the functions runSVB.m and runMCMC.m which are adapted for the OpenfMRI data ds105, available at https://openfmri.org/dataset/ds000105/. Use at own risk.

In the current version, various settings are defined in different files and some of these are described below:

- To not run SVB in parallel, in spm12/svb/2D/spm_spm_vb.m or spm12/svb/3D/spm_spm_vb.m, change the variable SPM.ParallelGMRFSampling to 0.
- Change the number of SVB iterations in spm12/svb/2D/spm_spm_vb.m or spm12/svb/3D/spm_spm_vb.m, variable SPM.PPM.maxits (default 50).
- In the beginning of spm12b/svb/spm_svb_init.m one can change some SVB settings, e.g. the number of expectation approximation samples N_s (default 100) and the PCG tolerance δ (default 10^{-8}).
- For the MCMC-method, settings are changed in runMCMC.m, e.g. the number of MCMC iterations, warmup iterations, thinning factor and PCG tolerance δ can be changed by changing the variables niter, warmup, thinningFactor and PCGTol.

 $Post-processing \verb| computePPMs.m| depends on the Tools | for NIfTI | and ANALYZE | image-package |$

(http://www.mathworks.com/matlabcentral/fileexchange/8797-tools-for-nifti-and-analyze-image). To compute joint PPMs, R is required and so is the excursions-package (Bolin and Lindgren, 2015), development version (https://bitbucket.org/davidbolin/excursions) and also the R-package R.matlab. Be aware that for large data sets the time and memory requirements can be quite demanding, especially for MCMC, which can be quick-fixed by limiting the number of iterations.

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