

## rsHRF: A Toolbox for Resting State HRF Deconvolution and Connectivity Analysis (MATLAB)

repo size 99.9 MB release **v2.2** downloads@v2.2 0 dependencies SPM open issues 2 closed issues 4 all contributors 3 License BSD 3-Clause

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**v2.2**

**MATLAB.** The current GitHub repository contains the MATLAB code for *rsHRF deconvolution and connectivity analysis*, both for 1) the MATLAB Standalone as well as 2) the SPM plugin (**v2.2**).

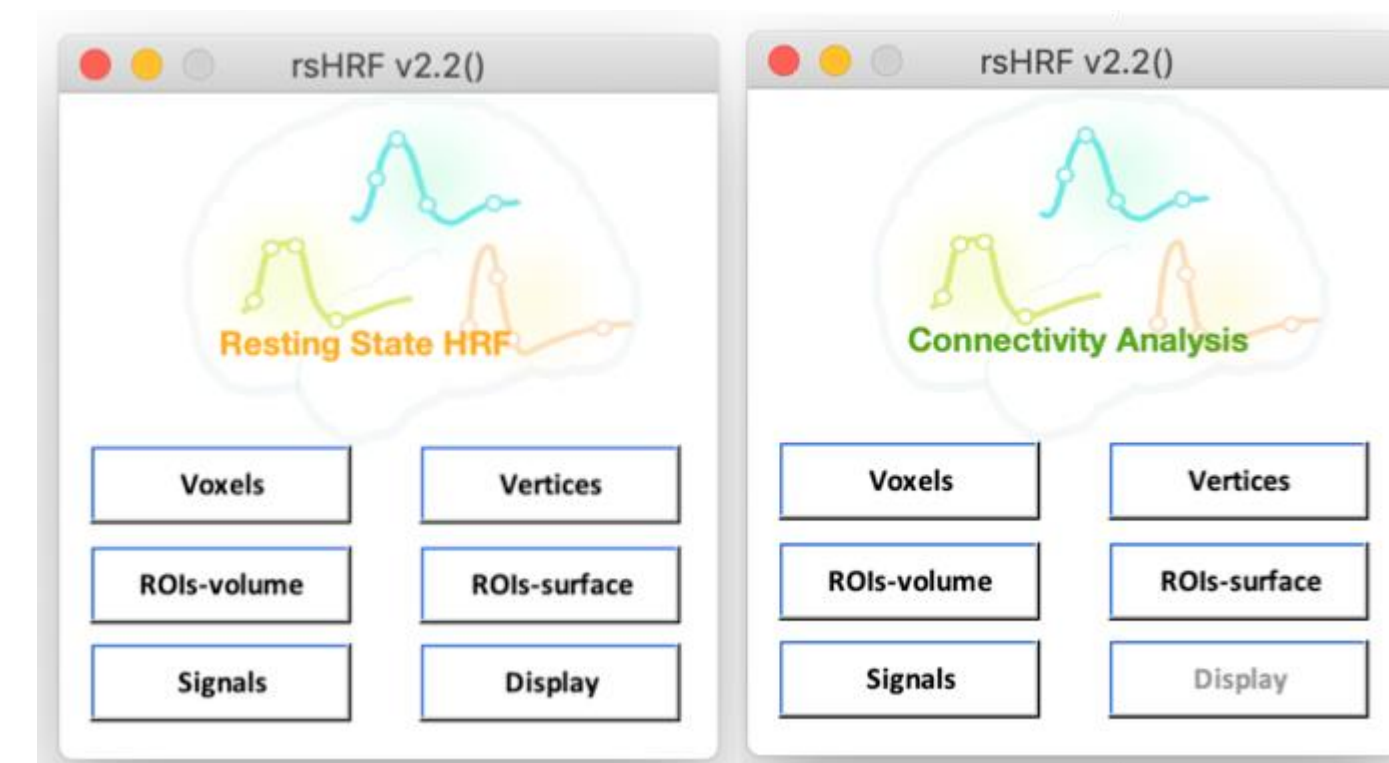
**Python.** For information concerning 1) the Python Standalone, along with 2) the BIDS-App through Dockers, head over to <https://github.com/BIDS-Apps/rsHRF>!

### v2.2 Additional features and analyses

rsHRF v2.2

! Main modifications (M):

- **surface-based analysis:** a surface-based analysis module has been added to the processing pipeline which you can select by clicking on either the **vertices** (whole-brain analysis) or **ROI-surface** (ROI analysis) panel in the GUI.
- **rsHRF estimation method:** the HRF basis functions have been updated, i.e. Canonical/Gamma/Fourier basis functions (`rsHRF_estimation_temporal_basis.m`), and an update of the (s)FIR model (`rsHRF_estimation_FIR.m`) using AR(k) for autocorrelated noise modeling has been added, along with a m-file (`rsHRF_estimation_impulseest.m`) for non-parametric impulse response estimation (which is not included in the rsHRF GUI).
- **visualization of rsHRF shapes:** the rsHRF shapes can be visualized by clicking on the **Display** panel in the GUI. The underlying script (`rsHRF_viewer.m`) has been added to the `rsHRF/code/` folder.
- **connectivity analysis:** a m-file (`rsHRF_mvgc.m`) for multivariate Granger causality analysis has been added to the processing pipeline.



A schematic overview of the rsHRF and connectivity analysis GUI, which are available as an SPM plugin.

### v2.2 Extended user documentation


- History and Development
- Installation
- Overview and Usage
- Workflow
- FAQ

#### Dependencies

To successfully run the MATLAB code for *rsHRF deconvolution and connectivity analysis*, **MATLAB** and **SPM** should be installed. SPM is still necessary because the MATLAB code uses some of its basis functions (e.g. `spm_vol.m`, `spm_read_vols.m`, ...). After completing the installation, open MATLAB and add the SPM directory including all its folders and subfolders to the MATLAB search path:

```
spmdir = '/path/to/spm12/';
addpath(genpath(spmdir));
```

#### Download the release version of your choice

To download the release version of your choice (i.e. either v1.0, v2.0, or v2.2) as a *rsHRF* zip folder in your `Downloads` folder, right-click on the corresponding  here below and open the link in a new tab. For each release version, the main code modifications are listed; open the collapsibles to have a closer look. For more information, head over to the [HISTORY PAGE](#)!

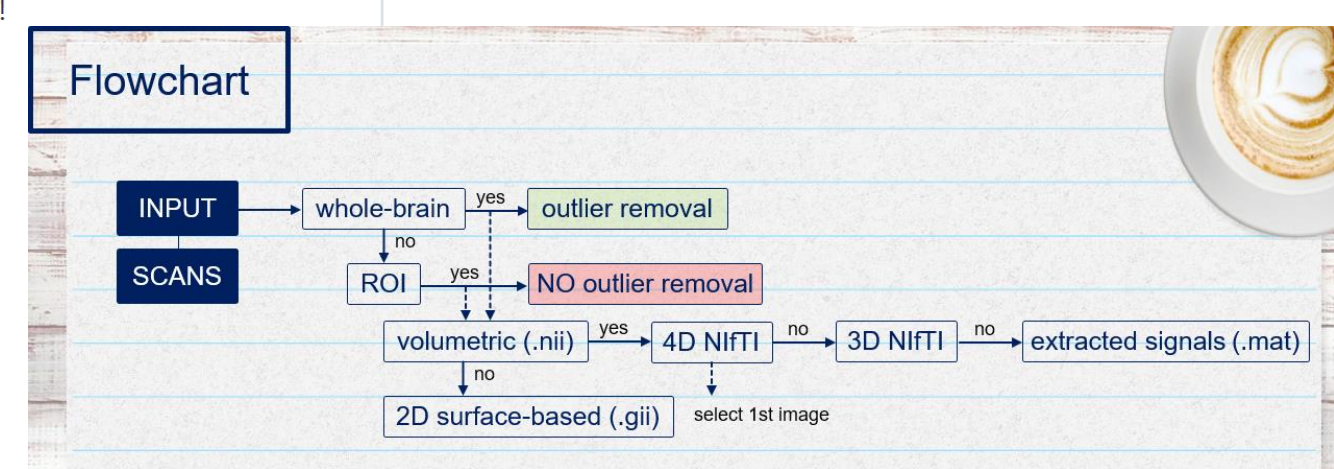
REMARK: Examples for *rsHRF connectivity analysis* (functional connectivity: Pearson/Spearman correlation, Pairwise/Conditional/Partially Conditioned Granger causality) are only provided for the rsHRF SPM plugin.

#### MATLAB Standalone

scripts located in  
`rsHRF/code/demo/`

#### SPM plugin

`rsHRF/documentation/demo/demo_jobs.zip`  
`rsHRF/documentation/rsHRF_toolbox.pptx`



## HRF estimation: fMRI - BOLD signal - General Linear Model (GLM)

Linear Time Invariant model

$$y(t) = s(t) \otimes h(t) + c + \varepsilon(t)$$

The processed BOLD signal at time  $t$ ,  $y(t)$ , is modeled as the convolution of:

- neural state  $s(t)$  and
- a hemodynamic response function (HRF)  $h(t)$ ,

where  $\otimes$  denotes convolution,  $\varepsilon(t)$  is the unexplained error and  $c$  indicates the baseline magnitude

**Goal:** retrieve the HRF by solving the equation for  $h(t)$

**Problem:**

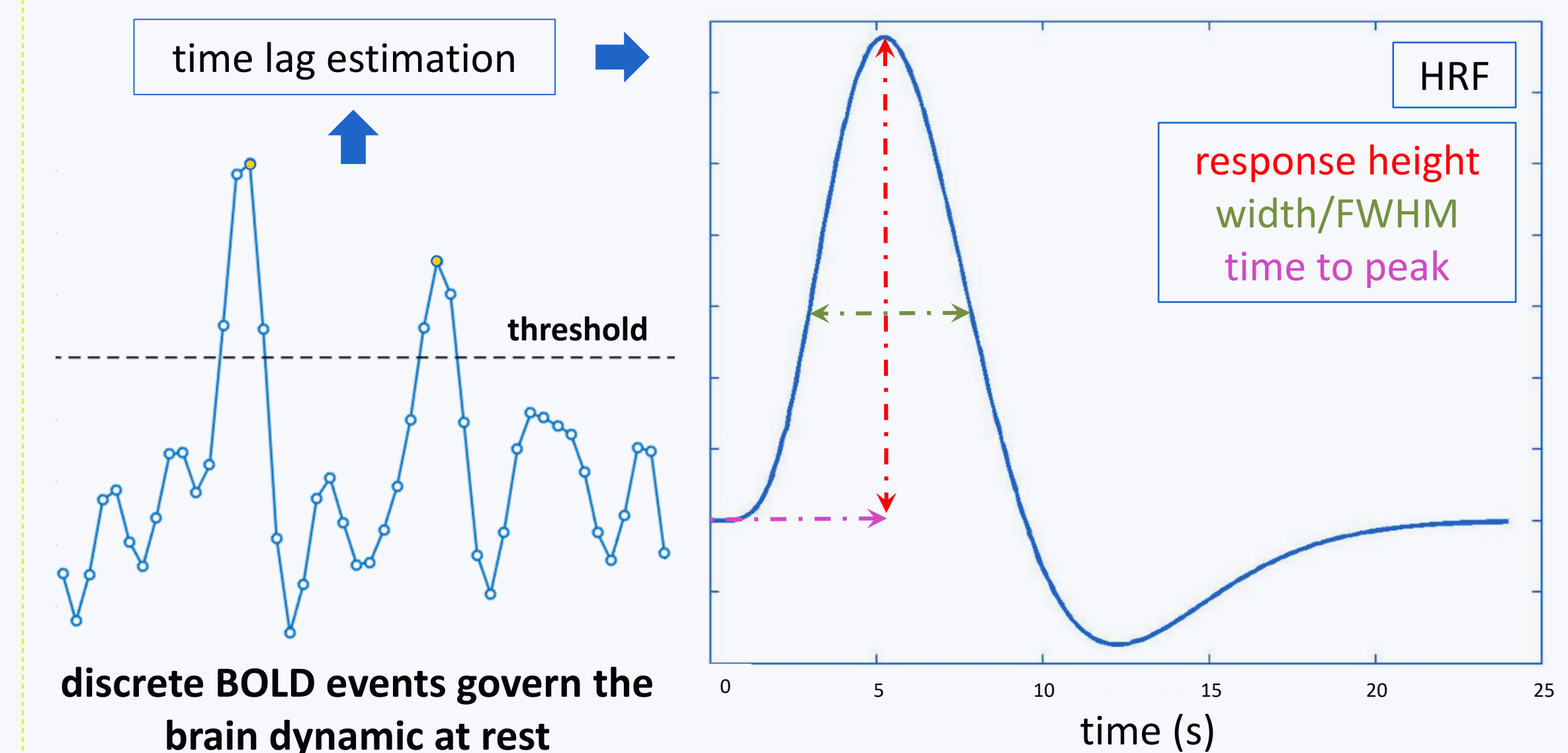
#### Task fMRI

$s(t)$  could be substituted with a hypothetical model of the neural activation for  $s(t)$ , i.e. stimulus function

#### rs-fMRI

no explicit stimulus and timing for HRF onset

**Solution:** estimate the shape of the rs-HRF using the rs-fMRI blind HRF retrieval approach developed by Wu and colleagues (2013)



Once the rs-HRF is retrieved, it can be used to:

1. map it onto the brain surface and look at its variability
2. deconvolve BOLD data in order to eliminate confounders on temporal precedence (connectivity analysis)

## !!! Contribute !!!

User feedback through GitHub or the NITRC fora ([https://www.nitrc.org/forum/?group\\_id=1304](https://www.nitrc.org/forum/?group_id=1304)) is encouraged to improve the toolbox and its user documentation even more; users' questions and suggestions will be addressed to our best ability and, when applicable, integrated into the toolbox and its user documentation.

#### Reference:

Wu, G. R., Liao, W., Stramaglia, S., Ding, J. R., Chen, H., & Marinazzo, D. (2013). A blind deconvolution approach to recover effective connectivity [...]. *Medical Image Analysis*, vol. 17, no. 3, pp. 365-374.