MarsBaR Documentation

Release 0.44

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March 17, 2016

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MarsBaR (MARSeille Boîte À Région d'Intérêt) is a toolbox for SPM which provides routines for region of interest analysis. Features include region of interest definition, combination of regions of interest with simple algebra, extraction of data for regions with and without SPM preprocessing (scaling, filtering), and statistical analyses of ROI data using the SPM statistics machinery.

CHAPTER

ONE

ABOUT MARSBAR

1.1 Citing MarsBaR

We presented an abstract to the Human Brain Mapping conference for 2002; this may be useful as a reference: MarsBaR HBM abstract. It should apparently be cited as:

> Matthew Brett, Jean-Luc Anton, Romain Valabregue, Jean-Baptiste Poline. Region of interest analysis using an SPM toolbox [abstract] Presented at the 8th International Conference on Functional Mapping of the Human Brain, June 2-6, 2002, Sendai, Japan. Available on CD-ROM in NeuroImage, Vol 16, No 2.

1.2 Thanks

For writing credits and some little jokes, see the marsbar.m file file in the MarsBaR release.

CHAPTER

TWO

DOWNLOAD AND INSTALL

All MarsBaR file releases are available via the MarsBaR project download page.

2.1 Installing MarsBaR

MarsBaR needs a version of SPM, so if you don't have SPM, please download and install that first. MarsBaR works with SPM versions 99, 2, 5, and 8.

For the current stable release of MarsBaR, look for the marsbar package; marsbar-devel is the development release. Releases consist of an archive which will unpack in a directory named after the MarsBaR version - for example `marsbar-0.42`. You then have two options for using MarsBaR within SPM.

1. You can add the new MarsBaR directory to your matlab path. To use MarsBaR, start it from the matlab prompt with the command "marsbar", or...
2. You could set up MarsBaR to run as an SPM toolbox. To do this, the contents of the new MarsBaR directory needs to be in a subdirectory "marsbar" of the SPM toolbox directory. Here is a worked example for Unix. Imagine SPM8 was in `/usr/local/spm/spm8`, and you had just unpacked the MarsBaR distribution, giving you a directory `/home/myhome/marsbar-0.42`. You could then create the marsbar SPM toolbox directory with:

```
mkdir /usr/local/spm/spm8/toolbox/marsbar
```

and copy the MarsBaR distribution into this directory with:

```
cp -r /home/myhome/marsbar-0.42/* /usr/local/spm/spm8/toolbox/marsbar
```

Alternatively, you could do the same job by making a symbolic link between the directories with something like:

```
ln -s /home/myhome/marsbar-0.42 /usr/local/spm/spm8/toolbox/marsbar
```

Either way, the next time you start spm you should be able to start the toolbox by selecting 'marsbar' from the toolbox button on the SPM interface.

2.2 Other MarsBaR downloads

2.2.1 Example dataset

You may want the example dataset to try out MarsBaR, or to run the *MarsBaR tutorial*.

Download the dataset from the MarsBaR project download page.

To install, unpack the archive in a directory you can write to. This will give you a subdirectory like `marsbar_example_data-0.3`, where 0.3 is the version number of the example data.

The example data are taken from an experiment described in an HBM2003 conference abstract:

> Matthew Brett, Ian Nimmo-Smith, Katja Osswald, Ed Bullmore (2003) Model fitting and power in fast event related designs. NeuroImage, 19(2) Supplement 1, abstract 791

The data consist of three EPI runs, all from one subject. In each run the subject watched a computer screen, and pressed a button when they saw a flashing checker board. An "event" in this design is one presentation of the flashing checker board.

We did this experiment because we were interested to see if events at fast presentation rates give different activation levels from events that are more widely spaced. Each run has a different presentation rate. We randomized the times between events in each run to give an average rate of 1 event every second in run 1, 1 event every 3 seconds for run 2, and 1 event every 10 seconds for run 3.

There are some automated pre-processing scripts for this dataset in the MarsBaR distribution, see *Starting the tutorial* for more details.

2.2.2 AAL structural ROIs

These ROIs can be useful as a standard set of anatomical definitions.

To install, download the AAL ROI archive file from the MarsBaR project download page. Unpack the archive somewhere; it will create a new directory, called something like `marsbar-aal-0.2`.

The AAL ROI library contains ROIs in MarsBaR format that were anatomically defined by hand on a single brain matched to the MNI / ICBM templates. The ROI definitions are described in:

> Tzourio-Mazoyer N, Landeau B, Papathanassiou D, Crivello F, Etard O, Delcroix N, et al. (2002). Automated anatomical labelling of activations in SPM using a macroscopic anatomical parcellation of the MNI MRI single subject brain. NeuroImage 15: 273-289.

CHAPTER

THREE

MARSBAR TUTORIAL

This is a short introduction to MarsBaR, a region of interest toolbox for SPM. It takes the form of a guided tour, showing the usage of MarsBaR with a standard dataset.

The tutorial assumes you have some experience using SPM

3.1 Getting started

3.1.1 How to read the tutorial

There are three threads in this tutorial. The first and most obvious is a step by step guide to running several standard ROI analyses. On the way, there are two sets of diversions. These are *interface summaries*, and *technical notes*. Interface summaries look like this:

An interface summary

with some interface description

and technical notes look like this:

A technical note

with some technical notes

If you just want to do the step-by-step tutorial, you can skip these diversions, and come back to them later. The interface summaries give you information on the range of things that MarsBaR can do; the technical notes are detailed explanations of the workings of MarsBaR, which can be useful in understanding the obscure parts of the interface.

3.1.2 Gearing up

To run all the examples in this tutorial you will need to download and install two packages:

1. MarsBaR: this tutorial assumes marsbar version 0.44;
2. the example dataset (version 0.3).

To install these packages, see *Download and install*

This tutorial assumes you are using SPM8, but you can run the tutorial with SPM versions 12, 8, 5, 2 or 99; the results will be very similar.

3.1.3 Plan of campaign

The *Example dataset* is from an experiment with three EPI runs of flashing checkerboard events. The first run was at a high presentation rate (average 1 per second), run 2 was at a medium rate (average 1 every 3 seconds) and run 3 was slow (1 every 10 seconds on average).

We are going to analyse the data to see if there is different activation for fast and slow presentation rates. ROI analysis is an obvious choice here, because we know where the activation is likely to be – in the primary visual cortex – but we are more interested in how much activation there will be. So, we will first need to define an ROI for the visual cortex, and then analyze the data within the ROI.

In this tutorial we will cover two methods of defining an ROI: first, a functional definition and second, an anatomical definition.

3.1.4 Defining a functional ROI

A key problem in an ROI analysis is finding the right ROI. This is easier for the visual cortex than for almost any other functional area, because the location of the visual cortex is fairly well predicted by the calcarine sulcus, in the occipital lobe, which is easy enough to define on a structural scan. However, there is a moderate degree of individual variation in the size and border of the primary visual cortex.

One approach to this problem is to use the subject's own activation pattern to define the ROI. We might ask the subject to do another visual task in the scanner, and use SPM to detect the activated areas. We find the subject's primary visual cortex from the activation map, and use this functional ROI to analyze other data from the same subject. This approach has been very fruitful for areas such as the fusiform face area, which vary a great deal in position between subjects.

For this dataset, we are most interested in the difference between the fast presentation rates of run 1, and the slow presentation rates of run 3. So, we can use an SPM analysis of run 2 to define the visual cortex, and use this as an ROI for our analysis of run 1 and run 3.

3.1.5 Functional ROIs usually need independent data

Using the recipe above, we are not using run 2 for the ROI analysis. Because we will use run 2 to define the ROI, if we extract data from this ROI for run 2, it will be biased to be more activated than the data from run 1 and run 3. Imagine that our experiment had not worked, and there was no real activation in any of the runs. We do an SPM analysis on run 2, and drop the threshold to find some voxels with higher signal than others due to noise. We define the ROI using this noise cluster, and extract data from the ROI for this session, and the other two sessions. The activation signal from the ROI in run 2 will probably appear to be higher than for the other sessions, because we selected these voxels beforehand to have high signal for run 2. The same argument applies if we select the ROI from a truly activated area; the exact choice of voxels will depend to some extent on the noise in this session, and so data extracted from this ROI, for this session, will be biased to have high signal.

3.1.6 Starting the tutorial

First you will need to run some processing on the example dataset. After you unpack the dataset archive, you should have four subdirectories in the main `marsbar_example_data` directory. Directories `sess1`, `sess2` and `sess3` contain the slice-time corrected and realigned, undistorted, spatially normalized data for the three sessions (runs) of the experiment. The `rois` directory contains pre-defined regions of interest.

To run the tutorial, find where your marsbar directory is. You can do this from the matlab prompt with `>> which marsbar` . If `<marsbar>` is the marsbar directory, then you should be able to see a directory called `<marsbar>/examples/batch`. This `batch` subdirectory contains Matlab program files to run the preprocessing. Change directory to `batch`, and start Matlab. From the Matlab prompt, run the command `run_preprocess`. This little script will smooth the images by 8mm FWHM, and run SPM models for each run.

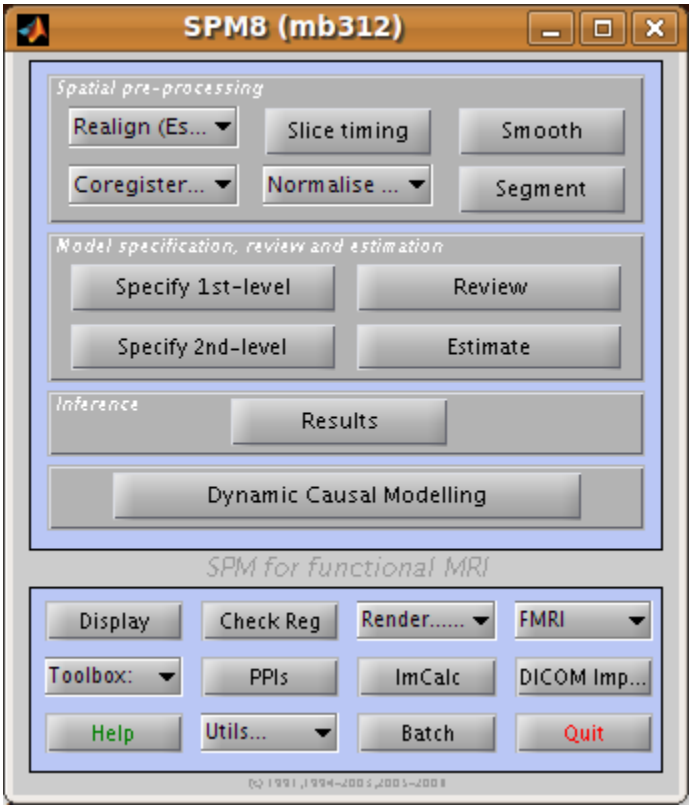
Now start MarsBaR. First, make sure the MarsBaR directory is on the Matlab path. If you are using the GUI to add marsbar to the path, add only the path containing `marsbar.m`, but *not* the subdirectories in this directory. Next, run the command `marsbar` from the Matlab >> prompt.

3.2 The MarsBaR / SPM interface

Let's begin by naming the windows used by SPM and MarsBaR. After you have started SPM and MarsBaR, you should have the following set of windows:

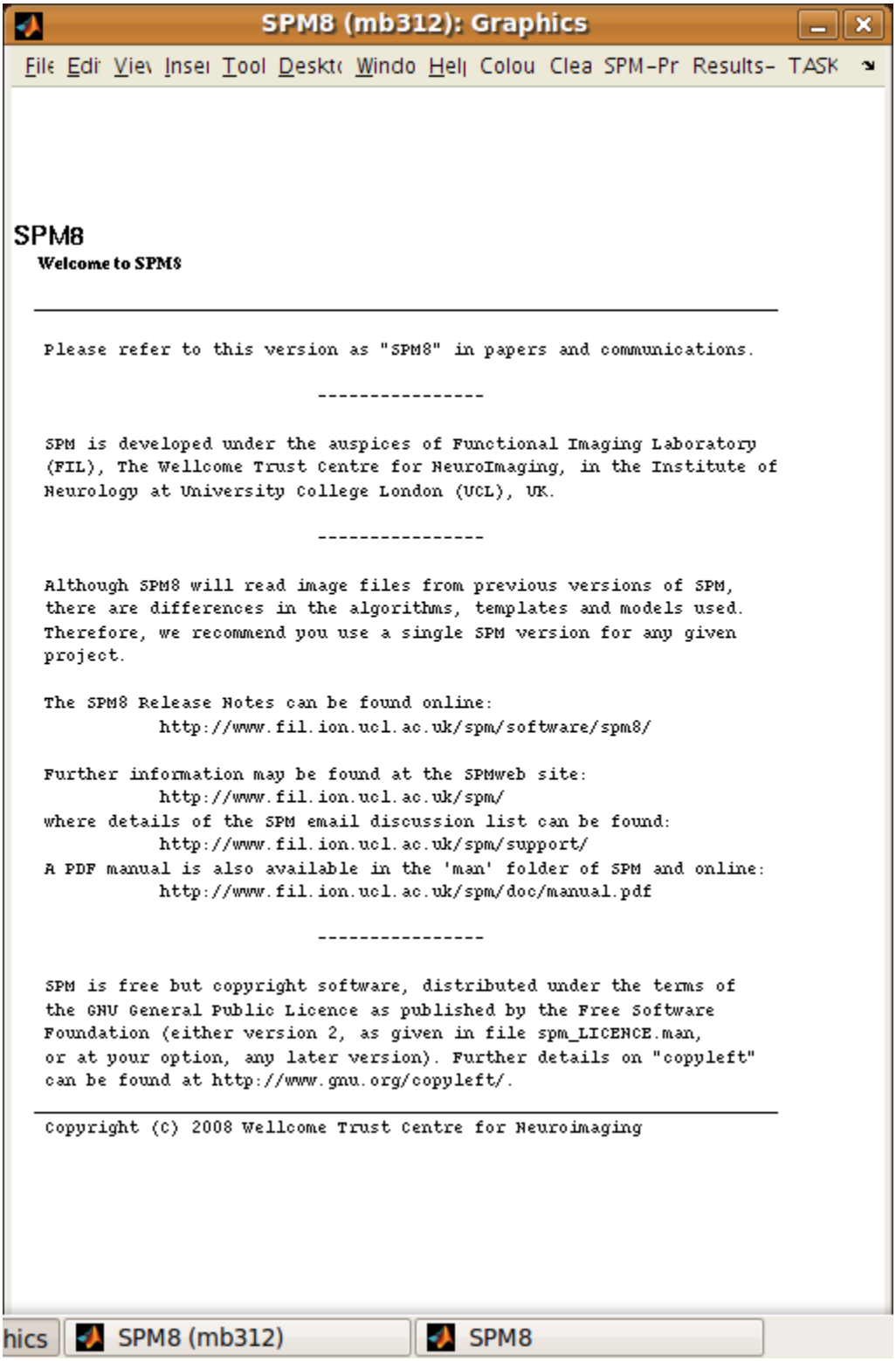
The MarsBaR window:

Then, at the top left of the screen, the SPM buttons window



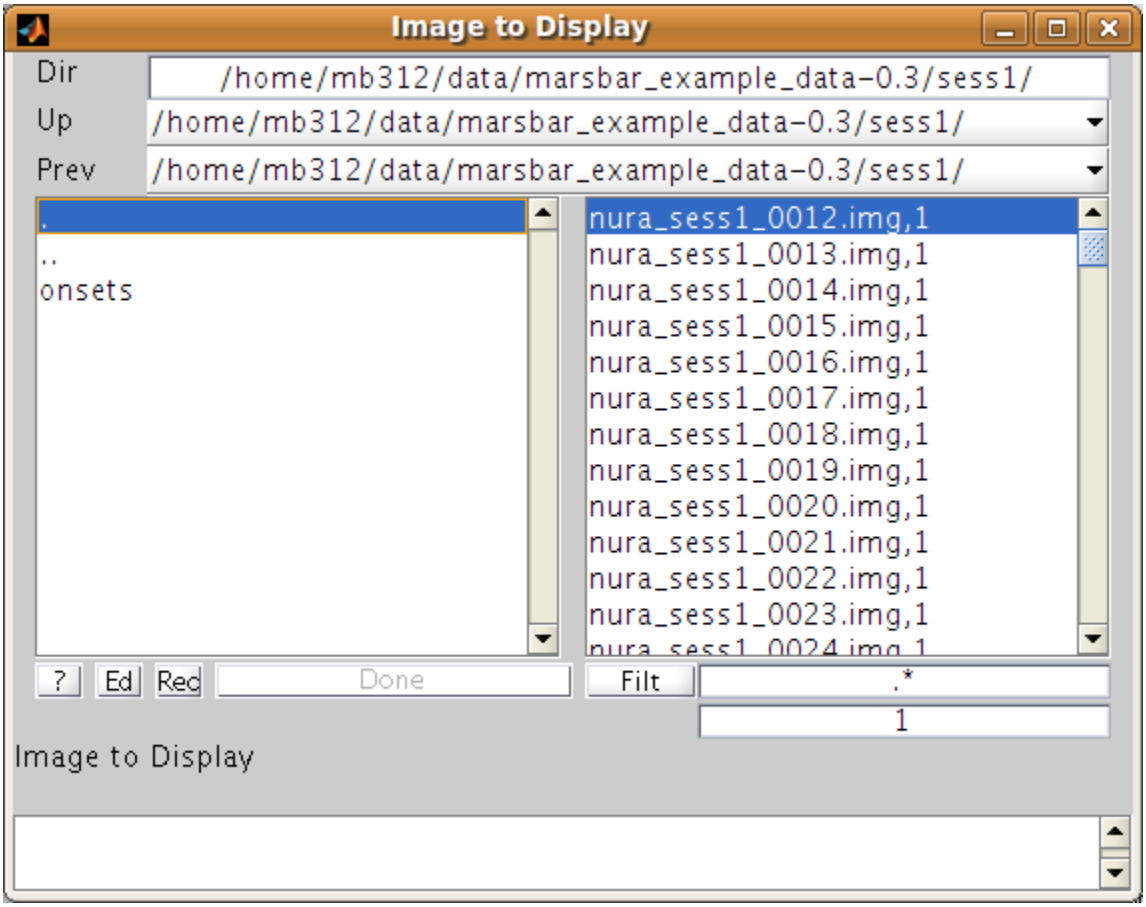
Underneath the SPM buttons window, at the bottom left of the screen, is the SPM input window:

SPM and MarsBaR use this window to get input from you, gentle user, such as text, numbers, or menu choices. Usually on the right hand side of the screen, there is the SPM graphics window:

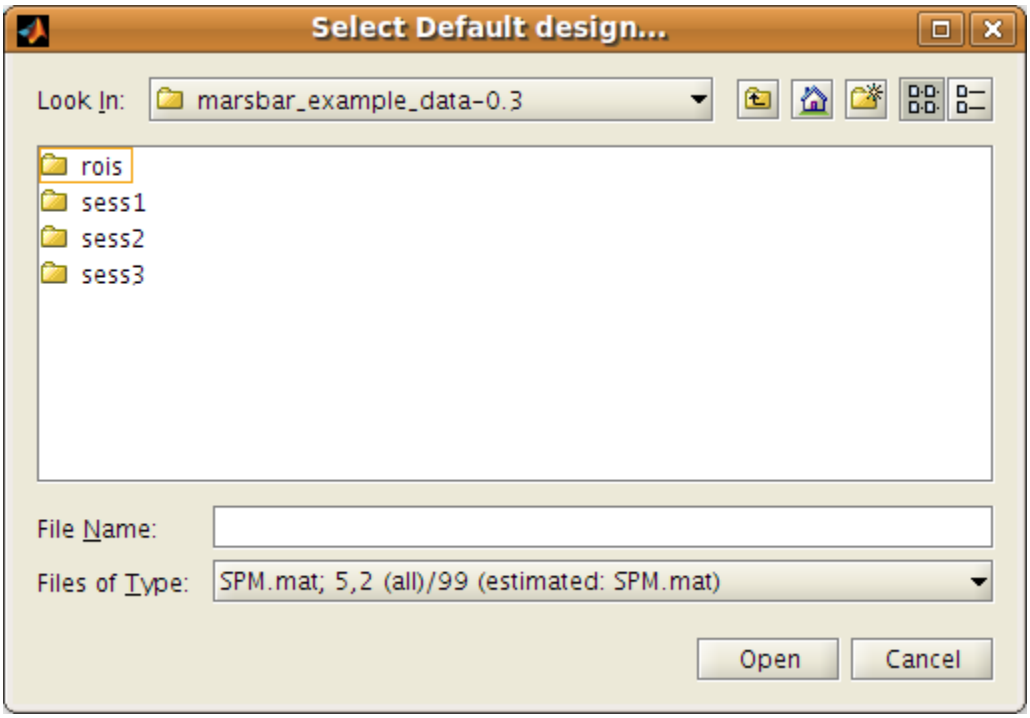


which is used to display results and other graphics.

When SPM and MarsBaR want file or directory names from you, they may use the file selection window:



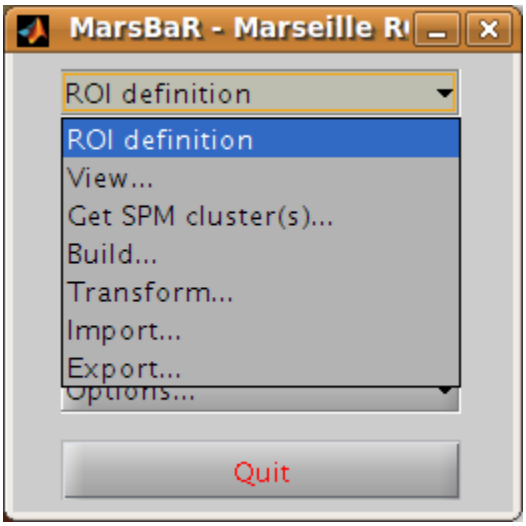
Sometimes MarsBaR does not use the SPM selection dialog above, but the standard Matlab dialog, that will differ for each platform (linux, windows, mac). Here's a linux version:



3.3 Defining ROIs

The preprocessing script has already run an SPM model for run 2 (and run 1 and run 3). Now we need to find an activation cluster in the visual cortex.

Go to the MarsBaR window, and click on ROI definition. You should get a menu like this:



Interface summary - the ROI definition menu

View displays one or ROIs on a structural image.

Get SPM cluster(s) uses the SPM results interface to select and save activation clusters as ROIs.

Build gives an interface to various methods for defining ROIs, using shapes (boxes, spheres), activation clusters, and binary images.

Transform offers a GUI for combining ROIs, and for flipping the orientation of an ROI to the right or left side of the brain.

Import allows you to import all SPM activations as ROIs, or to import ROIs from cluster images, such as those written by the SPM results interface, or from images where ROIs are defined by number labels (ROI 1 has value 1, ROI 2 has value 2, etc.). Similarly

Export writes ROIs as images for use in other packages, such as MRIcro.

3.3.1 Defining a functional ROI

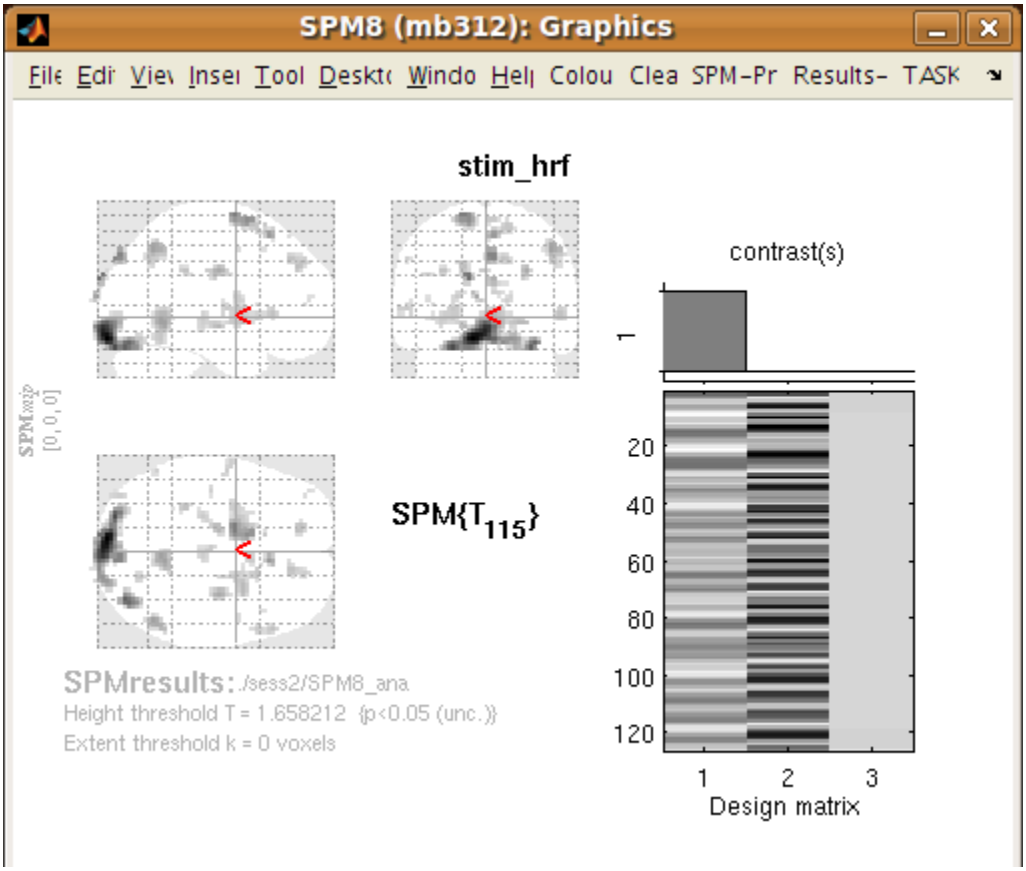
We are going to define the functional ROI using the SPM analysis for run 2. Select *Get SPM cluster(s)...*: from the menu. This runs the standard SPM results interface. Use the file selection window that SPM offers to navigate to the `sess2/SPM8_ana` directory. Select the SPM.mat file and click *Done*. Choose the `stim_hrf` t contrast from the SPM contrast manager, click *Done*. Then accept all the default answers from the interface, like this:

Prompt	Response
apply masking	none
title for comparison	stim_hrf
p value adjustment to control	none
threshold {T or p value}	0.05
& extent threshold {voxels}	0

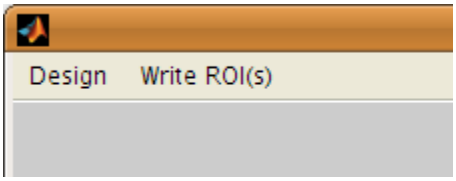
Technical note - MarsBaR and SPM designs

For the large majority of tasks, MarsBaR can use SPM designs interchangeably. For example, when running with SPM5, you can load SPM99 designs and estimate them in MarsBaR; you can also estimate SPM5 designs from MarsBaR, even if you are using - say - SPM99. However, MarsBaR uses the standard SPM routines for the 'Get SPM cluster(s)' routines. This means that if, for example, you are running SPM5 you can only get clusters from an SPM5 design and you can only get clusters from an SPM99 design if you are running SPM99.

Now you have run the *Get SPM cluster(s)* interface, you should have an SPM activation map in the graphics window:



Meanwhile, you may have noticed there is a new menu in the SPM input window:



Another thing you may not have noticed is that the matlab working directory has now changed to the `sess2/SPM8_ana`. SPM does this to be able to keep track of where its results files are.

Move the red arrow in the SPM graphics window to the activation cluster in the visual cortex. You can do this by dragging the arrow, or right-clicking to the right of the axial view and choosing `goto global maxima`.

When the red arrow is in the main cluster, click on the Write ROI(s) menu in the SPM input window and select Write one cluster.

Interface summary - Write ROI(s)

Write one cluster writes out a single cluster at the selected location.

Write all clusters writes all clusters from the SPM map; MarsBaR will ask for a directory to save the files, and a root name for the ROI files before saving each ROI as a separate file.

Rerun results UI restarts the SPM results interface as if you had clicked on the SPM results button; Clear clears the SPM graphics window.

After you have selected Write one cluster, MarsBaR asks for details to save with the ROI, which are a description, and a label. Both provide information about the ROI for statistical output and display. The label should be 20 characters or so, the description can be longer. For the moment, accept the defaults, which derive from the coordinates of the voxel under the red arrow and the title of the contrast:

Prompt	Response
Description of ROI	`stim_hrf` cluster at [-9.0 -93.0 -15.0]
Label for ROI	`stim_hrf_-9_-93_-15`

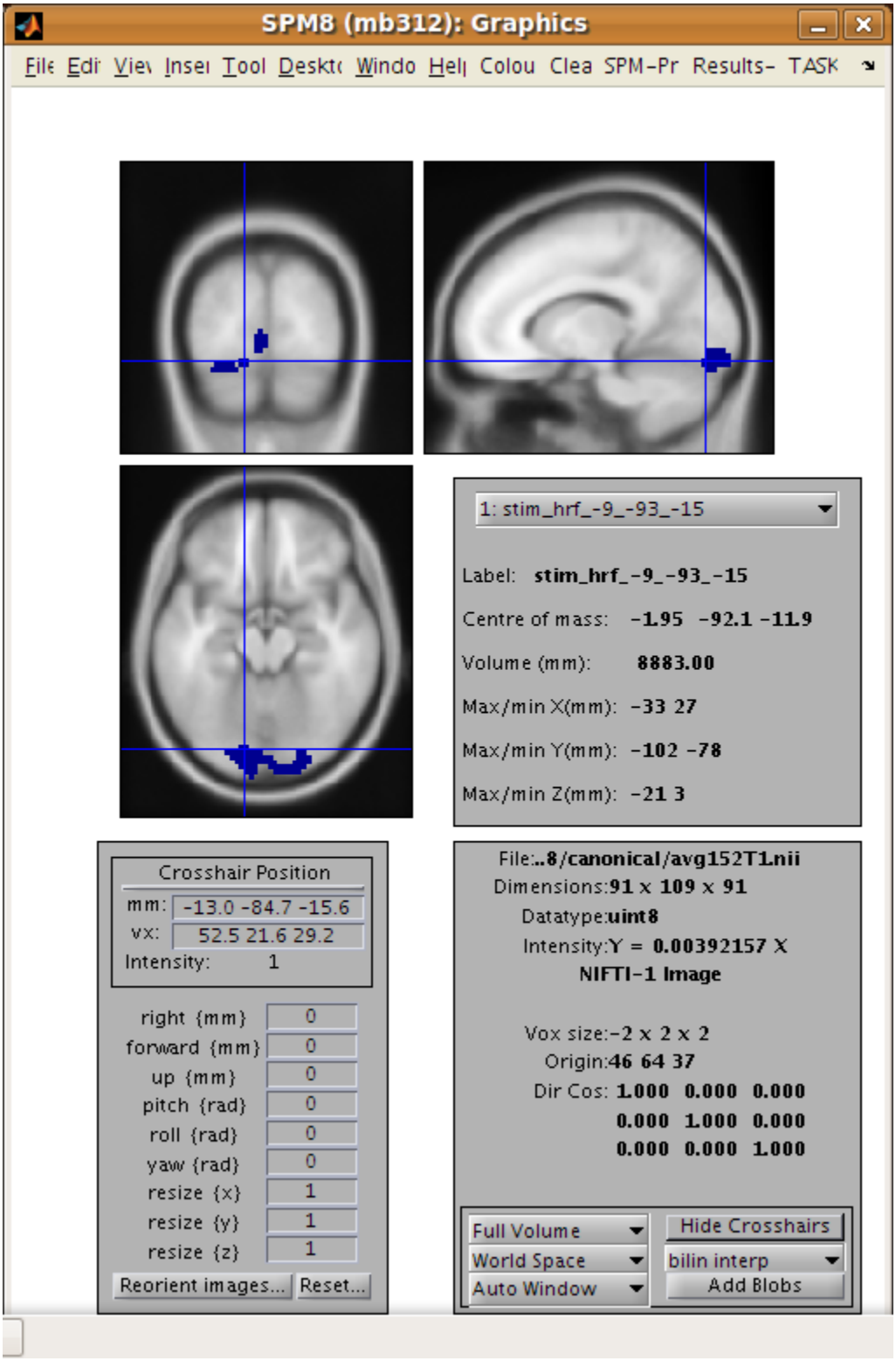
After this, MarsBaR offers a dialog box to give a filename for the ROI. By default the offered filename will be `stim_hrf_-9_-93_-15_roi.mat` in the `sess2/SPM8_ana` directory. For simplicity, why not accept the default name and click Save to save the ROI.

Technical note - ROIs and filenames

MarsBaR stores each ROI in a separate file. In fact, the files are in the Matlab `.mat` format. MarsBaR will accept any filename for the ROI, and can load ROIs from any file that you have saved them to, but it will suggest that you save the ROI with a filename that ends in `_roi.mat`. This is just for convenience, so that when you are asked to select ROIs, the MarsBaR GUI can assume that ROI files end with this suffix. It will probably make your life easier if you keep to this convention.

3.3.2 Review the ROI

We can now review this ROI to check if it is a good definition of the visual cortex. Click on the ROI definition menu in the MarsBaR window, and select View.... Choose the ROI and click Done. Your ROI should be displayed in blue on an average structural image:



Interface summary - the view utility

The view utility allows you to click around the image to review the ROI in the standard orthogonal views. You can select multiple ROIs to view on the same structural. The list box to the left of the axial view allows you to move to

a particular ROI (if you have more than one). When the cross-hairs are in the ROI, the information panel will show details for that ROI, such as centre of mass, and volume in mm. The default structural image is the MNI 152 T1 average brain; you can choose any image to display ROIs on by clicking on the Options... menu in the MarsBaR window, then choosing Edit Options..., followed by Default structural.

3.3.3 Refining the ROI

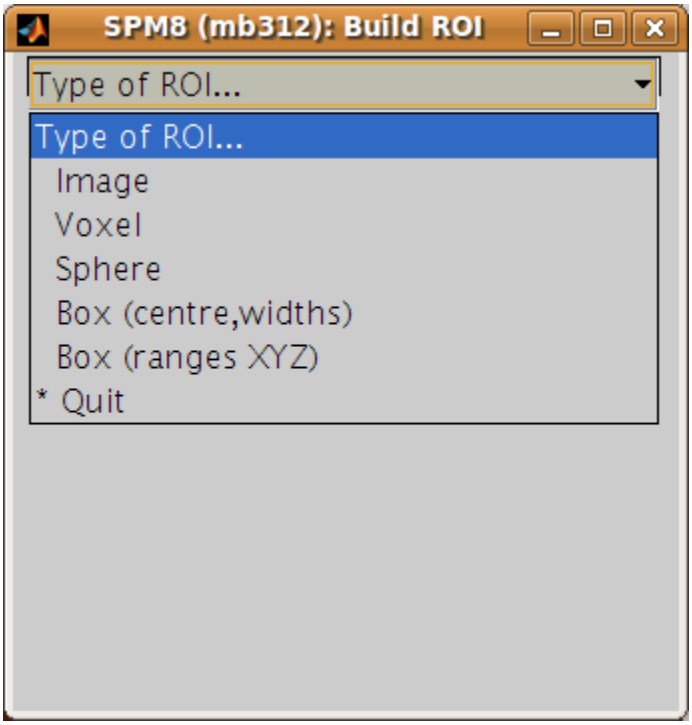
Now we have reviewed the ROI, we see that the cluster does include visual cortex, but there also seems to be some connected activation lateral and inferior to the primary visual cortex. The cross-hairs in the figure are at something like the border between primary visual cortex and more lateral voxels. Ideally we would like to restrict the ROI to voxels in the primary visual cortex.

We can do this by defining a box ROI that covers the area we are interested in, and combining this with the activation cluster.

Defining a box ROI

To decide on the box dimensions, click around the ROI in the view interface and note the coordinates of the cross-hairs that are shown at the top of the bottom left panel. This may suggest to you, as it did to us, that it would be good to restrict the ROI to between -20 and +20mm in X, -66 to -106mm in Y, and -20 to +7mm in Z.

To define this box ROI, click on ROI definition, and choose Build..., . You will see a new menu in the SPM input window:



From the menu, select Box (ranges XYZ). Answer the prompts like this:

Prompt	Response
[2] Range in X (mm)	-20 20
[2] Range in Y (mm)	-66 -106
[2] Range in Z (mm)	-20 7
Description of ROI	box at -20.0>X<20.0 -106.0>Y<-66.0 -20.0>Z<7.0
Label for ROI	`box_x_-20:20_y_-106:-66_z_-20:7`
Filename	`box_x_-20_20_y_-106_-66_z_-20_7_roi.mat`

The last three values here are the defaults.

To check this is as you want it, choose ROI Definition, View, select both of `box_x_-20_20_y_-106_-66_z_-20_7_roi.mat` and `stim_hrf_-9_-93_-12_roi.mat`, in that order, and click Done. You should see the box in blue, with the activation cluster overlaid in red.

We now need to combine the two ROIs, to select only those voxels that are shared by the box and the activation cluster.

Combining ROIs

Choose ROI Definition, Transform... A new menu comes up in the SPM input window. Choose Combine ROIs; select both the box and the cluster ROIs, click on Done. The prompt now asks for a function with which to combine the ROIs. In this function, the first ROI you selected is r1, and the second ROI is r2. Here we want to get the overlap, and this is represented by the logical AND operator, which is `&` in Matlab. Enter the function `r1 & r2`.

Technical note - combining ROIs

You can use most mathematical functions to combine ROIs. If you wanted to combine two ROIs, so the new ROI has all the voxels in ROI 1 and all the voxels in ROI2, you could use the function `r1 | r2` (read as "r1 or r2"). If you wanted only the voxels in ROI 1 that are not in ROI 2: `r1 & ~ r2`. Similarly, you can choose more than two ROIs and combine them. The function `(r1 & r2) & ~r3` gives all the voxels that in *both of* ROI 1 and ROI 2, but excluding those voxels that are in ROI 3.

Be careful: `r1 & r2` gives all the voxels that are in ROI 1 *and in* ROI 2 - so `r1 & r2` is the *intersection* of ROI 1 and ROI 2. `r1 | r2` gives the voxels that are in *either of* ROI 1 or ROI 2 - so `r1 | r2` is the *union* of ROI 1 and ROI 2.

After this, accept the default description, set the label to something like "Trimmed stim run 2", and save the ROI as `trim_stim_roi.mat`.

3.3.4 Writing the ROI as an image

Just for practice, let us write our new ROI as a binary image. You might want to do this so you can review the ROI using another program, such as the excellent MRIcro. Click on ROI definition, then Export.... Select image from the new menu in the SPM input window, and choose the new trim_stim_roi.mat as the ROI to export. Another menu appears, asking for a Space for ROI image. The three options are Base space for ROIs, From image, or ROI native space.

Technical note - ROIs and image spaces

An ROI can be one of two fundamental types: a shape (such as a box or sphere) or a list of points (such as an activation cluster or coordinates read in from an ROI in an image). Shape ROIs know nothing about such vulgarities as voxels, they are abstract concepts waiting to be applied. In order to display shapes, or write them to images, or combine them with other ROIs, we need to convert them to point lists in a certain space – with dimensions in X Y and Z, and voxels with specified sizes. For example, when MarsBaR combines ROIs, it needs some default space (dimensions, voxel sizes) in which to define the new point list ROI. By default, this is the space of the MNI template; so the Base space for

ROIs in the menu above will be MNI space. This is a good space to use if you are working with spatially normalized data, but ROIs are often defined on a subject's data before spatial normalization. In this case, it may be more useful to set the ROI base space to match the subject's own activation images, using Options, Edit options from the MarsBaR window.

The issue of the ROI space comes up here, because we need to define what dimensions and voxels we should use when writing the image. We can either write the image using the Base space, or we can use some arbitrary space defined by an image, or we can get the space directly from the ROI. Here, the ROI is an activation cluster, and the native ROI space for an activation cluster uses the minimum dimensions necessary to hold all the voxels in the ROI. An ROI image for this cluster using native space uses minimum disk storage, but does not give a good impression of the ROI location when displayed in, for example, MRIcro.

In our case, the data are spatially normalized, and so are in the space of the MNI template. The MNI template space is the default base space for ROIs, so select Base space for ROIs, choose a directory to save the image, and accept the default filename for the image, which should be trim_stim. You can check this has worked, by finding the SPM buttons window, selecting Display, and choosing the new trim_stim.img.

3.4 Running the ROI analysis

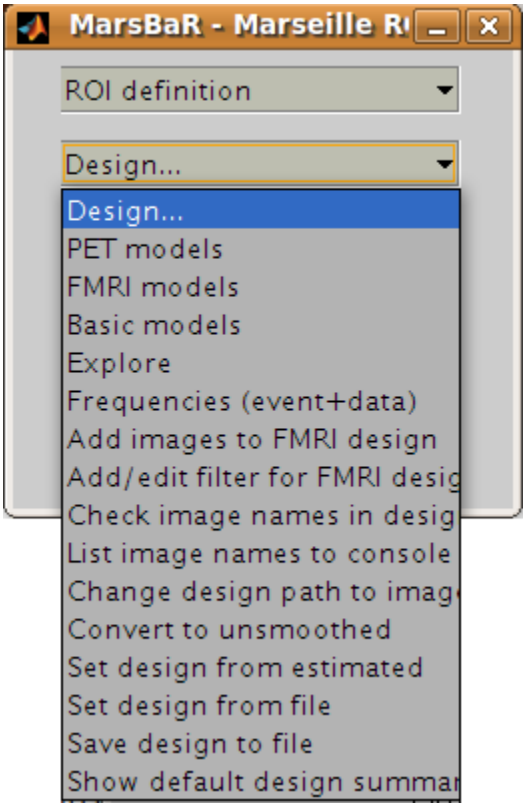
First, let us estimate the activation within the ROI for the first run. There are three stages to the analysis:

1. Choosing the design
2. Extracting the data
3. Estimating the design model with the data

The preprocessing for the example data created an SPM model for all three EPI runs, so we already have a design made for the first run. We are going to use this design and the `trim_stim` ROI to extract ROI data from the functional scans. Then we will use the design and the extracted data to estimate the model.

3.4.1 Stage 1: choosing the design

Click on the Design button in the MarsBaR window. You should get a menu like this:



Interface summary - design menu

The design menu offers options for creating, reviewing, estimating and processing SPM / MarsBaR designs.

Oddly, let us start at the end:

Show default design summary Displays a summary of the currently loaded design in the SPM graphics window

Set design from file will ask for a design file, and load the specified design into MarsBaR. The loaded design then becomes the default design. MarsBaR will from now on assume that you want to work with this design, unless you tell it otherwise by loading a different design.

Save design to file will save the current default design to a file.

Set design from estimated as we will see later, when MarsBaR estimates a design, it stores the estimated design in memory. Sometimes it is useful to take this estimated design and set it to be the default design, in order to be able to use the various of these menu options to review the design.

Now, from the top of the menu:

PET models, FMRI models, and Basic models will use the SPM design routines to make a design, and store it in memory as the default design.

Explore runs the SPM interface for reviewing and exploring designs.

Frequencies (event+data) can be useful for FMRI designs. The option gives a plot of the frequencies present in ROI data and the design regressors for a particular FMRI event. This allows you to choose a high-pass filter that will not remove much of the frequencies in the design, but will remove low frequencies in the data, which are usually dominated by noise.

Add images to FMRI design allows you to specify images for an FMRI design that does not yet contain images. SPM and MarsBaR can create FMRI designs without images. If you want to extract data using the design (see below), you may want to add images to the design using this menu item.

Add/edit filter for FMRI design gives menu options for specifying high pass and possibly (SPM99) low-pass filters, as well as autocorrelation options (SPM2 and later).

Check images in the design looks for the images names in a design, and simply checks if they exist on the disk, printing out a message on the matlab console window. A common problem in using saved SPM designs is that the images specified in the design have since moved or deleted; this option is a useful check to see it that has occurred.

Change path to images allows you to change the path of the image filenames saved in the SPM design, to deal with the situation when images have moved since the design was saved.

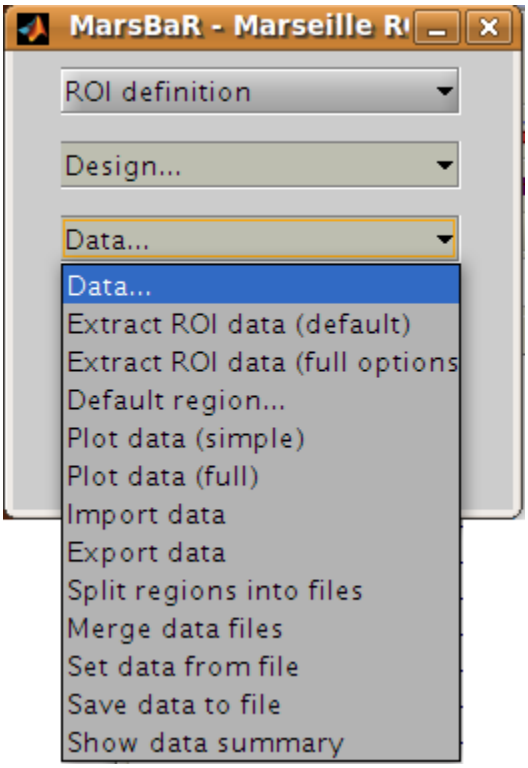
Convert to unsmoothed takes the image names in a design, and changes them so that they refer to the unsmoothed version of the same images – in fact it just removes the "s" prefix from the filenames. This can be useful when you want to use an SPM design that was originally run on smoothed images, but your ROI is very precise, so you want to avoid running the ROI analysis on smoothed data, which will blur unwanted signal into your ROI.

If you have been reading the interface summary, welcome back. Isn't it strange how time just seems to stop when you are reading about graphical user interfaces?

Our plan was to choose our design. Select the Set design from file option in the design menu and choose the `SPM.mat` file in the `sess1/SPM8_ana` directory. MarsBaR loads the design into memory and displays the design matrix in the SPM graphics window.

3.4.2 Stage 2: extracting the data

Before we can run the model, we need to extract the ROI data from the functional scans. This brings us to the data menu:



We are going to choose *Extract ROI data(default)*, and for simple analyses this may be all you will ever need. For those with a thirst for knowledge, here is the:

Interface summary - data menu

Extract ROI data (default) takes one or more ROI files and a design, and extracts the data within the ROI(s) for all the images in the design. As for the default design, MarsBaR stores the data in memory for further use.

Extract ROI data (full options) allows you to specify any set of images to extract data from, and will give you a full range of image scaling options for extracting the data.

Default region... is useful when you have extracted data for more than one ROI. In this case you may want to restrict the plotting functions (below) to look only at one of these regions; you can set which region to use with this option. If you do not specify, MarsBaR will assume you want to look at all regions.

Plot data (simple) draws time course plots of the ROI data to the SPM graphics window. Plot data (full) has options for filtering the data with the SPM design filter before plotting, and for other types of plots, such as Frequency plots or plots of autocorrelation coefficients.

Import data allows you to import data for analysis from matlab, text files or spreadsheets. With Export data you can export data to matlab variables, text files or spreadsheets.

Split regions into files is useful in the situation where you have extracted data from more than one ROI, but you want to estimate with the data from only one of these ROIs. This can be a good idea for SPM2 (and later) designs, because, like SPM2 (and later), MarsBaR will pool the data from all ROIs when calculating autocorrelation. This may not be valid, as different brain regions can have different levels of autocorrelation. Split regions into files takes the current set of data and saves the data for each ROI as a separate MarsBaR data file.

Merge data files reverses the process of *Split files* above, by taking a series of ROI data files and making them into one set of data with many ROIs.

Set data from file will ask for a MarsBaR data file (default suffix `_mdata.mat`) and load it into memory as the current set of data.

Save data to file will save the current set of data to a MarsBaR data file.

Show data summary outputs some summary text to the SPM graphics window

Again, welcome back to our linear readers. For the tutorial, we want to extract the data for our ROI, from the images in our design. Choose *Extract ROI data(default)*; the GUI will ask you to select one or more ROIs files; select the `trim_stim_roi.mat` file. MarsBaR starts to whirr. As it whirrs, it will:

1. Take each image in the design (you had already set the default design from the design menu);
2. Extract all the data within the ROI for each image, to give voxel time courses for each voxel in the ROI.

When it has finished, MarsBaR will calculate a new summary time course for each ROI. The summary time course has one value per scan, per ROI; by default, this new time course is made up of the means of all the voxel values in the ROI. For example, if there are only 5 voxels in the ROI, the first value in the summary time series will be the mean of the 5 voxel values for scan 1, the second value will be the mean of the 5 voxel values for scan 2, and so on. You can change the method of summarizing voxel data using the Statistics, Data summary function item in the MarsBaR options interface.

Technical note - the summary function

There are many ways to use ROI data, but the simplest approach, used by MarsBaR, is to treat the voxel values within the region of an image as many samples of the same signal. So, for each image, we find the voxels that are within the ROI, and calculate a single summary value to represent all the voxels in the ROI. This gives us one ROI summary value per image, and we can run the statistical model on this time-course of summary values.

The most obvious way of summarizing the values within the ROI is to take the mean. This is the default in MarsBaR. The mean can be greatly affected by outliers. If we suspect there may be outlier voxels in the ROI, the median may be

more robust as a summary function. The other option offered as a summary function is the weighted mean. Usually ROIs are binary – meaning that they contain ones within the ROI and zeros elsewhere. In this case the weighted mean will be identical to the mean. However, it is possible to define ROIs which contain weighting values, where high values represent high confidence that this voxel is within the region of interest, and values near zero represent low confidence. In this situation, it can be useful to use the ROI values to weight the mean value.

Earlier versions of MarsBaR also offered the option of taking the first eigenvector of the signal. We removed it for version 0.42 because it seemed as if it was replicating the behavior of the SPM VOI routines - but it was not.

As MarsBaR extracts the data you will see its progress printed to the matlab console. When the extraction is done, the data is kept in memory. You can save the data to disk if you want using the Save data to file option on the data menu.

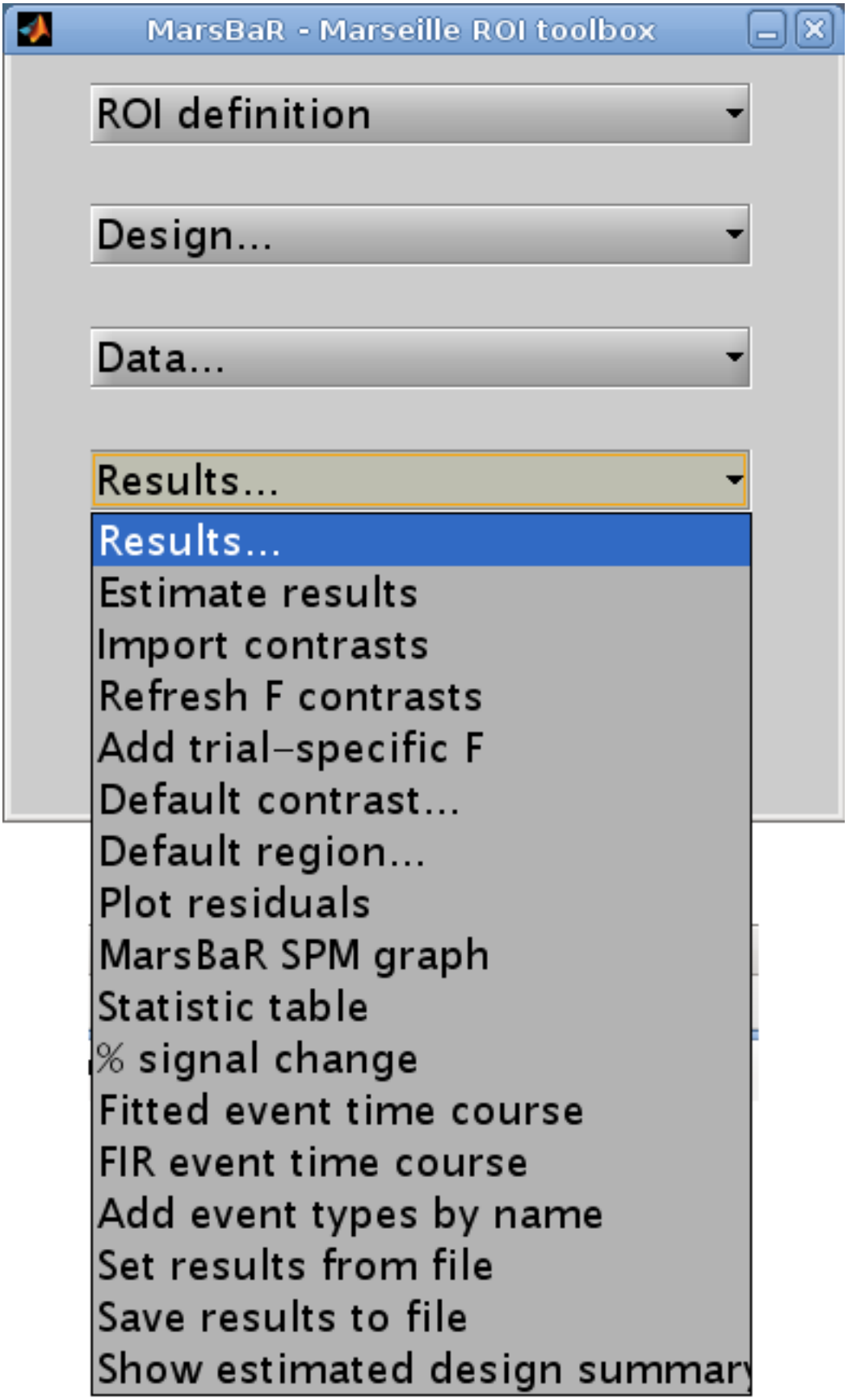
Now we have the design and the data we can estimate the model.

3.4.3 Stage 3: estimating the model

As the sweat pours from your brow, you click on the Results menu in the MarsBaR window. Scarcely believing it could be this easy, you choose the first item on the menu, *Estimate results*. It was that easy! MarsBaR takes the default design and the extracted data, and runs the model. There are more progress reports to the matlab console; finally you see the suggestion that you use the results section for assessment.

3.5 Basic results

Let us start the assessment by getting some t and F values for the effects in the design. Click on the Results button in the MarsBaR window:


MarsBaR - Marseille ROI toolbox
ROI definition
Design...
Data...
Results...
Results...
Estimate results
Import contrasts
Refresh F contrasts
Add trial-specific F
Default contrast...
Default region...
Plot residuals
MarsBaR SPM graph
Statistic table
% signal change
Fitted event time course
FIR event time course
Add event types by name
Set results from file
Save results to file
Show estimated design summary

Interface summary - the results menu

Estimate results as we know, takes the default design, and the ROI data, and estimates the model. MarsBaR stores the estimated results in memory as the estimated design.

Import contrasts gives an interface for you to select contrasts from other analyses, and import them into the list of contrasts for the current analysis.

Refresh F contrasts In earlier versions of marsbar (<= 0.42), F contrasts added from other designs (Import contrasts above) could give wrong results due to cached fields in the contrasts that were specific to the design from which they were imported. Unless you tell MarsBaR otherwise, it will automatically fix F contrasts in estimated designs when you load them so you should not need this menu option. If you have set MarsBaR not to refresh F contrasts on load (see Options: Statistics: Load updates F contrasts), then you can use this `Refresh F contrasts` menu option to refresh the contrasts.

Add trial specific F will add F contrasts for each trial, and each session, if they are not already present.

Default contrast will set one contrast as the default to use for other options on this menu, such as the MarsBaR SPM graph plotting function.

Default region applies only if the current results are for more than one region. It will select one region from the data to use for analysis and plots.

Plot residuals puts up various plots of the residual errors from the model, to check for violation of assumptions or major outliers.

MarsBaR SPM graph uses the SPM plotting functions to plot contrasts of parameter estimates, fitted and adjusted responses, estimates of event or block related response, and so on.

Statistic table shows various statistics for selected contrasts, as we will see in the tutorial.

% signal change will show an estimate for the percent signal change for a single event. There are many assumptions for this analysis; please treat it like you would treat your children: with a combination of great care and weary scepticism.

Set results from file allows you to choose the results you want to review. When you estimate a model in MarsBaR, the program will automatically set the new results to be current for the results menu. If you want to analyze some other set of MarsBaR results, you can use this option to select and load another analysis file. The default file suffix for MarsBaR estimated results is `_mres.mat`.

Save results to file will save the current estimated results, including the data used for the estimation, to a file on disk.

To continue with our analysis, we next need to specify a contrast. In our case the contrast is very simple: just a 1 in the column for the HRF regressor used to model the visual event. Usually the contrast will be more complicated, and you may have already entered it for a previous SPM or MarsBaR analysis. The Import contrasts option allows you to get contrasts from a previous analysis. To show how it works, click on this option. The SPM file selection window should appear. Navigate to the `sess1/SPM8_ana` directory, and select the `SPM.mat` file there. The SPM contrast manager comes up, showing all the F and t contrasts in the `SPM.mat` file. Select the `stim_hrf` t contrast, and click Done. MarsBaR will put this contrast into the current estimated design. Here we only selected one contrast, but you can select many contrasts by dragging the mouse, shift clicking etc. (depending on your system).

Now click on the Statistic table option in the MarsBaR results menu. Select the `stim_hrf` contrast and click Done. The results will print out in a rather ugly fashion in the Matlab window. You might want to enlarge your Matlab window to stop the text wrapping in an annoying way. Here is the output on my machine:

```
Contrast name   ROI name: Contrast value:    t statistic:  Uncorrected P:    Corrected P
-------------------------------------------------------------------------------------------


stim_hrf
```

```
-------------------------

      trimmed stim run 2:           2.21:           4.44:       0.000011:       0.000011
```

At the left you see the contrast name. Under this, and to the right, MarsBaR has printed the ROI label that you entered a while ago. The t statistic is self explanatory, and the uncorrected p value is just the one-tailed p value for this t statistic given the degrees of freedom for the analysis. The corrected p is the uncorrected p value, with a Bonferroni correction for the number of regions in the analysis. In this case, we only analyzed one region, so the corrected p value is the same as the uncorrected p value. MarsBaR (like SPM), will not attempt to correct the p value for the number of contrasts, because the contrasts may not be orthogonal, and this will make a Bonferroni correction too conservative.

There is also a column called *Contrast value*. For a t statistic, as here, this value is an effect size. Remember that a t statistic consists of an effect size, divided by the standard deviation of this effect. Here our contrast is very simple, containing only a single 1, so the contrast value is the same as the value of the first parameter in the model. The value of this parameter will be the best-fitting slope of the line relating the height of the HRF regressor to the FMRI signal. This effect size measure is the number that SPM stores for each voxel in the `con_0001.img`, `con_0002.img` ... series, and these are the values that are used for standard second level / random effect analyses.

Just for practice, let us also run an F contrast. Click Statistic table again, choose the effects of interest contrast, click Done:

```
Contrast name   ROI name:       Extra SS:    F statistic:  Uncorrected P:    Corrected P
-------------------------------------------------------------------------------------------

effects of interest
-------------------------

      trimmed stim run 2:          40.48:          25.01:       0.000000:       0.000000
```

Now the Contrast value has become the *Extra SS*. This is a measure of the variance that would be added to a model that does not contain the effects in the contrast. The F statistic is this measure, adjusted for the number of effects, and divided by the residual variance for the whole model. There is no simple way of using this *Extra SS* value in second level analyses.

3.5.1 Comparing fast and slow events

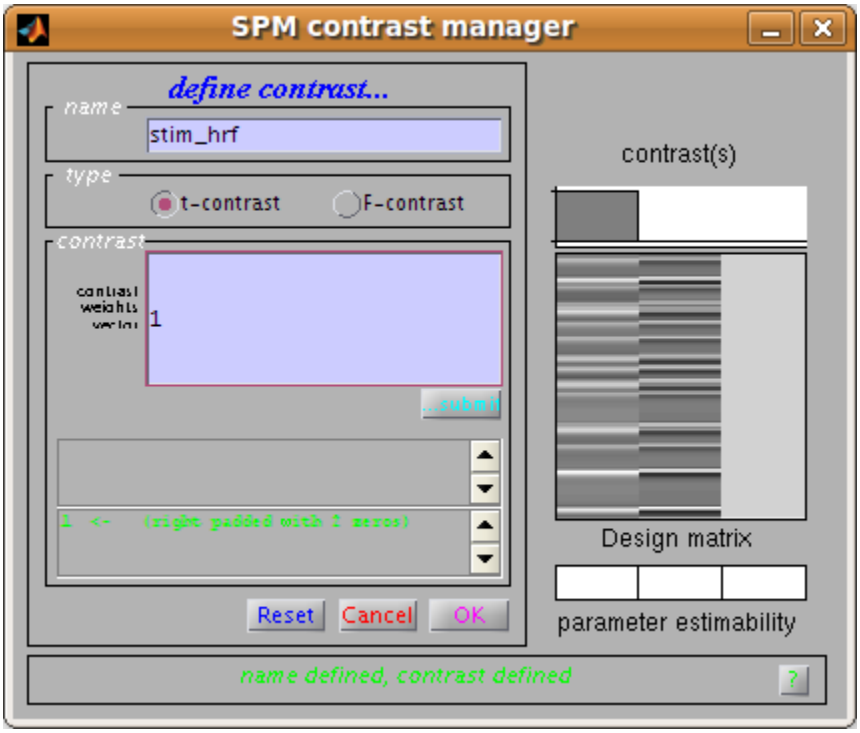
Our results so far show that there is indeed a highly significant effect of visual stimulation on the visual cortex, even for very frequent events. This is not a Nature paper so far. To make things a bit more interesting, we can compare this effect, from run 1, with the effect in run 3, for which the events were much less frequent.

Click on Design in the MarsBaR window, then Set design from file. Choose `SPM.mat` from `sess3/SPM8_ana`. Now we need to extract the data; select *Extract ROI data (default)* from the data menu. MarsBaR will ask you if you want to save the previous data. Why not say 'no' for the moment. Next choose `trim_stim_roi.mat` again. When that is done, run *Estimate results* from the Results menu. Again choose 'no' when asked if you want to save the previous estimated design.

Technical note - directories and saving results

MarsBaR, unlike SPM, does not need a new directory for each new set of results. Designs, results and data are kept in memory until you save them, and you can save them with any filename. This means you can keep many sets of results in the same directory.

When the estimation has finished, click on Results, *Statistic table*. Next you need to enter the HRF contrast. Earlier, we imported the HRF column contrast from an SPM model. To save time, why not enter this contrast directly using the contrast manager; it is just a t statistic with a single 1 in the first column:



In the end, you get a new statistic table:

```
Contrast name   ROI name: Contrast value:    t statistic:  Uncorrected P:    Corrected P
-----------------------------------------------------------------------------------------


stim_hrf
--------------------------


      trimmed stim run 2:           2.96:           3.98:       0.000061:       0.000061
```

You can see that the contrast value – which is proportional to the change in signal for a single event – is greater for run 3 than for run 1. Despite this, the t statistic for run 3 is lower than for run 1. One explanation for this is that there are many more events in run 1, so the estimate of signal change per event is more reliable (has less variance).

3.6 Using a structural ROI

So far we have used a functional ROI. This has the advantage that it is usually well tuned to the subject we are analysing. The disadvantages are that we have had to use a whole run of data to define the ROI, which we would have preferred to be able to analyze, and that functional ROIs can be noisy, when the activation signal is not strong. An alternative is to use the anatomy of the brain to estimate the location of functional areas.

Using anatomical ROIs can work well for areas that are naturally defined by brain structure, such as the subcortical nuclei, or the primary sensory and motor cortices, where the functional areas are closely linked to the position of large and relatively invariant sulci. Outside these areas, it can be difficult to define functional areas using anatomy alone. The problems are compounded when anatomical ROIs are defined on one subject, and applied to another, because there is great variability between subject in sulcal anatomy.

In the example experiment, subjects responded with a key-press each time they saw the flashing checker board. We might therefore be interested to know the level of activation in the putamen. This would be a good candidate for an anatomical ROI, because the putamen can be accurately defined on a structural scan, and does not vary much between subjects after spatial normalization. The AAL ROI library contains a definition of the left and right putamen for a

single subject after spatial normalization. The images from our subject have been spatially normalized, so the *AAL structural ROIs* definition of the putamen will probably give a reasonable approximation to the putamen in our data.

3.6.1 Running an analysis using structural ROIs

is exactly the same as running the analysis with the functional ROI. Select Design from the MarsBaR menu, and *Set design from file*. Choose `sess1/SPM8_ana/SPM.mat`. Click on Data, *Extract ROI data (default)*. When you are asked for ROI file, navigate to the MarsBaR *Example dataset* directory, then to the `rois` subdirectory, select `MNI_Putamen_L_roi.mat` and click Done. This is a copy of one of the *AAL structural ROIs*. When the data extraction is done, choose Results, *Estimate results* and wait till MarsBaR has done its thing. Select Results, *Statistic table*, enter the `stim_hrf` contrast, as shown in the figure above. Repeat the same procedure, using the copy of the AAL `MNI_Putamen_R_roi.mat` ROI. You will now have two tables.

One table for the left putamen:

```
Contrast name    ROI name: Contrast value:    t statistic:  Uncorrected P:    Corrected P
-------------------------------------------------------------------------------------------

stim_hrf
---------------------------

                 Putamen_L:           0.08:           0.77:       0.222894:       0.222894
```

and one for the right putamen:

```
Contrast name    ROI name: Contrast value:    t statistic:  Uncorrected P:    Corrected P
-------------------------------------------------------------------------------------------

stim_hrf
---------------------------

                 Putamen_R:           0.05:           0.50:       0.307312:       0.307312
```

The subject responded with their right hand, so we expected that the right putamen would have less signal than the left.

3.7 Batch mode

You can also run MarsBaR in batch mode. There is an example batch script in the `<marsbar>example/batch` directory, called `run_tutorial.m`. You won't be suprised to hear that this is a batch script that runs most of the steps in this tutorial, as well as extracting and plotting reconstructed event time courses.

3.8 The end

That is the end of this short guided tour. We haven't described the options interface, but then again, it isn't very interesting. As always, we would be very grateful to hear about any mistakes in this document or bugs in MarsBaR. You can find us on the MarsBaR mailing list - see *Support*.

May your regions always be as interesting as you hoped.

The MarsBaRistas

CHAPTER

FOUR

MARSBAR FAQ

4.1 What's with the fish?

When MarsBaR first starts, it flashes up a picture of a sardine. The sardine is a symbol of Marseille, the spiritual home of MarsBaR. To explain further, here's an excerpt from France Monthly online magazine, entitled **The Sardine That Blocked the Port Entrance**.

> "We" say, in France (understanding that the "we" excludes the people of Marseilles), that the people of Marseilles have a tendency to exaggerate their stories. And it is stated, by these local people, that one day a sardine (the little fish!) blocked the entrance to the port. But this is not said in jest, a slight distortion maybe! In 1778, the Viscount of Barras, officer of the marine infantry regiment from Pondichery in India was captured by the British. Benefiting from special accords for prisoner of war exchanges, he embarked the following year on a boat, named the "Sartine", which was not armed. To prevent potential attacks upon it, the captain would raise certain cartel flags that the enemy would recognize. However, the rule was not respected, because on May 1st, 10 months after being at sea without incident, a British war boat attacked the "Sartine" with two fatal canon volleys. The ship finished its trip and ran aground at the entrance to the old port. It is therefore not a "sardine" that blocked the port of Marseilles but a ship named "La Sartine", on a beautiful spring day in 1780!

4.2 Why do I get an error "Cant open image file" when estimating a design?

This occurs when the filenames in your SPM or MarsBaR design no longer point to valid files. For example, when you first estimated the design, the time series images might have been in a directory called `/now/dead/directory` - like this:

```
/now/dead/directory/subject1/sess1/image_01.img
/now/dead/directory/subject1/sess1/image_02.img
...
/now/dead/directory/subject1/sess2/image_01.img
...
/now/dead/directory/subject2/sess1/image_01.img
```

etc.

Time passed, you reorganized your files, and these images have now moved to another directory, like this:

```
/currently/extant/path/subject1/sess1/image_01.img
/currently/extant/path/subject1/sess1/image_02.img
...
/currently/extant/path/subject1/sess2/image_01.img
```

```
...
/currently/extant/path/subject2/sess1/image_01.img
```

etc.

When you ask MarsBaR to estimate the original design, it looks for `/now/dead/directory/subject1/sess1/image_01.img`, but the file does not exist. To fix this, you will need to change the filenames in the design to match the new image locations.

You can first check if this is the problem. Click on Design and choose *Check image names in design*. You should see an error message in the matlab console window if the images are not where the design says they are.

Next, you need to find the correct root path to the images. The root path is the shared common path for all the image names. In the above example, the shared common path for the correct image filenames is `/currently/extant/path`.

To do the fix, you click on Design and choose *Change design path to images*. In the SPM input window you will see the current root directory printed in bold text. In the example above, this would be: `/now/dead/directory`.

You select `/currently/extant/path` using the SPM file selection window that has just appeared. If all went well, you can check it has worked; click Design, choose *Check image names in design* and hope that you get the message `All images in design appear to exist` in the matlab window.

The same thing from the command line would be:

```
D = mardo('/path/to/spm/mat/SPM.mat');
D = cd_images(D, '/currently/extant/path');
save_spm(D);
```

4.3 How is the percent signal change calculated?

Good question. Let us imagine that you had an FMRI design with one event type, which is a flashing checkerboard. There is only one session of data. The events are all modeled with a haemodynamic response function (HRF) and the temporal derivative (TD). You run the MarsBaR model on these data, for an ROI in the visual cortex. Now you want the percent signal change.

Here's how it goes. You select the event using the MarsBaR percent signal change interface. MarsBaR does the following:

1. Finds the betas for this event. In this case the relevant betas are the first two betas, the beta for the HRF, and the beta for the TD.
2. Makes a new regressor for a single event. Remember that the best estimate of the signal due to the event is the beta values for this event multiplied by the regressors in the design matrix. So, to reconstruct the height of a single event of this type, we need to multiply the betas that we have calculated in the model by a regressor which is like the SPM design matrix regressor in scaling, but which is just for a single event. To do this we specify the duration of the event we want to estimate the height for, and run a single event of this duration back through the SPM design matrix machinery, to make the regressor(s) SPM would have used for just this single event. In this case we will get an HRF regressor and a TD regressor.
3. Next we multiply the betas that we have by the regressors (HRF beta * HRF regressor, TD beta * TD regressor), and sum up the two resulting time courses, to get the estimated event response for a single event of this event type. To get the size of the response, for now, we just take the maximum height of the reconstructed event. Let's say this is about 0.2 units.
4. We've said 0.2 units, but units of what? SPM scales the mean of all the in-brain voxels in the session to be 100 (see this SPM statistics tutorial for more detail on the scaling procedure). So, 0.2 units means 0.2 percent of the whole brain mean signal (in the rather strange SPM sense). The problem with this is, that gray matter has

a higher signal than the brain average. In fact, if the whole brain mean is 100, the gray matter signal tends to be about 180-200. We want to calculate signal change relative to the baseline in this ROI, so we do not want to use the value 100 as the baseline, we want to use the actual mean signal in this ROI, which will likely be in the range of 180-200. The next step is therefore to get the mean signal in the ROI. For this, we simply get the beta for the mean column for this session. You remember that SPM removes the mean signal within a session by using a session regressor which is just 1s in the scans for this session and zeros elsewhere. These columns are the last columns in the design matrix. In our case the mean column is the third (and last) column, so, to get the session mean, we just take the third (and last) beta. By doing this, we've ignored some complexities, to do with the mean-centering of the regressors in the design matrix, but let's just quietly sweep that under the carpet. There, all gone.

5. Let's say our session mean was 192. Now, to get percent signal change, we just divide 0.2 by 192. We get roughly 0.001. The last step is to multiply by 100 to get percent signal change - which gives (roughly) 0.1.

The values you get may be rather small compared to reported values for - say - signal change for a block of visual stimuation. In fact you may well get signal change values that are less than 0.1 percent. Your event may not be comparable to these reports. First, your events may be short, which will of course give less maximum signal change than a long block. Second, cognitive events usually give lower signal change than events affecting primary motor or sensory cortex.

4.4 How do I run a MarsBaR analysis in batch mode?

Here is a tiny example of a batch mode script. It assumes you have a design which has been estimated in SPM, and has a set of contrasts specified.

This example script assumes your design is stored in `/my/path/SPM.mat` and you have an ROI stored in `/my/path/my_roi.mat`:

```
spm_name = '/my/path/SPM.mat';
roi_file = '/my/path/my_roi.mat';

% Make marsbar design object
D  = mardo(spm_name);
% Make marsbar ROI object
R  = maroi(roi_file);
% Fetch data into marsbar data object
Y  = get_marsy(R, D, 'mean');
% Get contrasts from original design
xCon = get_contrasts(D);
% Estimate design on ROI data
E = estimate(D, Y);
% Put contrasts from original design back into design object
E = set_contrasts(E, xCon);
% get design betas
b = betas(E);
% get stats and stuff for all contrasts into statistics structure
marsS = compute_contrasts(E, 1:length(xCon));
```

See the help for the compute_contrasts function for details on the contents of the marsS structure.

4.5 How can I extract the percent of activated voxels from an ROI?

There is no easy way of doing this using the MarsBaR GUI, but you can do it using scipts like this one:

```
roi_file = 'my_roi.mat';
t_imgs = strvcat('spmT_0002.img', 'spmT_0003.img');
thresholds = [3.4 4.6];
roi_obj = maroi(roi_file);
y = getdata(roi_obj, t_imgs);
n_voxels = size(y, 2);
for i = 1:size(t_imgs, 1)
  pc_above_thresh(i) = sum(y(i,:) > thresholds(i)) / n_voxels * 100;
end
```

4.6 How do I get timecourses from images in an SPM design?

In the GUI, choose Data - Extract ROI data (default). Select your ROIs and your design (if you had not set it previously). MarsBaR extracts the data; you can then plot it or save it in various formats using Data - Export. In script form, this would be something like:

```
roi_files = spm_get(Inf,'*roi.mat', 'Select ROI files');
des_path = spm_get(1, 'SPM.mat', 'Select SPM.mat');
rois = maroi('load_cell', roi_files); % make maroi ROI objects
des = mardo(des_path);  % make mardo design object
mY = get_marsy(rois{:}, des, 'mean'); % extract data into marsy data object
y  = summary_data(mY);  % get summary time course(s)
```

4.7 I just want to get raw timecourses from some images; how do I do that?

This can be done from the GUI. Select Data - Extract ROI data (full options). Select the ROIs, say No to use SPM design, Other for type of images, 1 for number of subjects. Select the images you want to extract data from, Raw data for scaling, and 0 for grand mean. Now you can plot the data from the GUI, or save in various formats using Data - Export data. The script to do this might be:

```
roi_files = spm_get(Inf,'*roi.mat', 'Select ROI files');
P = spm_get(Inf,'*.img','Select images');
rois = maroi('load_cell', roi_files);  % make maroi ROI objects
mY = get_marsy(rois{:}, P, 'mean');  % extract data into marsy data object
y = summary_data(mY); % get summary time course(s)
```

4.8 I get errors using the SPM ReML estimation for FMRI designs. Can I try something else?

Why yes, in fact you can. MarsBaR includes the AR modelling from Keith Worsley's fmristat program, which is a good alternative to the standard SPM ReML for FMRI. To use this, load your design in the GUI, then choose Design - Add/Edit filter for SPM design. Set the high-pass filter as you wish, and then choose "fmristat AR(n)" for serial autocorrelations. Set the order of the model (AR(1), AR(2) etc) - 2 is a good choice. Estimate the model in the usual way.

In batch mode this would look like:

```
% Make marsbar design object
D  = mardo(spm_name);
% Set fmristat AR modelling
D = autocorr(D, 'fmristat', 2);
```

4.9 How is the FIR (or PSTH) calculated?

MarsBaR and SPM use FIR models to calculate the PSTH (peri-stimulus time histogram). By default, the FIR models have a time bin of one TR. Let us imagine your TR is one second, as is your FIR time-bin. You can then think of the FIR as calculating the best estimate of the signal 0 seconds, 1 seconds, 2 seconds after the event has occurred, and after adjusting for other effects in the model.

As this is just a very similar approach to averaging, there is no constraint that the signal should be at zero at 0 seconds. Just for example, random noise will mean than the average signal at 0 seconds will not be exactly zero.

For more information on the FIR method used for the PSTH, you might want to have a look at these papers:

> Ollinger JM, Shulman GL, Corbetta M. Separating processes within a trial in event-related functional MRI. Neuroimage. 2001 Jan;13(1):210-7.
>
> Dale AM. Optimal experimental design for event-related fMRI. Hum Brain Mapp. 1999;8(2-3):109-14.

Russ Poldrack also has a useful page on FIR modelling.

4.10 How do I extract all the FIR timecourses from my design?

You can of course do this via the GUI. The most efficient is to do it with a batch script. You have already run the batch script above up to `E = estimate(D, Y);`. Then:

```
% Get definitions of all events in model
[e_specs, e_names] = event_specs(E);
n_events = size(e_specs, 2);
% Bin size in seconds for FIR
bin_size = tr(E);
% Length of FIR in seconds
fir_length = 24;
% Number of FIR time bins to cover length of FIR
bin_no = fir_length / bin_size;
% Options - here 'single' FIR model, return estimated
opts = struct('single', 1, 'percent', 1);
% Return time courses for all events in fir_tc matrix
for e_s = 1:n_events
  fir_tc(:, e_s) = event_fitted_fir(E, e_specs(:,e_s), bin_size, ...
                                    bin_no, opts);
end
```

If your events have the same name across sessions, and you want to average across the events with the same name:

```
% Get compound event types structure
ets = event_types_named(E);
n_event_types = length(ets);
% Bin size in seconds for FIR
bin_size = tr(E);
% Length of FIR in seconds
fir_length = 24;
```

```
% Number of FIR time bins to cover length of FIR
bin_no = fir_length / bin_size;
% Options - here 'single' FIR model, return estimated % signal change
opts = struct('single', 1, 'percent', 1);
for e_t = 1:n_event_types
   fir_tc(:, e_t) = event_fitted_fir(E, ets(e_t).e_spec, bin_size, ...
      bin_no, opts);
end
```

4.11 How do I extract percent signal change from my design using batch?

Maybe something like this:

```
% Get definitions of all events in model
[e_specs, e_names] = event_specs(E);
n_events = size(e_specs, 2);
dur = 0;
% Return percent signal esimate for all events in design
for e_s = 1:n_events
  pct_ev(e_s) = event_signal(E, e_specs(:,e_s), dur);
end
```

See also the documentation for event_signal.m.

4.12 How do I do a random effect analysis in MarsBaR?

There are two ways to do this.

1. Do your ROI analysis for each subject. From the GUI, or via batch mode, extract the "contrast value" for your t contrast of interest. Put these values into a matlab matrix, with one value per subject (to take the simplest case). You have two ways to go from there. Either export this matrix to a spreadsheet or text file, and run the statistics using another statistics program, or load the SPM random effects design into MarsBaR, import your matlab matrix as the data, and run the random effects analysis in MarsBaR.
2. Run the full SPM analysis for each subject. Write out the contrast image for the contrast of interest. Run the random effects design in SPM. Then, import the random effects design into MarsBaR, and run it using your ROI. Here you are extracting the (e.g.) mean contrast value within the ROI for each subject, and using that as your estimate of the effect for that subject.

If you do ordinary least squares (OLS) analyses at the single-subject level, these two approaches will give you the exact same answer. OLS is the analysis that does not try to correct for auto-correlation in the data.

If you did not use OLS, then the first approach is more valid, as in this case, you have estimated the autocorrelation from the ROI itself, rather than the whole (activated) brain, which is the default SPM approach.

OLS at the single subject level is valid (is not biased), but is likely to be less powerful than the alternative (which is removing the autocorrelation - "whitening"). In practice the difference between using and not using OLS is often small.

The first approach also saves you having to run the SPM models at the single subject level, but you have often done this in any case.

4.13 Should I use MarsBaR ROI analysis, or small volume correction (SVC) in SPM?

Good question - thanks for asking. The two approaches will give answers to different questions. MarsBaR asks something like "does area A on average activate more for condition 1 than condition 2", whereas SVC asks "given I am only looking within the voxels of area A, are there any voxels in A that I can be confident are more active in condition 1 than condition 2". Thus, if you have a good idea of the region you are interested in, and believe that the response should be relatively homogenous across the region, then the MarsBaR question is likely to be the closest to the one you want to answer. However, if you do not have a good idea of the exact definition of the region you are interested in, and think there may will be different responses in different parts of the region that you define, then you might prefer SVC, which can detect peaks of activity even if the rest of the region is not activated, or even is negative.

Of course, the meaning of the results is slightly different. SVC allows you to say that some part of your candidate region is active (allowing for example that most of it could be deactivated). MarsBaR would likely find no significant change in that situation.

Summary: which you prefer depends on the exact question you want to answer, which in turn depends on the region definition that you are using.

4.14 Should I use smoothed or unsmoothed images for my MarsBaR analysis?

Of course, you can also think of using smoothed images as using a smoothed version of your ROI definition. Deciding whether to smooth is a trade-off between trying to:

1. increase voxel-to-voxel signal to noise, and
2. avoid polluting region signal by signal from nearby structures.

So, if your region definition is a conservative one in the centre of a large structure that you believe to be homogenous, then you might opt for image smoothing, on the basis that the risk from nearby signal is rather small. If your region was well-defined, and surrounded by other things such as CSF that you really wanted to avoid, you would probably choose unsmoothed images. The hippocampus strikes me as a good example of the latter...

4.15 Why can't I select files like SPM designs in the matlab GUI?

If you are running matlab 7 on Linux, you may have difficulty with the matlab GUI routines that MarsBaR uses to select files, like SPM designs and ROI data.

This is caused by a bug in matlab. You may find documentation for this by searching the Matlab site with the terms "uigetfile linux". It's a bizarre bug, which causes matlab to appear not to find files when you click on them in the matlab "uigetfile" interface that MarsBaR uses. If you are using the default method of running matlab, which uses the fancy Java desktop, you can get round it using the workaround documented at the link above, which is to run the following command:

```
setappdata(0,'UseNativeSystemDialogs',false)
```

in matlab, before you ever start a file selection dialog, such as those in MarsBaR. Future versions of MarsBaR will do this automatically. This fix doesn't work if you are running in non-Java mode - which is what you get if you start matlab with `matlab -nojvm`. In that case, you will need to either select the file using the keyboard, rather than the mouse, or type the file name directly into the file selection box. There are some other odd wrinkles to the behaviour of the uigetfile interface in matlab 7, which should be fixed in marsbar version 0.40 and above. For details, search for comments containing 'uigetfile' in mars_uifile.m.

4.16 Why do I get a "No valid data for roi" warning when extracting data?

You might run into a warning like this:

```
> Warning: No valid data for roi 1 ...
```

This is almost invariably because you are sampling from SPM results images, that have NaNs at the edges of the brain. Marsbar uses linear resampling by default to get the data from the images, so voxels at the edge of the brain disappear due to resampling with NaN values. The fix is to change the ROI resampling to nearest neighbour using something like:

```
roi_filename = 'my_roi.mat';
my_roi = maroi(roi_filename);
my_roi = spm_hold(my_roi, 0); % set NN resampling
saveroi(my_roi, roi_filename);
```

and then rerun the data extraction...

CHAPTER

FIVE

SUPPORT

We hope it is clear how to use MarsBaR, but please let us know if you have problems. In particular, we would be very glad to hear of any bugs or inconsistencies.

There is a mailing list for MarsBaR; list archives and instructions for posting are available via the MarsBaR users mailing list page. There is also a MarsBaR mailing list archive. Gmane also provides a nice interface to recent MarsBaR emails.

CHAPTER

SIX

READING AND WRITING MARSBAR CODE

Contents:

6.1 Getting the latest development code

MarsBaR code is on github - see marsbar github.

For instructions on getting the code, making patches or being a developer, see using-git.

6.2 API documentation

The MarsBaR code is reasonably well documented; we export this documentation as web pages using Guillaume Flandin's excellent m2html. The API documents are in the apidocs directory of the documentation.

CHAPTER

SEVEN

INDICES AND TABLES

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