SPM MATLAB TOOLBOX

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Abstract

The SPM toolbox is a noncommercial software for processing fMRI data. The toolbox is developed at the Department of Imaging Neuroscience, University College London. The common application of the SPM toolbox is the first level analysis consisting in the detection of active brain regions for one patient. The second level analysis, also covered by the SPM toolbox, is related to processing of fMRI data across the whole patients group. Besides these functions, the toolbox offers tools for DCM analysis, such as the parameters estimation routines, tools for comparison of resulting models, and a function for averaging models across the whole patients group.

1 Introduction

SPM toolbox serves for data processing, especially for fMRI, EEG and MEG data sets. It includes preprocessing steps, statistical analysis and DCM analysis. There exist several versions of this toolbox. The oldest available version was called SPM99, then SPM2 followed and nowadays version SPM5 is used.
fMRI abbreviates functional Magnetic Resonance Imaging. This method is able to create map of brain activity. The results of fMRI experiment are functional images and structural anatomical images which are useful as a base for localization of activated regions. The functional images are put through the statistical analysis and the result is statistically significant regions where the so-called haemodynamic responses were detected. But there appear some complications during this procedure for example some statistical discrepancies. The SPM toolbox try to correct them and to produce regular results.

2 fMRI analysis

2.1 Preprocessing

The first stage of fMRI data analysis is data preprocessing - preparation of data for statistical analysis. SPM toolbox offers these adjustments. *Realigning* corrects movement artifacts in data. Least squares approach and spatial transformation are used. Subsequently *slice timing correction* shifts the data (each voxel's time series) as if whole volume was acquired at exactly the same time. It is accomplished by a simple shift of the phase of the sines that make up signal [9]. Then there is *spatial normalization* for transformation of scans to standard space defined by template images (for instance Talairach standard space). This procedure employees the affine transformation and nonlinear deformation. It is very important step for the group statistics. Finally there is implemented *smoothing procedure* for noise suppression. The Gaussian filter is usually used.

2.2 1st level analysis

After the preprocessing steps the statistical analysis is carried on. Brain activity is mapped by detection of voxels activated by stimulation. This procedure is called the first level analysis. It can be carried out by correlation analysis or by predetermined haemodynamic response. This

statistical analysis is based on GLM - General Linear Model. It means to define so-called design matrix which embodies the fMRI experiment. Then the estimation of GLM parameters follows and finally the statistical parametric map is produced. It indicates the likeliest voxels associated with haemodynamic responses. The Fig.1 presents the result of the first level analysis. In this case the stimulus was left hand motion. The activated voxels are colorfully marked.

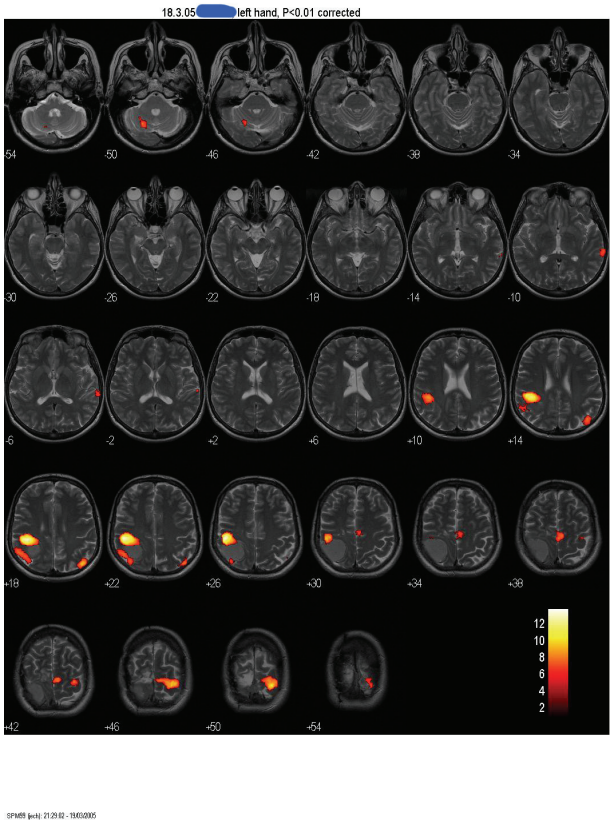
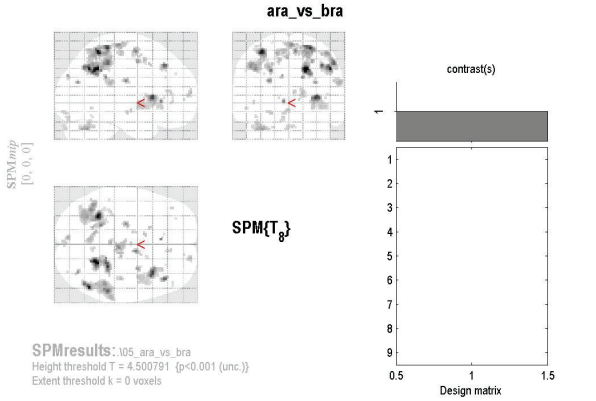


Figure 1: The statistical map - the first level analysis

2.3 2nd level analysis

The next type of analysis allows generalization of some conclusions to the whole group of patients [5]. There exist statistical methods for combining results across the subjects. The result is statistical map as well and it is valid for all patients from investigated group. These methods include "fixed-effects" and "random-effects" procedure. Fixed-effects allow inferences to be made about the particular subject in the experiment, while random-effects allows inferences to be made about the population. Random effects analysis is considered more appropriate for fMRI research because it deals with making inferences on the population [6]. The second level analysis can be useful for instance for selection of brain areas during DCM analysis.



Statistics: ***p-values adjusted for search volume***

set-level		cluster-level			voxel-level					mm mm mm		
p	c	$p_{corrected}$	k_E	$p_{uncorrected}$	$p_{FWE-corr}$	$p_{FDR-corr}$	T	(Z_e)	$p_{uncorrected}$			
0.000	**61**	**0.000**	**305**	**0.000**	**0.392**	**0.094**	**10.86**	**4.58**	**0.000**	**20**	**-50**	**40**
					0.841	0.094	9.35	4.34	0.000	26	-36	64
					0.994	0.094	7.35	3.94	0.000	26	-50	34
		0.000	**284**	**0.000**	**0.591**	**0.094**	**10.29**	**4.50**	**0.000**	**-32**	**-48**	**60**
					0.999	0.094	6.90	3.84	0.000	-40	-56	40
					1.000	0.094	5.65	3.49	0.000	-34	-56	46
		0.000	**303**	**0.000**	**0.721**	**0.094**	**10.01**	**4.45**	**0.000**	**50**	**-58**	**40**
					0.977	0.094	7.92	4.07	0.000	54	-36	46
					1.000	0.094	6.43	3.72	0.000	46	-40	58
		0.000	**200**	**0.000**	**0.899**	**0.094**	**8.89**	**4.26**	**0.000**	**32**	**18**	**6**
					1.000	0.094	5.33	3.39	0.000	38	2	-4
					1.000	0.094	5.06	3.30	0.000	44	10	-4
		0.706	**26**	**0.040**	**0.982**	**0.094**	**7.80**	**4.05**	**0.000**	**40**	**32**	**44**
		0.226	**47**	**0.008**	**0.996**	**0.094**	**7.24**	**3.92**	**0.000**	**-22**	**-44**	**38**
					1.000	0.094	5.77	3.53	0.000	-20	-54	38
		0.706	**26**	**0.040**	**0.996**	**0.094**	**7.21**	**3.91**	**0.000**	**8**	**-2**	**60**
		1.000	**4**	**0.395**	**0.999**	**0.094**	**6.87**	**3.83**	**0.000**	**-6**	**28**	**2**
		0.082	**64**	**0.003**	**0.999**	**0.094**	**6.86**	**3.83**	**0.000**	**4**	**-22**	**68**
					1.000	0.094	5.37	3.40	0.000	-2	-16	68
		0.974	**14**	**0.118**	**0.999**	**0.094**	**6.80**	**3.81**	**0.000**	**-24**	**-14**	**26**

table shows 3 local maxima more than 8.0mm apart

Height threshold: T = 4.50, p = 0.001 (1.000) {p<0.001 (unc.)}
Extent threshold: k = 0 voxels, p = 1.000 (1.000)
Expected voxels per cluster, <k> = 5.950
Expected number of clusters, <c> = 30.96
Expected false discovery rate, <= 0.09

Degrees of freedom = [1.0, 8.0]
FWHM = 10.2 10.7 10.3 mm mm mm; 5.1 5.3 5.2 {voxels};
Volume: 1374936 = 171867 voxels = 1140.7 resels
Voxel size: 2.0 2.0 2.0 mm mm mm; (resel = 140.52 voxels)
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Figure 2: The statistical map - the second level analysis

3 DCM analysis

The next type of fMRI processing is DCM analysis. It is a part of SPM toolbox as well. Dynamic Casual Modelling (DCM) is a statistical technique for detection of connections among selected brain areas [3]. The DCM procedure treats the brain as a deterministic nonlinear dynamic system. This system has some inputs and produces some outputs, measured by fMRI as the BOLD (Blood Oxygen Level Dependent) signals. The inputs to the system are the signals defining a certain fMRI experiment, i.e. time series representing some stimuli such as finger movement commands, projection of emotional pictures to the patients etc. Furthermore a model structure must be predefined before the DCM analysis is applied seeing Fig.3. Therefore certain special knowledge in brain organization is necessary. In addition, there are typically several structure candidates that must be processed and evaluated separately which can become time consuming.

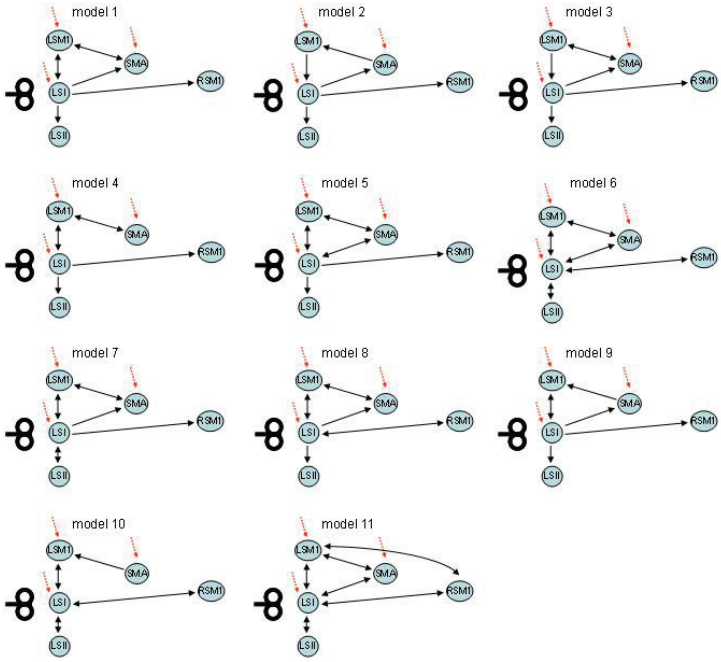

Figure 3: The predefined models

The DCM models are estimated using Bayesian estimators [8]. The inferences about connections are made using the posterior or conditional density [3]. The DCM result is the likeliest model accompanied by strength values of significant connections Fig.4. This figure was created by means of SPM toolbox [1].

3.0.1 DCM drawbacks

DCM is undoubtedly an established and commonly used method for identification of functional brain organization from fMRI data. DCM processing however can have some drawbacks from the user's point of view. They are explained in detail in the paper [2] and are based on experience of the authors with processing one particular fMRI experiment by DCM.
The predefinition of models is a complication not only for a user who does not have deep experience with fMRI, even educated experts have sometimes problems to establish the most appropriate model structure. As a result, a tedious trial-and-error loop must be performed to arrive at acceptable findings.
The DCM analysis of one model itself takes some time and the computation for a complete set of models can take a few days easily. Sometimes there is a specific additional uncertainty such as an alternative selection of a brain area coordinates which leads to additional structures to be considered. In the case of analysis of a therapy influence all these demands are doubled in principle (by data received after the therapy and their processing). These issues are discussed in detail in [2]. These troubles could be considerably reduced if an alternative identification procedure were used in place of DCM that would automatically detect the internal structure of the most appropriate dynamical model.
Methods for fitting measured data sets that do not require any particular assumptions on the system structure (apart of the order and linearity) are however commonly used in systems and signals identification routines, to estimate communication channels behavior, mechanical structures models, chemical processes etc. [4]. Our aim is therefore to try applicability of those methods in the fMRI case.
We expect some problems here related to small amount of data samples; the fMRI investigation does not allow fast sampling rates and the patients can be put subject to the experiment for a limited time period. The DCM features we present above as drawbacks certainly help on the

other hand to eliminate the lack of data (by incorporation of some a-priori information in fact).

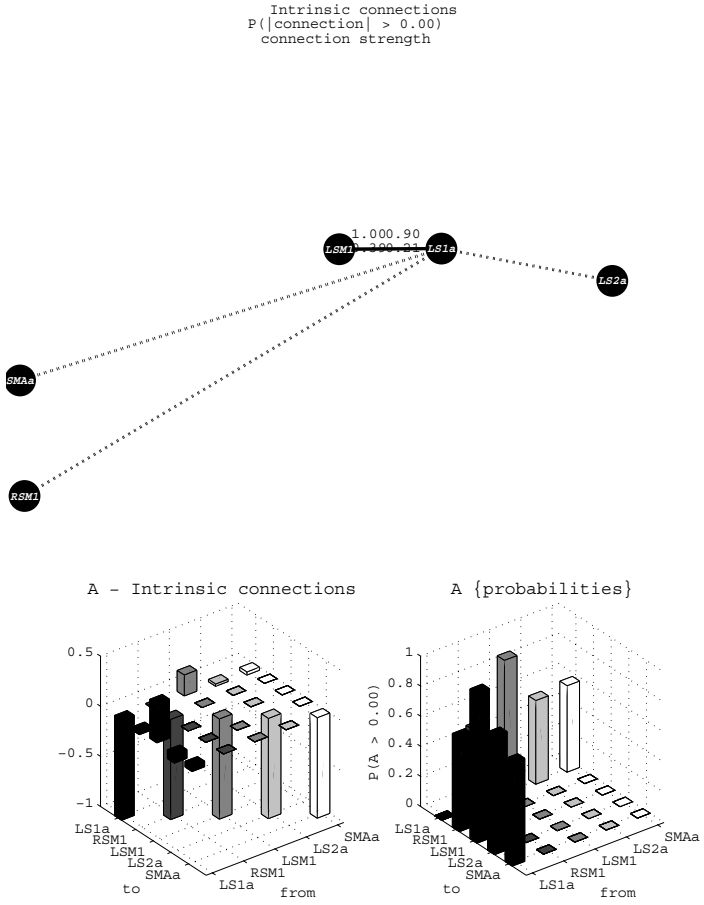

Figure 4: The significant connections

4 SPM simulator

The important part of SPM toolbox is data simulator which generates the fMRI DCM data on basis of our requirements. The simulator is started by means of function named *spm_dcm_create*. The function is able to generates simulated signals of selected brain regions with required parameters such as the signal-to-noise ratio, the number of regions, interscan interval (TR, sampling period in principle), number of scans (samples), number of conditions (stimulating inputs) and the vectors of onsets (starting instants) and durations for input signals (stimulations). The choice of the connectivity matrix A, the input matrix C and the modulatory matrix B follows.

5 Conclusion

The SPM toolbox is very useful software for fMRI data processing. It is suitable for doctors, for instance the version SPM5 permits batch data processing. And statistical analysis is not time-consuming for certain group of patients. The toolbox has also SPM simulator which is able to generate the typical fMRI data. It is very important for some experiments with fMRI data because we can define for instance very high quality of data or on the other hand very bad quality of data.

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