

# **HowTo: estimate HRF with RaBIDS**

User manual on how to estimate hemodynamic response function parameters using the inverse logit model (Lindquist & Wager, 2007) and marsbar (Brett et al., 2002).

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# 1 About

This manual explains how users of RaBIDS can use two toolboxes to estimate HRF parameters:

- Inverse logit HRF model: Code is available in the CanlabCore package (<https://canlab.github.io/>). The template code can be accessed here: CanlabCore\HRF\_Est\_Toolbox2\Example.m.
- Marsbar: Toolbox for ROI definition and parameter extraction, see <http://marsbar.sourceforge.net>

The scripts from this manual are available on my github, see RaBIDS project in the auxiliary tools directory (<https://github.com/christianparet/RaBIDS/tree/master/auxiliary%20tools>).

## Assumptions that must be met:

- fMRI derivative data (i.e., preprocessed data) is available in BIDS. The program has been developed with derivative data from fMRIPrep version 20.0.6 or later; note that data may look differently if you used other pipelines for preprocessing and the scripts may crash.
- A RaBIDS-datasheet is available and has the information that was used for import to BIDS (tested with RaBIDS version 0.2.2)
- Runs with spm12, tested with Matlab R2022a.
- The CanlabCore and/or the marsbar toolbox can be accessed by matlab. The path needs to be defined in the scripts.
- Works only for experiments with a single session (i.e., only one “scan”, in SPM terminology, enters the first level model for each subject)

## 2 Inverse logit HRF model

### 2.1 RaBIDS pipeline overview

You need to run firstlevel (i.e. subject-level) analysis on preprocessed, smoothed data first, using RaBIDS with SPM12. It is strongly recommended to use the program `SPManalysis_2_firstlevel.m` for firstlevel analysis, which is available in RaBIDS auxiliary tools. Contrast #1 of the resulting SPM-model has to be the contrast of your effects of interest (eoi). Usually, this is an F-contrast of all effects that you are going to analyse in subsequent analysis. Make sure to follow recommendations for contrast definition as explained in the RaBIDS manual.

When firstlevel data are available, download the two scripts to your code directory, which are available in the auxiliary tools:

1. `ROIanalysis_1_extract_eigenvariate.m`
2. `ROIanalysis_2_ilogitHRFmodel.m`

### 2.2 Extract eigenvariate

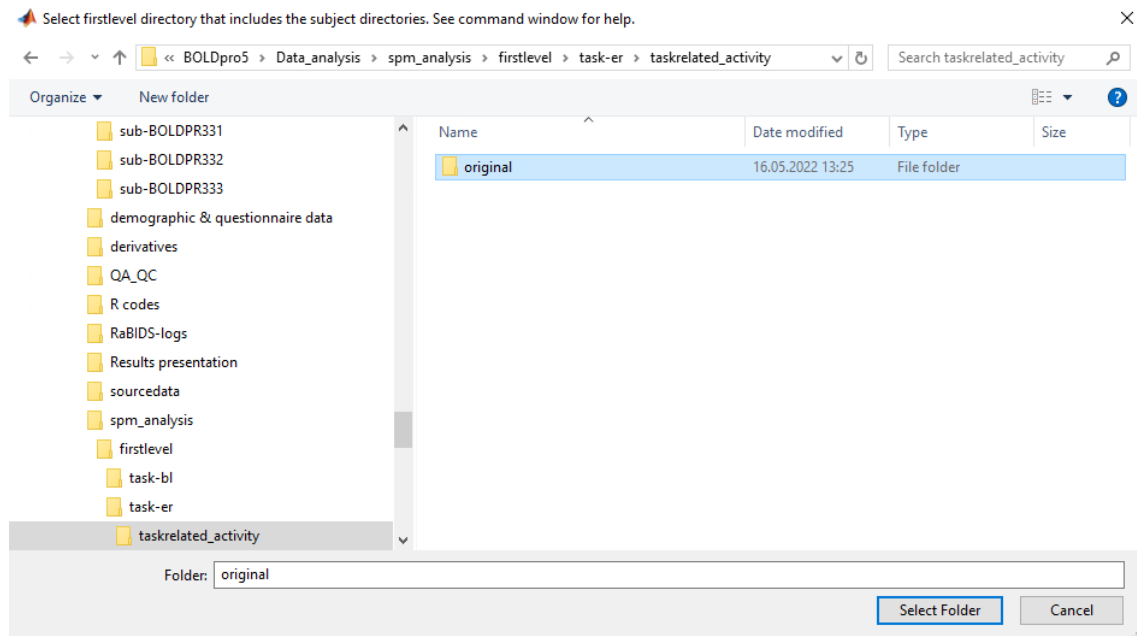
The first script named “`ROIanalysis_1_extract_eigenvariate.m`” uses SPM’s VOI utility tool to extract the Eigenvariate from defined brain voxels. To use the tool you need to provide one or more nifti-images defining the voxels in subject space (in this case it is MNI space). Such images can be prepared e.g. with the marsbar toolbox. Save the mask(s) in a separate directory.

The Eigenvariate corresponds to the BOLD time course, adusted for the eoi (i.e., confounds are regressed out). As a default, the eoi contrast is expected to be contrast number one in the SPM-model, but this can be changed in the script (search for variable “eoi”).

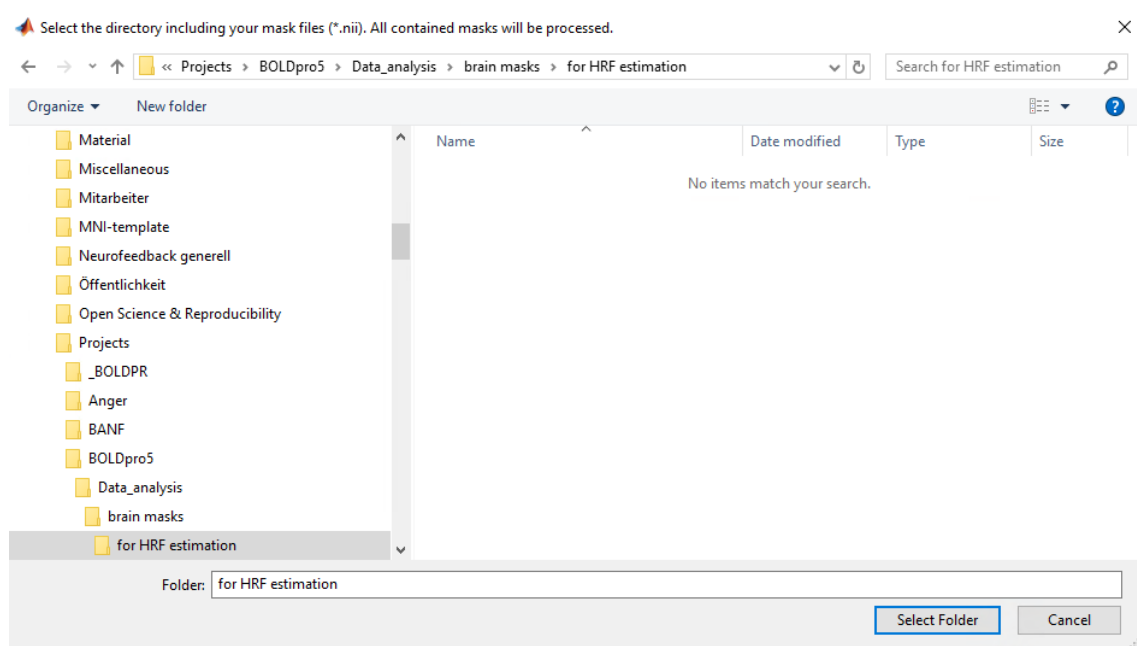
When you run the script it asks you to select the firstlevel directory including the subject directories. In RaBIDS file structure this is most often a directory such as YOUR-

PROJECT-DIRECTORY\Data\_analysis\spm\_analysis\firstlevel\task-TASKID\taskrelated\_activity\original.

See figure for an applied example; the Folder: “original” has been selected:



Once a folder has been selected, a second window pops up and asks for the directory including the mask files for signal extraction. Select the directory containing your mask file(s) and press “Select Folder”. Note: the dialogue does not display the mask files in your directory. Example:



For each subject, the script generates (a) nifti file(s) with a copy of the mask(s) and (a) matlab file(s) with the Eigenvariate data, e.g. “VOI\_mask-

RightAmygdala25\_sess\_1.mat”, where “RightAmygdala25” is the name of one of the masks used for signal extraction. The files can be found in the subject-directories.

## 2.3 Model HRF

Open the program “ROIanalysis\_2\_ilogitHRFmodel.m” and scroll to the “Settings” section. It looks sth like this:

```

25 %% Settings
26 VOIname = 'RightAmygdala25'; % enter VOI name; e.g. if file name is VOI_mask-visualcortex_sess_1.mat: VOIname = 'visualcortex';
27
28 origTR = 2; % original TR in seconds
29 resampleTR = 0.01; % resample to TR (seconds), should be in the order of stimulus onset time (SOT) resolution
30 interpolmeth = 'spline'; % spline, pchip or makima. Not clear which one is better
31 getFIR = 0; % FIR fitting fails with resampleTR<0.01
32 T = 30; % unit=seconds
33 FWHM = 4; % FWHM for residual scan
34 pval = 0.01;
35 df = 600;
36 alpha = 0.001;

```

Define the parameters according to your study:

- VOIname
- origTR
- resampleTR\*
- interpolmeth\*
- getFIR\*

Parameter with an asterisk are explained below.

The remaining parameters are default and were taken from the HRF\_Est\_Toolbox2 Example script.

### 2.3.1 resampleTR

It is only possible to use the HRF\_Est\_Toolbox2 toolbox with stimulus onset times (SOTs) defined at the resolution of the sampled timecourse (i.e., the eigenvariate, which has resolution=TR). This is not often the case. For precise modeling it is necessary to upsample the timecourse data using interpolation; otherwise SOTs are rounded to the next sample and HRF parameters would end up inaccurate. Define “resampleTR” according to requirements of your study. I do not see a reason to upsample higher than 0.01.

**CAVE:** The upsampling procedure has not yet been double-checked until 2022/05/16! It works, but whether results are prone to errors remains to be assessed.

### 2.3.2 Interpolmeth

Interpolation method used for upsampling. Currently, there are three methods available in matlab: spline, pchip, makima. To learn more about each method consult the matlab help center (<https://www.mathworks.com/help/matlab/ref/spline.html>).

**CAVE:** I did not assess pros/cons of each method and did not consult with experts what method may be better/worse. Before conclusions are drawn from data, it should be double-checked whether results change when a different interpolation method is used. Status from 2022/05/16.

### 2.3.3 getFIR

The program will not only return estimates from the ilogit model, but additionally returns HRF parameters from estimation with SPM's standard HRF model. Furthermore, it is possible to estimate HRF parameters using a smoothed FIR approach. However, this procedure crashes with high values for upsampling such as resampleTR=0.01 and higher. Therefore, getFIR should only be switched on (i.e., set to '1') if one resamples to a sufficiently low TR.

## 2.4 Cave: Warnings/preliminary status

There are still things that need to be double-checked (see also above), including warning messages. The "Warning: Matrix is close to singular or badly scaled. Results may be inaccurate" is not fully clear. My take is that it has to do with Power Loss estimation and probably does not affect parameter estimation. Also, the approach for AUC quantification should be reviewed by an expert.

## 2.5 Additional comments

- When you re-run the program with different settings it will overwrite previous data
- Firstlevel results are saved to subject directories

- Grouplevel results are saved next to the subject directories
- A readme file is saved next to the subject directories with meta-data
- A matlab-diary file is saved next to the subject directories for revision of e.g. warning messages

### **3 Marsbar**

Download “ROIanalysis\_1\_marsbar\_HRFmodel.m” to code directory. Firstlevel data need to be available as explained above. No eigenvariate extraction is necessary.

Steps for selection of firstlevel directory and mask files are similar as above. Note that marsbar needs the masks to be in a different format and they should end with “yourmaskname\_roi.mat”. Such files can be prepared with the marsbar toolbox.

## 4 References

Lindquist, M.A., Wager, T.D., 2007. Validity and Power in Hemodynamic Response Modeling: A Comparison Study and a New Approach. *Hum Brain Mapp* 28, 764–784. <https://doi.org/10.1002/hbm.20310>

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.