

# hMRI-toolbox: a user's tutorial with example data

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

# Purpose of workshop:

*Go through the main modules (maps & pipelines) of the hMRI toolbox by using the publicly available demo data and built-in standard defaults, fast-walking the users to start using the toolbox.*

- GitHub hMRI-toolbox – Wiki
- Tabelow K, Balteau E, Ashburner J, Callaghan MF, Draganski B, Helms G, Kherif F, Leutritz T, Lutti A, Phillips C, Reimer E, Ruthotto L, Seif M, Weiskopf N, Ziegler G, Mohammadi S (2019) hMRI – A toolbox for quantitative MRI in neuroscience and clinical research. *Neuroimage*.
- Callaghan MF, Lutti A, Ashburner J, Balteau E, Corbin N, Draganski B, Helms G, Kherif F, Leutritz T, Mohammadi S, Phillips C, Reimer E, Ruthotto L, Seif M, Tabelow K, Ziegler G, Weiskopf N (2019). Example dataset for the hMRI toolbox. *Data in Brief* 25:104132.

# hMRI-toolbox:

- *is state-of-the-art, easy-to-use and flexible tool, for qMRI data handling and processing.*
- *is open source. Hosted, maintained and further developed on GitHub.*
- *embedded in the Statistical Parametric Mapping (SPM) framework.*

# Motivation for hMRI (*in vivo histology*) in hMRI-toolbox

- Takes as input T1w, Pdw, MTw data (multi-contrast multi-echo FLASH protocol) and allows the estimation of high-quality multi-parameter qMRI maps (longitudinal and effective transverse relaxation rates R1 and R2\*, proton density PD and magnetisation transfer MT saturation) (Weiskopf et al. 2008 & 2013), followed by spatial registration in common space for statistical analysis (Draganski et al. 2011).
- Provides built-in B1 bias correction (3D EPI-Lutti A et al. 2012) with input: two different magnitude images with different TE (echo time) and presubtracted phase image.
- Provides built-in RF sensitivity bias correction (Unified Segmentation approach -Ashburner2005).
- Provides built-in post processing: Unified segmentation + DARTEL (Ashburner2007) + Gaussian smoothing.
- Sensitivity to micro-structural properties of brain tissue such as axon, myelin, iron and water concentration.
- Maps generated by the toolbox are key input parameters for biophysical models designed to estimate tissue microstructure properties such as the MR g-ratio and to derive standard and novel MRI biomarkers.

# Rereferences for motivation:

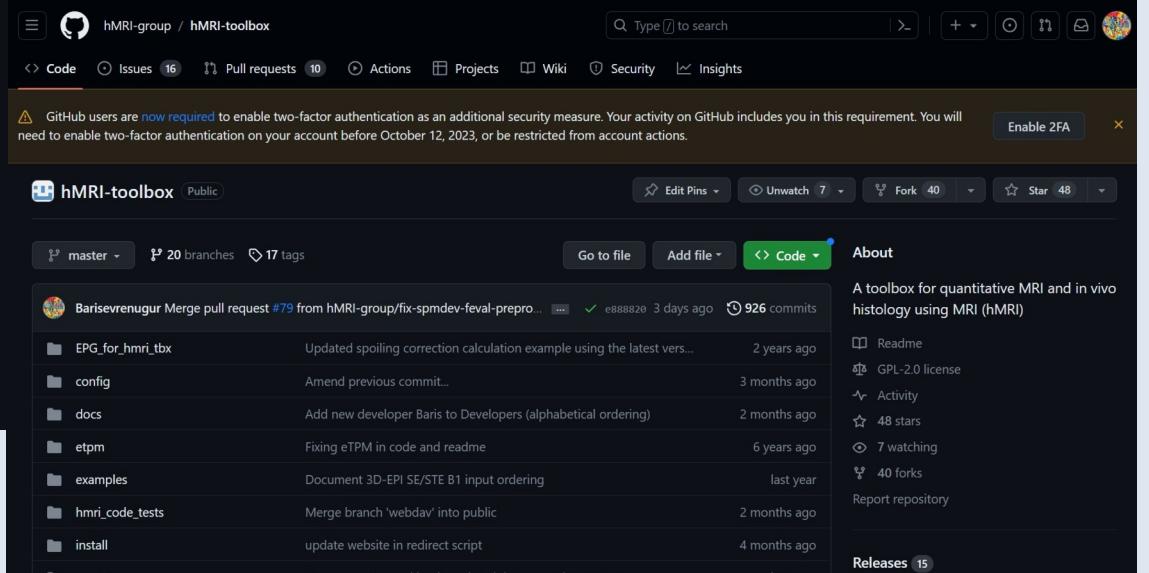
- McRobbie, Donald W., Elizabeth A. Moore, Martin J. Graves, and Martin R. Prince. MRI from Picture to Proton. Cambridge university press, 2017.
- Weiskopf, N., Edwards, L.J., Helms, G., Mohammadi, S. and Kirilina, E., 2021. Quantitative magnetic resonance imaging of brain anatomy and in vivo histology. *Nature Reviews Physics*, 3(8), pp.570-588.
- Tabelow K, Balteau E, Ashburner J, Callaghan MF, Draganski B, Helms G, Kherif F, Leutritz T, Lutti A, Phillips C, Reimer E, Ruthotto L, Seif M, Weiskopf N, Ziegler G, Mohammadi S (2019) hMRI – A toolbox for quantitative MRI in neuroscience and clinical research. *Neuroimage*.
- Weiskopf N, Callaghan MF, Josephs O, Lutti A, Mohammadi S (2014) Estimating the apparent transverse relaxation time ( $R2^*$ ) from images with different contrasts (ESTATICS) reduces motion artifacts. *Frontiers in Neuroscience* 8:278.
- Lutti A, Stadler J, Josephs O, Windischberger C, Speck O, Bernarding J, Hutton C, Weiskopf N (2012) Robust and fast whole brain mapping of the RF transmit field B1 at 7T. *PLoS One*. 7(3):e32379.
- Weiskopf N, Suckling J, Williams G, Correia MM, Inkster B, Tait R, Ooi C, Bullmore ET, Lutti A (2013) Quantitative multi-parameter mapping of R1, PD\*, MT, and R2\* at 3T: a multi-center validation. *Frontiers in Neuroscience* 7:95.
- Draganski B, Ashburner J, Hutton C, Kherif F, Frackowiak R, Helms G, Weiskopf N (2011) Regional specificity of MRI contrast parameter changes in normal ageing revealed by voxel-based quantification (VBQ). *Neuroimage* 55(4):1423–1434.
- Ashburner J and KJ Friston (2005) Unified segmentation. *NeuroImage* 26(3):839–851.
- Ashburner J. A (2007) fast diffeomorphic image registration algorithm. *NeuroImage* 38(1):95-113.

# hMRI toolbox-GitHub

## Developers of the hMRI-toolbox

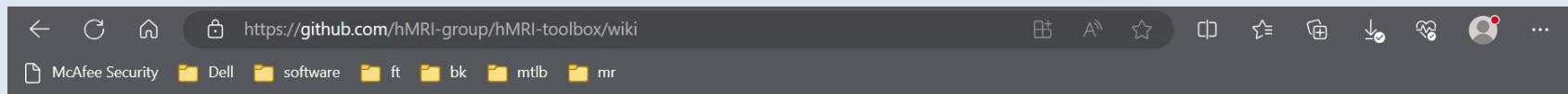
The development of the hMRI toolbox is an international collaborative effort including the following sites and developers:

- Luke J Edwards, Tobias Leutritz, Enrico Reimer, Baris Evren Ugurcan, Nikolaus Weiskopf (Max Planck Institute for Human Cognitive and Brain Sciences, Leipzig, Germany)
- Evelyne Balteau, Christophe Phillips ([University of Liege](#), Liege, Belgium)
- Siawoosh Mohammadi (Medical Center Hamburg-Eppendorf, Hamburg, Germany)
- Martina F Callaghan, John Ashburner (University College London, London, United Kingdom)
- Karsten Tabelow (Weierstrass Institute for Applied Analysis and Stochastics, Berlin, Germany)
- Bogdan Draganski, Ferath Kerif, Antoine Lutti (LREN, DNC - CHUV, University Lausanne, Lausanne, Switzerland)
- Maryam Seif (University of Zurich, Zurich, Switzerland)
- Gunther Helms (Department of Medical Radiation Physics, Lund University, Lund, Sweden)
- Lars Ruthotto (Emory University, Atlanta, GA, United States)
- Gabriel Ziegler (Otto-von-Guericke-University Magdeburg, Magdeburg, Germany)



The screenshot shows the GitHub repository page for 'hMRI-toolbox'. At the top, there's a banner with a warning about two-factor authentication. Below it, the repository name 'hMRI-toolbox' is shown with a 'Public' badge. The main interface includes a sidebar with options like 'About', 'Readme', 'GPL-2.0 license', 'Activity', '48 stars', '7 watching', '40 forks', and 'Report repository'. The main area displays the repository's structure with folders like 'EPG\_for\_hMRI\_tbx', 'config', 'docs', 'etpm', 'examples', 'hMRI\_code\_tests', and 'install'. Each folder has a brief description and the date of its last commit. The 'About' section provides a brief description of the toolbox: 'A toolbox for quantitative MRI and in vivo histology using MRI (hMRI)'.

# GitHub-wiki



## hMRI-toolbox - Wiki

The hMRI-toolbox is an easy-to-use open-source and flexible tool, for qMRI data handling and processing. It allows the estimation of high-quality multi-parameter qMRI maps (longitudinal and effective transverse relaxation rates R1 and R2\*, proton density PD and magnetisation transfer MT saturation) (Weiskopf *et al.* 2008 & 2013), followed by spatial registration in common space for statistical analysis (Draganski *et al.* 2011).

Embedded in the [Statistical Parametric Mapping](#) (SPM) framework, it can be readily combined with existing SPM toolboxes for estimating diffusion MRI parameter maps, and it benefits from the extensive range of established SPM tools for high-accuracy spatial registration and statistical inferences.

The qMRI maps generated by the toolbox can be used for quantitative parameter analysis and accurate delineation of subcortical brain structures. They are key input parameters for biophysical models designed to estimate tissue microstructure properties such as the MR g-ratio and to derive standard and novel MRI biomarkers (Mohammadi *et al.* 2015). The hMRI toolbox is therefore the first step towards *in vivo* histology using MRI (hMRI) and is being extended further in this direction.

The flexible and modular nature of the toolbox makes it usable for a [wide range of data types](#), from the full MPM protocol to subsets of it, including e.g. single contrast echo trains for mapping R2\* or variable flip angle data for R1 and PD mapping using multi-echo or single-echo data. The spatial processing part of the toolbox can be applied to [any set of rotationally-invariant qMRI maps](#), including diffusion MRI scalar parameter maps as well as the standard (R1, PD, MT and R2\*) MPM maps.

For a reference on the scientific background, methods and concepts please use the [hMRI-toolbox paper](#) and cite it when publishing results compiled with the hMRI-toolbox.

## About the wiki

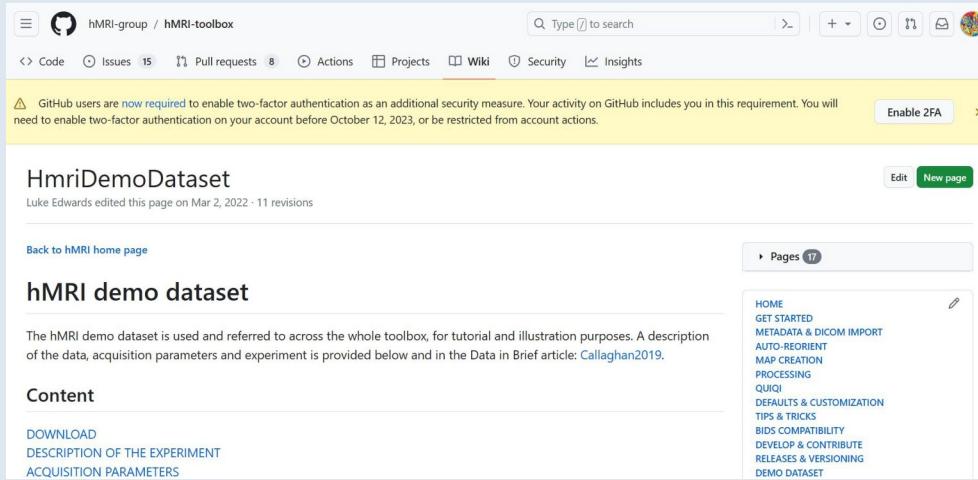
Pages 17

HOME  
GET STARTED  
METADATA & DICOM IMPORT  
AUTO-REORIENT  
MAP CREATION  
PROCESSING  
QUIQI  
DEFAULTS & CUSTOMIZATION  
TIPS & TRICKS  
BIDS COMPATIBILITY  
DEVELOP & CONTRIBUTE  
RELEASES & VERSIONING  
DEMO DATASET  
REFERENCES  
CONTACT

Clone this wiki locally

<https://github.com/hMRI-group/hMRI>

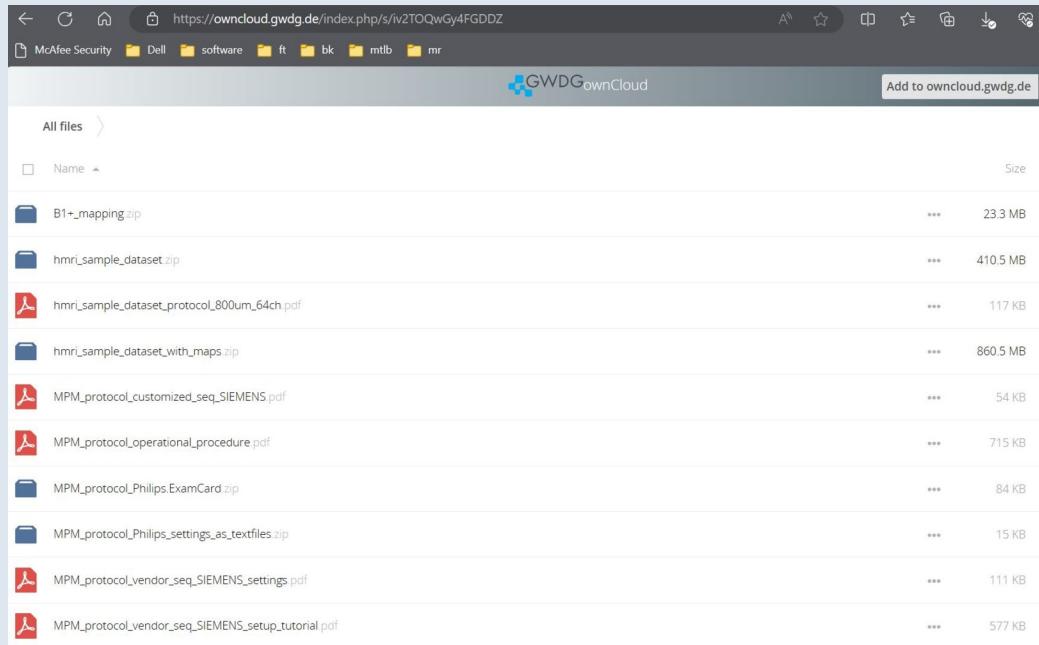
# hMRI demo dataset



The screenshot shows a GitHub repository page for 'hMRI-group / hMRI-toolbox'. The repository name is 'hMRI-demo-dataset'. The page includes a search bar, navigation links for Code, Issues (15), Pull requests (8), Actions, Projects, Wiki, Security, and Insights. A note at the top states: 'GitHub users are now required to enable two-factor authentication as an additional security measure. Your activity on GitHub includes you in this requirement. You will need to enable two-factor authentication on your account before October 12, 2023, or be restricted from account actions.' There is a 'Enable 2FA' button. Below the header, there's a 'Pages' section with a count of 17, a 'Edit' button, and a 'New page' button. The main content area contains a heading 'hMRI demo dataset', a description of the dataset, a 'Content' section with links to 'DOWNLOAD', 'DESCRIPTION OF THE EXPERIMENT', and 'ACQUISITION PARAMETERS', and a sidebar with a list of links: HOME, GET STARTED, METADATA & DICOM IMPORT, AUTO-REORIENT, MAP CREATION, PROCESSING, QUIQI, DEFAULTS & CUSTOMIZATION, TIPS & TRICKS, BIDS COMPATIBILITY, DEVELOP & CONTRIBUTE, RELEASES & VERSIONING, and 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

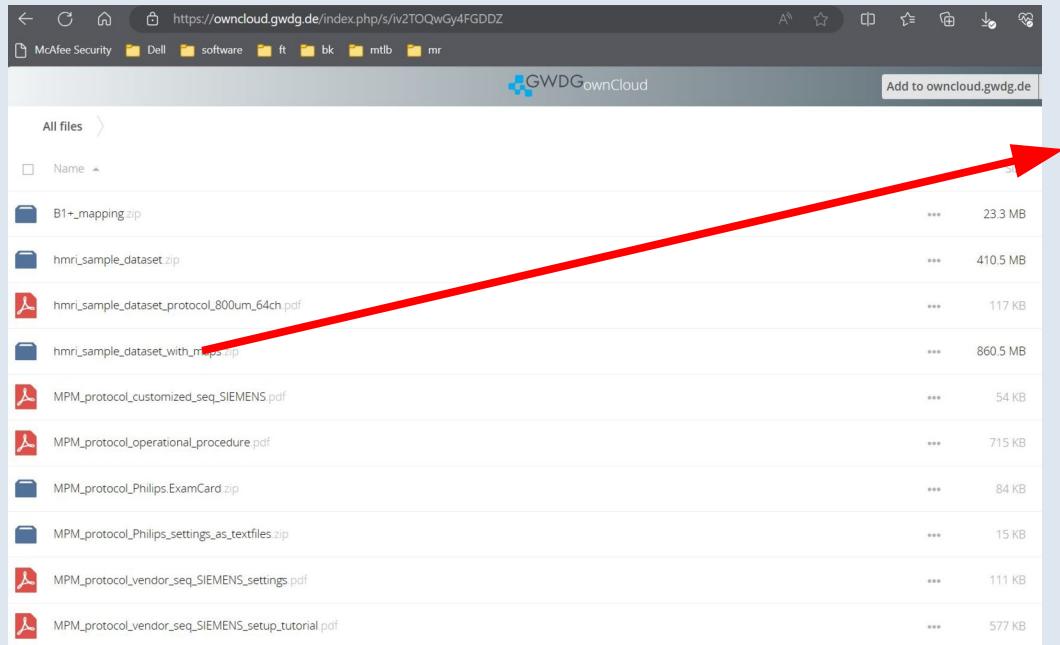


The screenshot shows a web browser window displaying a file list from GWDG ownCloud. The URL in the address bar is <https://owncloud.gwdg.de/index.php/s/iv2TOQwGy4FGDDZ>. The file list includes:

Name	Size
B1+_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



https://owncloud.gwdg.de/index.php/s/iv2TOQwGy4FGDDZ

McAfee Security Dell software ft bk mtb mr

GWGDG ownCloud Add to owncloud.gwdg.de

All files >

Name

	B1+_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_mfc.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

	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_smmaps_v1a_Array_0007	8/28/2023 12:23 PM	File folder
	mfc_smmaps_v1a_Array_0010	8/28/2023 12:23 PM	File folder
	mfc_smmaps_v1a_Array_0013	8/28/2023 12:23 PM	File folder
	mfc_smmaps_v1a_QBC_0008	8/28/2023 12:23 PM	File folder
	mfc_smmaps_v1a_QBC_0011	8/28/2023 12:23 PM	File folder
	mfc_smmaps_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

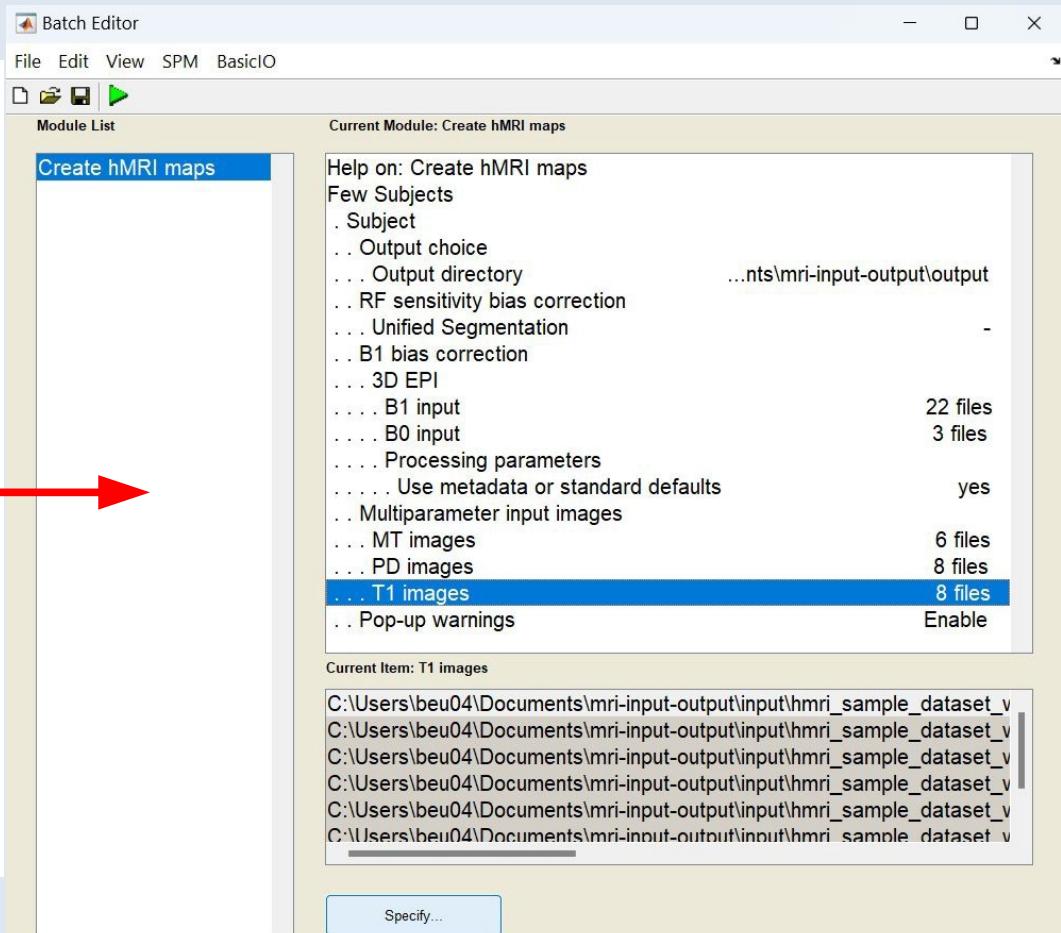
# Sample dataset

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_smmaps_v1a_Array_0007	8/28/2023 12:23 PM	File folder
mfc_smmaps_v1a_Array_0010	8/28/2023 12:23 PM	File folder
mfc_smmaps_v1a_Array_0013	8/28/2023 12:23 PM	File folder
mfc_smmaps_v1a_QBC_0008	8/28/2023 12:23 PM	File folder
mfc_smmaps_v1a_QBC_0011	8/28/2023 12:23 PM	File folder
mfc_smmaps_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

- mfc\_seste\_b1map\_v1e\_0004 : B1 mapping data (3D EPI SE/SESTE protocol)
- gre\_field\_mapping\_1acq\_rl\_0005 : B0 mapping data (2 magnitude images with different TE)
- gre\_field\_mapping\_1acq\_rl\_0006 : B0 mapping data (presubtracted phase image)
- mfc\_smmaps\_v1a\_Array\_0007 : RF sensitivity mapping data (64 channel head coil)
- mfc\_smmaps\_v1a\_QBC\_0008 : RF sensitivity mapping data (body coil)
- pdw\_mfc\_3dflash\_v1i\_R4\_0009 : 8 echoes with PD-weighting
- mfc\_smmaps\_v1a\_Array\_0010 : RF sensitivity mapping data (64 channel head coil)
- mfc\_smmaps\_v1a\_QBC\_0011 : RF sensitivity mapping data (body coil)
- mtw\_mfc\_3dflash\_v1i\_R4\_0012 : 6 echoes with MT-weighting
- mfc\_smmaps\_v1a\_Array\_0013 : RF sensitivity mapping data (64 channel head coil)
- mfc\_smmaps\_v1a\_QBC\_0014 : RF sensitivity mapping data (body coil)
- t1w\_mfc\_3dflash\_v1i\_R4\_0015 : 8 echoes with T1-weighting

# Toolbox input:

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_smmaps_v1a_Array_0007	8/28/2023 12:23 PM	File folder
mfc_smmaps_v1a_Array_0010	8/28/2023 12:23 PM	File folder
mfc_smmaps_v1a_Array_0013	8/28/2023 12:23 PM	File folder
mfc_smmaps_v1a_QBC_0008	8/28/2023 12:23 PM	File folder
mfc_smmaps_v1a_QBC_0011	8/28/2023 12:23 PM	File folder
mfc_smmaps_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



# pathToOutput/Results/\*



Supplementary

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

\_finished\_

# Results directory file descriptions:

## Results directory > Description ↵

- <firstPDfileName>\_MT.[nii|json] > Estimated magnetisation transfer map in p.u.
- <firstPDfileName>\_PD.[nii|json] > Estimated proton density PD map in p.u.
- <firstPDfileName>\_R1.[nii|json] > Estimated longitudinal relaxation rate R1 map in s<sup>-1</sup>
- <firstPDfileName>\_R2s\_<R2sMethod>.[nii|json] > Estimated transversal relaxation rate R2\* map in s<sup>-1</sup> (ESTATICS), where <R2sMethod> is the R2\* fitting method (e.g. OLS or WLS1 ; see [Create hMRI maps parameters](#)).

# pathToOutput/Results/ Supplementary

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

 anon_s2018-02-28_18-26-184837-0000-1-00001-1_B1map.son	 anon_s2018-02-28_18-26-184837-0000-1-00001-1_B1map.nii	 anon_s2018-02-28_18-26-184837-0000-1-00001-1_B1ref.json	 anon_s2018-02-28_18-26-184837-0000-1-00001-1_B1ref.nii	 anon_s2018-02-28_18-26-185345-0000-1-00224-1_MTw_OLSfit_TEzero.json	 anon_s2018-02-28_18-26-185345-0000-1-00224-1_MTw_OLSfit_TEzero.nii	 anon_s2018-02-28_18-26-185345-0000-1-00224-1_PDw_OLSfit_TEzero.json	 anon_s2018-02-28_18-26-185345-0000-1-00224-1_PDw_OLSfit_TEzero.nii	 anon_s2018-02-28_18-26-185345-0000-1-00224-1_R2s.json
 anon_s2018-02-28_18-26-185345-0000-1-00224-1_R2s.nii	 anon_s2018-02-28_18-26-185345-0000-1-00224-1_T1w_OLSfit_TEzero.json	 anon_s2018-02-28_18-26-185345-0000-1-00224-1_T1w_OLSfit_TEzero.nii	 hMRI_map_creation_b1map_params.json	 hMRI_map_creation_job_create_maps.json	 hMRI_map_creation_logfile.log	 hMRI_map_creation_mppm_params.json	 hMRI_map_creation_quality_assessment.json	

# Supplementary directory file descriptions:

Results/Supplementary directory > Description ↗

- `hMRI_map_creation_rfSens_params.json` > RF sensitivity bias correction parameters (measured sensitivity maps)
- `hMRI_map_creation_B1map_params.json` > B1 transmit map estimation: acquisition and processing parameters
- `hMRI_map_creation_job_create_maps.json` > Create hMRI maps: acquisition and processing parameters
- `hMRI_map_creation_ppm_params.json` > Acquisition and processing parameters used for the current job
- `hMRI_map_creation_quality_assessment.json` > Quality assessment results
- `<firstSESTEfileName>_B1map.[nii|json]` > Estimated B1 bias field  $fT$  map (p.u.)
- `<firstSESTEfileName>_B1ref.[nii|json]` > Anatomical reference for B1 bias field correction
- `<firstPDfileName>_MTw_<R2sMethod>fit_TEzero.[nii|json]` > MTw echoes extrapolated to TE=0, where `<R2sMethod>` is the R2\* fitting method
- `<firstPDfileName>_PDw_<R2sMethod>fit_TEzero.[nii|json]` > PDw echoes extrapolated to TE=0, where `<R2sMethod>` is the R2\* fitting method
- `<firstPDfileName>_R2s.[nii|json]` > Estimated R2\* map from simple exponential fit (PDw echoes)
- `<firstPDfileName>_T1w_<R2sMethod>fit_TEzero.[nii|json]` > T1w echoes extrapolated to TE=0, where `<R2sMethod>` is the R2\* fitting method

# SPM-download & install

- *The hMRI toolbox relies on SPM functionalities and has been developed starting from SPM12 (version 12.3 - r6906). It is recommended to have the latest release of SPM12 at hand and to make sure you have added the SPM root directory to your Matlab Path.*
- <https://www.fil.ion.ucl.ac.uk/spm/software/download/>
- *on Unix/Linux, use unzip SPM.zip or tar -xvfz SPM.tar.gz*
- *on Windows, use 7-Zip (any other archive software)*
- *on Mac, double-click to unpack the archive*

# hMRI-toolbox install

- <https://github.com/hMRI-group/hMRI-toolbox/releases>
- Download the latest release (currently v0.6.0)
- unzip the compressed file by the same instructions
- Create (empty) directory hMRI into <path-to-your-spm>/toolbox
- Copy hMRI-Toolbox/install/tbx\_cfg\_hmri\_redirect.m into <path-to-your-spm>/toolbox/hMRI
- launch MATLAB and add the hMRI-Toolbox root directory (containing the unzipped release or your local repository including the full implementation of the hMRI-Toolbox) to your Matlab Path
- add SPM to MATLAB's path, for example you can also use: `>>addpath C:/software/matlab/spm12`

# Opening the toolbox in Matlab

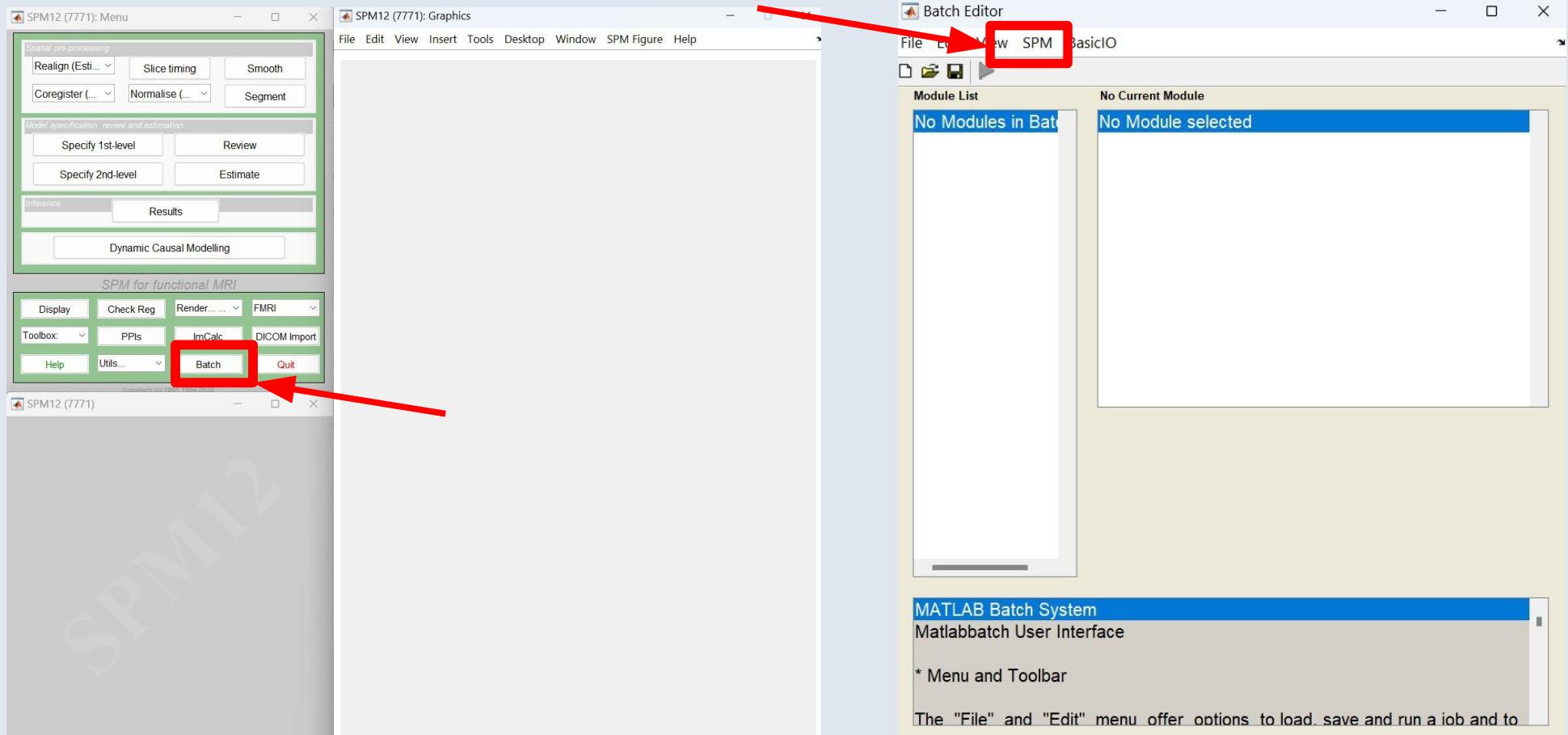
- You'll need Matlab to run the hMRI toolbox. Matlab versions from release R2018a (MATLAB 9.4) and up have been used to develop and test the software. Some functionality may still work in earlier versions of Matlab, but this is not officially supported. Please note that a single Matlab version should be used to process all of a given dataset, as results can differ slightly between versions due to changes in Matlab's internal algorithms.
- In the Matlab workspace type

```
>> spm fmri
```

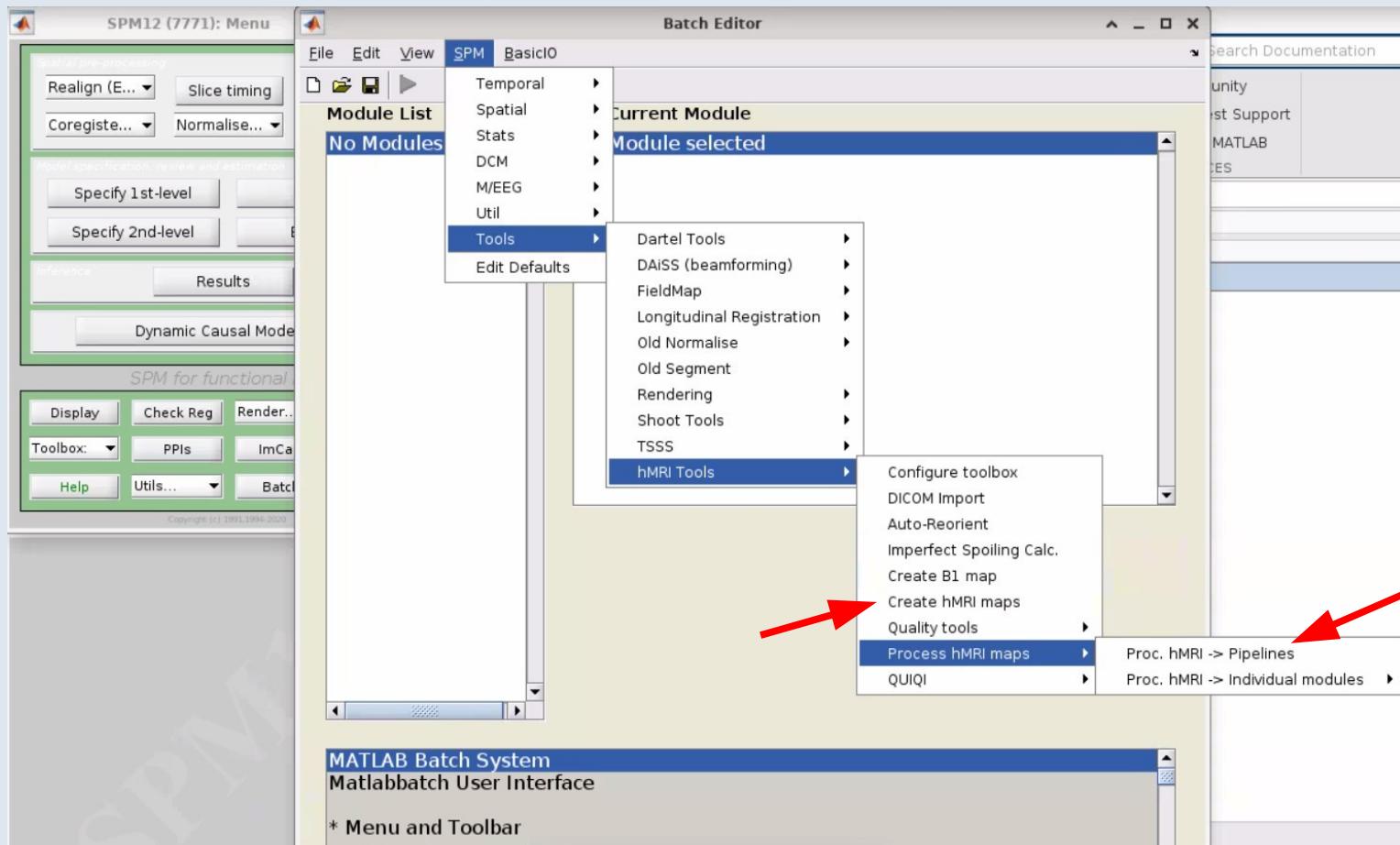
- Choose batch and then

SPM>Tools>hMRI toolbox

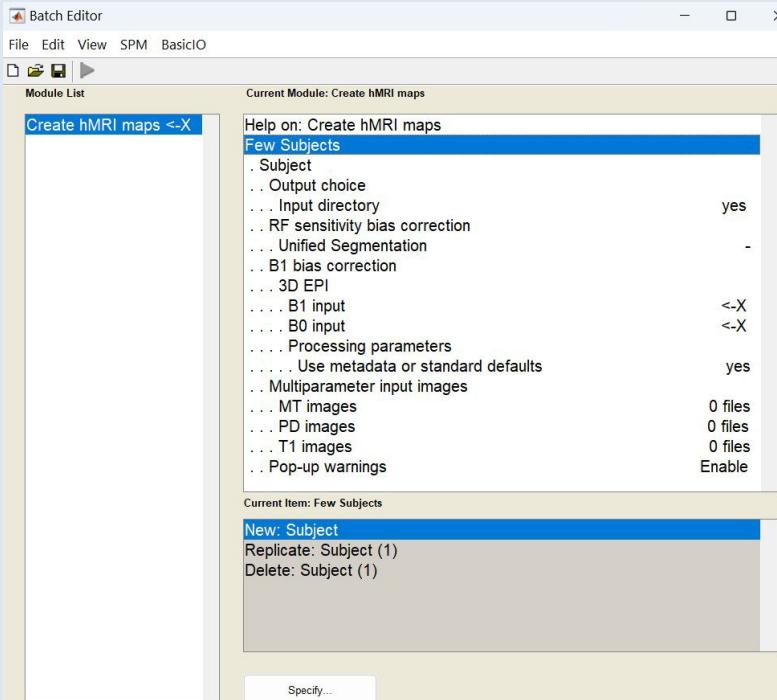
# SPM Batch editor



# Select from SPM



# Create hMRI Maps

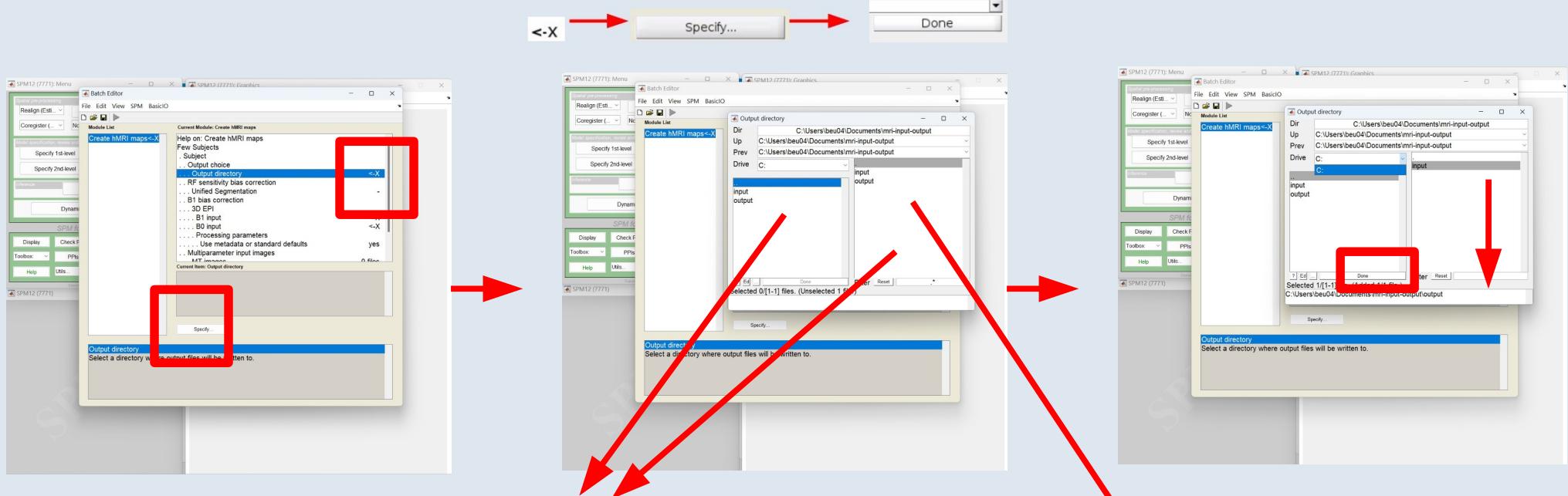


**Few Subjects**  
Specify the number of subjects.  
1 or more options must be selected from:  
\* Subject  
Currently selected options:  
\* "Subject"

- 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

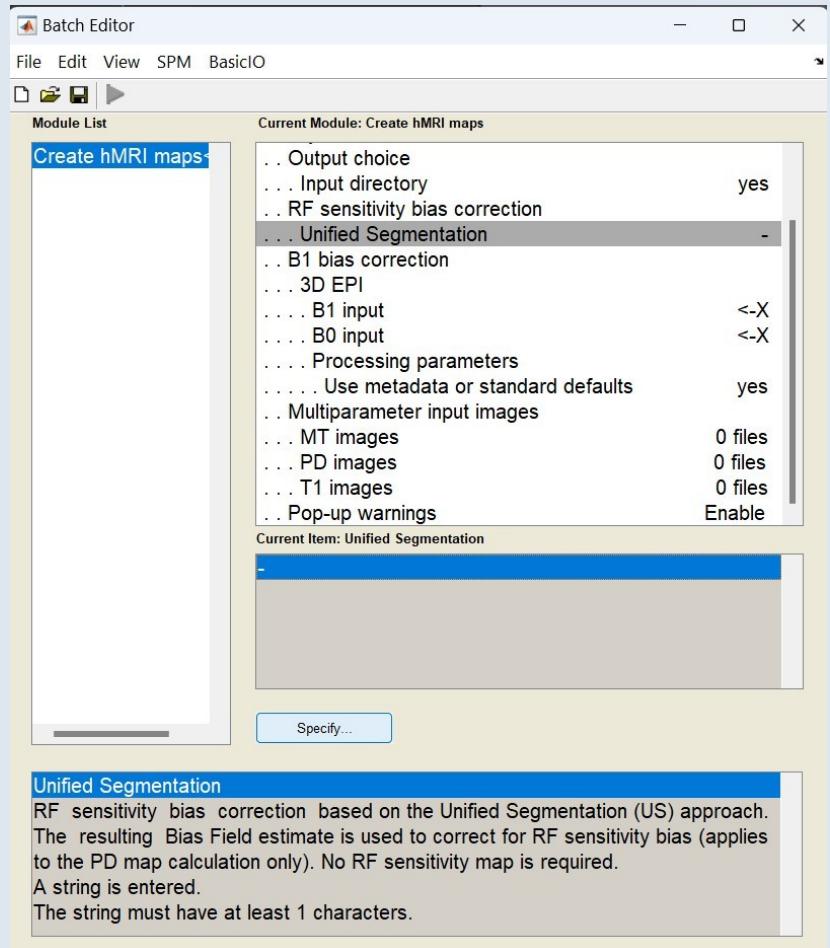


Sub-Dirs of Dir appears in left and right pane

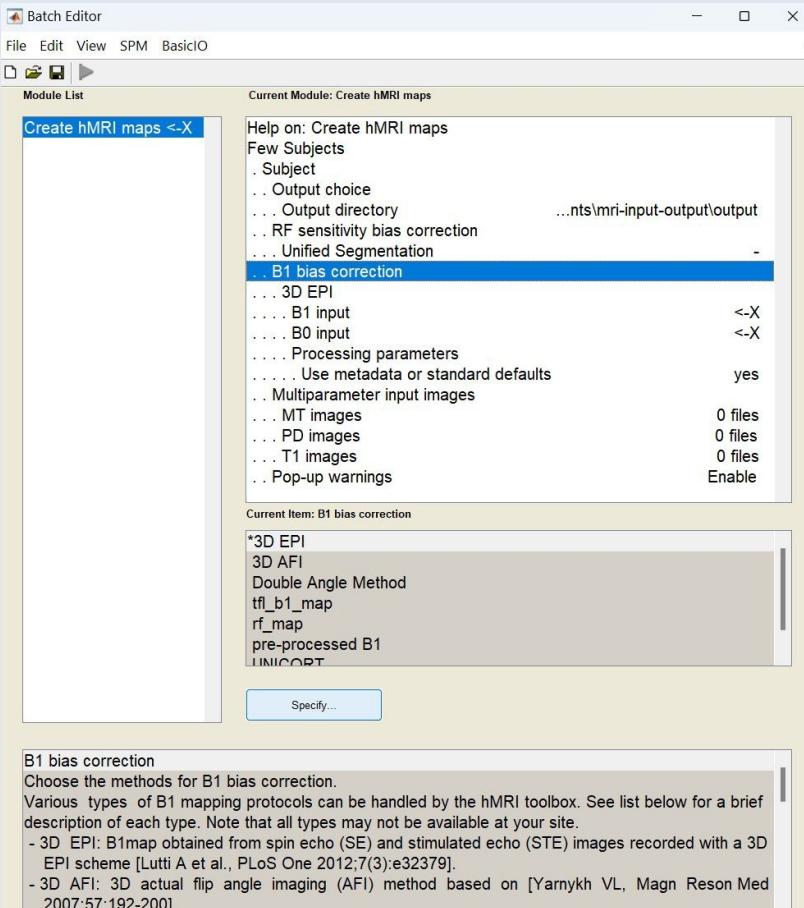
Once clicked in right pane, files transfer to 'selected'

# RF sensitivity bias correction

- Unified Segmentation approach (Ashburner2005) does not require receive field sensitivity maps and calculates the correction in a data driven way.



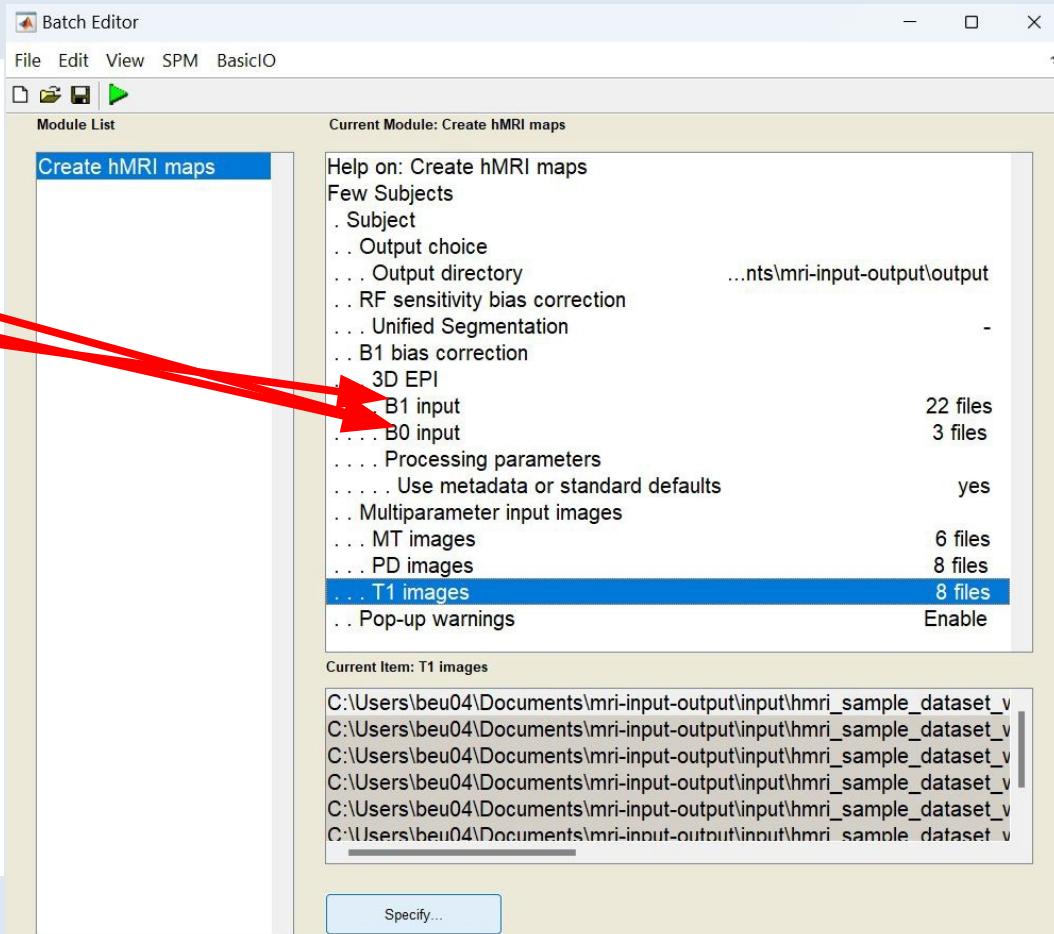
# B1 bias correction



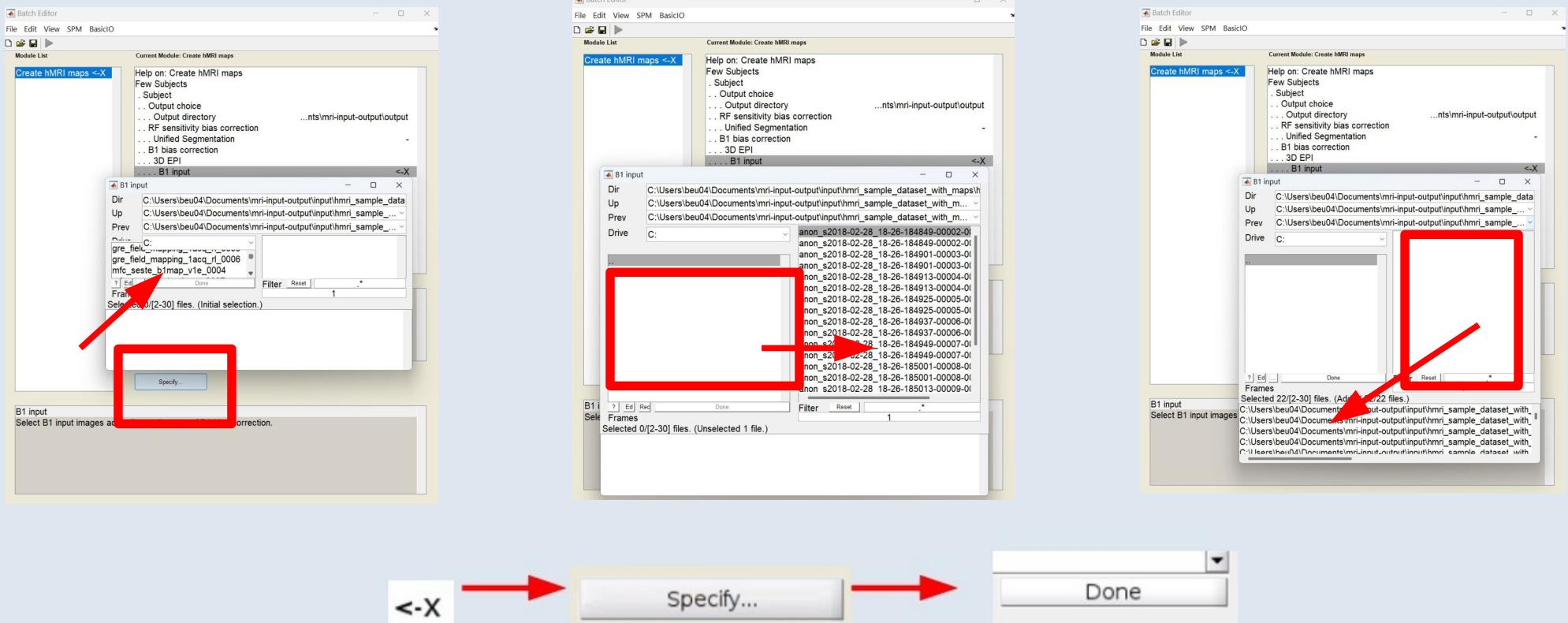
- B1 bias correction
- 3D EPI
- B1 input
- B0 input

# B1 bias correction input:

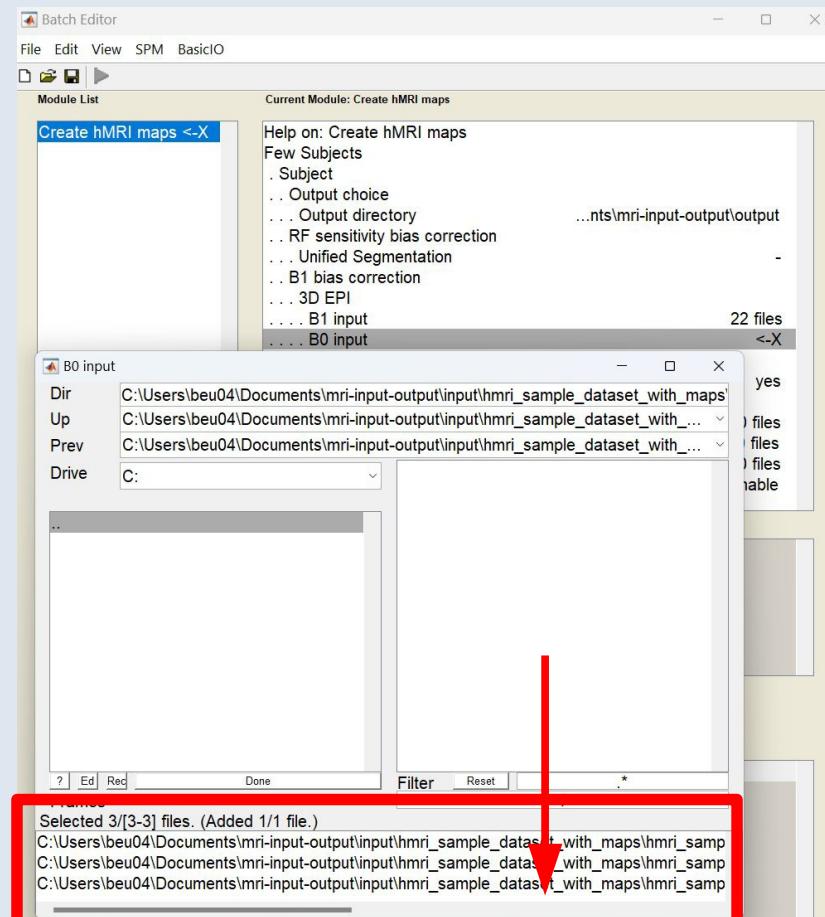
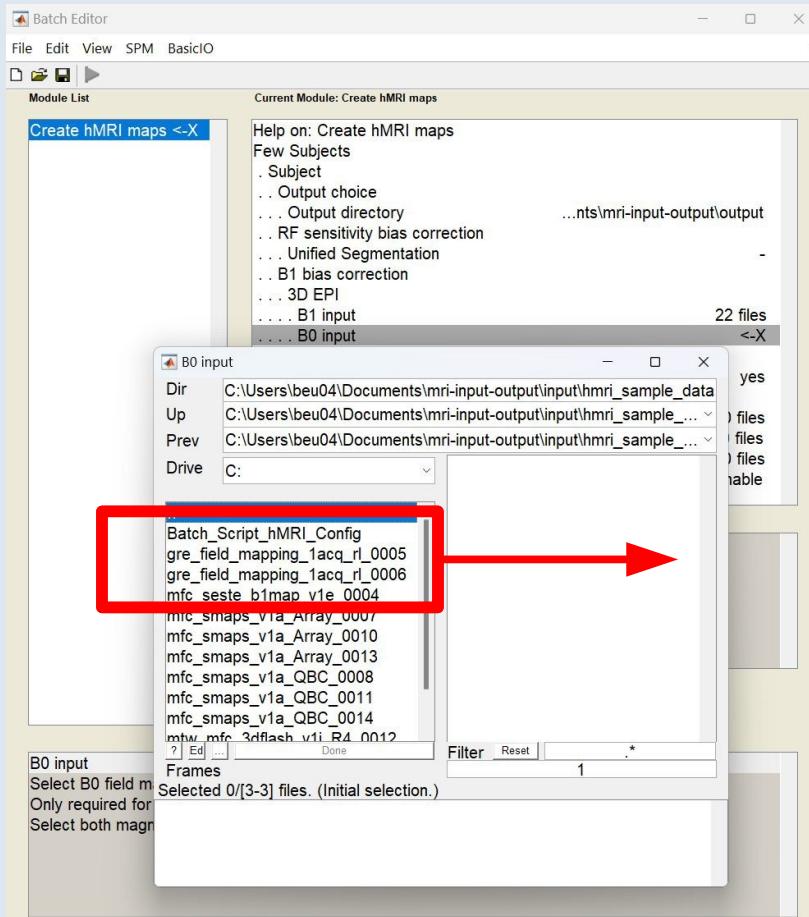
Batch_Script_hMRI_Config	8/28/2023 12:23 PM	File folder
gre_field_mapping_1acq_rl_0005	8/28/2023 12:23 PM	File folder
gre_field_mapping_1acq_rl_0006	8/28/2023 12:23 PM	File folder
mfc_seste_b1map_v1e_0004	8/28/2023 12:23 PM	File folder
mfc_smmaps_v1a_Array_0007	8/28/2023 12:23 PM	File folder
mfc_smmaps_v1a_Array_0010	8/28/2023 12:23 PM	File folder
mfc_smmaps_v1a_Array_0013	8/28/2023 12:23 PM	File folder
mfc_smmaps_v1a_QBC_0008	8/28/2023 12:23 PM	File folder
mfc_smmaps_v1a_QBC_0011	8/28/2023 12:23 PM	File folder
mfc_smmaps_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



# Choose B1 maps data

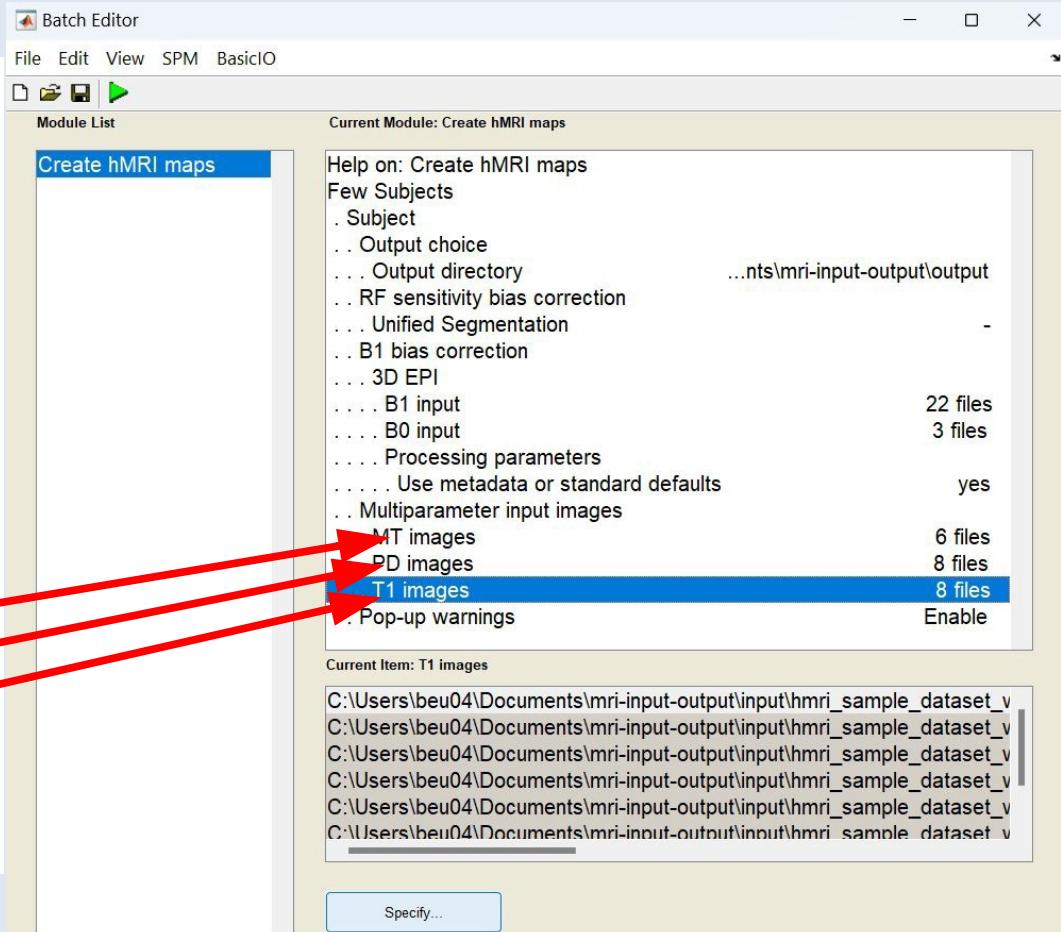


# B0 input add files



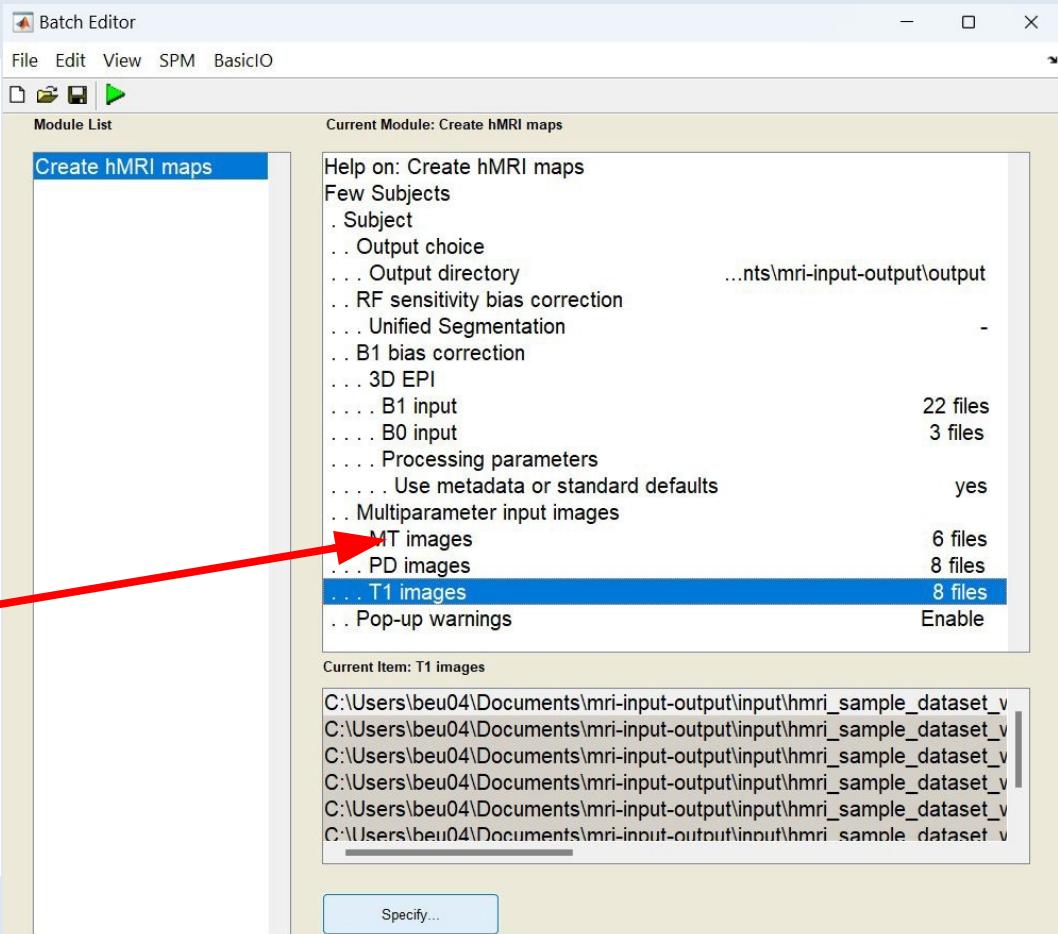
# Multiparameter input images

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_smmaps_v1a_Array_0007	8/28/2023 12:23 PM	File folder
mfc_smmaps_v1a_Array_0010	8/28/2023 12:23 PM	File folder
mfc_smmaps_v1a_Array_0013	8/28/2023 12:23 PM	File folder
mfc_smmaps_v1a_QBC_0008	8/28/2023 12:23 PM	File folder
mfc_smmaps_v1a_QBC_0011	8/28/2023 12:23 PM	File folder
mfc_smmaps_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	8/28/2022 12:24 PM	File folder
t1w_mfc_3dflash_v1i_R4_0015	8/28/2023 12:24 PM	File folder



# MTw images input:

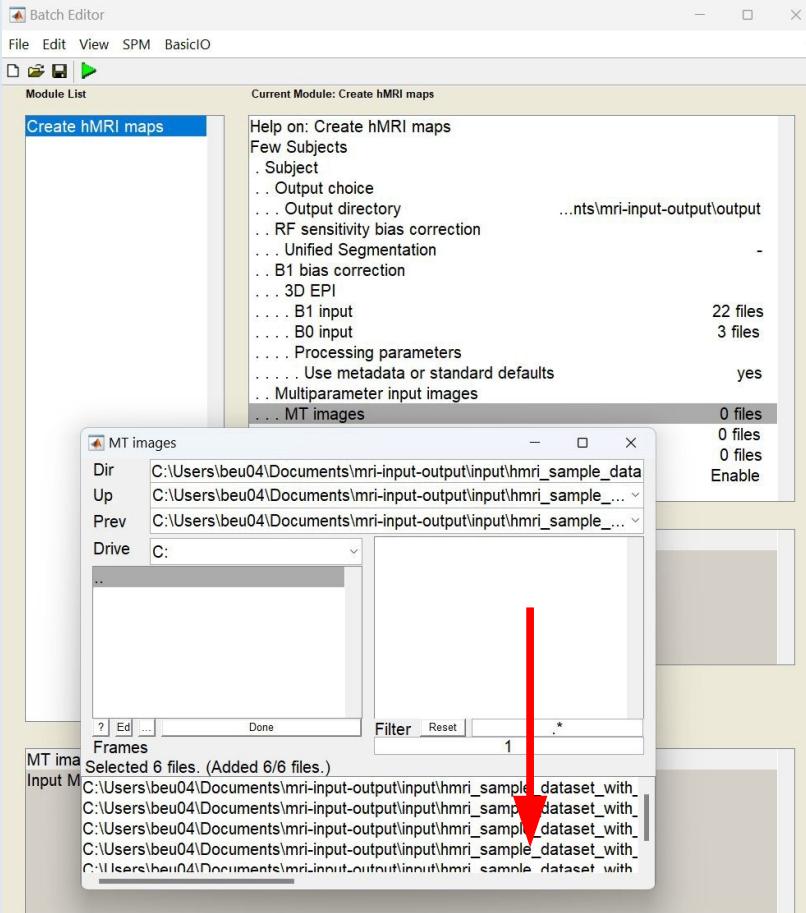
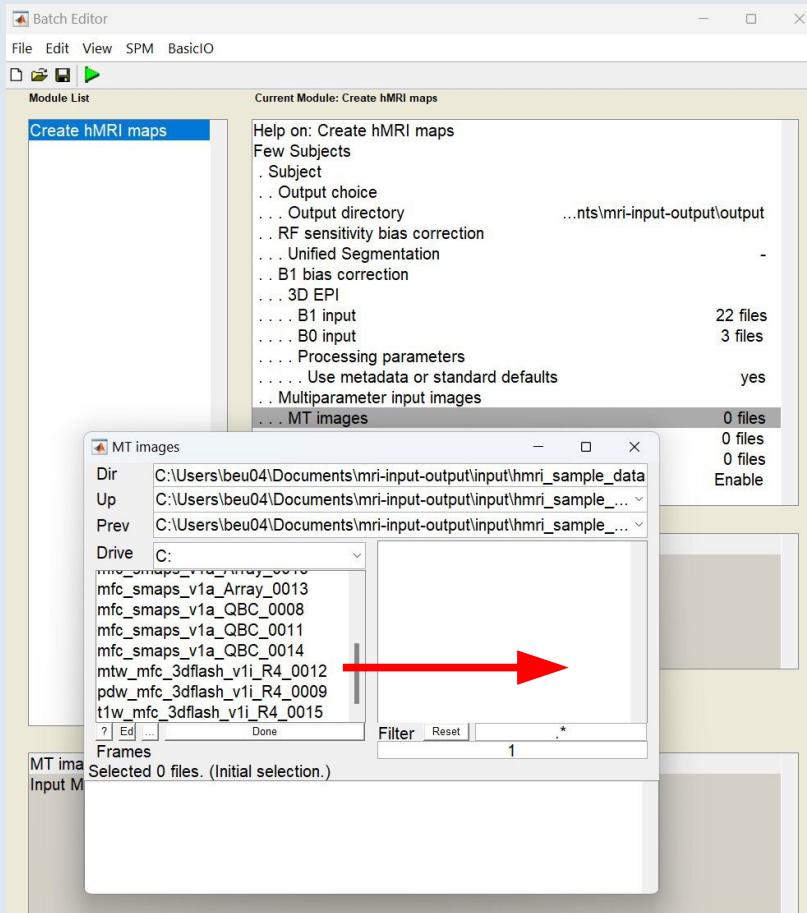
Batch_Script_hMRI_Config	8/28/2023 12:23 PM	File folder
gre_field_mapping_1acq_rl_0005	8/28/2023 12:23 PM	File folder
gre_field_mapping_1acq_rl_0006	8/28/2023 12:23 PM	File folder
mfc_seste_b1map_v1e_0004	8/28/2023 12:23 PM	File folder
mfc_smmaps_v1a_Array_0007	8/28/2023 12:23 PM	File folder
mfc_smmaps_v1a_Array_0010	8/28/2023 12:23 PM	File folder
mfc_smmaps_v1a_Array_0013	8/28/2023 12:23 PM	File folder
mfc_smmaps_v1a_QBC_0008	8/28/2023 12:23 PM	File folder
mfc_smmaps_v1a_QBC_0011	8/28/2023 12:23 PM	File folder
mfc_smmaps_v1a_QBC_0014	8/28/2023 12:23 PM	File folder
mtw_mfc_3dflash_v1i_R4_001	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



# MT image files folder

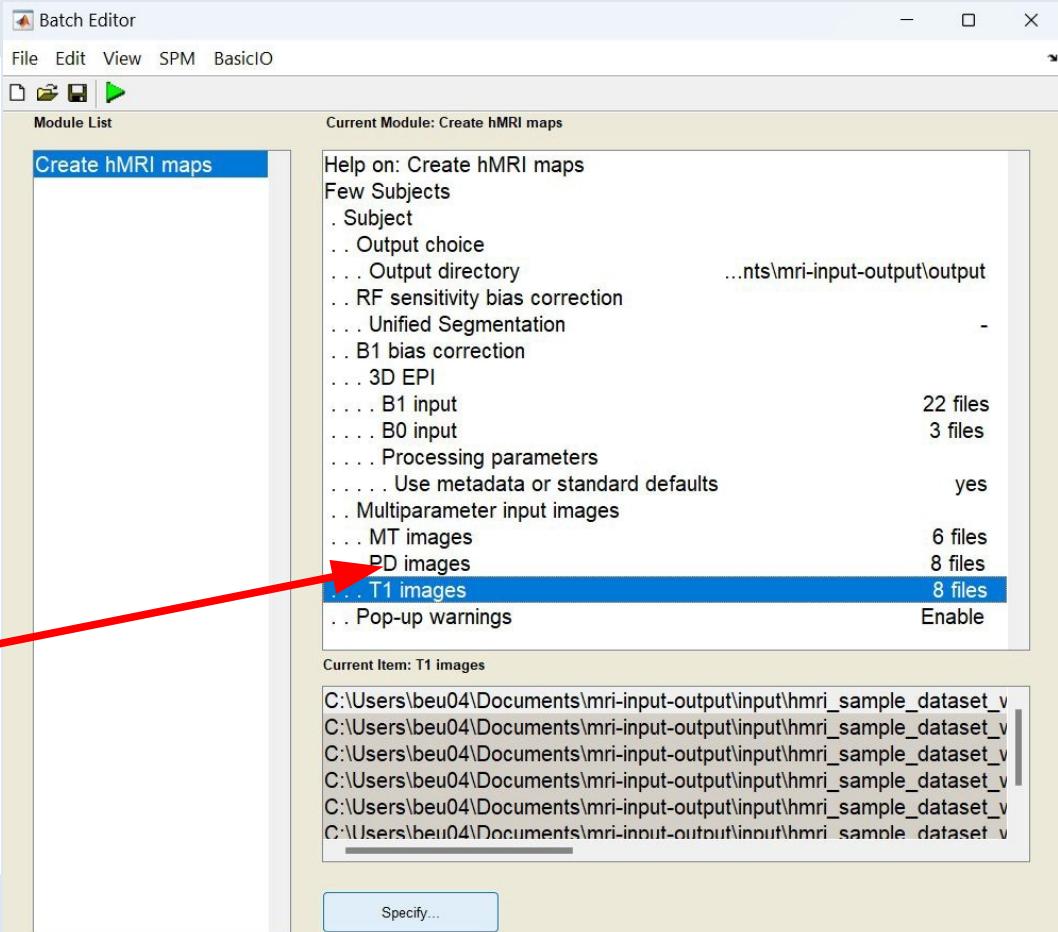
Name
anon_s2018-02-28_18-26-190132-00001-00224-1.json
anon_s2018-02-28_18-26-190132-00001-00224-1.nii
anon_s2018-02-28_18-26-190132-00001-00448-2.json
anon_s2018-02-28_18-26-190132-00001-00448-2.nii
anon_s2018-02-28_18-26-190132-00001-00672-3.json
anon_s2018-02-28_18-26-190132-00001-00672-3.nii
anon_s2018-02-28_18-26-190132-00001-00896-4.json
anon_s2018-02-28_18-26-190132-00001-00896-4.nii
anon_s2018-02-28_18-26-190132-00001-01120-5.json
anon_s2018-02-28_18-26-190132-00001-01120-5.nii
anon_s2018-02-28_18-26-190132-00001-01344-6.json
anon_s2018-02-28_18-26-190132-00001-01344-6.nii

# Multiparameter images: MT

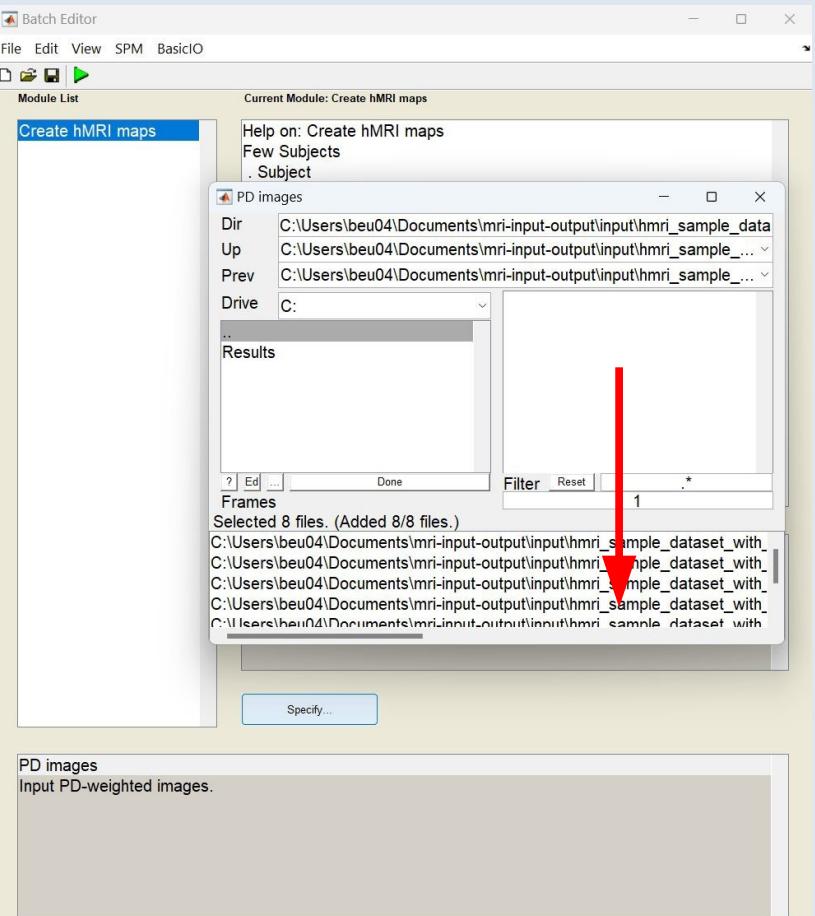
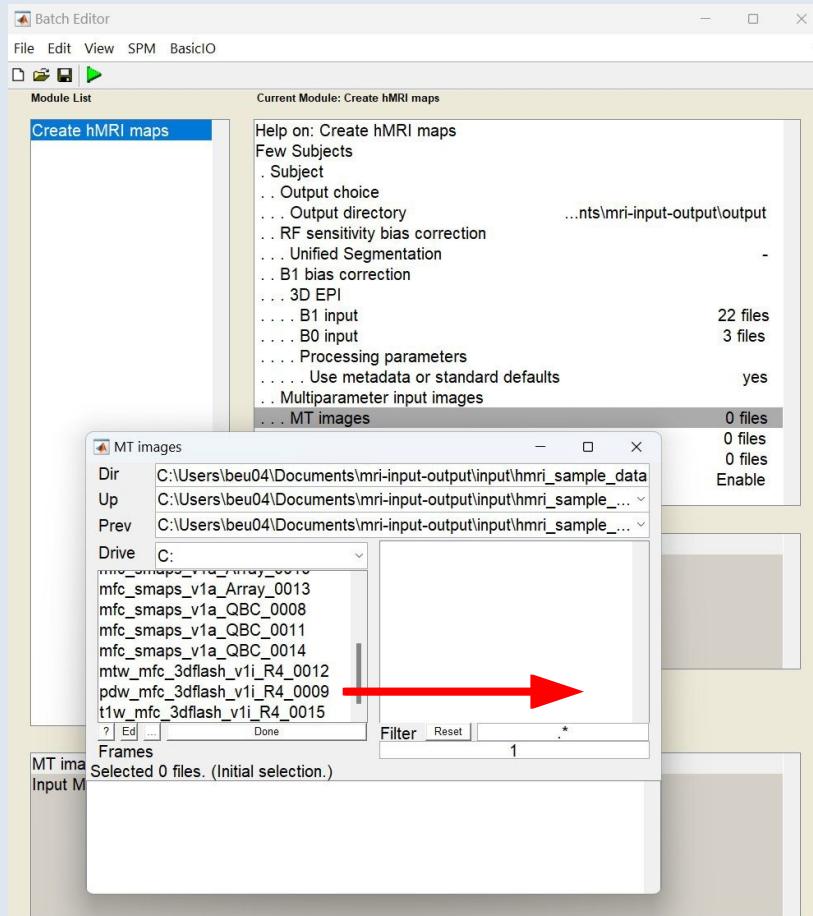


# PDw images input:

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_smmaps_v1a_Array_0007	8/28/2023 12:23 PM	File folder
mfc_smmaps_v1a_Array_0010	8/28/2023 12:23 PM	File folder
mfc_smmaps_v1a_Array_0013	8/28/2023 12:23 PM	File folder
mfc_smmaps_v1a_QBC_0008	8/28/2023 12:23 PM	File folder
mfc_smmaps_v1a_QBC_0011	8/28/2023 12:23 PM	File folder
mfc_smmaps_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

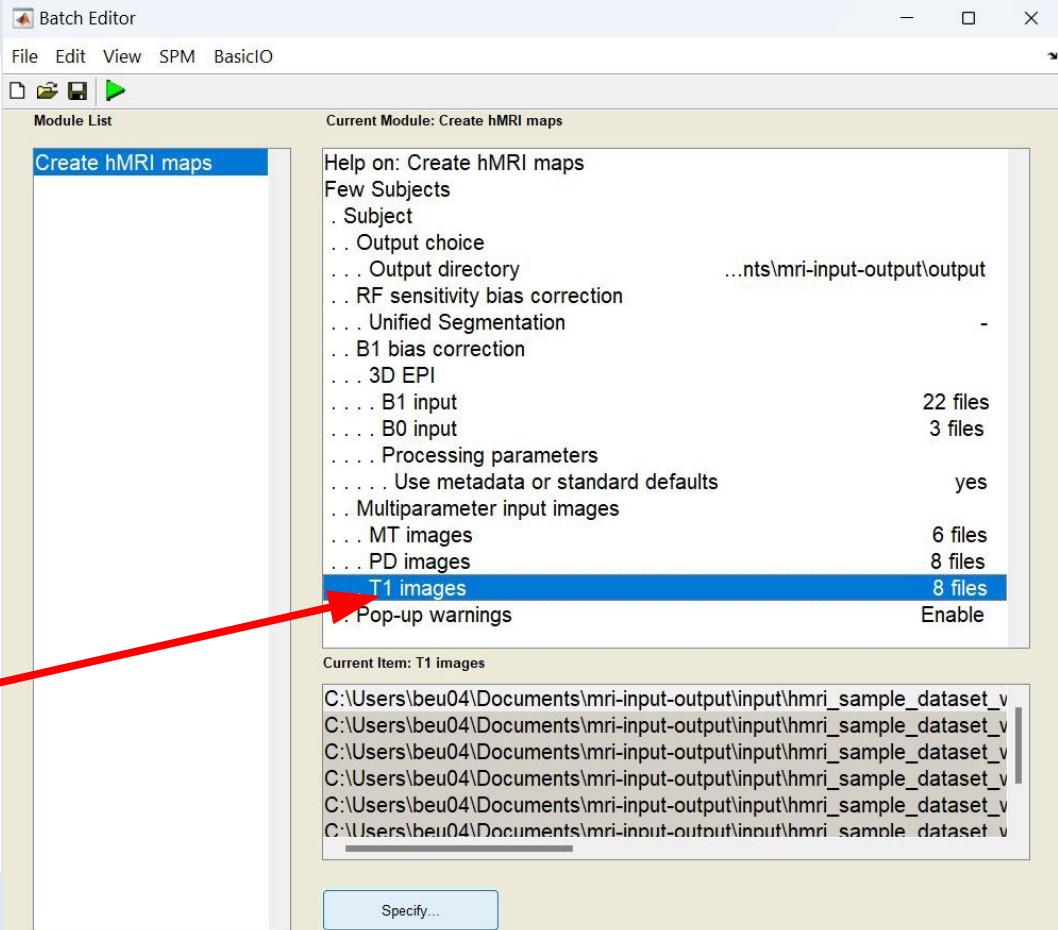


# Multiparameter images: PD

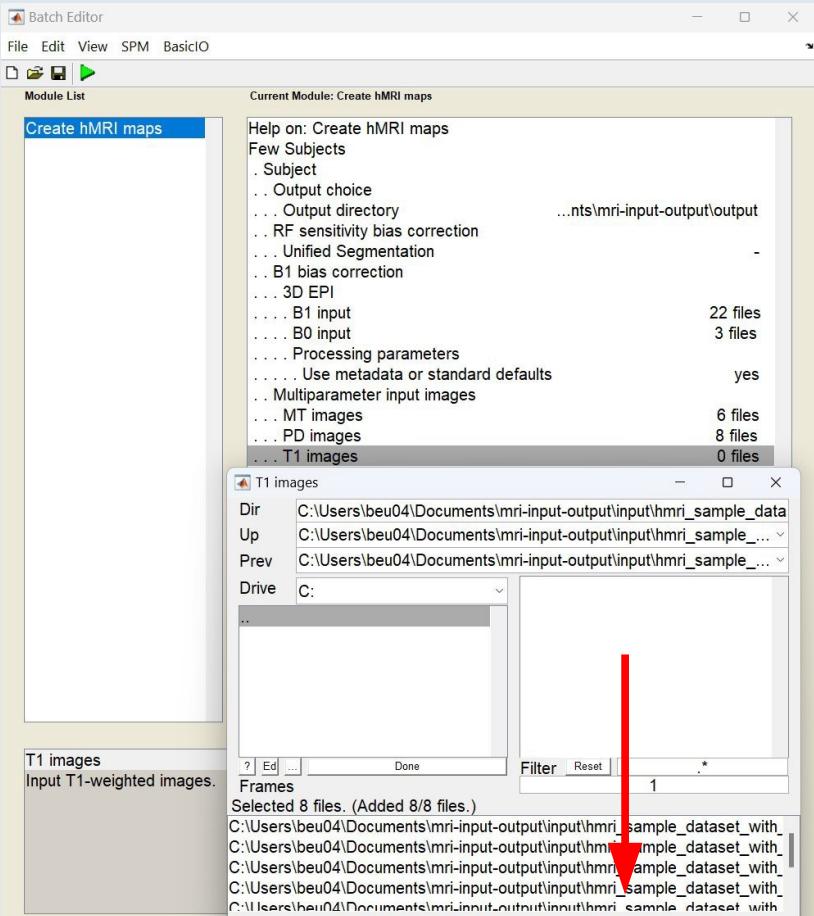
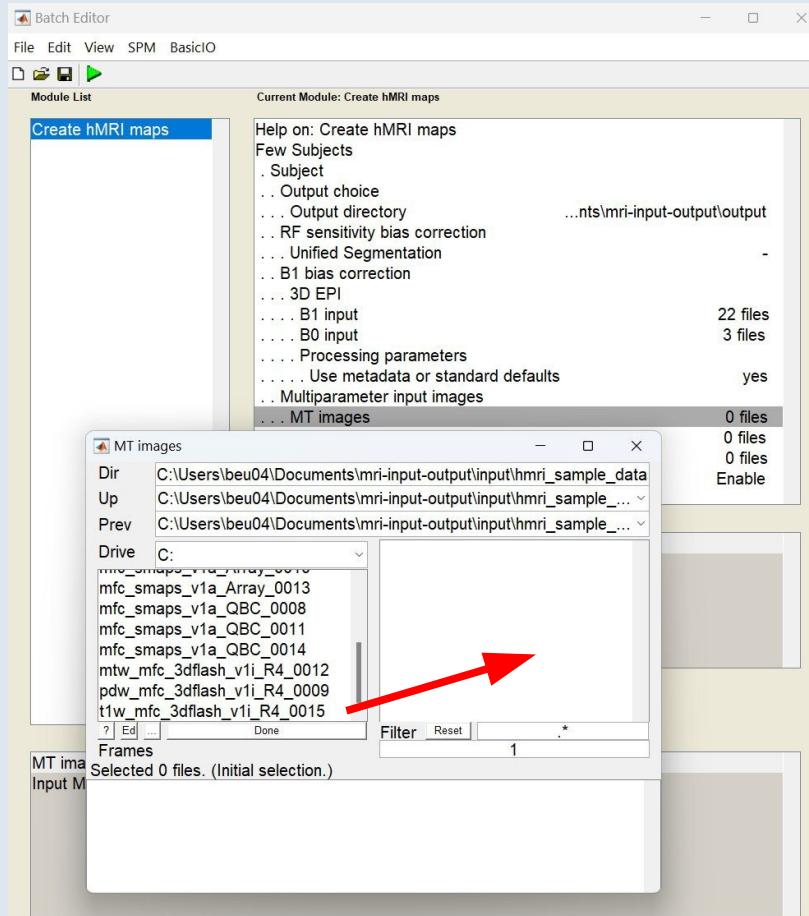


# T1w images input:

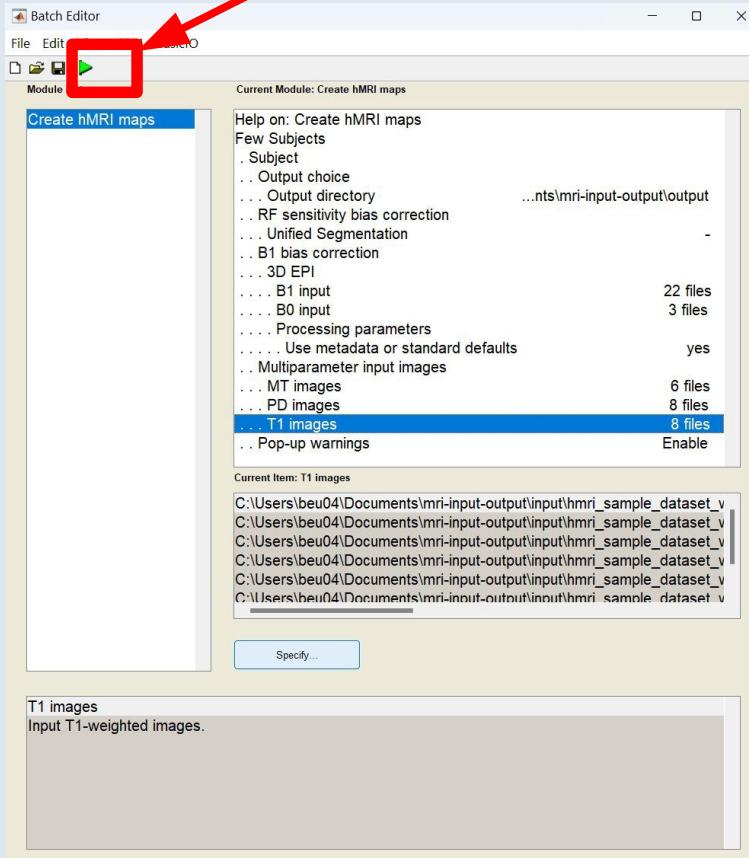
📁	Batch_Script_hMRI_Config	8/28/2023 12:23 PM
📁	gre_field_mapping_1acq_rl_0005	8/28/2023 12:23 PM
📁	gre_field_mapping_1acq_rl_0006	8/28/2023 12:23 PM
📁	mfc_seste_b1map_v1e_0004	8/28/2023 12:23 PM
📁	mfc_smmaps_v1a_Array_0007	8/28/2023 12:23 PM
📁	mfc_smmaps_v1a_Array_0010	8/28/2023 12:23 PM
📁	mfc_smmaps_v1a_Array_0013	8/28/2023 12:23 PM
📁	mfc_smmaps_v1a_QBC_0008	8/28/2023 12:23 PM
📁	mfc_smmaps_v1a_QBC_0011	8/28/2023 12:23 PM
📁	mfc_smmaps_v1a_QBC_0014	8/28/2023 12:23 PM
📁	mtw_mfc_3dflash_v1i_R4_0012	8/28/2023 12:24 PM
📁	pdw_mfc_3dflash_v1i_R4_0009	8/28/2023 12:24 PM
📁	t1w_mfc_3dflash_v1i_R4_0015	8/28/2023 12:24 PM



# Multiparameter images: T1



# Time to hit run...



# pathToOutput/Results/\*



Supplementary

anon\_s2018-02-28\_  
18-26-185345-0000  
1-00224-1\_MTsat.js  
onanon\_s2018-02-28\_  
18-26-185345-0000  
1-00224-1\_MTsat.niianon\_s2018-02-28\_  
18-26-185345-0000  
1-00224-1\_PD.jsonanon\_s2018-02-28\_  
18-26-185345-0000  
1-00224-1\_PD.niianon\_s2018-02-28\_  
18-26-185345-0000  
1-00224-1\_R1.jsonanon\_s2018-02-28\_  
18-26-185345-0000  
1-00224-1\_R1.niianon\_s2018-02-28\_  
18-26-185345-0000  
1-00224-1\_R2s\_OLS  
.jsonanon\_s2018-02-28\_  
18-26-185345-0000  
1-00224-1\_R2s\_OLS  
.nii

\_finished\_

# pathToOutput/Results/ Supplementary

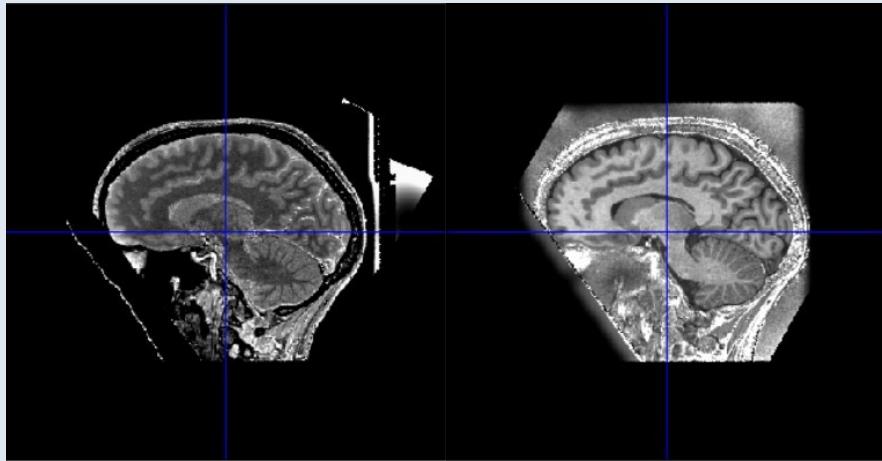
/data/u\_ugurcan\_software/output/compiled-v6-fulltest/Results/Supplementary/

 anon_s2018-02-28_18-26-184837-0000-1-00001-1_B1map.son	 anon_s2018-02-28_18-26-184837-0000-1-00001-1_B1map.nii	 anon_s2018-02-28_18-26-184837-0000-1-00001-1_B1ref.json	 anon_s2018-02-28_18-26-184837-0000-1-00001-1_B1ref.nii	 anon_s2018-02-28_18-26-185345-0000-1-00224-1_MTw_OL_Sfit_TEzero.json	 anon_s2018-02-28_18-26-185345-0000-1-00224-1_MTw_OL_Sfit_TEzero.nii	 anon_s2018-02-28_18-26-185345-0000-1-00224-1_PDw_OL_Sfit_TEzero.json	 anon_s2018-02-28_18-26-185345-0000-1-00224-1_PDw_OL_Sfit_TEzero.nii	 anon_s2018-02-28_18-26-185345-0000-1-00224-1_R2s.json
 anon_s2018-02-28_18-26-185345-0000-1-00224-1_R2s.nii	 anon_s2018-02-28_18-26-185345-0000-1-00224-1_T1w_OLS_fit_TEzero.json	 anon_s2018-02-28_18-26-185345-0000-1-00224-1_T1w_OLS_fit_TEzero.nii	 hMRI_map_creation_b1map_params.json	 hMRI_map_creation_job_create_maps.json	 hMRI_map_creation_logfile.log	 hMRI_map_creation_mppm_params.json	 hMRI_map_creation_quality_assessment.json	

# Visualization software

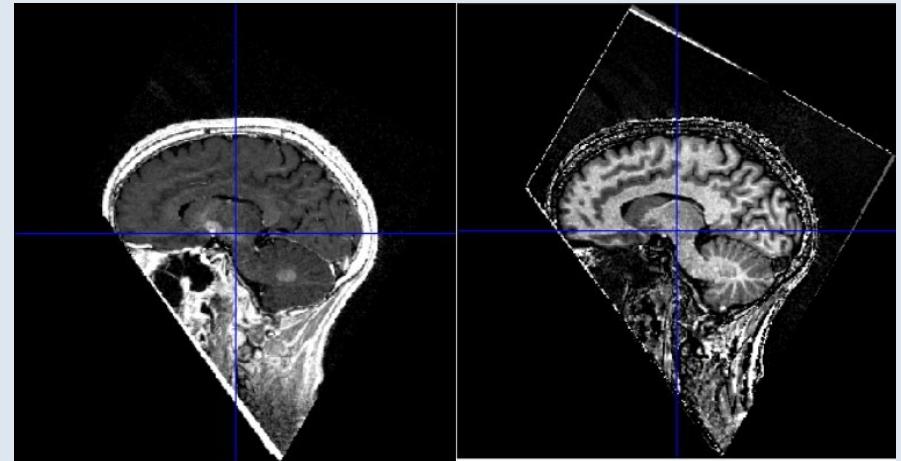


# Intensity ranges for maps



Intensity range  
[50 120]

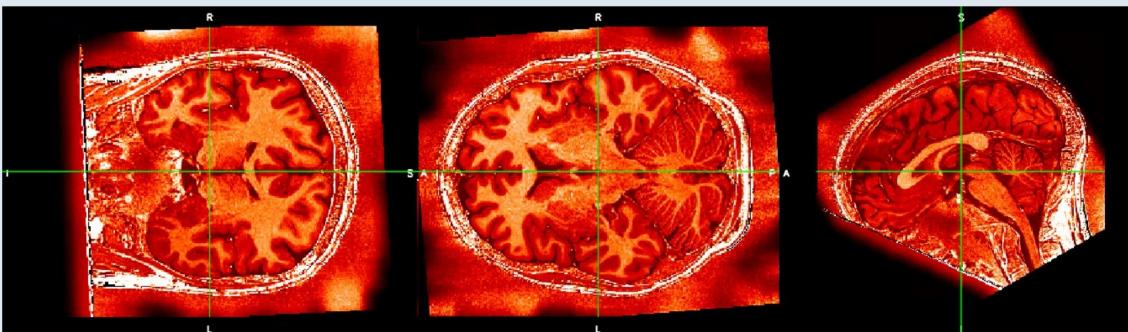
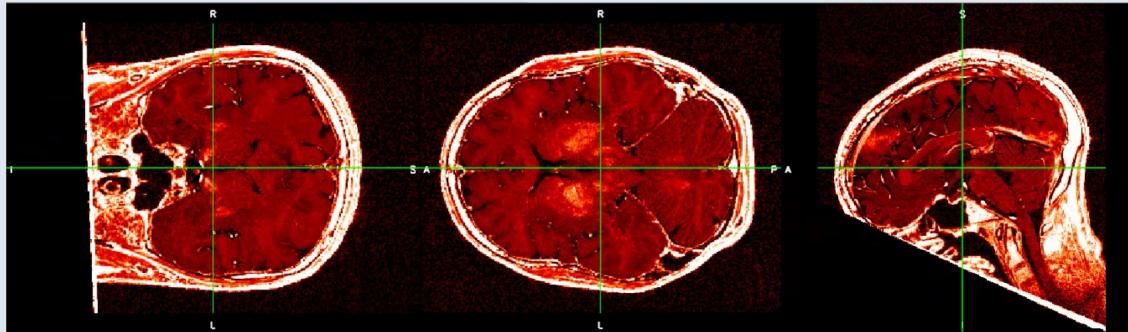
Intensity range  
[0.0 1.4]



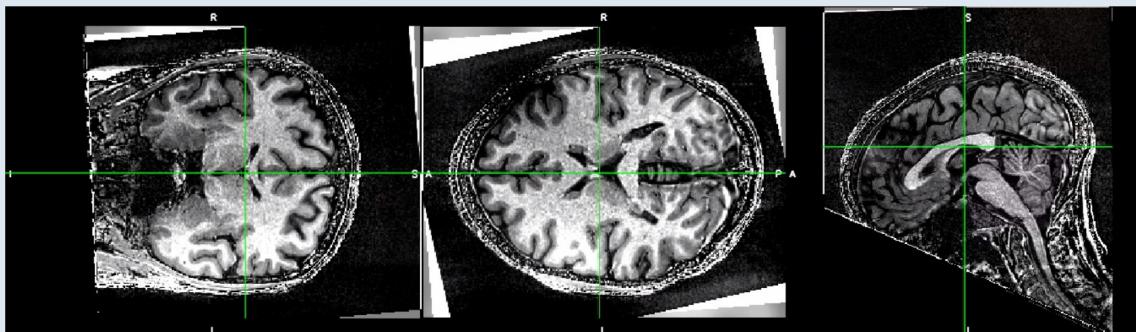
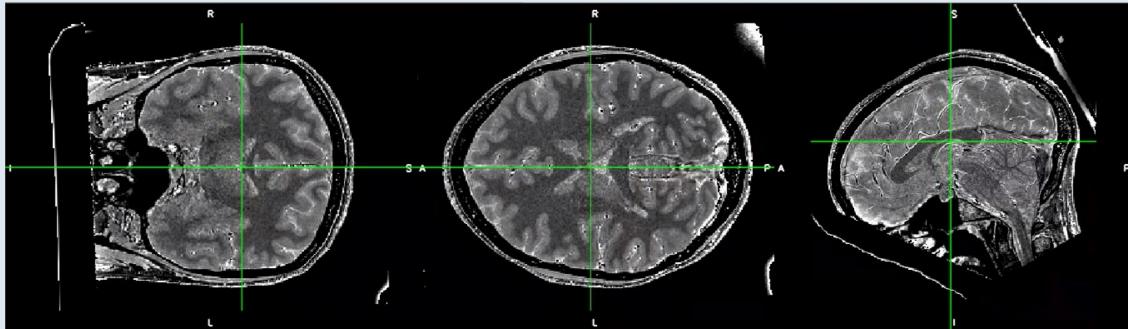
Intensity range  
[0 70]

Intensity range  
[0 2]

# R2s and R1 Maps

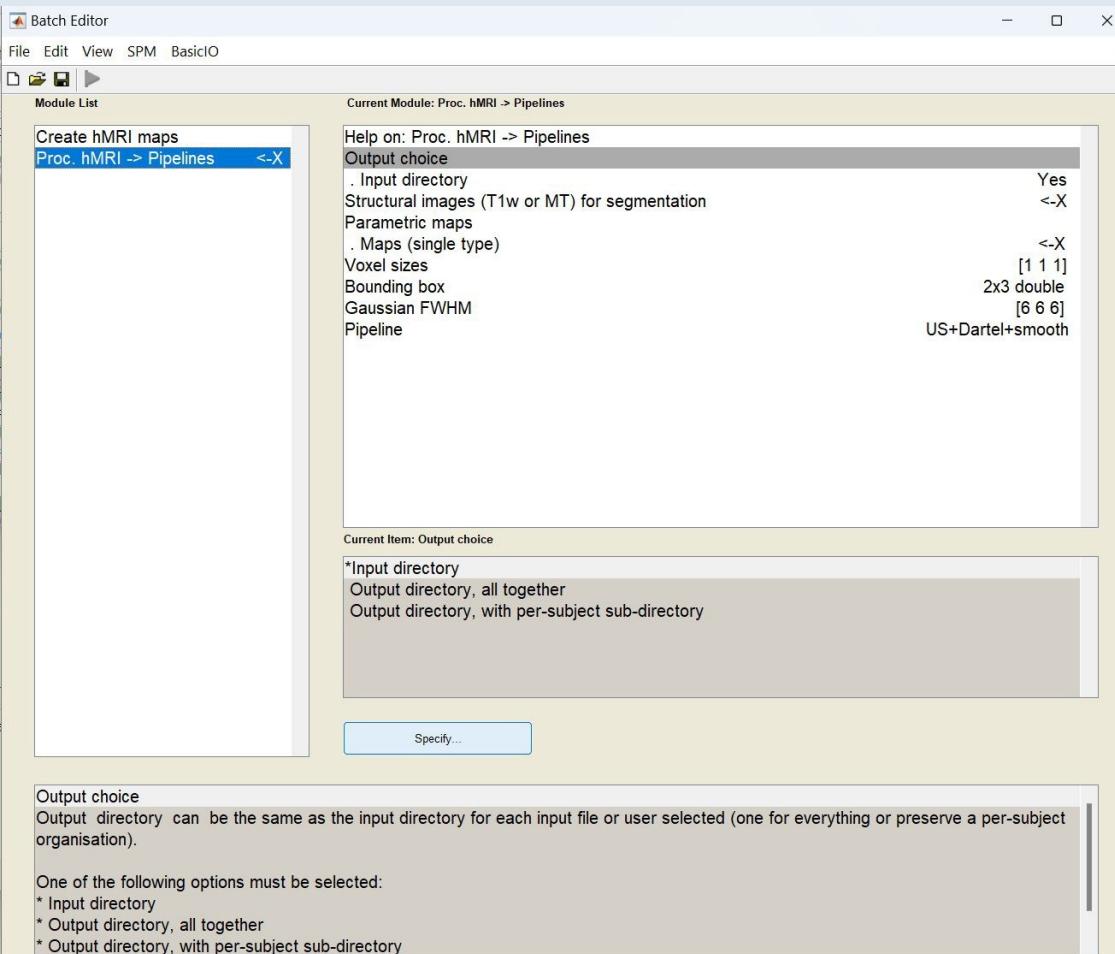
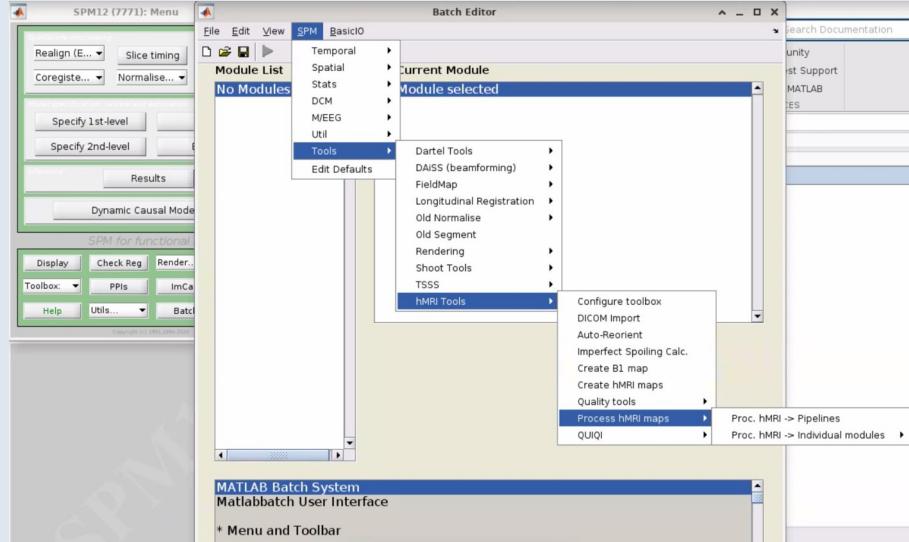


# PD and Mtsat

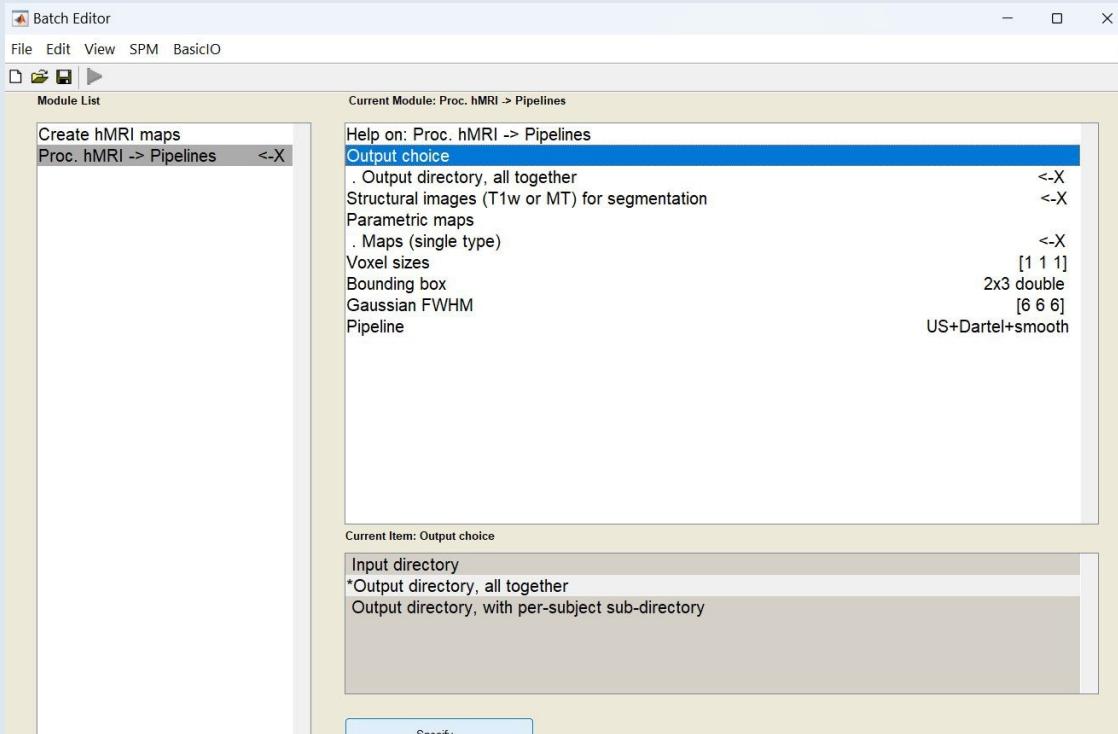


# Spatial processing: pipeline

# SPM>Tools>hMRI tools> Process hMRI maps> Proc. hMRI → Pipelines



# Output directory choice



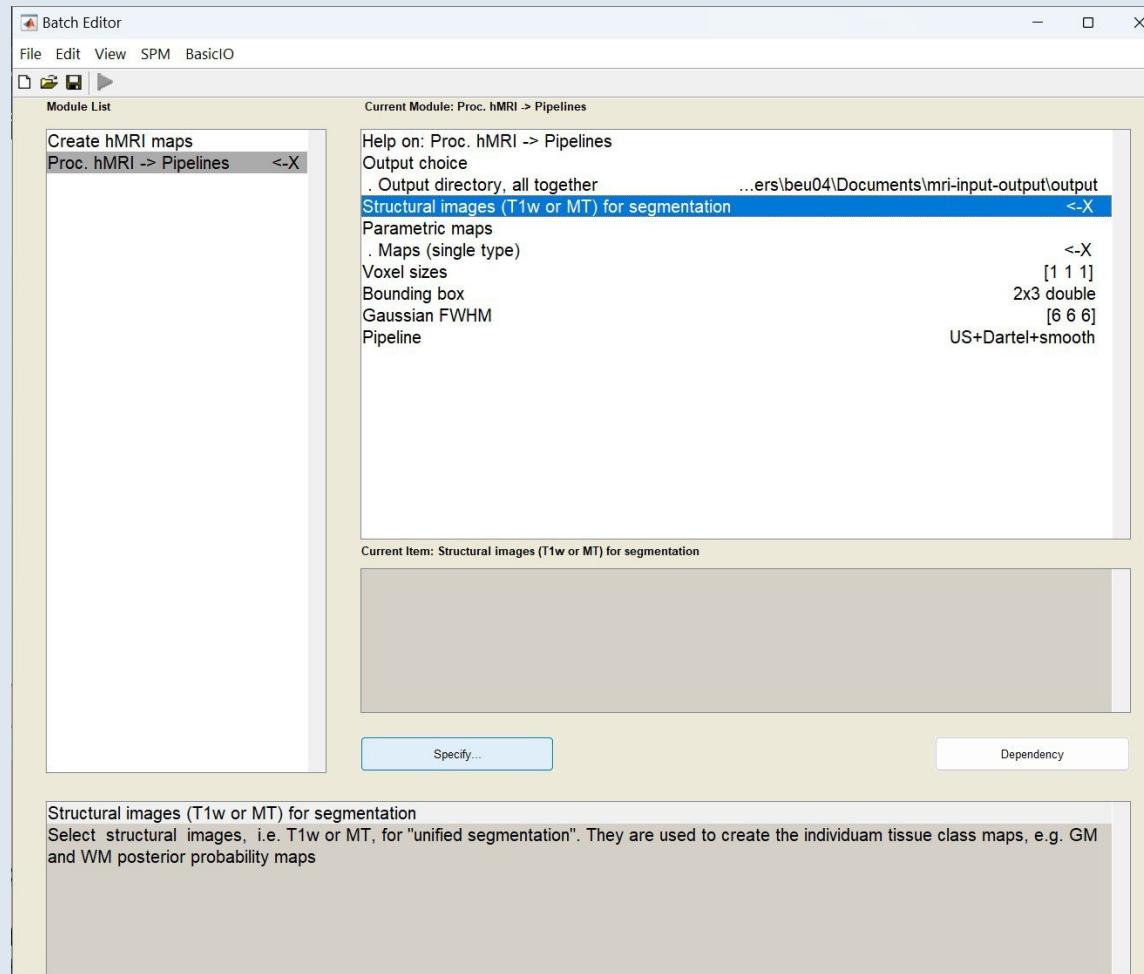
## Output choice

Output directory can be the same as the input directory for each input file or user selected (one for everything or preserve a per-subject organisation).

One of the following options must be selected:

- \* Input directory
- \* Output directory, all together
- \* Output directory, with per-subject sub-directory

# Add T1w images for each subject



# hMRI-toolbox demo data

Name

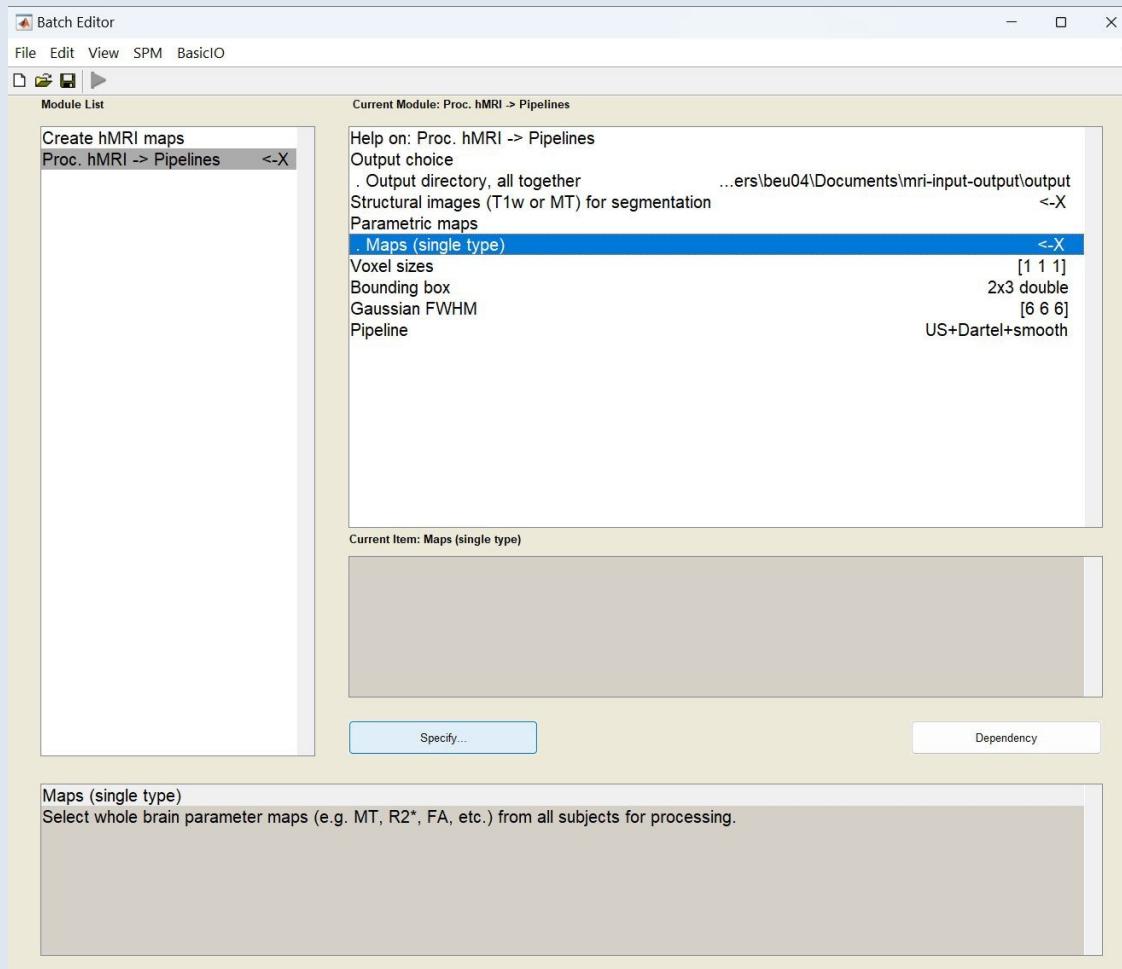
- 📁 Batch\_Script\_hMRI\_Config
- 📁 gre\_field\_mapping\_1acq\_rl\_0005
- 📁 gre\_field\_mapping\_1acq\_rl\_0006
- 📁 mfc\_seste\_b1map\_v1e\_0004
- 📁 mfc\_smmaps\_v1a\_Array\_0007
- 📁 mfc\_smmaps\_v1a\_Array\_0010
- 📁 mfc\_smmaps\_v1a\_Array\_0013
- 📁 mfc\_smmaps\_v1a\_QBC\_0008
- 📁 mfc\_smmaps\_v1a\_QBC\_0011
- 📁 mfc\_smmaps\_v1a\_QBC\_0014
- 📁 mtw\_mfc\_3dflash\_v1i\_R4\_0012
- 📁 pdw\_mfc\_3dflash\_v1i\_R4\_0009
- 📁 t1w\_mfc\_3dflash\_v1i\_R4\_0015

Name

- 📄 anon\_s2018-02-28\_18-26-190921-00001-00224-1.json
- 📄 anon\_s2018-02-28\_18-26-190921-00001-00224-1.nii
- 📄 anon\_s2018-02-28\_18-26-190921-00001-00448-2.json
- 📄 anon\_s2018-02-28\_18-26-190921-00001-00448-2.nii
- 📄 anon\_s2018-02-28\_18-26-190921-00001-00672-3.json
- 📄 anon\_s2018-02-28\_18-26-190921-00001-00672-3.nii
- 📄 anon\_s2018-02-28\_18-26-190921-00001-00896-4.json
- 📄 anon\_s2018-02-28\_18-26-190921-00001-00896-4.nii
- 📄 anon\_s2018-02-28\_18-26-190921-00001-01120-5.json
- 📄 anon\_s2018-02-28\_18-26-190921-00001-01120-5.nii
- 📄 anon\_s2018-02-28\_18-26-190921-00001-01344-6.json
- 📄 anon\_s2018-02-28\_18-26-190921-00001-01344-6.nii
- 📄 anon\_s2018-02-28\_18-26-190921-00001-01568-7.json
- 📄 anon\_s2018-02-28\_18-26-190921-00001-01568-7.nii
- 📄 anon\_s2018-02-28\_18-26-190921-00001-01792-8.json
- 📄 anon\_s2018-02-28\_18-26-190921-00001-01792-8.nii



# Add R2s for each subject



# From Results folder



Supplementary



anon\_s2018-02-28\_18-26-185345-0000\_1-00224-1\_MTsat.json



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

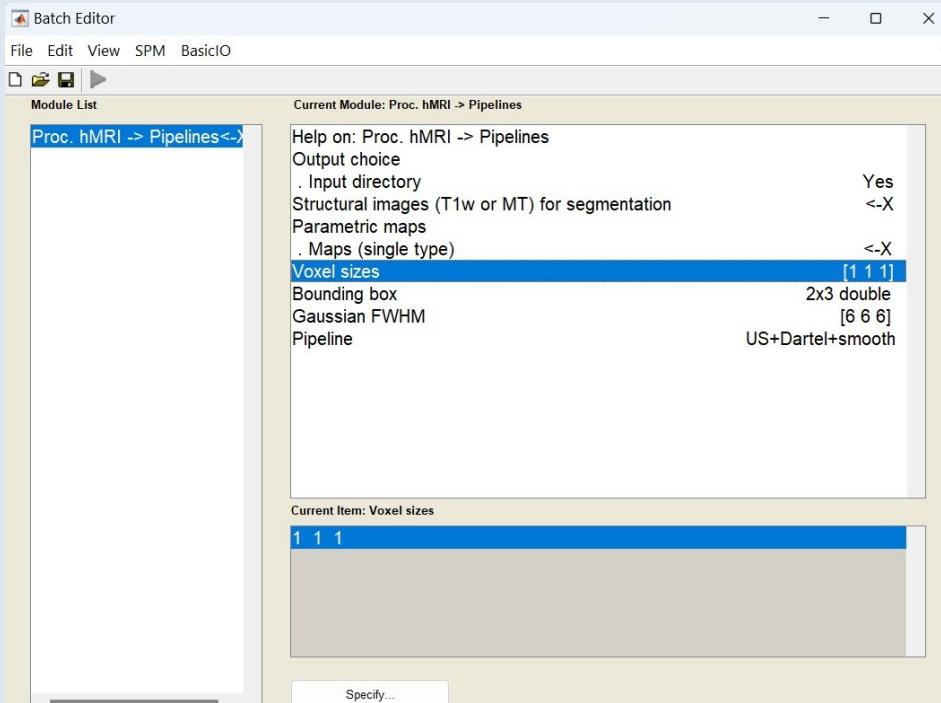


anon\_s2018-02-28\_18-26-185345-0000\_1-00224-1\_R2s\_OLS.nii



\_finished\_

# Voxel size & bounding box

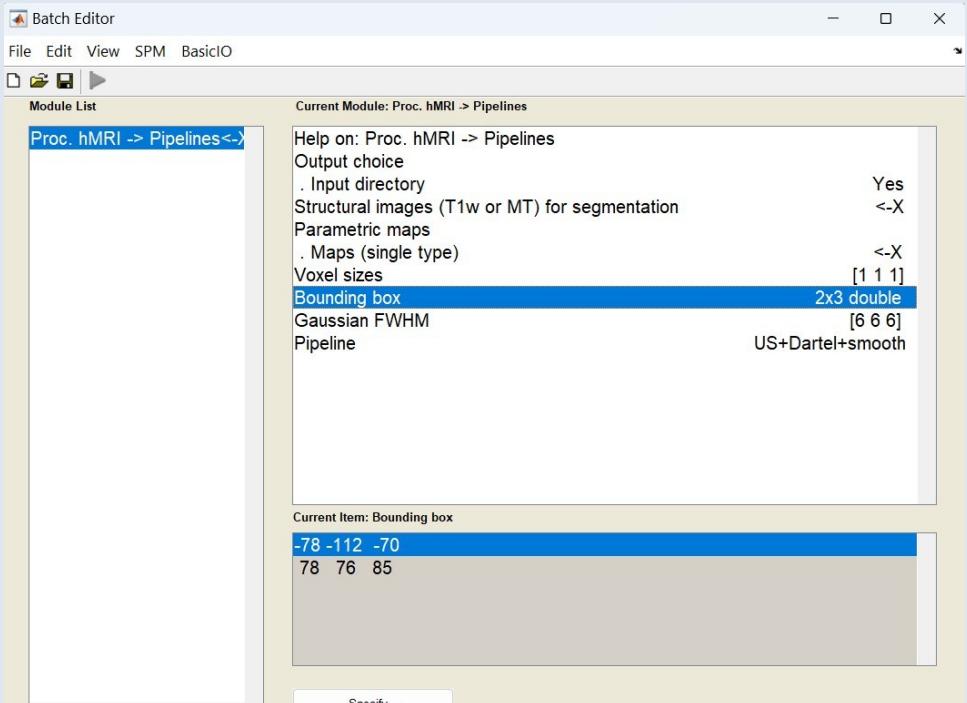


## Voxel sizes

Specify the voxel sizes of the deformation field and tissue classes to be produced. Non-finite values will default to the voxel sizes of the template image that was originally used to estimate the deformation.

Evaluated statements are entered.

An 1-by-3 array must be entered.



## Bounding box

The bounding box (in mm) of the volume which is to be written (relative to the anterior commissure).

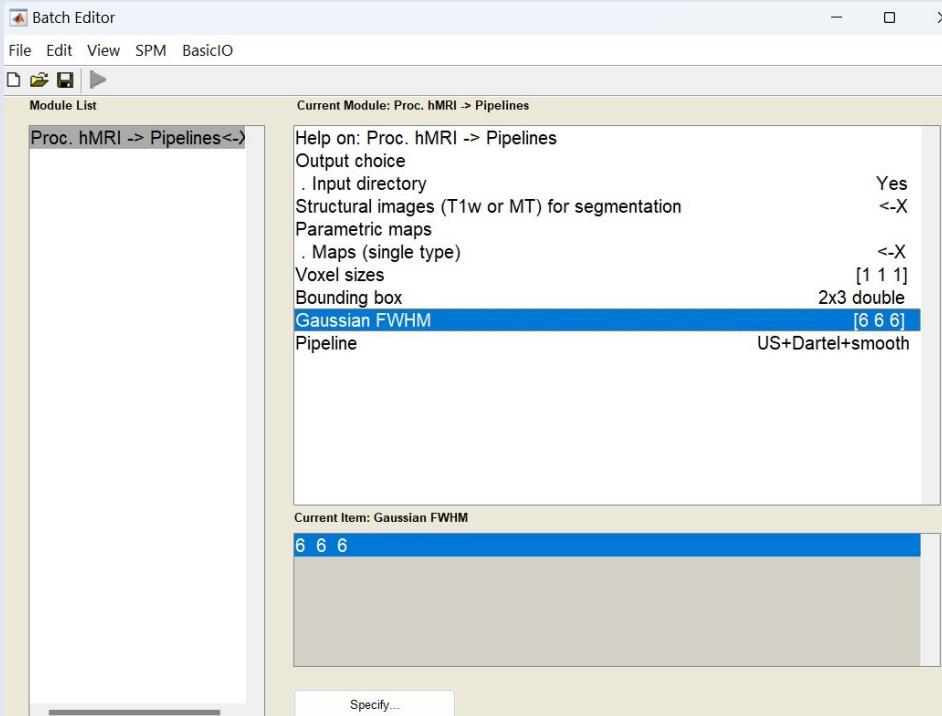
This item has a default value, set via a call to function

```
@(val)spm_get_defaults('normalise.write.bb',val{})
```

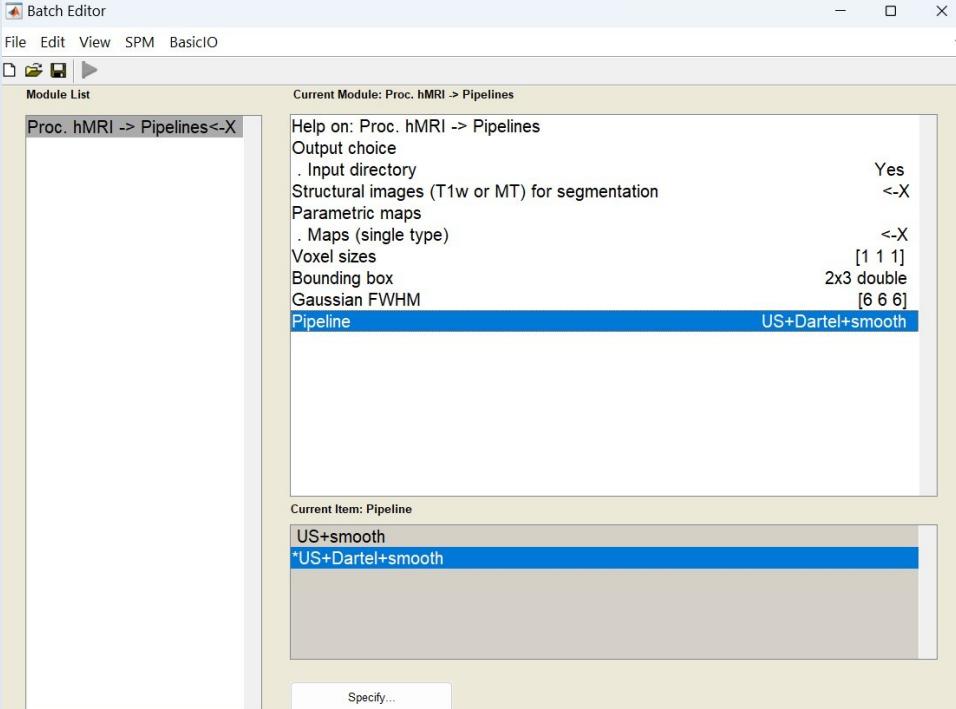
Real numbers are entered.

An 2-by-3 array must be entered.

# Gaussian FWHM & pipeline

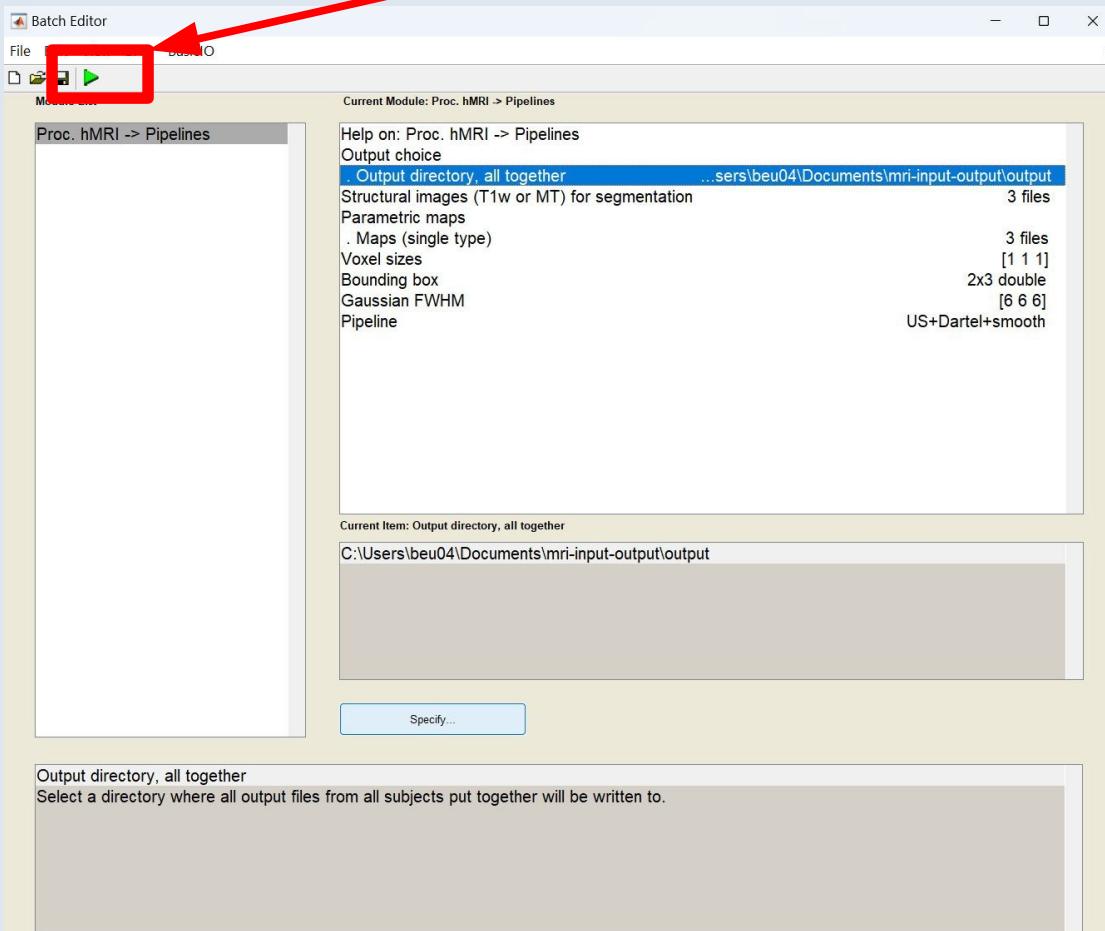


**Gaussian FWHM**  
Specify the full-width at half maximum (FWHM) of the Gaussian blurring kernel in mm. Three values should be entered denoting the FWHM in the x, y and z directions.  
Evaluated statements are entered.  
An 1-by-3 array must be entered.



**Pipeline**  
Chose the predefined pipeline that you prefer:  
- US+Smooth -> applies US, warps into MNI, then smoothes (weighted-average)  
- US+Dartel+Smooth -> applies US, builds Dartel template and warps into MNI, then smoothes (weighted-average)  
One of the following options must be selected:  
\* US+smooth  
\* US+Dartel+smooth

# Finally hit run...

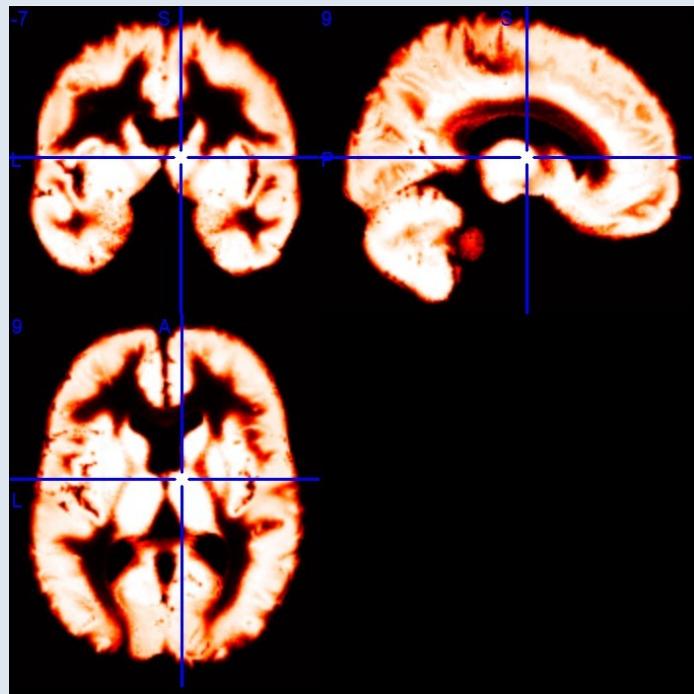
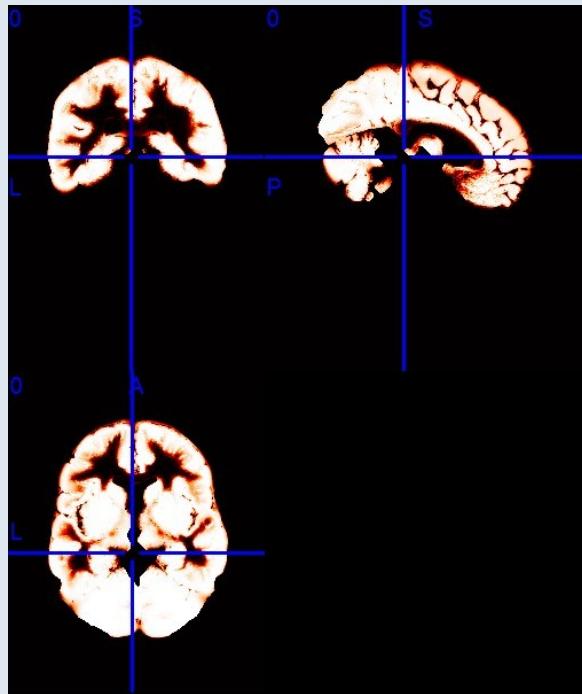


# Results: all together

c1s27703c5-153119-00001-00224-1.nii	Template_6_2mnni.mat
c1s268240f-082409-00001-00224-1.nii	u_rc1s27703c5-153119-00001-00224-1_Template.nii
c1s3120485-082744-00001-00224-1.nii	u_rc1s268240f-082409-00001-00224-1_Template.nii
c2s27703c5-153119-00001-00224-1.nii	u_rc1s3120485-082744-00001-00224-1_Template.nii
c2s268240f-082409-00001-00224-1.nii	wap1_ws27703c5-153918-00001-00224-1_R2s_OLS.nii
c2s3120485-082744-00001-00224-1.nii	wap1_ws268240f-083155-00001-00224-1_R2s_OLS.nii
c3s27703c5-153119-00001-00224-1.nii	wap1_ws3120485-083655-00001-00224-1_R2s_OLS.nii
c3s268240f-082409-00001-00224-1.nii	wap2_ws27703c5-153918-00001-00224-1_R2s_OLS.nii
c3s3120485-082744-00001-00224-1.nii	wap2_ws268240f-083155-00001-00224-1_R2s_OLS.nii
mwc1s27703c5-153119-00001-00224-1.nii	wap2_ws3120485-083655-00001-00224-1_R2s_OLS.nii
mwc1s268240f-082409-00001-00224-1.nii	wcl1s27703c5-153119-00001-00224-1.nii
mwc1s3120485-082744-00001-00224-1.nii	wcl1s268240f-082409-00001-00224-1.nii
mwc2s27703c5-153119-00001-00224-1.nii	wcl1s20485-082744-00001-00224-1.nii
mwc2s268240f-082409-00001-00224-1.nii	wc1s27703c5-153119-00001-00224-1.nii
mwc2s3120485-082744-00001-00224-1.nii	wc1s268240f-082409-00001-00224-1.nii
rc1s27703c5-153119-00001-00224-1.nii	wc2s3120485-082744-00001-00224-1.nii
rc1s268240f-082409-00001-00224-1.nii	ws27703c5-153918-00001-00224-1_R2s_OLS.nii
rc1s3120485-082744-00001-00224-1.nii	ws268240f-083155-00001-00224-1_R2s_OLS.nii
rc2s27703c5-153119-00001-00224-1.nii	ws3120485-083655-00001-00224-1_R2s_OLS.nii
rc2s268240f-082409-00001-00224-1.nii	y_s27703c5-153119-00001-00224-1.nii
rc2s3120485-082744-00001-00224-1.nii	y_s268240f-082409-00001-00224-1.nii
s27703c5-153119-00001-00224-1_seg8.nii	y_s3120485-082744-00001-00224-1.nii
s268240f-082409-00001-00224-1_seg8.nii	
s3120485-082744-00001-00224-1_seg8.nii	
Template_0.nii	
Template_1.nii	
Template_2.nii	
Template_3.nii	
Template_4.nii	
Template_5.nii	
Template_6.nii	

File name	Description
<i>Unified Segmentation (US)</i> (Proc. hMRI -> Segmentation)	
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 <i>US</i> . 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 <i>US</i> , 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 <i>US</i>
<segmInputFileName>_seg8.mat	Segmentation and warping parameters, obtained from <i>US</i>
Diffeomorphic registration (Proc. hMRI -> Dartel -> Run Dartel (create Templates))	
u_rc1_-Template.nii	Flow field images 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.
Diffeomorphic registration (Proc. hMRI -> Dartel -> Normalise to MNI space)	
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.
<i>Tissue-weighted smoothing</i> (Proc. hMRI -> Smoothing)	
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



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# Thank you!