

# -hMRI-toolbox-

## Session II: summary & demonstration & compiled version

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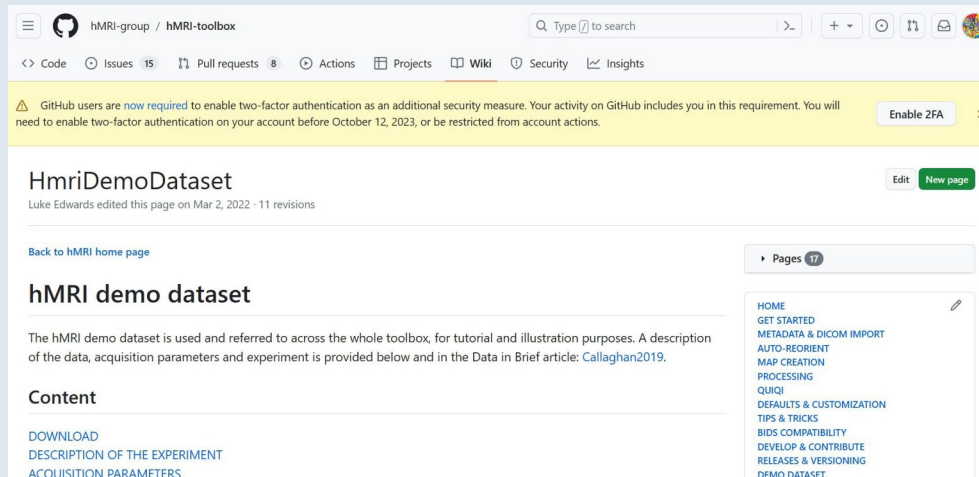
**MAX-PLANCK-INSTITUT**  
FÜR KOGNITIONS- UND NEUROWISSENSCHAFTEN



## **Session-I (19.10.2023) and abstract:**

The hMRI-toolbox is a state-of-the-art software tool for processing MRI data. In this workshop-tutorial for users, we will quickly cover the structure of the input data, output data, the main processing workflow and the filesystem (that involves the files that carry metadata information) created by the toolbox at the end of the runtime. We will give several examples of visualizations of the output image data with different color maps. Afterwards, we will demonstrate the main functionality of the latest release (v0.6.0) by using the publicly available data. Time permitting, we will also introduce the compiled version and explain the steps of compilation of the toolbox which can be run directly on the Linux command line by calling the Matlab runtime.

# hMRI demo dataset



- acquired on a whole body 3T Prisma system (Siemens Healthcare, Erlangen, Germany).
- to illustrate the hMRI-toolbox features and provide the users with a full MPM dataset used in the tutorial and examples.
- study was approved by the local ethics committee and informed written consent was obtained from the participant prior to scanning.

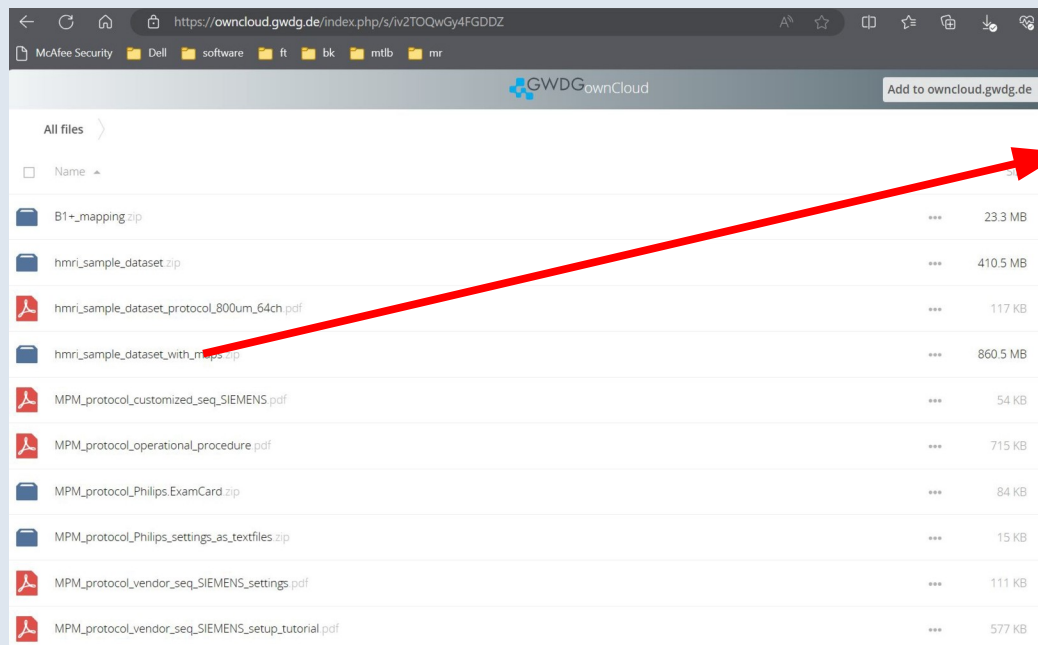
# Sample dataset website

The screenshot shows a web browser window with the URL <https://owncloud.gwdg.de/index.php/s/tv2TOQwGy4FGDDZ>. The page displays a list of files and folders available for download. The table below summarizes the content shown in the screenshot.

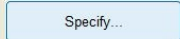
Name	Size
B1+ <sub>-</sub> mapping.zip	23.3 MB
hmri_sample_dataset.zip	410.5 MB
hmri_sample_dataset_protocol_800um_64ch.pdf	117 KB
hmri_sample_dataset_with_maps.zip	860.5 MB
MPM_protocol_customized_seq_SIEMENS.pdf	54 KB
MPM_protocol_operational_procedure.pdf	715 KB
MPM_protocol_Philips_ExamCard.zip	84 KB
MPM_protocol_Philips_settings_as_textfiles.zip	15 KB
MPM_protocol_vendor_seq_SIEMENS_settings.pdf	111 KB
MPM_protocol_vendor_seq_SIEMENS_setup_tutorial.pdf	577 KB

- Demo dataset ([ZIP archive](#)).
- Corresponding protocol `hmri_sample_dataset_protocol_800um_64ch.pdf`
- Other MPM protocol examples, including Siemens and Philips scanners.

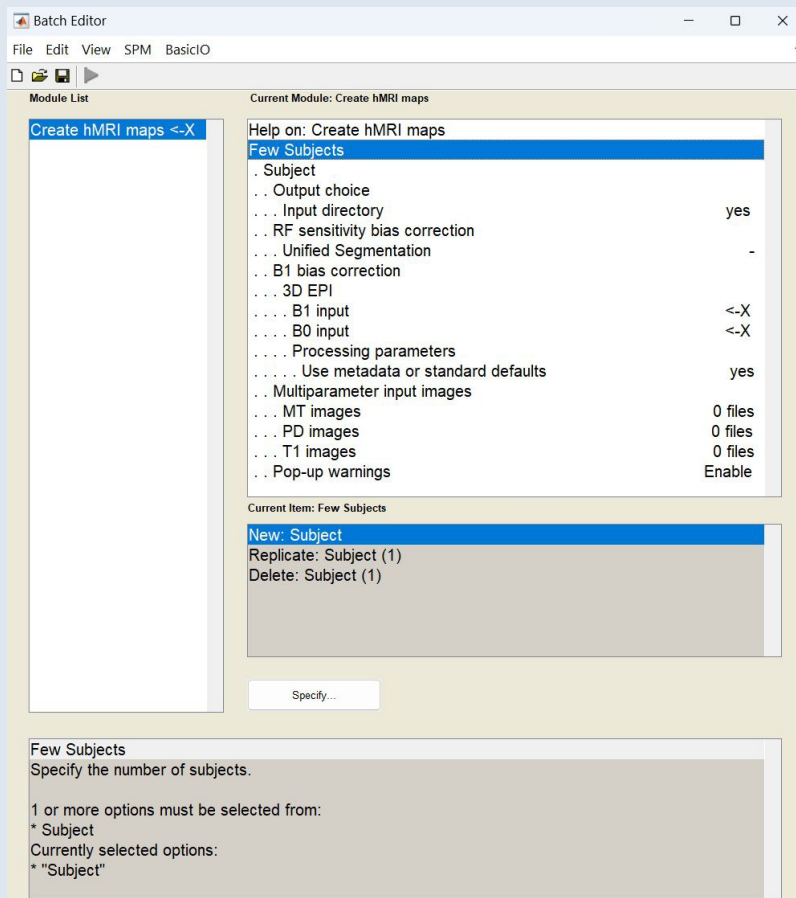
# Sample dataset



Batch_Script_hMRI_Config	8/28/2023 12:23 PM	File folder
gre_field_mapping_1acq_rl_0005	8/28/2023 12:23 PM	File folder
gre_field_mapping_1acq_rl_0006	8/28/2023 12:23 PM	File folder
mfc_seste_b1map_v1e_0004	8/28/2023 12:23 PM	File folder
mfc_smaps_v1a_Array_0007	8/28/2023 12:23 PM	File folder
mfc_smaps_v1a_Array_0010	8/28/2023 12:23 PM	File folder
mfc_smaps_v1a_Array_0013	8/28/2023 12:23 PM	File folder
mfc_smaps_v1a_QBC_0008	8/28/2023 12:23 PM	File folder
mfc_smaps_v1a_QBC_0011	8/28/2023 12:23 PM	File folder
mfc_smaps_v1a_QBC_0014	8/28/2023 12:23 PM	File folder
mtw_mfc_3dflash_v1i_R4_0012	8/28/2023 12:24 PM	File folder
pdw_mfc_3dflash_v1i_R4_0009	8/28/2023 12:24 PM	File folder
t1w_mfc_3dflash_v1i_R4_0015	8/28/2023 12:24 PM	File folder



# Create hMRI Maps

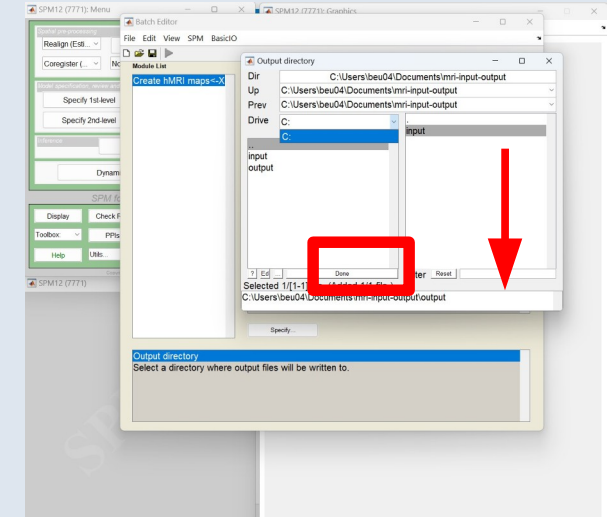
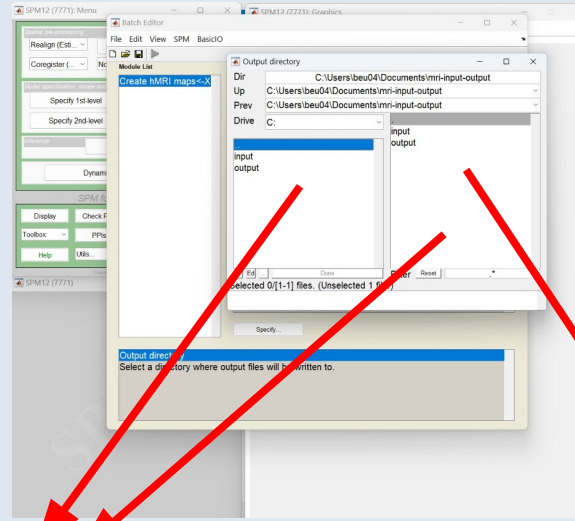
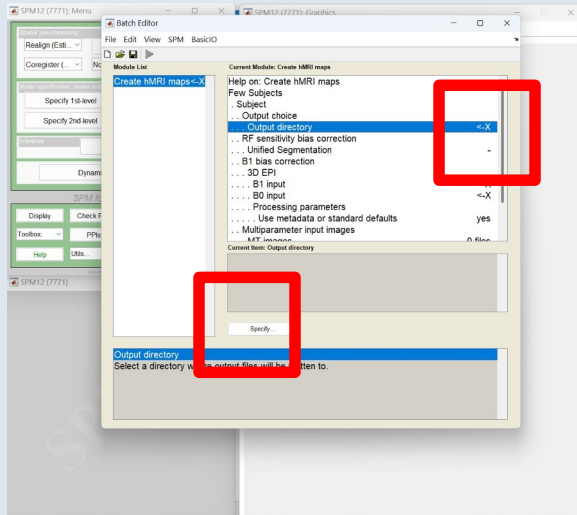
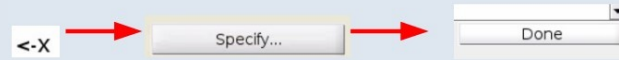


- Specify -output dir- input
- RF sensitivity bias correction (choose US-no input)
- B1 input
- B0 input
- MT images input
- PD images input
- T1 images input





# Choose output directory



Sub-Dirs of Dir appears in left and right pane

Once clicked in right pane, files transfer to 'selected'



Demostration with demodata...

# pathToOutput/Results/\*



Supplementary



anon\_s2018-02-28\_  
18-26-185345-0000  
1-00224-1\_MTsat.js  
on



anon\_s2018-02-28\_  
18-26-185345-0000  
1-00224-1\_MTsat.nii



anon\_s2018-02-28\_  
18-26-185345-0000  
1-00224-1\_PD.json



anon\_s2018-02-28\_  
18-26-185345-0000  
1-00224-1\_PD.nii



anon\_s2018-02-28\_  
18-26-185345-0000  
1-00224-1\_R1.json



anon\_s2018-02-28\_  
18-26-185345-0000  
1-00224-1\_R1.nii



anon\_s2018-02-28\_  
18-26-185345-0000  
1-00224-1\_R2s\_OLS  
.json



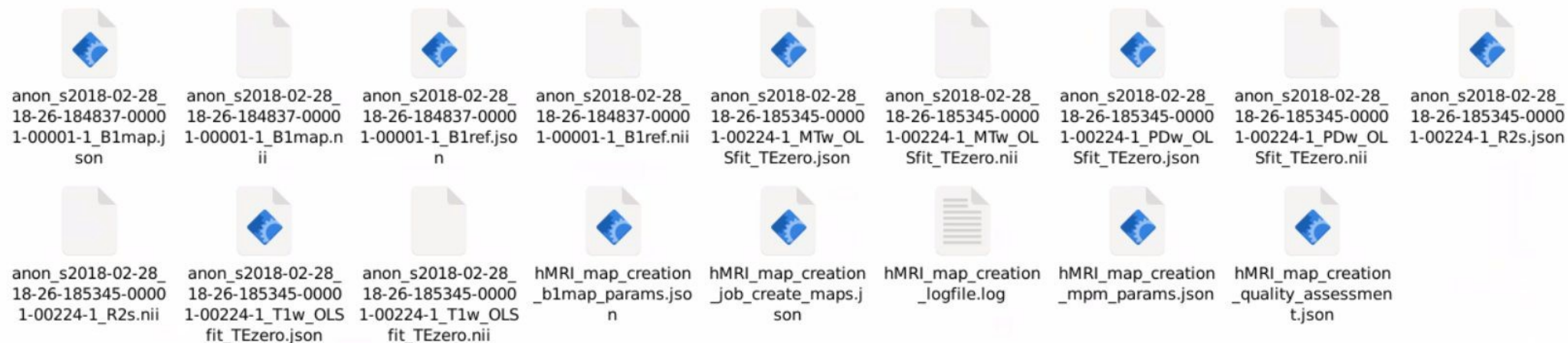
anon\_s2018-02-28\_  
18-26-185345-0000  
1-00224-1\_R2s\_OLS  
.nii



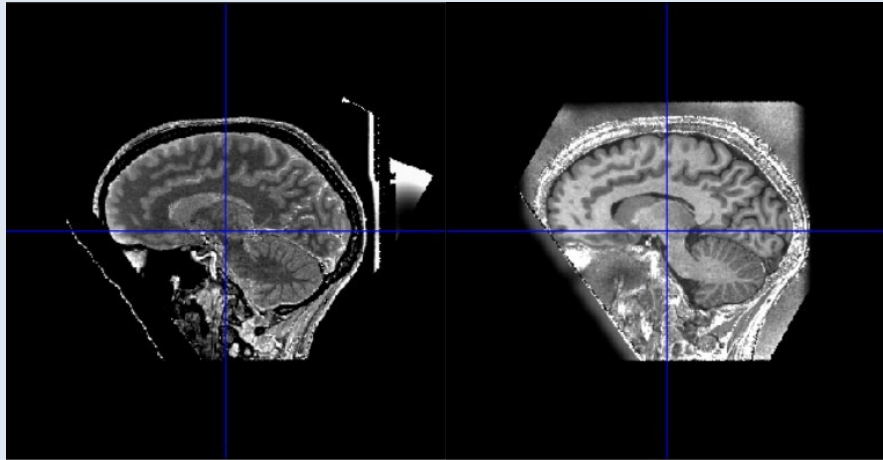
\_finished\_

# pathToOutput/Results/ Supplementary

/data/u\_ugurcan\_software/output/compiled-v6-fulltest/Results/Supplementary/



# Intensity ranges for maps

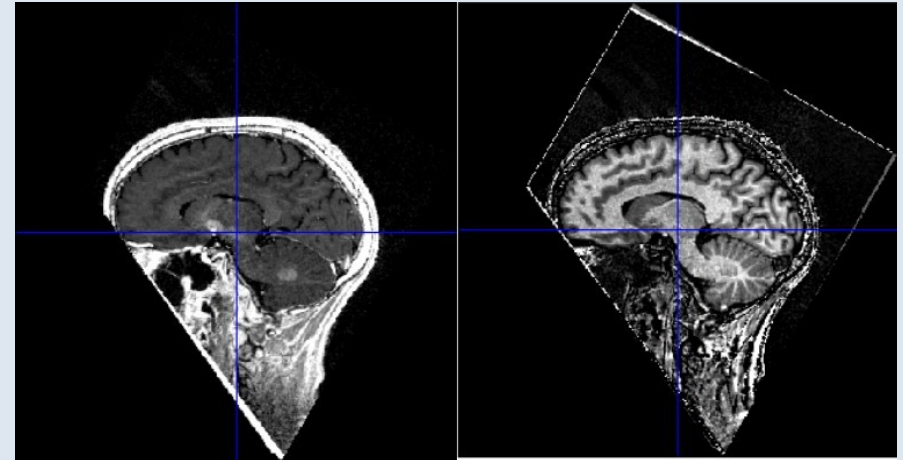


PD map (water  
concentration)  
[p.u.]

Intensity range  
[50 120]

R1 map [s-1]

Intensity range  
[0.0 1.4]



R2\* map [s-1]

Intensity range  
[0 70]

MT saturation map  
[p.u.]

Intensity range  
[0 2]

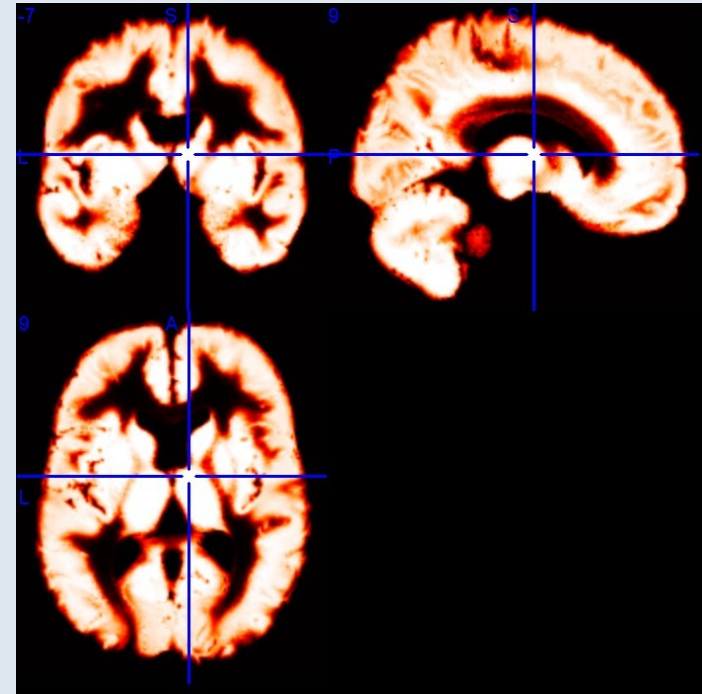
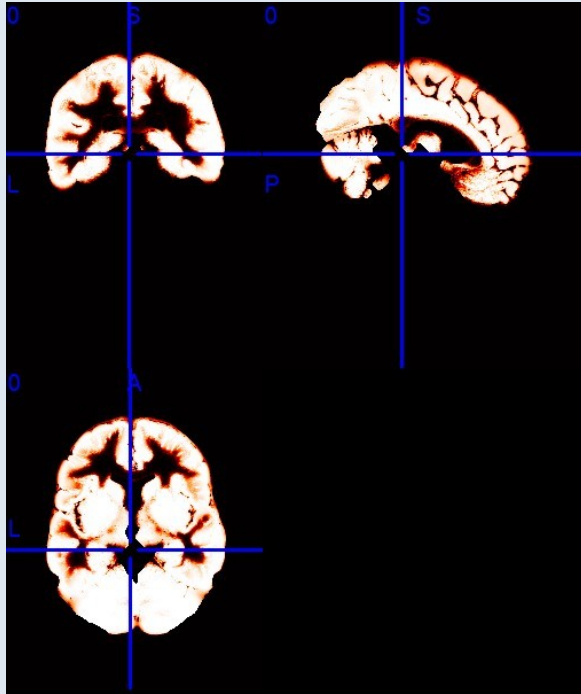
# Results: all together

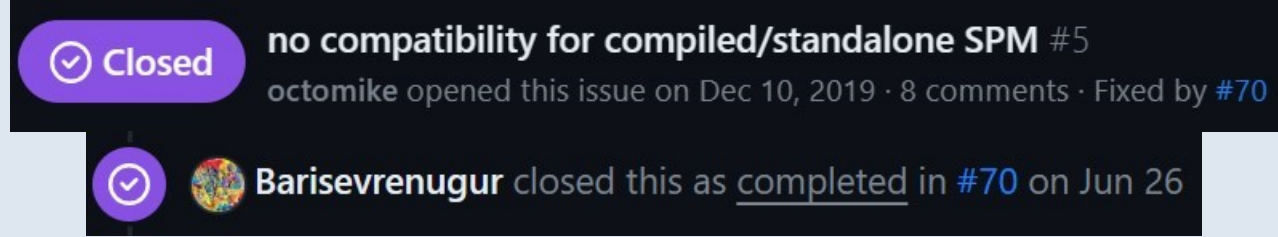
c1s27703c5-153119-00001-00224-1.nii  
 c1s268240f-082409-00001-00224-1.nii  
 c1s3120485-082744-00001-00224-1.nii  
 c2s27703c5-153119-00001-00224-1.nii  
 c2s268240f-082409-00001-00224-1.nii  
 c2s3120485-082744-00001-00224-1.nii  
 c3s27703c5-153119-00001-00224-1.nii  
 c3s268240f-082409-00001-00224-1.nii  
 c3s3120485-082744-00001-00224-1.nii  
 mwc1s27703c5-153119-00001-00224-1.nii  
 mwc1s268240f-082409-00001-00224-1.nii  
 mwc1s3120485-082744-00001-00224-1.nii  
 mwc2s27703c5-153119-00001-00224-1.nii  
 mwc2s268240f-082409-00001-00224-1.nii  
 mwc2s3120485-082744-00001-00224-1.nii  
 rc1s27703c5-153119-00001-00224-1.nii  
 rc1s268240f-082409-00001-00224-1.nii  
 rc1s3120485-082744-00001-00224-1.nii  
 rc2s27703c5-153119-00001-00224-1.nii  
 rc2s268240f-082409-00001-00224-1.nii  
 rc2s3120485-082744-00001-00224-1.nii  
 s27703c5-153119-00001-00224-1\_seg8.mat  
 s268240f-082409-00001-00224-1\_seg8.mat  
 s3120485-082744-00001-00224-1\_seg8.mat  
 Template\_0.nii  
 Template\_1.nii  
 Template\_2.nii  
 Template\_3.nii  
 Template\_4.nii  
 Template\_5.nii  
 Template\_6.nii

Template\_6\_2mni.mat  
 u\_rc1s27703c5-153119-00001-00224-1\_Template.nii  
 u\_rc1s268240f-082409-00001-00224-1\_Template.nii  
 u\_rc1s3120485-082744-00001-00224-1\_Template.nii  
 wap1\_ws27703c5-153918-00001-00224-1\_R2s\_OLS.nii  
 wap1\_ws268240f-083155-00001-00224-1\_R2s\_OLS.nii  
 wap1\_ws3120485-083655-00001-00224-1\_R2s\_OLS.nii  
 wap2\_ws27703c5-153918-00001-00224-1\_R2s\_OLS.nii  
 wap2\_ws268240f-083155-00001-00224-1\_R2s\_OLS.nii  
 wap2\_ws3120485-083655-00001-00224-1\_R2s\_OLS.nii  
 wc1s27703c5-153119-00001-00224-1.nii  
 wc1s268240f-082409-00001-00224-1.nii  
 wc1s3120485-082744-00001-00224-1.nii  
 wc2s27703c5-153119-00001-00224-1.nii  
 wc2s268240f-082409-00001-00224-1.nii  
 wc2s3120485-082744-00001-00224-1.nii  
 ws27703c5-153918-00001-00224-1\_R2s\_OLS.nii  
 ws268240f-083155-00001-00224-1\_R2s\_OLS.nii  
 ws3120485-083655-00001-00224-1\_R2s\_OLS.nii  
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 y\_s268240f-082409-00001-00224-1.nii  
 y\_s3120485-082744-00001-00224-1.nii

File name	Description
<b>Unified Segmentation (US) (Proc. hMRI -&gt; Segmentation)</b>	
c1<segmInputFileName>.[nii json]	Tissue class 1 in subject space. Prefixes c1/c2/c3 correspond to GM/WM/CSF respectively.
rc1<segmInputFileName>.[nii json]	Tissue class 1 in subject space, resliced and imported for Dartel processing. Dartel usually relies on rc1/rc2 images (GM/WM) only.
wc1<segmInputFileName>.[nii json]	Tissue class 1 warped into MNI space, with the simple warp obtained with the US. Prefixes wc1/wc2 correspond to GM/WM respectively.
mwc1<segmInputFileName>.[nii json]	Tissue class 1 warped into MNI space, with the simple warp obtained with the US, and modulated by the determinant of the Jacobian, i.e. accounting for local change of volume. Prefixes mwc1/mwc2 correspond to GM/WM respectively.
y_<segmInputFileName>.[nii]	Deformation field, i.e. warps, obtained from US
<segmInputFileName>_seg8.mat	Segmentation and warping parameters, obtained from US
<b>Diffeomorphic registration (Proc. hMRI -&gt; Dartel -&gt; Run Dartel (create Templates))</b>	
u_rc1*_Template.nii	Flow field image, one per subject, estimated by Dartel from the rc1/rc2 images.
Template_*.nii	7 template images, numbered from 0 to 6, created by Dartel from the rc1/rc2 images of all the subjects.
<b>Diffeomorphic registration (Proc. hMRI -&gt; Dartel -&gt; Normalise to MNI space)</b>	
w*<normInputFileName>.[nii json]	Image warped into MNI space following Dartel, using the estimated <i>flow field</i> and an affine transformation. This would be typically a qMRI map that should <i>not</i> be modulated to account for volume changes.
mw*<normInputFileName>.[nii json]	Image warped into MNI space and modulated by the determinant of the Jacobian, i.e. accounting for local change of volume. This would typically be any tissue probability map (i.e. image with a measure whose total amount over the brain volume should be preserved) to be used after smoothing for a VBM analysis.
<b>Tissue-weighted smoothing (Proc. hMRI -&gt; Smoothing)</b>	
wap1_<smooFileName>.[nii json]	Tissue-weighted smoothing for tissue class 1.
s*<FileName>.[nii json]	(Any) image smoothed with a standard Gaussian filter (here for comparison, <i>not</i> in hMRI).

# Spatial process images:c1 and wc1





- hMRI-toolbox compiled version: new update within the development of hMRI toolbox, has been developed & tested & documented and in use since the release:



- Matlab compiler: produces executables that can be run directly with the Matlab runtime environment without the need for an installation of Matlab.
- Compilation can be run directly from the Linux command line without need of an installed Matlab but requires an installed Matlab runtime environment.



# Running the compiled version

1. `git clone https://github.com/spm/spm12.git` that clones the spm12.
2. follow the directions in the documentation and get the hMRI toolbox.
3. copy the hMRI-toolbox folder to `spm12/toolbox`
4. on matlab obtain the compilation of spm12 by executing: `spm_make_standalone`

After these steps the standalone version is located in the standalone folder in the same directory as SPM12.

In our example, we were able to run the compiled version of hMRI toolbox by typing in the linux commandline:

```
/path/to/standalone > ./run_spm12.sh /data/u_ugurcan_software fmri
```



Of course, before doing all these, you need to check that your matlab already has the runtime environment. In order to check for this, go to your matlab folder and check whether you have the runtime folder containing the directory glnxa64. In the above example our runtime folder was located in `/data/u_ugurcan_software`



Thank you!